

STUDY TITLE

Supplemental Information for Potential Allergenicity Assessment of AAD-12 Protein Expressed
in Soybean Event DAS-68416-4 by Bioinformatics Analysis (Update, March, 2010)

DATA REQUIREMENTS

N/A

AUTHOR(S)

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STUDY COMPLETED ON

23-April-2010

PERFORMING LABORATORY

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LABORATORY STUDY ID

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```

72      12      12:+AD0APQAg-
74      10      10:+AD0-+AD0AKg-
76      3       7:+AD0AKg-
78      4       6:+AD0AKg-
80      3       4:+ACo-
82      2       3:+ACo-
84      1       3:+ACo-
86      2       2:+ACo-
88      2       2:+ACo-          inset +AD0- represents 1 library sequences
90      2       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.70320.00357+ADs- mu+AD0- 3.1488
0.185
mean+AF8-var+AD0-45.600412.910, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.189928
Kolmogorov-Smirnov statistic: 0.0668 (N+AD0-29) at 56

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
63 22.9      5.3
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
63 22.9      5.3
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k l pollen allerge ( 339)
63 22.9      5.3
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 22.1      5.8
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.8      7.3
gi+AHw-51242679+AHw-gb+AHw-AAT99258.1+AHw- pectin-methyltransferas ( 362)
61 22.3      8.3

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 63 Z-score: 89.4 bits: 22.9 E(): 5.3

```

Smith-Waterman score: 63+ADs- 27.778+ACU- identity (55.556+ACU- similar)
in 54 aa overlap (1-54:218-270)

```

                                10      20      30
AAD-12                          MAQTTLQITPTGATLGATVTGVHLATLDDA
                                ... : .  ..  ...  . : : .  .
gi+AHw-598 CYIEGTVDLIFGEARSLYLNTELHVVPDPMAMITAHARKNADGVGG-YSFVHCKVVTGTG
              190      200      210      220      230      240
    
```

```

                                40      50      60      70      80
AAD-12 GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISN
              : : :  :... : ...  :...
gi+AHw-598 GTALLGRAWFEEARVVFSYCNLSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKR
              250      260      270      280      290      300
    
```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 63 Z-score: 89.4 bits: 22.9 E(): 5.3
Smith-Waterman score: 63+ADs- 27.778+ACU- identity (55.556+ACU- similar)
in 54 aa overlap (1-54:218-270)

```

                                10      20      30
AAD-12                          MAQTTLQITPTGATLGATVTGVHLATLDDA
                                ... : .  ..  ...  . : : .  .
gi+AHw-598 CYIEGTVDLIFGEARSLYLNTELHVVPDPMAMITAHARKNADGVGG-YSFVHCKVVTGTG
              190      200      210      220      230      240
    
```

```

                                40      50      60      70      80
AAD-12 GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISN
              : : :  :... : ...  :...
gi+AHw-598 GTALLGRAWFEEARVVFSYCNLSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKR
              250      260      270      280      290      300
    
```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 63 Z-score: 89.4 bits: 22.9 E(): 5.3
Smith-Waterman score: 63+ADs- 27.778+ACU- identity (55.556+ACU- similar)
in 54 aa overlap (1-54:218-270)

```

                                10      20      30
AAD-12                          MAQTTLQITPTGATLGATVTGVHLATLDDA
                                ... : .  ..  ...  . : : .  .
gi+AHw-225 CYIEGTVDLIFGEARSLYLNTELHVVPDPMAMITAHARKNADGVGG-YSFVHCKVVTGTG
              190      200      210      220      230      240
    
```

```

                                40      50      60      70      80
AAD-12 GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISN
              : : :  :... : ...  :...
gi+AHw-225 GTALLGRAWFEEARVVFSYCNLSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKR
              250      260      270      280      290      300
    
```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)

initn: 43 init1: 43 opt: 60 Z-score: 88.7 bits: 22.1 E(): 5.8

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (47-78:133-160)

```

      20      30      40      50      60      70
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      : : : : : : : : : : : :
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSORPPRRFQGGDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150

```

```

      80
AAD-12 AISN
      :
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)
initn: 39 initl: 39 opt: 59 Z-score: 86.8 bits: 21.8 E(): 7.3
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (15-63:3-55)

```

      10      20      30      40      50
AAD-12 MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQ
      : : : : : : : : : : : :
gi+AHw-886 FALIAVVATSTIAQMETSICIPGLERPWQQQPLPPQQTLPFQQQPFPPQQ
      10      20      30      40

```

```

      60      70      80
AAD-12 QITFAKRFGAIERIGGGDIVAISN
      : : : :
gi+AHw-886 QPPFSQQQPSFSQQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPQQQQQLP
      50      60      70      80      90      100

```

+AD4APg-gi+AHw-51242679+AHw-gb+AHw-AAT99258.1+AHw- pectin-
methyltransferase pr (362 aa)
initn: 59 initl: 59 opt: 61 Z-score: 85.9 bits: 22.3 E(): 8.3
Smith-Waterman score: 61+ADs- 27.778+ACU- identity (55.556+ACU- similar)
in 54 aa overlap (1-54:241-293)

```

      10      20      30
AAD-12 MAQTTLQITPTGATLGATVTGVHLATLDDA
      : : : : : : : :
gi+AHw-512 CYTEGTVDFIFGEARSLYLNTELHVVPDPMAMITAHARKNADGVGG--YSFVHCKVVTGTG
      220      230      240      250      260

```

```

      40      50      60      70      80
AAD-12 GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISN
      : : : : : : : :
gi+AHw-512 GTALLGRAWFDAARVVFVSYCNLSDAKPEGWSDNNKPEAQKTILFGEYKNTGPGAAPDKR
      270      280      290      300      310      320

```

80 residues in 1 query sequences


```

60      66      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
62      90
40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
64      44      32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      28      25:+AD0APQA9AD0APQA9ACo-
68      21      20:+AD0APQA9AD0AKgA9-
70      33      16:+AD0APQA9ACoAPQA9AD0APQA9-
72      9       12:+AD0APQ-+ACo-
74      11      10:+AD0APQAq-
76      6       7:+AD0AKg-
78      1       6:+AD0AKg-
80      4       4:+ACo-
82      2       3:+ACo-
84      2       3:+ACo-
86      4       2:+ACo-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120  0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.63820.00354+ADs- mu+AD0- 3.5421
0.183
mean+AF8-var+AD0-44.819412.556, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.191576
Kolmogorov-Smirnov statistic: 0.0662 (N+AD0-29) at 56

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 22.1      5.6
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.9      7.1
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.4      7.4
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.4      7.4
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.4      7.4

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 88.9 bits: 22.1 E(): 5.6
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (46-77:133-160)

```

                20          30          40          50          60          70
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                : :: :...: . : ...: :...
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRRRFQGGDQSQQQQDSHQK----VHRFDEGDLI
                110          120          130          140          150

```

```

                80
AAD-12 AISNV
                :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                160          170          180          190          200          210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
 gluteni (229 aa)
 initn: 39 initl: 39 opt: 59 Z-score: 87.1 bits: 21.9 E(): 7.1
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
 in 53 aa overlap (14-62:3-55)

```

                10          20          30          40          50
AAD-12 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQ
                : :... :. . . . : : : : : : : : : : : :
gi+AHw-886          FALIAVVATSTIAQMETSICIPGLERPWQQQPLPPQQTLFPQQQPPFPQQQ
                10          20          30          40

```

```

                60          70          80
AAD-12 ITFAKRFGAIERIGGGDIVAISNV
                :...
gi+AHw-886 PPFsQQQPSFSQQQPPFSQQQPILPEPPFSLQQQPVLFPQQSPFSQQQLVLPQQQQQLPQ
                50          60          70          80          90          100

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 86.8 bits: 22.4 E(): 7.4
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (21-53:238-270)

```

                10          20          30          40          50
AAD-12          AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                : : . : : : : : : : : : : : : : : .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVGTGTTALLGRAWFEARVVFSYCN
                210          220          230          240          250          260

```

```

                60          70          80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNV
                :..
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270          280          290          300          310          320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allergen +AFs-S (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 86.8 bits: 22.4 E(): 7.4
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (21-53:238-270)

```

                10         20         30         40         50
AAD-12          AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210         220         230         240         250         260
    
```

```

                60         70         80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNV
                ::.
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270         280         290         300         310         320
    
```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase aller (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 86.8 bits: 22.4 E(): 7.4
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (21-53:238-270)

```

                10         20         30         40         50
AAD-12          AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210         220         230         240         250         260
    
```

```

                60         70         80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNV
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270         280         290         300         310         320
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:33 2010 done: Fri Feb 5 12:55:33 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

66      20      25:+AD0APQA9AD0APQA9AD0- +ACo-
68      21      20:+AD0APQA9AD0APQA9ACo-
70      32      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      11      12:+AD0APQA9ACo-
74      10      10:+AD0APQA9ACo-
76      6       7:+AD0APQAq-
78      2       6:+AD0AKg-
80      3       4:+AD0AKg-
82      1       3:+ACo-
84      2       3:+ACo-
86      4       2:+ACoAPQ-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.66860.00352+ADs- mu+AD0- 3.7091
0.182
mean+AF8-var+AD0-43.840912.063, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.193702
Kolmogorov-Smirnov statistic: 0.0573 (N+AD0-29) at 56

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.1 5.6

gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229) 59 21.8 7.2

gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.3 7.5

gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339) 61 22.3 7.5

gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.3 7.5

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 init1: 43 opt: 60 Z-score: 88.9 bits: 22.1 E(): 5.6

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (45-76:133-160)

```

                20          30          40          50          60          70
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                :  ::  :...:  .  :  ...  :...
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSRPPRRFQGDQSQQQQDSHQK----VHRFDEGDLI
                110          120          130          140          150
    
```

```

                80
AAD-12 AISNVK
                :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                160          170          180          190          200          210
    
```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)
initn: 39 init1: 39 opt: 59 Z-score: 87.0 bits: 21.8 E(): 7.2
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (13-61:3-55)

```

                10          20          30          40          50
AAD-12 QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQI
                :  :...  :.  .  .  .  .  :  :.  :  .  :.  :.  :.
gi+AHw-886                FALIAVVATSTIAQMETSICIPGLERPWQQQPLPPQQTLPQQQPPFPQQQP
                10          20          30          40          50
    
```

```

                60          70          80
AAD-12 TFAKRFGAIERIGGGDIVAISNVK
                :...
gi+AHw-886 PFSQQQPSFSQQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPQQQQQLPQQ
                60          70          80          90          100          110
    
```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (20-52:238-270)

```

                10          20          30          40
AAD-12                QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :  .  .  :  :  :  :...  :  :.  .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVVTGTGGTALLGRAWFEEARVVFSYCN
                210          220          230          240          250          260
    
```

```

                50          60          70          80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVK
                :..
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270          280          290          300          310          320
    
```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.5

Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (20-52:238-270)

```

                10      20      30      40
AAD-12          QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: .  :: : :  ::.. : ..  .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

                50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVK
                ::.
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (20-52:238-270)

```

                10      20      30      40
AAD-12          QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: .  :: : :  ::.. : ..  .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

                50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVK
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:33 2010 done: Fri Feb 5 12:55:33 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 4 - 83 80 aa - 80 aa


```

74      6      10:+AD0APQ- +ACo-
76      6      7:+AD0APQAq-
78      2      6:+AD0AKg-
80      3      4:+AD0AKg-
82      2      3:+ACo-
84      1      3:+ACo-
86      4      2:+ACoAPQ-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.69180.00355+ADs- mu+AD0- 3.5856
0.184
mean+AF8-var+AD0-43.914412.062, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.193540
Kolmogorov-Smirnov statistic: 0.0525 (N+AD0-29) at 56

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 22.1      5.7
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.8      7.2
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.3      7.6
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k l pollen allerge ( 339)
61 22.3      7.6
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.3      7.6

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 init1: 43 opt: 60 Z-score: 88.8 bits: 22.1 E(): 5.7
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (44-75:133-160)

```

20

30

40

50

60

70

```

AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      :  ::  :...:  .  :  ....  :...
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSORPPRRFQGDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150

```

```

      80
AAD-12 AISNVKA
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)
initn: 39 initl: 39 opt: 59 Z-score: 87.0 bits: 21.8 E(): 7.2
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (12-60:3-55)

```

      10      20      30      40      50
AAD-12 TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQIT
      :  :...  .:  . . . . . :  :  :  :...  :  :...
gi+AHw-886      FALIAVVATSTIAQMETSICIPGLERPWQQQPLPPQQTLFPQQQPPFQQQPP
      10      20      30      40      50

```

```

      60      70      80
AAD-12 FAKRFGAIERIGGGDIVAISNVKA
      :...
gi+AHw-886 FSQQQPSFSQQQPPFSQQQPILPEPPFSLQQQPVLFPQQSPFSQQQLVLPQQQQQLFPQQQ
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 initl: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (19-51:238-270)

```

      10      20      30      40
AAD-12      TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      :  .  .:  :  :  :...  :  :...  .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFSYCN
      210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKA
      :..
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)
initn: 61 initl: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (19-51:238-270)

```

      10      20      30      40

```

```

AAD-12          TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKA
                :::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (19-51:238-270)

```

                10      20      30      40
AAD-12          TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKA
                :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:35 2010 done: Fri Feb 5 12:55:35 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 5 - 84 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

                opt      E()
+ADw- 20      2      0:+AD0-

```



```

82      3      3:+ACo-
84      1      3:+ACo-
86      3      2:+ACo-
88      1      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120  0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.80460.00358+ADs- mu+AD0- 2.7946
0.186
mean+AF8-var+AD0-45.908712.867, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.189290
Kolmogorov-Smirnov statistic: 0.0525 (N+AD0-29) at 56

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.100

The best scores are: opt bits E(1471)

```

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 22.0      6.1
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.7      7.7
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.2      8.2
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.2      8.2
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.2      8.2

```

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 88.3 bits: 22.0 E(): 6.1
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (43-74:133-160)

```

```

                20          30          40          50          60          70
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                : :: :...: . : :... :...
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSORPPRRFQGDQSQQQQDSHQK----VHRFDEGDLI
                110          120          130          140          150

```



```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      :::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 86.0 bits: 22.2 E(): 8.2
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (18-50:238-270)

```

                                10      20      30      40
AAD-12 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFVSYCN
      210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:35 2010 done: Fri Feb 5 12:55:35 2010
 Total Scan time: 0.100 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 6 - 85 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      3      0:+AD0-

```



```

 96      0      1:+ACo-          :+ACo-
 98      0      0:              +ACo-
100      0      0:              +ACo-
102      0      0:              +ACo-
104      0      0:              +ACo-
106      0      0:              +ACo-
108      0      0:              +ACo-
110      0      0:              +ACo-
112      0      0:              +ACo-
114      0      0:              +ACo-
116      0      0:              +ACo-
118      0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.94690.00361+ADs- mu+AD0- 2.2455
0.187
mean+AF8-var+AD0-46.955213.181, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.187168
Kolmogorov-Smirnov statistic: 0.0525 (N+AD0-28) at 56

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 21.9 6.7

gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229) 59 21.6 8.5

gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.1 9.1

gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339) 61 22.1 9.1

gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.1 9.1

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 init1: 43 opt: 60 Z-score: 87.5 bits: 21.9 E(): 6.7

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar) in 32 aa overlap (42-73:133-160)

```

                20          30          40          50          60          70
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                : :: :...: . : ...: :...
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSORPPRRFQGGDQSQQQDQSHQK----VHRFDEGDLI
                110          120          130          140          150

                80
AAD-12 AISNVKADG
                :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFRRRNLAGNHEQEFLRYQQQSRRR
                160          170          180          190          200          210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
 gluteni (229 aa)
 initn: 39 init1: 39 opt: 59 Z-score: 85.7 bits: 21.6 E(): 8.5
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
 in 53 aa overlap (10-58:3-55)

```

                10         20         30         40         50
AAD-12 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFA
                : :.:. .: . . . .: :. : .: :. .: :.
gi+AHw-886      FALIAVVATSTIAQMETSICIPGLERPWQQQPLPPQQTLFPQQQPPFPQQPPFS
                10         20         30         40         50
    
```

```

                60         70         80
AAD-12 KRFGAIERIGGGDIVAISNVKADG
                ..
gi+AHw-886 QQQPSFSQQQPPFSQQQPILPEPPFSLQQQPVLPPQSPFSQQQLVLPQQQQQLPQQQIS
                60         70         80         90         100         110
    
```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (17-49:238-270)

```

                10         20         30         40
AAD-12          LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                : : . . : : : : :. . : :. .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210        220        230        240        250        260
    
```

```

                50         60         70         80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADG
                :.:.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270        280        290        300        310        320
    
```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (17-49:238-270)

```

                10         20         30         40
AAD-12          LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                : : . . : : : : :. . : :. .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210        220        230        240        250        260
    
```

```

                50         60         70         80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADG
                :.:.
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270        280        290        300        310        320
    
```



```

108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.92780.00359+ADs- mu+AD0- 2.3831
0.186
mean+AF8-var+AD0-46.847613.124, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.187383
Kolmogorov-Smirnov statistic: 0.0498 (N+AD0-28) at 56

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 21.9 6.7

gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229) 59 21.6 8.5

gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.1 9.1

gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339) 61 22.1 9.1

gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.1 9.1

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 init1: 43 opt: 60 Z-score: 87.5 bits: 21.9 E(): 6.7

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar) in 32 aa overlap (41-72:133-160)

```

                20          30          40          50          60          70
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                : :: :...: . :   ...: :...
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSRPPRRFQGQDQSQQQQDSHQK----VHRFDEGDLI
                110          120          130          140          150

```

```

                80
AAD-12 AISNVKADGT
                :.

```

```

gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNDNDQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                160          170          180          190          200          210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight gluteni (229 aa)

initn: 39 init1: 39 opt: 59 Z-score: 85.7 bits: 21.6 E(): 8.5

Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar) in 53 aa overlap (9-57:3-55)

```

      10      20      30      40      50
AAD-12 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAK
      : :.:. .: . . . . .: :. . : :.:. . .: :.:. . .
gi+AHw-886 FALIAVVATSTIAQMETSICIPGLERPWQQQPLPPQQTLFPQQQPPFPQQQPPFSQ
      10      20      30      40      50

```

```

      60      70      80
AAD-12 RFGAIERIGGGDIVAISNVKADGT
      .
gi+AHw-886 QQPSFSQQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPQQQQQLPQQQISI
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (16-48:238-270)

```

      10      20      30      40
AAD-12 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      : : . . : : : : :.:. . .: .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
      210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGT
      :.:.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (16-48:238-270)

```

      10      20      30      40
AAD-12 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      : : . . : : : : :.:. . .: .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
      210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGT
      :.:.
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (16-48:238-270)

```

                10         20         30         40
AAD-12          QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . .: : : :... : ..: .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVVTGTGGTALLGLRAWFEAARVVFSYCN
                210         220         230         240         250         260

                50         60         70         80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGT
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270         280         290         300         310         320

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:35 2010 done: Fri Feb 5 12:55:35 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 8 - 87 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      3      0:+AD0-
      30      4      2:+ACoAPQ-
      32     10      8:+AD0APQAqAD0-
      34     32     21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
      36     69
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
      38     77
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
-
      40     86    101:+AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      42    128
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-

```


+AD4-120 0 0: +ACo-
 331323 residues in 1471 sequences
 Expectation+AF8-n fit: rho(ln(x))+AD0- 5.87940.00357+ADs- mu+AD0- 2.8634
 0.185
 mean+AF8-var+AD0-46.540612.935, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
 Lambda+AD0- 0.188000
 Kolmogorov-Smirnov statistic: 0.0485 (N+AD0-28) at 56

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1
 join: 42, opt: 30, open/ext: -10/-2, width: 32
 Scan time: 0.090

The best scores are: opt bits E(1471)
 gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 21.8 6.9
 gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229) 59 21.6 8.7
 gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.0 9.3
 gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339) 61 22.0 9.3
 gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.0 9.3

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 init1: 43 opt: 60 Z-score: 87.3 bits: 21.8 E(): 6.9
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (40-71:133-160)

```

      10      20      30      40      50      60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRPFRFQGGDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150

```

```

      70      80
AAD-12 AISNVKADGTV
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
 gluteni (229 aa)
 initn: 39 init1: 39 opt: 59 Z-score: 85.5 bits: 21.6 E(): 8.7
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
 in 53 aa overlap (8-56:3-55)

```

      10      20      30      40      50
AAD-12 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-886 FALIAVVATSTIAQMETSICIPGLERPWQQQPLPPQQTLPFQQQPPFQQQPPFSQQ
      10      20      30      40      50

```

60 70 80
 AAD-12 FGAIERIGGGDIVAISNVKADGTV

gi+AHw-886 QPSFSQQQPPFSQQQPILPEPPFSLQQQPVLPPQSPFSQQQLVLPQQQQQLPQQQISIV
 60 70 80 90 100 110

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
 aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.0 bits: 22.0 E(): 9.3
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (15-47:238-270)

10 20 30 40
 AAD-12 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
 :: . : : : : : : : :
 gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
 210 220 230 240 250 260

50 60 70 80
 AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTV

:::
 gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
 270 280 290 300 310 320

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.0 bits: 22.0 E(): 9.3
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (15-47:238-270)

10 20 30 40
 AAD-12 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
 :: . : : : : : : : :
 gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
 210 220 230 240 250 260

50 60 70 80
 AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTV

:::
 gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
 270 280 290 300 310 320

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.0 bits: 22.0 E(): 9.3
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (15-47:238-270)

10 20 30 40
 AAD-12 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
 :: . : : : : : : : :
 gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
 210 220 230 240 250 260

```

          50          60          70          80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTV
      :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
          270          280          290          300          310          320
    
```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:35 2010 done: Fri Feb 5 12:55:36 2010
Total Scan time: 0.090 Total Display time: 0.010
    
```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
    
```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
    
```

```

1+AD4APgA+-AAD-12: 9 - 88 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
    
```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      1      0:+AD0-          one +AD0- represents 3 library sequences
      24      0      0:
      26      1      0:+AD0-
      28      3      0:+AD0-
      30      4      2:+ACoAPQ-
      32      9      8:+AD0APQAq-
      34      32     21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
      36      71
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
      38      75
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
      40      93
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0- +ACo-
      42      105
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      44      133
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
      46      137
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
    
```


Kolmogorov-Smirnov statistic: 0.0498 (N+AD0-28) at 56

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 21.9 6.6

gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229) 59 21.6 8.4

gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.1 9.1

gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k l pollen allerge (339) 61 22.1 9.1

gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.1 9.1

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 87.6 bits: 21.9 E(): 6.6
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (39-70:133-160)

```

      10      20      30      40      50      60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      : : : : : : : : : : : :
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRPFRFQGGDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150
    
```

```

      70      80
AAD-12 AISNVKADGTVR
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210
    
```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight gluteni (229 aa)

initn: 39 initl: 39 opt: 59 Z-score: 85.7 bits: 21.6 E(): 8.4
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (7-55:3-55)

```

      10      20      30      40      50
AAD-12 TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKRF
      : : : : : : : : : : : :
gi+AHw-886 FALIAVVATSTIAQMETSCIPGLERPWQQQPLPPQQTLPFQQQPFPPQQPPFSQQQ
      10      20      30      40      50
    
```

```

      60      70      80
AAD-12 GAIERIGGGDIVAISNVKADGTVR
      :.
gi+AHw-886 PSFSQQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPQQQQQLPQQQISIVQ
      60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (14-46:238-270)

```

                                10      20      30      40
AAD-12      TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: .  :: : :  ::.. : ..  .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFSYCN
                210      220      230      240      250      260

```

```

                    50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                    ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (14-46:238-270)

```

                                10      20      30      40
AAD-12      TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: .  :: : :  ::.. : ..  .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFSYCN
                210      220      230      240      250      260

```

```

                    50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                    ::.
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (14-46:238-270)

```

                                10      20      30      40
AAD-12      TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: .  :: : :  ::.. : ..  .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFSYCN
                210      220      230      240      250      260

```

```

                    50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                    ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```


52 67
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
54 99
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0-+AD0APQAqAD0APQ-
56 78
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58 102
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9AD0APQA9AD0APQA9AD0-
60 53 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
62 57 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
64 33 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66 18 25:+AD0APQA9AD0APQA9- +ACo-
68 32 20:+AD0-+AD0APQA9AD0APQAqAD0APQA9AD0-
70 30 16:+AD0APQA9AD0APQAqAD0APQA9AD0-
72 11 12:+AD0APQA9ACo-
74 3 10:+AD0- +ACo-
76 5 7:+AD0APQAq-
78 4 6:+AD0AKg-
80 3 4:+AD0AKg-
82 3 3:+ACo-
84 3 3:+ACo-
86 4 2:+ACoAPQ-
88 0 2:+ACo- inset +AD0- represents 1 library sequences
90 0 1:+ACo-
92 0 1:+ACo- :+ACo-
94 0 1:+ACo- :+ACo-
96 0 1:+ACo- :+ACo-
98 0 0: +ACo-
100 0 0: +ACo-
102 0 0: +ACo-
104 0 0: +ACo-
106 0 0: +ACo-
108 0 0: +ACo-
110 0 0: +ACo-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.70890.00314+ADs- mu+AD0- 3.6476
0.162
mean+AF8-var+AD0-46.298212.950, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.188492
Kolmogorov-Smirnov statistic: 0.0496 (N+AD0-28) at 52

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 21.9 6.6
 gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229) 59 21.6 8.4
 gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.1 8.8
 gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k l pollen allerge (339) 61 22.1 8.8
 gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.1 8.8
 gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase inhib (217) 58 21.3 9.6
 gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName: Full+AD0-S (221) 58 21.3 9.8

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 87.6 bits: 21.9 E(): 6.6
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (38-69:133-160)

```

      10      20      30      40      50      60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      : : : . . . . . : . . . . : : :
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRRPFRFQGGDQSQQQQDQSHQK----VHRFDEGDLI
      110      120      130      140      150

      70      80
AAD-12 AISNVKADGTVRQ
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210
    
```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight gluteni (229 aa)
 initn: 39 initl: 39 opt: 59 Z-score: 85.8 bits: 21.6 E(): 8.4
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
 in 53 aa overlap (6-54:3-55)

```

      10      20      30      40      50
AAD-12 PTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKRFG
      : : : . . : . . . . : : : : : : : . : : : . : : : . : :
gi+AHw-886 FALIAVVATSTIAQMETSICIPGLERPWQQQPLPPQQTLFPQQQPFPPQQPPFSQQQP
      10      20      30      40      50

      60      70      80
AAD-12 AIERIGGGDIVAISNVKADGTVRQ

gi+AHw-886 SFSQQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPQQQQQLPQQQISIVQP
      60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.4 bits: 22.1 E(): 8.8
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (13-45:238-270)

```

                                10      20      30      40
AAD-12      PTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                    50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQ
                :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 85.4 bits: 22.1 E(): 8.8
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (13-45:238-270)

```

                                10      20      30      40
AAD-12      PTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                    50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQ
                :::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 85.4 bits: 22.1 E(): 8.8
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (13-45:238-270)

```

                                10      20      30      40
AAD-12      PTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                    50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQ
                :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4-+AD4-gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase
 inhibitor (217 aa)

initn: 37 initl: 37 opt: 58 Z-score: 84.7 bits: 21.3 E(): 9.6
 Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
 in 84 aa overlap (4-80:134-215)

```

                                10          20          30
AAD-12          PTGATLGATV--TGVHLATLDDAGFAALHAAWL
                   :.:. . . :. . :. . :. . . .
gi+AHw-214 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
              110          120          130          140          150          160
    
```

```

                                40          50          60          70          80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQ
                   . :. : . . :. :. :. : . :. :. : . . . . : . . :
gi+AHw-214 GYNLLYCPVTSTMSCPFSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFKQVQ
              170          180          190          200          210
    
```

+AD4APg-gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName:
 Full+AD0-Serin (221 aa)

initn: 37 initl: 37 opt: 58 Z-score: 84.6 bits: 21.3 E(): 9.8
 Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
 in 84 aa overlap (4-80:138-219)

```

                                10          20          30
AAD-12          PTGATLGATV--TGVHLATLDDAGFAALHAAWL
                   :.:. . . :. . :. . :. . . .
gi+AHw-201 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
              110          120          130          140          150          160
    
```

```

                                40          50          60          70          80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQ
                   . :. : . . :. :. :. : . :. :. : . . . . : . . :
gi+AHw-201 GYNLLYCPVTSTMSCPFSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFKQVQ
              170          180          190          200          210          220
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:36 2010 done: Fri Feb 5 12:55:36 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

76      5      7:+AD0APQAg-
78      1      6:+AD0AKg-
80      4      4:+AD0AKg-
82      3      3:+ACo-
84      2      3:+ACo-
86      6      2:+ACoAPQ-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120  0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.74630.00326+ADs- mu+AD0- 3.0558
0.168
mean+AF8-var+AD0-43.781711.657, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.193833
Kolmogorov-Smirnov statistic: 0.0394 (N+AD0-29) at 52

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:          opt bits E(1471)
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 22.2  5.4
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.9  6.9
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.4  7.2
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k l pollen allerge ( 339)
61 22.4  7.2
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.4  7.2
gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase inhib ( 217)
58 21.6  7.8
gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName: Full+AD0-S
( 221)  58 21.6  8

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 init1: 43 opt: 60 Z-score: 89.3 bits: 22.2 E(): 5.4

```

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (37-68:133-160)

```

      10      20      30      40      50      60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSORPPRRFQGDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150

```

```

      70      80
AAD-12 AISNVKADGTVRQH
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)
initn: 39 init1: 39 opt: 59 Z-score: 87.4 bits: 21.9 E(): 6.9
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (5-53:3-55)

```

      10      20      30      40      50
AAD-12 TGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKRFGA
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-886 FALIAVVATSTIAQMETSICIPGLERPWQQQPLPPQQTLPFPQQQPFPPQQQPPFSQQQPS
      10      20      30      40      50

```

```

      60      70      80
AAD-12 IERIGGGDIVAISNVKADGTVRQH
gi+AHw-886 FSQQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPQQQQQLPQQQISIVQPS
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 87.0 bits: 22.4 E(): 7.2
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (12-44:238-270)

```

      10      20      30      40
AAD-12 TGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
      210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH
      :.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 87.0 bits: 22.4 E(): 7.2

Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (12-44:238-270)

```

                                10      20      30      40
AAD-12      TGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: .  :: : :  ::.. : ...
gi+AHw-225  TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVGTGGTALLGRAWFEEARVVFSYCN
            210      220      230      240      250      260
    
```

```

                    50      60      70      80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH
        :::
gi+AHw-225  LSDAVKPEGWSDNNKPAAQKTIFFGHEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
            270      280      290      300      310      320
    
```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 87.0 bits: 22.4 E(): 7.2
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (12-44:238-270)

```

                                10      20      30      40
AAD-12      TGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: .  :: : :  ::.. : ...
gi+AHw-598  TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVGTGGTALLGRAWFEEARVVFSYCN
            210      220      230      240      250      260
    
```

```

                    50      60      70      80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH
        :::
gi+AHw-598  LSDAVKPEGWSDNNKPAAQKTIFFGHEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
            270      280      290      300      310      320
    
```

+AD4APg-gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase
inhibitor (217 aa)

initn: 37 initl: 37 opt: 58 Z-score: 86.3 bits: 21.6 E(): 7.8
Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
in 84 aa overlap (3-79:134-215)

```

                                10      20      30
AAD-12      TGATLGATV--TGVHLATLDDAGFAALHAAWL
                                ::.. .  :: ..  ::. :  ::... .
gi+AHw-214  FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
            110      120      130      140      150      160
    
```

```

                    40      50      60      70      80
AAD-12  QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH
        . :: : .  ::..: : .  ::... :  .. ... : .  ::
gi+AHw-214  GYNLLYCPVTSTMSCPFSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFKQVQ
            170      180      190      200      210
    
```

+AD4APg-gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName:
Full+AD0-Serin (221 aa)

initn: 37 initl: 37 opt: 58 Z-score: 86.2 bits: 21.6 E(): 8

Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
in 84 aa overlap (3-79:138-219)

```

                                10      20      30
AAD-12                        TGATLGATV--TGVHLATLDDAGFAALHAAWL
                                :.:. . . :. . :. . . .
gi+AHw-201 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
                110      120      130      140      150      160

                                40      50      60      70      80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH
                . :. : . . :. :. : . :. . . : . . :
gi+AHw-201 GYNLLYCPVTSTMSCPFSSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFKQVQ
                170      180      190      200      210      220

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:36 2010 done: Fri Feb 5 12:55:36 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 12 - 91 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      2      0:+AD0-
      30      7      2:+ACoAPQA9-
      32     10      8:+AD0APQAqAD0-
      34     25     21:+AD0APQA9AD0APQA9ACoAPQA9-
      36     85
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQ-
      38     70
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
      40     85     101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-

```



```

114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.69370.00338+ADs- mu+AD0- 3.4584
0.175
mean+AF8-var+AD0-44.175411.947, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.192967
Kolmogorov-Smirnov statistic: 0.0380 (N+AD0-29) at 36

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 22.1 5.6
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.8 7.2
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.3 7.5
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.3 7.5
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.3 7.5
gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase inhib ( 217)
58 21.6 8.2
gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName: Full+AD0-S
( 221) 58 21.6 8.4

```

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 init1: 43 opt: 60 Z-score: 88.9 bits: 22.1 E(): 5.6
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (36-67:133-160)

```

```

          10          20          30          40          50          60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
          : :: :...: . : ...: :...
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSRPPRRFQGDQSQQQDQSHQK----VHRFDEGDLI
          110          120          130          140          150

          70          80
AAD-12 AISNVKADGTVRQHS
          :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPPRRFNLAGNHEQEFLRYQQQSRRR
          160          170          180          190          200          210

```

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)
initn: 39 init1: 39 opt: 59 Z-score: 87.0 bits: 21.8 E(): 7.2
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (4-52:3-55)

```

```
          10          20          30          40          50
AAD-12  GATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKRFGAI
          : :.:. .: . . .: . . .: . . .: . . .: . . .: . . .: . . .: . . .
gi+AHw-886  FALIAVVATSTIAQMETSCIPGLERPWQQQPLPPQQTLPFPQQQPFPPQQQPPFSQQQPSF
          10          20          30          40          50
```

```
          60          70          80
AAD-12  ERIGGGDIVAISNVKADGTVRQHS

gi+AHw-886  SQQQPPFSQQQPILPEPPFSLQQQPVLPPQSPFSQQQLVLPQQQQQLPQQQISIVQPSV
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 86.7 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (11-43:238-270)

```
          10          20          30          40
AAD-12  GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
          : : . .: : : : :.:. .: . . .: . . .: . . .: . . .: . . .: . . .
gi+AHw-598  TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
          210          220          230          240          250          260
```

```
          50          60          70          80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS
          :.:.
gi+AHw-598  LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
          270          280          290          300          310          320
```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 86.7 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (11-43:238-270)

```
          10          20          30          40
AAD-12  GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
          : : . .: : : : :.:. .: . . .: . . .: . . .: . . .: . . .
gi+AHw-225  TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
          210          220          230          240          250          260
```

```
          50          60          70          80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS
          :.:.
gi+AHw-225  LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
          270          280          290          300          310          320
```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 86.7 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (11-43:238-270)

```

                                10      20      30      40
AAD-12      GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: .  :: : :  ::.. :  :: .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFVSYCN
                210      220      230      240      250      260
    
```

```

                                50      60      70      80
AAD-12      LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320
    
```

+AD4APg-gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase inhibitor (217 aa)
 initn: 37 initl: 37 opt: 58 Z-score: 86.0 bits: 21.6 E(): 8.2
 Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
 in 84 aa overlap (2-78:134-215)

```

                                10      20
AAD-12      GATLGATV--TGVHLATLDDAGFAALHAAWL
                                ::.. .  :: ..  ::. :  ::.. .
gi+AHw-214 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
                110      120      130      140      150      160
    
```

```

                                30      40      50      60      70      80
AAD-12      QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS
                . :: :  .  ::::: :  . :.... :  .. ...  :  . :
gi+AHw-214 GYNLLYCPVTSTMSCPFSSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFKQVQ
                170      180      190      200      210
    
```

+AD4APg-gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName: Full+AD0-Serin (221 aa)
 initn: 37 initl: 37 opt: 58 Z-score: 85.8 bits: 21.6 E(): 8.4
 Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
 in 84 aa overlap (2-78:138-219)

```

                                10      20
AAD-12      GATLGATV--TGVHLATLDDAGFAALHAAWL
                                ::.. .  :: ..  ::. :  ::.. .
gi+AHw-201 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
                110      120      130      140      150      160
    
```

```

                                30      40      50      60      70      80
AAD-12      QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS
                . :: :  .  ::::: :  . :.... :  .. ...  :  . :
gi+AHw-201 GYNLLYCPVTSTMSCPFSSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFKQVQ
                170      180      190      200      210      220
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-

54 111 91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
56 69
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
58 69
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60 64
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
62 51 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
64 42 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66 10 25:+AD0APQA9AD0- +ACo-
68 25 20:+AD0APQA9AD0APQA9ACoAPQA9-
70 27 16:+AD0APQA9AD0APQAqAD0APQA9-
72 7 12:+AD0APQA9ACo-
74 11 10:+AD0APQA9ACo-
76 4 7:+AD0APQAq-
78 2 6:+AD0AKg-
80 4 4:+AD0AKg-
82 2 3:+ACo-
84 3 3:+ACo-
86 3 2:+ACo-
88 4 2:+ACoAPQ- inset +AD0- represents 1 library

sequences

90 0 1:+ACo-
92 0 1:+ACo- :+ACo-
94 0 1:+ACo- :+ACo-
96 0 1:+ACo- :+ACo-
98 0 0: +ACo-
100 0 0: +ACo-
102 0 0: +ACo-
104 0 0: +ACo-
106 0 0: +ACo-
108 0 0: +ACo-
110 0 0: +ACo-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 5.43100.00331+ADs- mu+AD0- 4.9373
0.170

mean+AF8-var+AD0-42.130011.266, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43

Lambda+AD0- 0.197596

Kolmogorov-Smirnov statistic: 0.0453 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 22.3 5.1

gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229)
 59 22.0 6.5
 gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339)
 61 22.5 6.6
 gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339)
 61 22.5 6.6
 gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339)
 61 22.5 6.6
 gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase inhib (217)
 58 21.7 7.4
 gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName: Full+AD0-S
 (221) 58 21.7 7.6
 gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen Ana (457)
 61 22.5 9.1
 gi+AHw-21591547+AHw-gb+AHw-AAM64112.1+AHw- gelsolin-like allergen (480)
 61 22.5 9.6

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
 Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 89.7 bits: 22.3 E(): 5.1
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (35-66:133-160)

```

                10         20         30         40         50         60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRRPRRFQGGDQSQQQQDQSHQK----VHRFDEGDLI
                110         120         130         140         150

                70         80
AAD-12 AISNVKADGTVRQHSP
                :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNDNDQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                160         170         180         190         200         210
    
```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
 gluteni (229 aa)
 initn: 39 initl: 39 opt: 59 Z-score: 87.8 bits: 22.0 E(): 6.5
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
 in 53 aa overlap (3-51:3-55)

```

                10         20         30         40         50
AAD-12 ATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKRFGAIE
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-886 FALIAVVATSTIAQMETSCIPGLERPWQQQPLPPQQTLFPQQQPPFQQQPPFSQQQPSFS
                10         20         30         40         50         60

                60         70         80
AAD-12 RIGGGDIVAISNVKADGTVRQHSP

gi+AHw-886 QQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPQQQQQLPQQQISIVQPSVL
                70         80         90         100         110         120
    
```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 87.6 bits: 22.5 E(): 6.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (10-42:238-270)

```

                                10      20      30
AAD-12                        ATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSP
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 87.6 bits: 22.5 E(): 6.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (10-42:238-270)

```

                                10      20      30
AAD-12                        ATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSP
                ::.
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4-+AD4-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 87.6 bits: 22.5 E(): 6.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (10-42:238-270)

```

                                10      20      30
AAD-12                        ATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSP
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase inhibitor (217 aa)
 initn: 37 initl: 37 opt: 58 Z-score: 86.7 bits: 21.7 E(): 7.4
 Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
 in 84 aa overlap (1-77:134-215)

```

                                10      20
AAD-12          ATLGGATV--TGVHLATLDDAGFAALHAAWL
                                :.:. . . :. . :. . . .
gi+AHw-214 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
            110      120      130      140      150      160

            30      40      50      60      70      80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSP
            . :. : . . :. :. : . :. :. : . . . . : . . :
gi+AHw-214 GYNLLYCPVTSTMSCPFSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFQVQ
            170      180      190      200      210
    
```

+AD4APg-gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName: Full+AD0-Serin (221 aa)
 initn: 37 initl: 37 opt: 58 Z-score: 86.6 bits: 21.7 E(): 7.6
 Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
 in 84 aa overlap (1-77:138-219)

```

                                10      20
AAD-12          ATLGGATV--TGVHLATLDDAGFAALHAAWL
                                :.:. . . :. . :. . . .
gi+AHw-201 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
            110      120      130      140      150      160

            30      40      50      60      70      80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSP
            . :. : . . :. :. : . :. :. : . . . . : . . :
gi+AHw-201 GYNLLYCPVTSTMSCPFSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFQVQ
            170      180      190      200      210      220
    
```

+AD4APg-gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen Ana o 2 (457 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 85.1 bits: 22.5 E(): 9.1
 Smith-Waterman score: 61+ADs- 38.710+ACU- identity (58.065+ACU- similar)
 in 31 aa overlap (36-66:108-138)

```

            10      20      30      40      50      60
AAD-12 TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA
            : : . . : : :. . :. . :
gi+AHw-259 YSNAPQLIYVVQEGGMTGISYPGCPETYQAPQQGRQQQSGRFQDRHQKIRRFRRGDIIA
            80      90      100      110      120      130

            70      80
AAD-12 ISNVKADGTVRQHSP
            :
gi+AHw-259 IPAGVAHWCYNEGNSPVVTVTLLDVSNSQNQLDRTPRKFHLAGNPKDVFQQQQHQSRGR
            140      150      160      170      180      190
    
```

+AD4APg-gi+AHw-21591547+AHw-gb+AHw-AAM64112.1+AHw- gelsolin-like allergen
 Der (480 aa)
 initn: 60 init1: 60 opt: 61 Z-score: 84.7 bits: 22.5 E(): 9.6
 Smith-Waterman score: 61+ADs- 32.692+ACU- identity (59.615+ACU- similar)
 in 52 aa overlap (13-60:83-134)

```

                                10      20      30      40
AAD-12                        ATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH--L
                                .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-215 NPTGGHSMKESKPILNHGYCHIHFWIGSESTKDEAGVAAIKSVELDDFLGGYPVQHREI
                                60      70      80      90      100     110

                                50      60      70      80
AAD-12 SNDQQITFAKRF--GAIERIGGGDIVAISNVKADGTVRQHSP
                                . . . : . : : : :
gi+AHw-215 EEFESRQFSSYFKNGIYKGGYESGFTKMIDELKPSLLHVKGKRRPIVYECAEISWKVM
                                120     130     140     150     160     170

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:36 2010 done: Fri Feb 5 12:55:36 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 14 - 93 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      1      0:+AD0-
      30      5      2:+ACoAPQ-
      32     16      8:+AD0APQAqAD0APQA9-
      34     29     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36     57     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
      38     74
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-

```



```

108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.37420.00333+ADs- mu+AD0- 5.2757
0.172
mean+AF8-var+AD0-42.213611.314, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.197400
Kolmogorov-Smirnov statistic: 0.0446 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.3 5.1

gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229) 59 22.0 6.5

gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.5 6.7

gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339) 61 22.5 6.7

gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.5 6.7

gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen Ana (457) 61 22.5 9.2

gi+AHw-21591547+AHw-gb+AHw-AAM64112.1+AHw- gelsolin-like allergen (480) 61 22.5 9.6

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 init1: 43 opt: 60 Z-score: 89.7 bits: 22.3 E(): 5.1
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (34-65:133-160)

```

          10          20          30          40          50          60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
          :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRPFRFQGDQSQQQQDSHQK----VHRFDEGDLI
          110          120          130          140          150

```

```

          70          80
AAD-12 AISNVKADGTVRQHSPA
          :  :
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNDNDQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
          160          170          180          190          200          210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight gluteni (229 aa)

initn: 39 init1: 39 opt: 59 Z-score: 87.7 bits: 22.0 E(): 6.5
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
 in 53 aa overlap (2-50:3-55)

```

                10      20      30      40      50
AAD-12  TLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKRFGAIE
          : : : . . : . . . . : : : : : : : : : : : : : : : : : :
gi+AHw-886 FALIAVVATSTIAQMETSCIPGLERPWQQQPLPPQQTLFPQQQPFPPQQQPPFSQQQPSFS
          10      20      30      40      50      60
    
```

```

                60      70      80
AAD-12  RIGGGDIVAISNVKADGTVRQHSPA

gi+AHw-886 QQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPQQQQQLPQQQISIVQPSVL
          70      80      90      100     110     120
    
```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
 aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 87.6 bits: 22.5 E(): 6.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (9-41:238-270)

```

                10      20      30
AAD-12  TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
          : : . . : : : : : : : : : : : : .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
          210     220     230     240     250     260
    
```

```

                40      50      60      70      80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA
          : : .
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
          270     280     290     300     310     320
    
```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 87.6 bits: 22.5 E(): 6.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (9-41:238-270)

```

                10      20      30
AAD-12  TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
          : : . . : : : : : : : : : : .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
          210     220     230     240     250     260
    
```

```

                40      50      60      70      80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA
          : : .
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
          270     280     290     300     310     320
    
```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 87.6 bits: 22.5 E(): 6.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (9-41:238-270)

```

                                10      20      30
AAD-12                        TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: .  :: : :  ::.. : ..  .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen
 Ana o 2 (457 aa)

initn: 61 initl: 61 opt: 61 Z-score: 85.1 bits: 22.5 E(): 9.2
 Smith-Waterman score: 61+ADs- 38.710+ACU- identity (58.065+ACU- similar)
 in 31 aa overlap (35-65:108-138)

```

                10      20      30      40      50      60
AAD-12 TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA
                                : :  .. : :  : :  ::.. ::::
gi+AHw-259 YSNAPQLIYVVQEGEMTGISYPGCPETYQAPQQGRQQQSGRFQDRHQKIRRFRRGDI IA
                80      90      100      110      120      130

                70      80
AAD-12 ISNVKADGTVRQHSPA
                :
gi+AHw-259 IPAGVAHWCYNEGNSPVVTVTLLDVSNSQNQLDRTPRKFHLAGNPKDVFQQQQHQSRGR
                140      150      160      170      180      190

```

+AD4APg-gi+AHw-21591547+AHw-gb+AHw-AAM64112.1+AHw- gelsolin-like allergen
 Der (480 aa)

initn: 60 initl: 60 opt: 61 Z-score: 84.7 bits: 22.5 E(): 9.6
 Smith-Waterman score: 61+ADs- 32.692+ACU- identity (59.615+ACU- similar)
 in 52 aa overlap (12-59:83-134)

```

                                10      20      30
AAD-12                        TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH--L
                                :: :::: :..... :. :  :: :.
gi+AHw-215 NPTGGHSMKESKPILNGHYCHIHFWIGSESTKDEAGVAAIKSVELDDFLGGYPVQHREI
                60      70      80      90      100      110

                40      50      60      70      80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA
                . . .  . :  : :  ::
gi+AHw-215 EEFESRQFSSYFKNGI IYLGKGYESGFTKMIDELKPSLLHVKGKKRP IYVECAEISWKVM
                120      130      140      150      160      170

```


The best scores are:

opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.3 5.2

gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229) 59 22.0 6.6

gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.5 6.7

gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339) 61 22.5 6.7

gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.5 6.7

gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen Ana (457) 61 22.5 9.2

gi+AHw-21591547+AHw-gb+AHw-AAM64112.1+AHw- gelsolin-like allergen (480) 61 22.5 9.7

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 89.6 bits: 22.3 E(): 5.2

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar) in 32 aa overlap (33-64:133-160)

```

                10         20         30         40         50         60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRRPRRFQGGDQSQQQQDQSHQK----VHRFDEGLI
                110         120         130         140         150

                70         80
AAD-12 AISNVKADGTVRQHSPAE
                :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                160         170         180         190         200         210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight gluteni (229 aa)

initn: 39 initl: 39 opt: 59 Z-score: 87.7 bits: 22.0 E(): 6.6

Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar) in 53 aa overlap (1-49:3-55)

```

                10         20         30         40         50
AAD-12 LGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKRFGAIE
                :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-886 FALIAVVATSTIAQMETSCIPGLERPWQQQPLPPQQTLFPQQQPPFPQQQPPFSQQQPSFS
                10         20         30         40         50         60

                60         70         80
AAD-12 RIGGGDIVAISNVKADGTVRQHSPAE

gi+AHw-886 QQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPQQQQQLPQQQISIVQPSVL
                70         80         90         100         110         120

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 87.5 bits: 22.5 E(): 6.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (8-40:238-270)

```

                                10      20      30
AAD-12                        LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAE
                :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 87.5 bits: 22.5 E(): 6.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (8-40:238-270)

```

                                10      20      30
AAD-12                        LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAE
                :::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 87.5 bits: 22.5 E(): 6.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (8-40:238-270)

```

                                10      20      30
AAD-12                        LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAE
                :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen
 Ana o 2 (457 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.0 bits: 22.5 E(): 9.2
 Smith-Waterman score: 61+ADs- 38.710+ACU- identity (58.065+ACU- similar)
 in 31 aa overlap (34-64:108-138)

```

          10          20          30          40          50          60
AAD-12 TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA
          : : .. : : : : : : : : : :
gi+AHw-259 YSNAPQLIYVVQEGEGMTGISYPGCPETYQAPQQGRQQQSGRFGQDRHQKIRRFRRGGDIIA
          80          90          100          110          120          130
    
```

```

          70          80
AAD-12 ISNVKADGTVRQHSPA
          :
gi+AHw-259 IPAGVAHWCYNEGNSPVVTVTLLDVSNSQNQLDRTPRKFHLAGNPKDVFQQQQHQSRGR
          140          150          160          170          180          190
    
```

+AD4APg-gi+AHw-21591547+AHw-gb+AHw-AAM64112.1+AHw- gelsolin-like allergen
 Der (480 aa)

initn: 60 init1: 60 opt: 61 Z-score: 84.6 bits: 22.5 E(): 9.7
 Smith-Waterman score: 61+ADs- 32.692+ACU- identity (59.615+ACU- similar)
 in 52 aa overlap (11-58:83-134)

```

          10          20          30
AAD-12 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH--L
          . : : : : : : : : : : :
gi+AHw-215 NPTGGHSMESKPIILNGHYCHIFWIGSESTKDEAGVAAIKSVELDDFLGGYPVQHREI
          60          70          80          90          100          110
    
```

```

          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA
          . . : : : : : :
gi+AHw-215 EEFESRQFSSYFKNGIYLYLGGYESGFTKMIDELKPSLLHVKGKKRPVYECAEISWKVM
          120          130          140          150          160          170
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:37 2010 done: Fri Feb 5 12:55:37 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

76      9      7:+AD0APQAq-
78      2      6:+AD0AKg-
80      3      4:+AD0AKg-
82      2      3:+ACo-
84      2      3:+ACo-
86      3      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-

```

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 5.34590.00343+ADs- mu+AD0- 5.5817
0.176

mean+AF8-var+AD0-43.259511.506, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42

Lambda+AD0- 0.195000

Kolmogorov-Smirnov statistic: 0.0555 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.1 5.6

gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.4 7.3

gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.4 7.3

gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339) 61 22.4 7.3

gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen Ana (457) 61 22.4 9.9

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 init1: 43 opt: 60 Z-score: 88.9 bits: 22.1 E(): 5.6

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar) in 32 aa overlap (32-63:133-160)

```

                10          20          30          40          50          60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSDQITFAKRFGAIERIGGGDIV

```



```

gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
          210          220          230          240          250          260

```

```

          40          50          60          70          80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEW

```

```

          270          280          290          300          310          320
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVVPYTKQLTEADAKTFTSLEYI

```

+AD4APg-gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen
Ana o 2 (457 aa)
initn: 61 initl: 61 opt: 61 Z-score: 84.5 bits: 22.4 E(): 9.9
Smith-Waterman score: 61+ADs- 38.710+ACU- identity (58.065+ACU- similar)
in 31 aa overlap (33-63:108-138)

```

          10          20          30          40          50          60
AAD-12 TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA
          : : .. : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-259 YSNAPQLIYVVQEGEGMTGISYPGCPETYQAPQQGRQQGQSGRFQDRHQKIRRFRRGDIIA
          80          90          100          110          120          130

```

```

          70          80
AAD-12 ISNVKADGTVRQHSPAEW
          :
gi+AHw-259 IPAGVAHWCYNEGNSPVVTVTLLDVSNSQNQLDRTPRKFHLAGNPKDVFQQQQHQSRGR
          140          150          160          170          180          190

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:37 2010 done: Fri Feb 5 12:55:37 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 17 - 96 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

          opt          E()
+ADw- 20          2          0:+AD0-
          22          0          0:          one +AD0- represents 3 library sequences

```



```

88      1      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.38670.00341+ADs- mu+AD0- 5.4933
0.176
mean+AF8-var+AD0-43.426911.513, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.194623
Kolmogorov-Smirnov statistic: 0.0582 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.1 5.8

gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.3 7.5

gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.3 7.5

gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339) 61 22.3 7.5

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 88.7 bits: 22.1 E(): 5.8

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar) in 32 aa overlap (31-62:133-160)

```

                10          20          30          40          50          60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                : :: :...: . : ...: :...
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGGDQSQQQQDSHQK----VHRFDEGLI
                110          120          130          140          150

                70          80
AAD-12 AISNVKADGTVRQHSPAEDW
                :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR

```

160 170 180 190 200 210

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (6-38:238-270)

```

                                10      20      30
AAD-12                        ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFVSYCN
                210      220      230      240      250      260

```

```

                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDW
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (6-38:238-270)

```

                                10      20      30
AAD-12                        ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFVSYCN
                210      220      230      240      250      260

```

```

                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDW
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (6-38:238-270)

```

                                10      20      30
AAD-12                        ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFVSYCN
                210      220      230      240      250      260

```

```

                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDW
                ::.
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI

```


join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.1 5.7
 gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.4 7.4
 gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.4 7.4
 gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k l pollen allerge (339) 61 22.4 7.4

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 88.8 bits: 22.1 E(): 5.7
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar) in 32 aa overlap (30-61:133-160)

```

                10      20      30      40      50
AAD-12  TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                ::  ::  ::  ::  ::
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRPFRFQGDQSQQQQDSHQK----VHRFDEGDLI
                110      120      130      140      150
    
```

```

        60      70      80
AAD-12  AISNVKADGTVRQHSPAEWDD
        ::
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
        160      170      180      190      200      210
    
```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 86.7 bits: 22.4 E(): 7.4
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar) in 33 aa overlap (5-37:238-270)

```

                10      20      30
AAD-12  TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                ::  ::  ::
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFSYCN
                210      220      230      240      250      260
    
```

```

        40      50      60      70      80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDD
        ::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320
    
```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 86.7 bits: 22.4 E(): 7.4
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar) in 33 aa overlap (5-37:238-270)

```

                                10      20      30
AAD-12      TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598  TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVGTGGTALLGRAWFEARVVFVSYCN
                210      220      230      240      250      260

```

```

                40      50      60      70      80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDD
                ::.
gi+AHw-598  LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allergen +AFs-S (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 86.7 bits: 22.4 E(): 7.4
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar) in 33 aa overlap (5-37:238-270)

```

                                10      20      30
AAD-12      TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-225  TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVGTGGTALLGRAWFEARVVFVSYCN
                210      220      230      240      250      260

```

```

                40      50      60      70      80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDD
                ::.
gi+AHw-225  LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:37 2010 done: Fri Feb 5 12:55:37 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 19 - 98 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

opt E()


```

84      2      3:+ACo-
86      4      2:+ACoAPQ-
88      1      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.32380.00343+ADs- mu+AD0- 5.7987
0.177
mean+AF8-var+AD0-43.431211.6666, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.194614
Kolmogorov-Smirnov statistic: 0.0528 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are: opt bits E(1471)
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.1 5.8
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.4 7.5
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.4 7.5
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339) 61 22.4 7.5
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po (97) 54 20.4 8

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 88.7 bits: 22.1 E(): 5.8
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (29-60:133-160)

```

                10      20      30      40      50
AAD-12      VTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                : ::  :::: . :  .... :...
gi+AHw-221  FGLIFPGCPSTYEEPAQQGRRHQSORPPRRFQGDQSQQQQDSHQK----VHRFDEGDLI
                110      120      130      140      150

```

```

      60      70      80
AAD-12 AISNVKADGTVRQHSPAEWDDM
      ::
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 86.7 bits: 22.4 E(): 7.5
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (4-36:238-270)

```

                                10      20      30
AAD-12                          VTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : .: .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
      210      220      230      240      250      260

```

```

      40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDM
      ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 86.7 bits: 22.4 E(): 7.5
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (4-36:238-270)

```

                                10      20      30
AAD-12                          VTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : .: .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
      210      220      230      240      250      260

```

```

      40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDM
      ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 86.7 bits: 22.4 E(): 7.5
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (4-36:238-270)

```

                                10      20      30
AAD-12                          VTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : .: .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
      210      220      230      240      250      260

```

```

      40          50          60          70          80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDM
      :::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVYPYTKQLTEADAKTFTSLEYI
      270          280          290          300          310          320

```

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
  initn: 54 initl: 54 opt: 54 Z-score: 86.2 bits: 20.4 E(): 8
Smith-Waterman score: 54+ADs- 43.750+ACU- identity (68.750+ACU- similar)
in 16 aa overlap (65-80:30-45)

```

```

      40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDM
      .. .:::. ::: :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAKP
      10          20          30          40          50

```

```

gi+AHw-126 LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60          70          80          90

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:37 2010 done: Fri Feb 5 12:55:37 2010
Total Scan time: 0.090 Total Display time: 0.000

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

1+AD4APgA+-AAD-12: 20 - 99 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      1      0:+AD0-
      28      2      0:+AD0-
      30      3      2:+ACo-
      32      19     8:+AD0APQAqAD0APQA9AD0-
      34      25     21:+AD0APQA9AD0APQA9ACoAPQA9-
      36      56     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-

```



```

102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.27690.00346+ADs- mu+AD0- 6.0403
0.178
mean+AF8-var+AD0-43.854411.795, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193672
Kolmogorov-Smirnov statistic: 0.0507 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 22.1 5.9
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.3 7.6
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.3 7.6
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.3 7.6
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134) 56 21.0 7.7
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 54 20.4 8.2

```

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 init1: 43 opt: 60 Z-score: 88.5 bits: 22.1 E(): 5.9
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (28-59:133-160)

```

```

          10          20          30          40          50
AAD-12      TGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
          : :: :...: . : ...: :...
gi+AHw-221  FGLIFPGCPSTYEEPAQQGRRHQSORPPRRFQGDQSQQQDQSHQK----VHRFDEGLI
          110          120          130          140          150

          60          70          80
AAD-12  AISNVKADGTVRQHSPAEWDDMM
          :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVVAVSLTDTNNDNDQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
          160          170          180          190          200          210

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (3-35:238-270)

```

                                10      20      30
AAD-12                        TGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: .  .: : : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMM
                :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (3-35:238-270)

```

                                10      20      30
AAD-12                        TGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: .  .: : : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMM
                :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (3-35:238-270)

```

                                10      20      30
AAD-12                        TGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: .  .: : : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMM
                :::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)
 initn: 36 init1: 36 opt: 56 Z-score: 86.4 bits: 21.0 E(): 7.7
 Smith-Waterman score: 56+ADs- 26.866+ACU- identity (49.254+ACU- similar)
 in 67 aa overlap (19-80:33-99)

```

                10         20         30         40
AAD-12          TGVHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                : .:: . . : : : . :: : . :
gi+AHw-273 MEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
                10         20         30         40         50         60

                50         60         70         80
AAD-12 IERIGG--GD--IVAI SNVKADGTVRQHSPA EWDDMM
                . : .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-273 KMLLKG VIGEEKVVELRN MKEAGADIQELQQVEKMLSEVTDEKQKEKVHEYGPACKKIF
                70         80         90         100        110        120

gi+AHw-273 GATTLQHRRRR
                130

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 54 init1: 54 opt: 54 Z-score: 86.0 bits: 20.4 E(): 8.2
 Smith-Waterman score: 54+ADs- 43.750+ACU- identity (68.750+ACU- similar)
 in 16 aa overlap (64-79:30-45)

```

                40         50         60         70         80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMM
                .. .::: .:: :
gi+AHw-126 TKVDLTVEKGSDAKTLVLN IKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAP
                10         20         30         40         50

gi+AHw-126 LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60         70         80         90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:37 2010 done: Fri Feb 5 12:55:37 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

72      19      12:+AD0APQA9ACoAPQA9AD0-
74      7       10:+AD0APQA9ACo-
76      7       7:+AD0APQAq-
78      0       6: +ACo-
80      8       4:+AD0AKgA9-
82      2       3:+ACo-
84      1       3:+ACo-
86      5       2:+ACoAPQ-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      1       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.33880.0036+ADs- mu+AD0- 5.7902
0.186
mean+AF8-var+AD0-43.734911.708, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193937
Kolmogorov-Smirnov statistic: 0.0480 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  59 21.8      3.1
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 22.0      5.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  55 20.7      6.7
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.3      7.7
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.3      7.7
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.3      7.7
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)  56 21.0      7.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

```

initn: 59 init1: 59 opt: 59 Z-score: 93.5 bits: 21.8 E(): 3.1
 Smith-Waterman score: 59+ADs- 44.444+ACU- identity (66.667+ACU- similar)
 in 18 aa overlap (63-80:30-47)

```

          40          50          60          70          80
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMK
          ..  .::::  :::  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAKP
          10          20          30          40          50

gi+AHw-126  LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
          60          70          80          90

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
 Arachis (219 aa)
 initn: 43 init1: 43 opt: 60 Z-score: 88.5 bits: 22.0 E(): 5.9
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (27-58:133-160)

```

          10          20          30          40          50
AAD-12  GVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
          :  :  .::::  .  :  .:::  :..
gi+AHw-221  FGLIFPGCPSTYEEPAQQGRRHQSQRPFRFQGGDQSQQQQDSHQK----VHRFDEGDLI
          110          120          130          140          150

          60          70          80
AAD-12  AISNVKADGTVRQHSPEAWDDMMK
          :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
          160          170          180          190          200          210

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 55 Z-score: 87.6 bits: 20.7 E(): 6.7
 Smith-Waterman score: 55+ADs- 38.889+ACU- identity (66.667+ACU- similar)
 in 18 aa overlap (63-80:30-47)

```

          40          50          60          70          80
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMK
          ..  .::::  :::  :
gi+AHw-144  VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSSKP
          10          20          30          40          50

gi+AHw-144  LTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
          60          70          80          90

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 86.5 bits: 22.3 E(): 7.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (2-34:238-270)

```

          10          20          30
AAD-12  GVHLATLDDAGFAALHAAWLQHALLIFPGQH

```

```

                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVGTGGTALLGRAWFEEARVVFSYCN
           210         220         230         240         250         260

```

```

           40         50         60         70         80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMK
      ::.

```

```

gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
           270         280         290         300         310         320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.5 bits: 22.3 E(): 7.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (2-34:238-270)

```

                               10         20         30
AAD-12                               GVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVGTGGTALLGRAWFEEARVVFSYCN
           210         220         230         240         250         260

```

```

           40         50         60         70         80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMK
      ::.

```

```

gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
           270         280         290         300         310         320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.5 bits: 22.3 E(): 7.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (2-34:238-270)

```

                               10         20         30
AAD-12                               GVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVGTGGTALLGRAWFEEARVVFSYCN
           210         220         230         240         250         260

```

```

           40         50         60         70         80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMK
      ::.

```

```

gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
           270         280         290         300         310         320

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)

initn: 36 init1: 36 opt: 56 Z-score: 86.4 bits: 21.0 E(): 7.8
 Smith-Waterman score: 56+ADs- 26.866+ACU- identity (49.254+ACU- similar)
 in 67 aa overlap (18-79:33-99)

```

                               10         20         30         40
AAD-12                               GVHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA

```



```

114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.27310.00363+ADs- mu+AD0- 6.0666
0.187
mean+AF8-var+AD0-43.804311.712, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193783
Kolmogorov-Smirnov statistic: 0.0534 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 59 21.8 3.1
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 22.1 5.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 55 20.7 6.7
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.3 7.6
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.3 7.6
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.3 7.6
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134) 56 21.0 7.7

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 59 Z-score: 93.5 bits: 21.8 E(): 3.1
Smith-Waterman score: 59+ADs- 44.444+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (62-79:30-47)

```

                40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKV
                ..  .:.:.  .:.  .:
gi+AHw-126  TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAP
                10          20          30          40          50

gi+AHw-126  LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60          70          80          90

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 88.6 bits: 22.1 E(): 5.9
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (26-57:133-160)

```

                10          20          30          40          50
AAD-12      VHLATLDDAGFAALHAAWLQHALLIFPGQHLSDNDQQITFAKRFGAIERIGGGDIV

```

```

                                : :: :...: . : ...: :...
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSORPPRRFQGDQSQQQDQSHQK----VHRFDEGDLI
                110          120          130          140          150

```

```

        60          70          80
AAD-12 AISNVKADGTVRQHSPAEWDDMMKV
      :.

```

```

gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
        160          170          180          190          200          210

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 init1: 55 opt: 55 Z-score: 87.6 bits: 20.7 E(): 6.7
Smith-Waterman score: 55+ADs- 38.889+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (62-79:30-47)

```

                40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKV
                                .. :...: :... :
gi+AHw-144 VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPLTKKGNLWEVKSSKP
                10          20          30          40          50

```

```

gi+AHw-144 LTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
        60          70          80          90

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (1-33:238-270)

```

                                10          20          30
AAD-12                                VHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
        210          220          230          240          250          260

```

```

                40          50          60          70          80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKV
      :.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFGGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
        270          280          290          300          310          320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (1-33:238-270)

```

                                10          20          30
AAD-12                                VHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
        210          220          230          240          250          260

```

```

                40          50          60          70          80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKV
      :::
gi+AHw-598  LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTKQLTEADAKTFTSLEYI
          270          280          290          300          310          320
    
```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allergen +AFs-S (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (1-33:238-270)

```

                                10          20          30
AAD-12                                VHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : : :: . .: .
gi+AHw-225  TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEAARVVFVSYCN
          210          220          230          240          250          260
    
```

```

                40          50          60          70          80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKV
      :::
gi+AHw-225  LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTKQLTEADAKTFTSLEYI
          270          280          290          300          310          320
    
```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs- Ascaris lumb (134 aa)
 initn: 36 init1: 36 opt: 56 Z-score: 86.4 bits: 21.0 E(): 7.7
 Smith-Waterman score: 56+ADs- 26.866+ACU- identity (49.254+ACU- similar)
 in 67 aa overlap (17-78:33-99)

```

                                10          20          30          40
AAD-12                                VHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                                : .:: . . : : : . :: : . :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQA TEKLVGC
          10          20          30          40          50          60
    
```

```

                50          60          70          80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPA EWDDMMKV
      . : :. .: . :: :. :. . . :.
gi+AHw-273  KMLLKGVI GEEKVVELLRNMKEAGADIQELQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
          70          80          90          100          110          120
    
```

```

gi+AHw-273  GATTLQHRRRR
          130
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:38 2010 done: Fri Feb 5 12:55:38 2010
 Total Scan time: 0.090 Total Display time: 0.010


```

58      67
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60      63
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
62      67
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
64      27      32:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
66      19      25:+AD0APQA9AD0APQA9AD0- +ACo-
68      29      20:+AD0APQA9AD0APQA9ACoAPQA9AD0-
70      20      16:+AD0APQA9AD0APQAqAD0-
72      16      12:+AD0APQA9ACoAPQA9-
74      9       10:+AD0APQA9ACo-
76      5       7:+AD0APQAq-
78      4       6:+AD0AKg-
80      7       4:+AD0AKgA9-
82      1       3:+ACo-
84      2       3:+ACo-
86      1       2:+ACo-
88      2       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      1       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120  0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.21120.00364+ADs- mu+AD0- 6.4473
0.188
mean+AF8-var+AD0-43.771711.792, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193855
Kolmogorov-Smirnov statistic: 0.0616 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  59 21.8      3.2
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 22.1      5.9
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)  57 21.2      6.5

```

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0- (96) 55 20.7 6.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 59 Z-score: 93.4 bits: 21.8 E(): 3.2
Smith-Waterman score: 59+ADs- 44.444+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (61-78:30-47)

40 50 60 70 80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVI
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAPK
10 20 30 40 50

gi+AHw-126 LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs- Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 88.5 bits: 22.1 E(): 5.9
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (25-56:133-160)

10 20 30 40 50
AAD-12 HLATLDDAGFAALHAAWLQHALLIFPGQHLSDNDQQITFAKRFGAIERIGGGDIV
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRRPRRFQGGQDQSQQQQDSHQK----VHRFDEGDLI
110 120 130 140 150

60 70 80
AAD-12 AISNVKADGTVRQHSPEAWDDMMKVI
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
160 170 180 190 200 210

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs- Ascaris lumb (134 aa)
initn: 36 initl: 36 opt: 57 Z-score: 87.8 bits: 21.2 E(): 6.5
Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
in 70 aa overlap (16-80:33-102)

10 20 30 40
AAD-12 HLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
gi+AHw-273 MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQOATEKLVGC
10 20 30 40 50 60

50 60 70 80
AAD-12 IERIGG--GD--IVAISNVKADGTVRQHSPEAWDDMMKVI
gi+AHw-273 KMLLKGVI GEEKVVELRNMKEAGADIQELQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
70 80 90 100 110 120

gi+AHw-273 GATTLQHRRRR
130

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 55 Z-score: 87.4 bits: 20.7 E(): 6.8
Smith-Waterman score: 55+ADs- 38.889+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (61-78:30-47)

	40	50	60	70	80
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVI				
			
gi+AHw-144	VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEWEPLTKKGNLWEVKSSKP				
	10	20	30	40	50

gi+AHw-144	LTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE			
	60	70	80	90

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:38 2010 done: Fri Feb 5 12:55:38 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 24 - 103 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	1	0:+AD0-	
30	5	2:+ACoAPQ-	
32	20	8:+AD0APQAqAD0APQA9AD0-	
34	27	21:+AD0APQA9AD0-+AD0APQAqAD0APQ-	
36	62		

44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-


```

100      0      0:      +ACo-
102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.29960.00371+ADs- mu+AD0- 6.0233
0.191
mean+AF8-var+AD0-44.174211.942, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.192970
Kolmogorov-Smirnov statistic: 0.0630 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 59 21.8 3.2

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.0 6.1

gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134) 57 21.2 6.6

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 55 20.6 6.9

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 59 Z-score: 93.2 bits: 21.8 E(): 3.2
Smith-Waterman score: 59+ADs- 44.444+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (60-77:30-47)

```

      30      40      50      60      70      80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIV
      .. .::::. ::: : :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAP
      10      20      30      40      50

```

```

gi+AHw-126 LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 init1: 43 opt: 60 Z-score: 88.2 bits: 22.0 E(): 6.1
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (24-55:133-160)

10 20 30 40 50

```

AAD-12          LATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                :  ::  :...: .  :  ....  :...
gi+AHw-221 FGLIFPGCPSTYEPEPAQQGRRHQSQRPPRRFQGDQSQQQDSSHQK---VHRFDEGDLI
            110          120          130          140          150

```

```

                60          70          80
AAD-12 AISNVKADGTVRQHSPAEWDDMMKVIV
                :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
            160          170          180          190          200          210

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 87.6 bits: 21.2 E(): 6.6
 Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
 in 70 aa overlap (15-79:33-102)

```

                10          20          30          40
AAD-12          LATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                :  ::  .  :  :  :  .  ::  :  .  :
gi+AHw-273 MEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVKVC
            10          20          30          40          50          60

```

```

                50          60          70          80
AAD-12 IERIGG--GD--IVAISNVKADGTVRQHSPAEWDDMMKVIV
                .  :  .  .  :  .  :  :  .  :  .  .  :  .  .
gi+AHw-273 KMLLKGVIGEEKVVELLRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
            70          80          90          100          110          120

```

```

gi+AHw-273 GATTLQHRRRR
            130

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 55 Z-score: 87.3 bits: 20.6 E(): 6.9
 Smith-Waterman score: 55+ADs- 38.889+ACU- identity (66.667+ACU- similar)
 in 18 aa overlap (60-77:30-47)

```

                30          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIV
                :.  :...:  :...  :
gi+AHw-144 VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEP LTKKGNLWEVKSSKP
            10          20          30          40          50

```

```

gi+AHw-144 LTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
            60          70          80          90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scmplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:38 2010 done: Fri Feb 5 12:55:38 2010
 Total Scan time: 0.090 Total Display time: 0.000

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.0 6
 gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134) 57 21.2 6.4
 gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0- (96) 55 20.7 6.6

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 59 Z-score: 93.6 bits: 21.8 E(): 3.1
 Smith-Waterman score: 59+ADs- 44.444+ACU- identity (66.667+ACU- similar) in 18 aa overlap (59-76:30-47)

	30	40	50	60	70	80
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVG					
			 :
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKKNLWEVKSAP					
	10	20	30	40	50	

gi+AHw-126 LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 88.4 bits: 22.0 E(): 6
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar) in 32 aa overlap (23-54:133-160)

		10	20	30	40	50
AAD-12	ATLDDAGFAALHAAWLQHALLIFPGQHLSDNDQQITFAKRFGAIERIGGGDIV					
				:: :
gi+AHw-221	FGLIFPGCPSTYEEPAQQGRRHQSQRPFRFQGGDQSQQQQDSHQK----VHRFDEGDLI					
	110	120	130	140	150	

	60	70	80
AAD-12	AISNVKADGTVRQHSPEAWDDMMKVIVG		
	..		
gi+AHw-221	AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR		
	160	170	180 190 200 210

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 87.9 bits: 21.2 E(): 6.4
 Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar) in 70 aa overlap (14-78:33-102)

		10	20	30	40
AAD-12	ATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA				
			::	..	: : : . : : . :
gi+AHw-273	MEHYLKTYLSWLTEEQKEKLEKEMKEAGTKAEIQHEVMHFYDQLHGEEKQQAATEKLVGC				
	10	20	30	40	50 60

	50	60	70	80
AAD-12	IERIGG--GD--IVAISNVKADGTVRQHSPEAWDDMMKVIVG			


```

  98      0      0:      +ACo-
 100      0      0:      +ACo-
 102      0      0:      +ACo-
 104      0      0:      +ACo-
 106      0      0:      +ACo-
 108      0      0:      +ACo-
 110      0      0:      +ACo-
 112      0      0:      +ACo-
 114      0      0:      +ACo-
 116      0      0:      +ACo-
 118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.46400.00375+ADs- mu+AD0- 5.0984
0.193
mean+AF8-var+AD0-43.770711.813, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193857
Kolmogorov-Smirnov statistic: 0.0487 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  59 21.8      3
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 22.0      5.9
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)  57 21.3      6.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  55 20.7      6.5

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 init1: 59 opt: 59 Z-score: 93.7 bits: 21.8 E(): 3
Smith-Waterman score: 59+ADs- 44.444+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (58-75:30-47)

      30      40      50      60      70      80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGN
      ..  .::::  :::  ::
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAP
      10      20      30      40      50

gi+AHw-126 LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 init1: 43 opt: 60 Z-score: 88.5 bits: 22.0 E(): 5.9
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (22-53:133-160)

```

```

                10      20      30      40      50
AAD-12      TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                :  ::  :...:  .  :  ...  :...
gi+AHw-221  FGLIFPGCPSTYEEPAQQGRRHQSQRPPRRFQGDQSQQQDQSHQK----VHRFDEGDLI
                110      120      130      140      150

```

```

                60      70      80
AAD-12  AISNVKADGTVRQHSPAEWDDMMKVIVGN
                :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                160      170      180      190      200      210

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 88.0 bits: 21.3 E(): 6.3
 Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
 in 70 aa overlap (13-77:33-102)

```

                10      20      30      40
AAD-12      TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                :  ::  .  :  :  :  .  ::  :  .  :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
                10      20      30      40      50      60

```

```

                50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPAEWDDMMKVIVGN
                .  :  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-273  KMLLLKGVIGEEKVVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
                70      80      90      100      110      120

```

```

gi+AHw-273  GATTLQHRRRR
                130

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 55 Z-score: 87.7 bits: 20.7 E(): 6.5
 Smith-Waterman score: 55+ADs- 38.889+ACU- identity (66.667+ACU- similar)
 in 18 aa overlap (58-75:30-47)

```

                30      40      50      60      70      80
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGN
                :.  :...  :...  :
gi+AHw-144  VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWELTKKGNLWEVKSSKP
                10      20      30      40      50

```

```

gi+AHw-144  LTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                60      70      80      90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:38 2010 done: Fri Feb 5 12:55:38 2010


```

56      59      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
58      72
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
60      63
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
62      70
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9-
64      29      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      21      25:+AD0APQA9AD0APQA9AD0- +ACo-
68      33      20:+AD0APQA9-+AD0APQA9ACoAPQA9AD0APQ-
70      19      16:+AD0APQA9AD0APQAqAD0-
72      21      12:+AD0APQA9ACoAPQA9AD0-
74      7       10:+AD0APQA9ACo-
76      4       7:+AD0APQAq-
78      2       6:+AD0AKg-
80      6       4:+AD0AKg-
82      2       3:+ACo-
84      1       3:+ACo-
86      0       2:+ACo-
88      3       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      1       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:           +ACo-
100     0       0:           +ACo-
102     0       0:           +ACo-
104     0       0:           +ACo-
106     0       0:           +ACo-
108     0       0:           +ACo-
110     0       0:           +ACo-
112     0       0:           +ACo-
114     0       0:           +ACo-
116     0       0:           +ACo-
118     0       0:           +ACo-
+AD4-120 0       0:           +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.53540.00374+ADs- mu+AD0- 4.7046
0.193
mean+AF8-var+AD0-43.527011.684, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.194399
Kolmogorov-Smirnov statistic: 0.0432 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 60 22.2 2.4
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 56 21.0 5.2

```

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.1 5.8
 gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134) 57 21.3 6.2

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 60 Z-score: 95.4 bits: 22.2 E(): 2.4
 Smith-Waterman score: 60+ADs- 41.667+ACU- identity (62.500+ACU- similar) in 24 aa overlap (57-80:30-51)

```

      30      40      50      60      70      80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNM
      .. .: : : : :
gi+AHw-126 TKVDLTVEKGS DAKTLVLN IKYTRPGDTLAEVELRQH GSEEWEPMTKK--GNLWEVKSA
      10      20      30      40      50

```

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 56 Z-score: 89.5 bits: 21.0 E(): 5.2
 Smith-Waterman score: 56+ADs- 37.500+ACU- identity (62.500+ACU- similar) in 24 aa overlap (57-80:30-51)

```

      30      40      50      60      70      80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNM
      .. .: : : : :
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEEWEPMTKK--GNLWEVKSS
      10      20      30      40      50

```

```

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTYYTPEE
      60      70      80      90

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 init1: 43 opt: 60 Z-score: 88.6 bits: 22.1 E(): 5.8
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar) in 32 aa overlap (21-52:133-160)

```

      10      20      30      40      50
AAD-12 LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      : : : : : : : : : :
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRP RRFFQGDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150

```

```

      60      70      80
AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIVGNM
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFRRRNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210

```



```

  98      0      0:      +ACo-
 100      0      0:      +ACo-
 102      0      0:      +ACo-
 104      0      0:      +ACo-
 106      0      0:      +ACo-
 108      0      0:      +ACo-
 110      0      0:      +ACo-
 112      0      0:      +ACo-
 114      0      0:      +ACo-
 116      0      0:      +ACo-
 118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.52170.0037+ADs- mu+AD0- 4.7768
0.191
mean+AF8-var+AD0-43.563311.711, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.194318
Kolmogorov-Smirnov statistic: 0.0419 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 60 22.2 2.4

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 56 21.0 5.3

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219)
60 22.1 5.9

gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134)
57 21.3 6.2

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 60 Z-score: 95.4 bits: 22.2 E(): 2.4

Smith-Waterman score: 60+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (56-79:30-51)

```

          30          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMA
          ..  .::::  :::  :  :  :::
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNLWEVKSA
          10          20          30          40          50

```

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
          60          70          80          90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)

initn: 55 init1: 55 opt: 56 Z-score: 89.4 bits: 21.0 E(): 5.3

Smith-Waterman score: 56+ADs- 37.500+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (56-79:30-51)

```

      30      40      50      60      70      80
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMA
      ..  .:..:  :..  .  :  :..
gi+AHw-144  VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWELTKK--GNLWEVKSS
      10      20      30      40      50

```

```

gi+AHw-144  KPLTGFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
      60      70      80      90

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
 Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 88.6 bits: 22.1 E(): 5.9
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (20-51:133-160)

```

      10      20      30      40
AAD-12  DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      :  :  :..:  .  :  :..  :..
gi+AHw-221  FGLIFPGCPSTYEEPAQQGRRHQSRPPRRFQGDQSQQQQDSHQK----VHRFDEGLI
      110      120      130      140      150

```

```

      50      60      70      80
AAD-12  AISNVKADGTVRQHSPEAWDDMMKVIVGNMA
      :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 88.1 bits: 21.3 E(): 6.2
 Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
 in 70 aa overlap (11-75:33-102)

```

      10      20      30
AAD-12  DDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
      :  :..  .  :  :  :  :  :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQAATEKLVGC
      10      20      30      40      50      60

```

```

      40      50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPEAWDDMMKVIVGNMA
      .  :  :.  :.  :..  :.  :.  .  :..  .
gi+AHw-273  KMLLKGVIGEEKVVELLRNMKEAGADIQELQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
      70      80      90      100      110      120

```

```

gi+AHw-273  GATTLQHRRRR
      130

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:38 2010 done: Fri Feb 5 12:55:39 2010

54 74
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56 61 76:+AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
58 76
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
-
60 57 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62 68
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
64 28 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66 25 25:+AD0APQA9AD0APQA9AD0APQA9-
68 34 20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
70 23 16:+AD0-+AD0APQA9AD0AKgA9AD0-
72 20 12:+AD0APQA9ACoAPQA9AD0-
74 5 10:+AD0APQ- +ACo-
76 4 7:+AD0APQA9-
78 1 6:+AD0AKg-
80 7 4:+AD0AKgA9-
82 1 3:+ACo-
84 1 3:+ACo-
86 0 2:+ACo-
88 2 2:+ACo- inset +AD0- represents 1 library sequences
90 0 1:+ACo-
92 1 1:+ACo- :+ACo-
94 0 1:+ACo- :+ACo-
96 0 1:+ACo- :+ACo-
98 1 0:+AD0- +ACoAPQ-
100 0 0: +ACo-
102 0 0: +ACo-
104 0 0: +ACo-
106 0 0: +ACo-
108 0 0: +ACo-
110 0 0: +ACo-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.45900.00374+ADs- mu+AD0- 5.1700
0.193
mean+AF8-var+AD0-44.058411.784, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193223
Kolmogorov-Smirnov statistic: 0.0466 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 63 22.9 1.4

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
 (96) 59 21.8 3.1
 gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219)
 60 22.0 6.1
 gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134)
 57 21.2 6.5

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 63 Z-score: 99.5 bits: 22.9 E(): 1.4
 Smith-Waterman score: 63+ADs- 42.308+ACU- identity (61.538+ACU- similar)
 in 26 aa overlap (55-80:30-52)

	30	40	50	60	70	80
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW					
				::: : : ::: :
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNL-WEVKS					
	10	20	30	40	50	

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 59 Z-score: 93.6 bits: 21.8 E(): 3.1
 Smith-Waterman score: 59+ADs- 38.462+ACU- identity (61.538+ACU- similar)
 in 26 aa overlap (55-80:30-52)

	30	40	50	60	70	80
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW					
				::: . : ::: :
gi+AHw-144	VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEP LTKK--GNL-WEVKS					
	10	20	30	40	50	

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
 60 70 80 90

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
 Arachis (219 aa)
 initn: 43 init1: 43 opt: 60 Z-score: 88.3 bits: 22.0 E(): 6.1
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (19-50:133-160)

		10	20	30	40
AAD-12	DAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV				
		::
gi+AHw-221	FGLIFPGCPSTYEEPAQQGRRHQSQRPFRFQGDQSQQQQDSHQK---VHRFDEGDLI				
	110	120	130	140	150

	50	60	70	80
AAD-12	AISNVKADGTVRQHSPA EWDDMMKVIVGNMAW			
	..			
gi+AHw-221	AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR			
	160	170	180	210

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 87.8 bits: 21.2 E(): 6.5
 Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
 in 70 aa overlap (10-74:33-102)

```

                                10      20      30
AAD-12      DAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                                :  .:  .:  :  :  .  :  :  .  :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
                                10      20      30      40      50      60

                                40      50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPEWDDMMKVIVGNMAW
                                .  :  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-273  KMLLKGVIGEEKVVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
                                70      80      90      100     110     120

gi+AHw-273  GATTLQHRRRR
                                130
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:39 2010 done: Fri Feb 5 12:55:39 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 30 - 109 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
	22	0	0: one +AD0- represents 3 library sequences
	24	0	0:
	26	0	0:
	28	2	0:+AD0-
	30	6	2:+ACoAPQ-
	32	21	8:+AD0APQAqAD0APQA9AD0-
	34	25	21:+AD0APQA9AD0APQA9ACoAPQA9-


```

100      0      0:      +ACo-
102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.33500.00368+ADs- mu+AD0- 5.8232
0.190
mean+AF8-var+AD0-44.662411.986, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.191913
Kolmogorov-Smirnov statistic: 0.0480 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.070

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 63 22.8 1.5

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 59 21.7 3.3

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219)
60 22.0 6.3

gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134)
57 21.2 6.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 63 Z-score: 99.0 bits: 22.8 E(): 1.5
Smith-Waterman score: 63+ADs- 42.308+ACU- identity (61.538+ACU- similar)
in 26 aa overlap (54-79:30-52)

```

          30          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWH
          ..  .::::  :::  :  :  :::  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNL-WEVK
          10          20          30          40          50

```

```

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
          60          70          80          90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)

initn: 55 init1: 55 opt: 59 Z-score: 93.1 bits: 21.7 E(): 3.3
Smith-Waterman score: 59+ADs- 38.462+ACU- identity (61.538+ACU- similar)
in 26 aa overlap (54-79:30-52)

```

          30          40          50          60          70          80

```

```

AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPPAEWDDMMKVIVGNMAWH
          ..  .::::.  :::  .  :  :::  :
gi+AHw-144  VKVTFKVEKGSDPKKLVLVDIKYTRPGDTLAEVELRQHGSEEWELTKK--GNL-WEVKS
          10          20          30          40          50

```

```

gi+AHw-144  SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPPE
          60          70          80          90

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
 Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 88.0 bits: 22.0 E(): 6.3
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (18-49:133-160)

```

          10          20          30          40
AAD-12      AGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
          :  :  .::::.  .  :  .::::.  :...
gi+AHw-221  FGLIFPGCPSTYEEPAQQGRRHQSQRRRFQGDQSQQQQDSHQK----VHRFDEGLI
          110          120          130          140          150

```

```

          50          60          70          80
AAD-12  AISNVKADGTVRQHSPPAEWDDMMKVIVGNMAWH
          :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
          160          170          180          190          200          210

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 87.5 bits: 21.2 E(): 6.8
 Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
 in 70 aa overlap (9-73:33-102)

```

          10          20          30
AAD-12      AGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
          :  :  :  .  :  :  :  .  :  :  .  :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
          10          20          30          40          50          60

```

```

          40          50          60          70          80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPPAEWDDMMKVIVGNMAWH
          .  :  :.  .:  .:::  :.  :.  .  :...
gi+AHw-273  KMLLKGVIGEEKVVELLRNMKEAGADIQELQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
          70          80          90          100          110          120

```

```

gi+AHw-273  GATTLQHRRRR
          130

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:40 2010 done: Fri Feb 5 12:55:40 2010
 Total Scan time: 0.070 Total Display time: 0.010


```

56      58      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
58      68
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60      57      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      66
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
64      31      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      28      25:+AD0APQA9AD0APQA9AD0APQAqAD0-
68      36      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
70      18      16:+AD0APQA9AD0APQAq-
72      15      12:+AD0APQA9ACoAPQ-
74      3      10:+AD0- +ACo-
76      3      7:+AD0- +ACo-
78      9      6:+AD0AKgA9-
80      6      4:+AD0AKg-
82      2      3:+ACo-
84      0      3:+ACo-
86      1      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      1      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120  0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.46220.00363+ADs- mu+AD0- 5.2174
0.187
mean+AF8-var+AD0-44.786411.931, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.191647
Kolmogorov-Smirnov statistic: 0.0425 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 63 22.8 1.5
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 59 21.7 3.3
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 21.9 6.4

```

gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134) 57 21.1 6.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 63 Z-score: 99.0 bits: 22.8 E(): 1.5
 Smith-Waterman score: 63+ADs- 42.308+ACU- identity (61.538+ACU- similar)
 in 26 aa overlap (53-78:30-52)

```

                30          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA
                ..  .::::.  :::  :  :  ::.  :
gi+AHw-126 TKVDLTVEKGS DAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNL-WEVKS
                10          20          30          40          50

```

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 59 Z-score: 93.1 bits: 21.7 E(): 3.3
 Smith-Waterman score: 59+ADs- 38.462+ACU- identity (61.538+ACU- similar)
 in 26 aa overlap (53-78:30-52)

```

                30          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA
                ..  .::::.  :::  .  :  ::.  :
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNL-WEVKS
                10          20          30          40          50

```

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
 60 70 80 90

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 init1: 43 opt: 60 Z-score: 87.9 bits: 21.9 E(): 6.4
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (17-48:133-160)

```

                10          20          30          40
AAD-12          GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                :  :  .::::.  .  :  .::::.  :...
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSRPPRRFQGDQSQQQQDSHQK----VHRFDEGDLI
                110          120          130          140          150

```

```

                50          60          70          80
AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA
                :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNDNDQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                160          170          180          190          200          210

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris lumb (134 aa)
 initn: 36 init1: 36 opt: 57 Z-score: 87.4 bits: 21.1 E(): 6.8

Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar) in 70 aa overlap (8-72:33-102)

```

                                10      20      30
AAD-12      GFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                                :  ::  ..  :  :  .  ::  :  .  :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
                10      20      30      40      50      60

                40      50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHA
                .  :  ::  ..  .  ::  ::  ..  .  .  ::  .
gi+AHw-273  KMLLKGVIGEEKVVELLRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
                70      80      90      100      110      120

gi+AHw-273  GATTLQHRRRR
                130

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:41 2010 done: Fri Feb 5 12:55:42 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 32 - 111 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      8      2:+ACoAPQA9-
      32      15     8:+AD0APQAqAD0APQ-
      34      29     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36      68
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
      38      63
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-

```



```

112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.54240.00366+ADs- mu+AD0- 4.9212
0.189
mean+AF8-var+AD0-48.425113.884, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.184306
Kolmogorov-Smirnov statistic: 0.0371 (N+AD0-27) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 63 22.5 2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 59 21.4 4.1
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 21.6 7.9
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134) 57 20.9 8.3

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
initn: 59 init1: 59 opt: 63 Z-score: 97.0 bits: 22.5 E(): 2
Smith-Waterman score: 63+ADs- 42.308+ACU- identity (61.538+ACU- similar) in 26 aa overlap (52-77:30-52)

```

          30          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPPAEWDDMMKVIVGNMAWHAD
          ..  .:..:  .:..:  .:..:  .:..:
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNL-WEVKS
          10          20          30          40          50

```

```

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
          60          70          80          90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
initn: 55 init1: 55 opt: 59 Z-score: 91.4 bits: 21.4 E(): 4.1
Smith-Waterman score: 59+ADs- 38.462+ACU- identity (61.538+ACU- similar) in 26 aa overlap (52-77:30-52)

```

          30          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPPAEWDDMMKVIVGNMAWHAD
          ..  .:..:  .:..:  .:..:  .:..:
gi+AHw-144 VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNL-WEVKS
          10          20          30          40          50

```

```

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE

```

60 70 80 90

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 86.2 bits: 21.6 E(): 7.9
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (16-47:133-160)

```

                                10      20      30      40
AAD-12      FAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                                :  ::  ::  ::  .  :  .  ::  ::  ::
gi+AHw-221  FGLIFPGCPSTYEEPAQQGRRHQSQRRRFQGDQSQQQQDSHQK----VHRFDEGLI
                                110      120      130      140      150
    
```

```

                                50      60      70      80
AAD-12  AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD
                                :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                                160      170      180      190      200      210
    
```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris lumb (134 aa)

initn: 36 initl: 36 opt: 57 Z-score: 85.8 bits: 20.9 E(): 8.3
 Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
 in 70 aa overlap (7-71:33-102)

```

                                10      20      30
AAD-12      FAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                                :  ::  ..  :  :  :  .  ::  :  .  :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
                                10      20      30      40      50      60
    
```

```

                                40      50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAD
                                .  :  .  .  ::  ::  .  .  .  .  .
gi+AHw-273  KMLLLKGVIGEEKVVELLRNMKEAGADIQELQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
                                70      80      90      100      110      120
    
```

gi+AHw-273 GATTLQHRRRR
 130

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:42 2010 done: Fri Feb 5 12:55:42 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006


```

64      30      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      38      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
68      30      20:+AD0APQA9AD0APQA9ACoAPQA9AD0-
70      33      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72       8      12:+AD0APQA9ACo-
74       7      10:+AD0APQ-+AD0AKg-
76      12      7:+AD0APQAqAD0-
78       2      6:+AD0AKg-
80       2      4:+AD0AKg-
82       1      3:+ACo-
84       4      3:+ACoAPQ-
86       2      2:+ACo-
88       0      2:+ACo-          inset +AD0- represents 1 library sequences
90       0      1:+ACo-
92       0      1:+ACo-          :+ACo-
94       0      1:+ACo-          :+ACo-
96       1      1:+ACo-          :+ACo-
98       0      0:              +ACo-
100      1      0:+AD0-          +ACoAPQ-
102      0      0:              +ACo-
104      0      0:              +ACo-
106      0      0:              +ACo-
108      0      0:              +ACo-
110      0      0:              +ACo-
112      0      0:              +ACo-
114      0      0:              +ACo-
116      0      0:              +ACo-
118      0      0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.47430.00367+ADs- mu+AD0- 5.3943
0.189
mean+AF8-var+AD0-50.328914.482, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.180786
Kolmogorov-Smirnov statistic: 0.0357 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po

(97) 67 23.3 1.1

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-

(96) 63 22.2 2.3

gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)

57 20.7 8.5

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)

57 20.7 8.5

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P

(122) 57 20.7 8.5

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)

57 20.7 8.5

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 21.5 8.8
 gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134) 57 20.7 9.3

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 101.5 bits: 23.3 E(): 1.1
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (51-80:30-56)

```

                30         40         50         60         70         80
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                ..  .: : : : : : : : : : : :
gi+AHw-126  TKVDLTVEKGS DAKTLVLN IKYTRPGDTLAEVELRQH GSEEWEPMTK--KGNL-WEVKS
                10         20         30         40         50

```

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 63 Z-score: 96.0 bits: 22.2 E(): 2.3
 Smith-Waterman score: 63+ADs- 36.667+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (51-80:30-56)

```

                30         40         50         60         70         80
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                ..  .: : : : : : : : : : : :
gi+AHw-144  VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEEWEPMTK--KGNL-WEVKS
                10         20         30         40         50

```

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
 60 70 80 90

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.7 bits: 20.7 E(): 8.5
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (25-80:29-82)

```

                10         20         30         40         50
AAD-12  AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..  .: : : : : : : : : : : :
gi+AHw-400  MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
                10         20         30         40         50         60

```

```

                60         70         80
AAD-12  QHSPA EWDDMMKVIVGNMAWHADS
                ..  : : : : : : : :
gi+AHw-400  EHGSD E VWAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                70         80         90         100        110

```



```

68      32      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
70      31      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      9       12:+AD0APQA9ACo-
74      7       10:+AD0APQA9ACo-
76      12      7:+AD0APQAqAD0-
78      2       6:+AD0AKg-
80      2       4:+AD0AKg-
82      1       3:+ACo-
84      4       3:+ACoAPQ-
86      2       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120  0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.54220.00367+ADs- mu+AD0- 5.0367
0.190
mean+AF8-var+AD0-50.508214.517, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.180465
Kolmogorov-Smirnov statistic: 0.0385 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.3      1.1
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.8      1.6
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.7      8.5
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.7      8.5
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.7      8.5
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.7      8.5
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 21.5      8.9

```

gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134) 57 20.7 9.4

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 101.5 bits: 23.3 E(): 1.1
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (50-79:30-56)

20 30 40 50 60 70
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
gi+AHw-126 TKVDLTVEKGS DAKTLVLN IKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
10 20 30 40 50

80
AAD-12 T

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 98.8 bits: 22.8 E(): 1.6
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (50-80:30-57)

20 30 40 50 60 70
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
10 20 30 40 50

80
AAD-12 T

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
60 70 80 90

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
initn: 52 initl: 52 opt: 57 Z-score: 85.7 bits: 20.7 E(): 8.5
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (24-79:29-82)

10 20 30 40 50
AAD-12 ALHAAWLQHALLIFPGQHL SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
gi+AHw-400 MSMASSSSSGLLAMAVL AALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
10 20 30 40 50 60

60 70 80
AAD-12 QHSPA EWDDMMKVIVGNMAWHADST
... :: : : : .: ::

gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.7 bits: 20.7 E(): 8.5
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (24-79:29-82)

10 20 30 40 50
AAD-12 ALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... :. :. :. :.
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
10 20 30 40 50 60

60 70 80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADST
.. :: : : : .: ::
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-Polle (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 85.7 bits: 20.7 E(): 8.5
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (24-79:29-82)

10 20 30 40 50
AAD-12 ALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... :. :. :. :.
gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
10 20 30 40 50 60

60 70 80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADST
.. :: : : : .: ::
gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 85.7 bits: 20.7 E(): 8.5
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (24-79:29-82)

10 20 30 40 50
AAD-12 ALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... :. :. :. :.
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
10 20 30 40 50 60

60 70 80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADST
.. :: : : : .: ::

gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 85.3 bits: 21.5 E(): 8.9
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (14-45:133-160)

AAD-12 ALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
: : : : : : : : : : : :
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSRPPRRFQGDQSQQQQDSHQK----VHRFDEGDLI
110 120 130 140 150

AAD-12 AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
:.
gi+AHw-221 AVPTGVAFWMYNDHDTDVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
160 170 180 190 200 210

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
Ascaris lumb (134 aa)
initn: 36 initl: 36 opt: 57 Z-score: 84.9 bits: 20.7 E(): 9.4
Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
in 70 aa overlap (5-69:33-102)

AAD-12 ALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
: : : : : : : : : :
gi+AHw-273 MEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
10 20 30 40 50 60

AAD-12 IERIGG--GD--IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
. : . : . : : : . : . : . :
gi+AHw-273 KMLLKGVIGEEKVVELLRNMKEAGADIQELQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
70 80 90 100 110 120

gi+AHw-273 GATTLQHRRRR
130

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:43 2010 done: Fri Feb 5 12:55:43 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank


```

60      61
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
62      28      40:+AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
64      26      32:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
66      44      25:+AD0-+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
68      23      20:+AD0APQA9AD0APQA9ACoAPQ-
70      33      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      9       12:+AD0APQA9ACo-
74      6       10:+AD0APQ- +ACo-
76      11      7:+AD0APQAqAD0-
78      5       6:+AD0AKg-
80      3       4:+AD0AKg-
82      1       3:+ACo-
84      7       3:+ACoAPQA9-
86      2       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0 0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.60300.00371+ADs- mu+AD0- 4.7526
0.191
mean+AF8-var+AD0-53.865115.304, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.174751
Kolmogorov-Smirnov statistic: 0.0323 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:          opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 23.0 1.4
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.5 1.9
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0 7.3
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.8 8
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.8 8.7

```

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
 (122) 57 20.5 9.9
 gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 57 20.5 9.9
 gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
 57 20.5 9.9
 gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 57 20.5 9.9

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 99.9 bits: 23.0 E(): 1.4
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (49-78:30-56)

	20	30	40	50	60	70
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS					
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS					
	10	20	30	40	50	

80
 AAD-12 TY

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 65 Z-score: 97.2 bits: 22.5 E(): 1.9
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (49-79:30-57)

	20	30	40	50	60	70
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS					
gi+AHw-144	VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKS					
	10	20	30	40	50	

80
 AAD-12 TY

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
 60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
 +AFs-Phl (263 aa)
 initn: 44 init1: 44 opt: 63 Z-score: 86.8 bits: 22.0 E(): 7.3
 Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (21-80:207-260)

		10	20	30	40	50
AAD-12	LHAAWLQHALLIFPGQHLSDQQITFAKRFGAIERIGGGDIVAISNVKAD					

gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGGKDKWIALKESWGAIWRIDTPEVL-----KGP
 180 190 200 210 220 230

60 70 80
 AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTY
 ::: . . :

gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
 240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
 product +AFs-P (240 aa)
 initn: 44 initl: 44 opt: 62 Z-score: 86.2 bits: 21.8 E(): 8
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
 in 60 aa overlap (21-80:184-237)

10 20 30 40 50
 AAD-12 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD

gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGGKDKWIALKESWGAIWRIDTPEVL-----KGP
 160 170 180 190 200

60 70 80
 AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTY
 ::: . . :

gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
 210 220 230 240

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
 (262 aa)
 initn: 44 initl: 44 opt: 62 Z-score: 85.5 bits: 21.8 E(): 8.7
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (21-80:206-259)

10 20 30 40 50
 AAD-12 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD

gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGGKDKWIALKESWGAIWRIDTPEVL-----KGP
 180 190 200 210 220 230

60 70 80
 AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTY
 ::: . . :

gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
 240 250 260

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)
 initn: 52 initl: 52 opt: 57 Z-score: 84.5 bits: 20.5 E(): 9.9
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (23-78:29-82)

10 20 30 40 50
 AAD-12 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR

gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
10 20 30 40 50 60

60 70 80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTY
... :: : : : .: ::

gi+AHw-117 EHGSDSEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 84.5 bits: 20.5 E(): 9.9
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (23-78:29-82)

10 20 30 40 50
AAD-12 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... . :. :. :. :.
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
10 20 30 40 50 60

60 70 80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTY
... :: : : : .: ::
gi+AHw-400 EHGSDSEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 84.5 bits: 20.5 E(): 9.9
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (23-78:29-82)

10 20 30 40 50
AAD-12 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... . :. :. :. :.
gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
10 20 30 40 50 60

60 70 80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTY
... :: : : : .: ::
gi+AHw-400 EHGSDSEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 84.5 bits: 20.5 E(): 9.9
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (23-78:29-82)

10 20 30 40 50
AAD-12 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... . :. :. :. :.


```

                10      20      30      40
AAD-12      HAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                .. ... . : : : : : : : : : : : :
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                180      190      200      210      220      230

```

```

                50      60      70      80
AAD-12      GTVRQHSPAEWDDMMKVIVGNMAWHADSTYM
                ::: . . : .. . : : : : : : : : :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
                240      250      260

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 84.5 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (22-77:29-82)

```

                10      20      30      40      50
AAD-12      HAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..... : : : . . . . : :
gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                10      20      30      40      50      60

```

```

                60      70      80
AAD-12      QHSPAEWDDMMKVIVGNMAWHADSTYM
                .. :: : : : : : :
gi+AHw-117 EHGSDSEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                70      80      90      100      110

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
 II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 84.5 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (22-77:29-82)

```

                10      20      30      40      50
AAD-12      HAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..... : : : . . . . : :
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                10      20      30      40      50      60

```

```

                60      70      80
AAD-12      QHSPAEWDDMMKVIVGNMAWHADSTYM
                .. :: : : : : : :
gi+AHw-400 EHGSDSEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                70      80      90      100      110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
 II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 84.5 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (22-77:29-82)

```

                10         20         30         40         50
AAD-12      HAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..... :. :. . . . . :. :.
gi+AHw-400  MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELR
                10         20         30         40         50         60

```

```

                60         70         80
AAD-12      QHSPAEWDDMMKVIVGNMAWHADSTYM
                ... :: : : : .: ::
gi+AHw-400  EHGSDEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                70         80         90         100        110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 initl: 52 opt: 57 Z-score: 84.5 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (22-77:29-82)

```

                10         20         30         40         50
AAD-12      HAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..... :. :. . . . . :. :.
gi+AHw-400  MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELR
                10         20         30         40         50         60

```

```

                60         70         80
AAD-12      QHSPAEWDDMMKVIVGNMAWHADSTYM
                ... :: : : : .: ::
gi+AHw-400  EHGSDEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                70         80         90         100        110

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:43 2010 done: Fri Feb 5 12:55:43 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 37 - 116 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

opt E()


```

86      2      2:+ACo-
88      0      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      1      0:+AD0-      +ACoAPQ-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120  0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.58210.00377+ADs- mu+AD0- 4.8582
0.194
mean+AF8-var+AD0-54.479415.446, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.173763
Kolmogorov-Smirnov statistic: 0.0357 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

```

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 22.9      1.4
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.4      2
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0      7.5
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.7      8.2
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.7      8.9
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)  58 20.7      9.3

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 67 Z-score: 99.6 bits: 22.9 E(): 1.4

Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar) in 30 aa overlap (47-76:30-56)

```

          20          30          40          50          60          70
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPPAEWDDMMKVIVGNMAWHADS
          ..  .....  ...  :  :  ...  ...  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVK
          10          20          30          40          50

```



```

      50      60      70      80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
      ::: . . : . . . . . :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
      210      220      230      240
    
```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen Phi p I
 (262 aa)
 initn: 44 initl: 44 opt: 62 Z-score: 85.3 bits: 21.7 E(): 8.9
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (19-78:206-259)

```

      10      20      30      40
AAD-12  AAWLQHALLIFPGQHLSNDQQITFAKRFGA IERIGGGDIVAISNVKAD
      . . . . . : . . . . . :
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      180      190      200      210      220      230
    
```

```

      50      60      70      80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
      ::: . . : . . . . . :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
      240      250      260
    
```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)
 initn: 39 initl: 39 opt: 58 Z-score: 85.0 bits: 20.7 E(): 9.3
 Smith-Waterman score: 58+ADs- 23.810+ACU- identity (47.619+ACU- similar)
 in 84 aa overlap (2-80:33-116)

```

      10      20      30
AAD-12  AAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
      . . . . . : . . . . . :
gi+AHw-273 MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
      10      20      30      40      50      60
    
```

```

      40      50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
      . : . : . : . : . : . : . : . :
gi+AHw-273 KMLLKGVIGEEKVVELLRNMKEAGADIQELQOKVEKMLSEVTDEKQKEKVHEYGPACKKIF
      70      80      90      100      110      120
    
```

```

gi+AHw-273 GATTLQHRRRR
      130
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:44 2010 done: Fri Feb 5 12:55:44 2010
 Total Scan time: 0.080 Total Display time: 0.010


```

56      61
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
58      66
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
60      53      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-+AD0APQAqAD0-
62      31      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
64      30      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      43      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
68      23      20:+AD0APQA9AD0APQA9ACoAPQ-
70      36      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
72      8      12:+AD0APQA9ACo-
74      8      10:+AD0APQA9ACo-
76      8      7:+AD0APQAq-
78      3      6:+AD0AKg-
80      4      4:+AD0AKg-
82      1      3:+ACo-
84      7      3:+ACoAPQA9-
86      2      2:+ACo-
88      0      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     1      0:+AD0-      +ACoAPQ-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120     0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.73250.0037+ADs- mu+AD0- 4.1430
0.191
mean+AF8-var+AD0-53.410415.308, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.175494
Kolmogorov-Smirnov statistic: 0.0344 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 23.0 1.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.5 1.9
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0 7.3

```

gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc (240)
 62 21.8 8
 gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen Phi p I (262)
 62 21.8 8.7
 gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134)
 58 20.7 9
 gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 57 20.5 9.7
 gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
 (122) 57 20.5 9.7
 gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 57 20.5 9.7
 gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
 57 20.5 9.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 100.1 bits: 23.0 E(): 1.3
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (46-75:30-56)

```

      20      30      40      50      60      70
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
      ..  .::::  :::  . :  :::  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
      10      20      30      40      50

```

80
 AAD-12 TYMPV

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 65 Z-score: 97.5 bits: 22.5 E(): 1.9
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (46-76:30-57)

```

      20      30      40      50      60      70
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
      ..  .::::  :::  . :  :::  ...  :
gi+AHw-144 VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKS
      10      20      30      40      50

```

80
 AAD-12 TYMPV

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
 60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phi p I
 +AFs-Phi (263 aa)
 initn: 44 init1: 44 opt: 63 Z-score: 86.8 bits: 22.0 E(): 7.3

Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (18-77:207-260)

```

                                10      20      30      40
AAD-12      AWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. ... . .::: ::  ...  ..
gi+AHw-390  GSNPNYLALLVKFVAGDGDVVAVDIKEKGDKDWIALKESWGAIWRIDTPEVL-----KGP
                                180      190      200      210      220      230

```

```

                                50      60      70      80
AAD-12  GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
                                ::: . . : .. . .::: . . :
gi+AHw-390  FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
                                240      250      260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)

initn: 44 init1: 44 opt: 62 Z-score: 86.2 bits: 21.8 E(): 8
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (18-77:184-237)

```

                                10      20      30      40
AAD-12      AWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. ... . .::: ::  ...  ..
gi+AHw-458  GSNPNYLALLVKFVAGDGDVVAVDIKEKGDKDWIALKESWGAIWRIDTPEVL-----KGP
                                160      170      180      190      200

```

```

                                50      60      70      80
AAD-12  GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
                                ::: . . : .. . .::: . . :
gi+AHw-458  FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
                                210      220      230      240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen Phi p I
(262 aa)

initn: 44 init1: 44 opt: 62 Z-score: 85.5 bits: 21.8 E(): 8.7
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (18-77:206-259)

```

                                10      20      30      40
AAD-12      AWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. ... . .::: ::  ...  ..
gi+AHw-158  KGSNPNYLALLVKFSGDGDVVAVDIKEKGDKDWIALKESWGAIWRIDTPEVL-----KGP
                                180      190      200      210      220      230

```

```

                                50      60      70      80
AAD-12  GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
                                ::: . . : .. . .::: . . :
gi+AHw-158  FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
                                240      250      260

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
Ascaris lumb (134 aa)

initn: 39 init1: 39 opt: 58 Z-score: 85.3 bits: 20.7 E(): 9

Smith-Waterman score: 58+ADs- 23.810+ACU- identity (47.619+ACU- similar)
in 84 aa overlap (1-79:33-116)

```

                                10      20
AAD-12      AWLQHALLIFPGQ-HLSNDQQITFAKRFGA
              : .:. .: : : . :. : . :
gi+AHw-273 MEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
              10      20      30      40      50      60

              30      40      50      60      70      80
AAD-12      IERIGG--GD--IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPV
              . : .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-273 KMLLKGVIGEEKVVVELRNMKEAGADIQELQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
              70      80      90      100     110     120

gi+AHw-273 GATTLQHRRRR
              130
    
```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 84.6 bits: 20.5 E(): 9.7
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (20-75:29-82)

```

                                10      20      30      40      50
AAD-12      AWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
              .:. .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
              10      20      30      40      50      60

              60      70      80
AAD-12      QHSPAEWDDMMKVIVGNMAWHADSTYMPV
              .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-400 EHGSDVWAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70      80      90      100     110
    
```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-Polle (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 84.6 bits: 20.5 E(): 9.7
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (20-75:29-82)

```

                                10      20      30      40      50
AAD-12      AWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
              .:. .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
              10      20      30      40      50      60

              60      70      80
AAD-12      QHSPAEWDDMMKVIVGNMAWHADSTYMPV
              .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-117 EHGSDVWAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70      80      90      100     110
    
```



```

72      11      12:+AD0APQA9ACo-
74      7       10:+AD0APQA9ACo-
76      6       7:+AD0APQAq-
78      4       6:+AD0AKg-
80      3       4:+AD0AKg-
82      3       3:+ACo-
84      6       3:+ACoAPQ-
86      2       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.75990.00368+ADs- mu+AD0- 4.0059
0.189
mean+AF8-var+AD0-53.117415.091, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.175977
Kolmogorov-Smirnov statistic: 0.0323 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.1      1.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.6      1.8
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0      7.3
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.8      7.9
gi+AHw-1582250+AHw-prf+AHwAfa-2118271A allergen PhI p I ( 262)
62 21.8      8.6
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.5      9.6
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.5      9.6
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.5      9.6

```

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
57 20.5 9.6

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 100.3 bits: 23.1 E(): 1.3
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (45-74:30-56)

```

                20          30          40          50          60          70
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS
                ..  .:..:  .:..:  .:  .:  .:..:  .:..:  .:
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
                10          20          30          40          50
```

80
AAD-12 TYMPVM

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 97.6 bits: 22.6 E(): 1.8
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (45-75:30-57)

```

                20          30          40          50          60          70
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS
                ..  .:..:  .:..:  .:  .:  .:..:  .:..:  .:
gi+AHw-144 VKVTFKVEKGSDDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
                10          20          30          40          50
```

80
AAD-12 TYMPVM

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 86.9 bits: 22.0 E(): 7.3
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (17-76:207-260)

```

                10          20          30          40
AAD-12 WLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                ..  .:..:  .:..:  .:  .:  .:..:  .:..:  .:
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGDKDWIALKESWGAIWRIDTPEVL-----KGP
                180          190          200          210          220          230
```

50 60 70 80
AAD-12 GTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVM
::: . . : . . .:~::~:

gi+AHw-117 EHGSDWEVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (19-74:29-82)

10 20 30 40 50
 AAD-12 WLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
 :. :. :. :.
 gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
 10 20 30 40 50 60

60 70 80
 AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 .. :: : : : .: ::
 gi+AHw-400 EHGSDWEVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (19-74:29-82)

10 20 30 40 50
 AAD-12 WLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
 :. :. :. :.
 gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
 10 20 30 40 50 60

60 70 80
 AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 .. :: : : : .: ::
 gi+AHw-400 EHGSDWEVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (19-74:29-82)

10 20 30 40 50
 AAD-12 WLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
 :. :. :. :.
 gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
 10 20 30 40 50 60

60 70 80
 AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 .. :: : : : .: ::

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po

(97) 67 23.1 1.3

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-

(96) 65 22.5 1.8

gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen PhI pI (263)

63 22.0 7.2

gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc (240)

62 21.8 7.9

gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I (262)

62 21.8 8.6

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P

(122) 57 20.5 9.6

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)

57 20.5 9.6

gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)

57 20.5 9.6

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)

57 20.5 9.6

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:

Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 67 Z-score: 100.3 bits: 23.1 E(): 1.3

Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)

in 30 aa overlap (44-73:30-56)

```

                20          30          40          50          60          70
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
                ..  .:.:.  .:.  :  :  .:.  .:.  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
                10          20          30          40          50

```

80
AAD-12 TYMPVMA

```

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60          70          80          90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:

Full+AD0-Poll (96 aa)

initn: 55 init1: 55 opt: 65 Z-score: 97.6 bits: 22.5 E(): 1.8

Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)

in 31 aa overlap (44-74:30-57)

```

                20          30          40          50          60          70
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
                ..  .:.:.  .:.  .  :  .:.  .:.  :
gi+AHw-144  VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKS
                10          20          30          40          50

```

80

AAD-12 TYMPVMA

```

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPPEE
           60          70          80          90

```

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 87.0 bits: 22.0 E(): 7.2
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (16-75:207-260)

```

AAD-12          10          20          30          40
              LQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
              .. ... . .::: :: ... ..
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
           180          190          200          210          220          230

```

```

AAD-12          50          60          70          80
              GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
              ::: . . : . . .::: . . .
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
           240          250          260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.3 bits: 21.8 E(): 7.9
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (16-75:184-237)

```

AAD-12          10          20          30          40
              LQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
              .. ... . .::: :: ... ..
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
           160          170          180          190          200

```

```

AAD-12          50          60          70          80
              GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
              ::: . . : . . .::: . . .
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
           210          220          230          240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen Phi p I
(262 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.6 bits: 21.8 E(): 8.6
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (16-75:206-259)

```

AAD-12          10          20          30          40
              LQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
              .. ... . .::: :: ... ..
gi+AHw-158 KGNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
           180          190          200          210          220          230

```

```

      50      60      70      80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA
      ::: . . . : . . . : . . . : . . . : . . . :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
      240      250      260

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (18-73:29-82)

```

      10      20      30      40
AAD-12  LQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
      . . . . . : . : . . . : . : . . . : . : . . . :
gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
      10      20      30      40      50      60

```

```

      50      60      70      80
AAD-12  QHSPA EWDDMMKVIVGNMAWHADSTYMPVMA
      . . : : : : : : : :
gi+AHw-117 EHGSD EWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
      70      80      90      100      110

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (18-73:29-82)

```

      10      20      30      40
AAD-12  LQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
      . . . . . : . : . . . : . : . . . : . : . . . :
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
      10      20      30      40      50      60

```

```

      50      60      70      80
AAD-12  QHSPA EWDDMMKVIVGNMAWHADSTYMPVMA
      . . : : : : : : : :
gi+AHw-400 EHGSD EWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
      70      80      90      100      110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (18-73:29-82)

```

      10      20      30      40
AAD-12  LQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
      . . . . . : . : . . . : . : . . . : . : . . . :
gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
      10      20      30      40      50      60

```


32 9 8:+AD0APQAq-
 34 36 21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
 36 73
 44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
 38 67
 72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
 40 92 101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
 +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 42 117
 123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 44 153
 136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
 46 128
 138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
 48 110
 132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
 +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
 50 120
 121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
 52 92
 106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0- +ACo-
 54 86
 91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
 A9AD0APQ- +ACo-
 56 61
 76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 58 74 62:+AD0APQA9AD0APQA9AD0-
 +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
 60 44 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 62 38 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
 64 34 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
 66 32 25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
 68 25 20:+AD0APQA9AD0APQA9ACoAPQA9-
 70 30 16:+AD0APQA9AD0APQAqAD0APQA9AD0-
 72 11 12:+AD0APQA9ACo-
 74 7 10:+AD0APQA9ACo-
 76 4 7:+AD0APQAq-
 78 5 6:+AD0AKg-
 80 5 4:+AD0AKg-
 82 1 3:+ACo-
 84 7 3:+ACoAPQA9-
 86 2 2:+ACo-
 88 0 2:+ACo- inset +AD0- represents 1 library sequences
 90 0 1:+ACo-
 92 0 1:+ACo- :+ACo-
 94 0 1:+ACo- :+ACo-
 96 0 1:+ACo- :+ACo-
 98 1 0:+AD0- +ACoAPQ-
 100 1 0:+AD0- +ACoAPQ-

```

102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.78560.00371+ADs- mu+AD0- 3.9736
0.191
mean+AF8-var+AD0-52.183614.682, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.177545
Kolmogorov-Smirnov statistic: 0.0319 (N+AD0-28) at 36

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 23.1 1.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.6 1.8
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.1 7.1
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.8 7.7
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.8 8.4
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 57 20.5 9.4
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.5 9.4
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.5 9.4
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.5 9.4

```

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 init1: 59 opt: 67 Z-score: 100.6 bits: 23.1 E(): 1.3
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (43-72:30-56)

```

```

                20          30          40          50          60          70
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS
                ..  .:.:.  .:.  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVK
                10          20          30          40          50

```

AAD-12 TYMPVMAQ

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 97.9 bits: 22.6 E(): 1.8
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (43-73:30-57)

20 30 40 50 60 70
 AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
 .. .:.. :. . : :. :. :
 gi+AHw-144 VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPLTKK--GNL-WEVKS
 10 20 30 40 50

80
 AAD-12 TYMPVMAQ

.
 gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
 60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
 +AFs-Phl (263 aa)

initn: 44 initl: 44 opt: 63 Z-score: 87.1 bits: 22.1 E(): 7.1
 Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (15-74:207-260)

10 20 30 40
 AAD-12 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
 .. :. . :. :. :.
 gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
 180 190 200 210 220 230

50 60 70 80
 AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
 ::: . . : . . :.:.:.
 gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
 240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
 product +AFs-P (240 aa)

initn: 44 initl: 44 opt: 62 Z-score: 86.4 bits: 21.8 E(): 7.7
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
 in 60 aa overlap (15-74:184-237)

10 20 30 40
 AAD-12 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
 .. :. . :. :. :.
 gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
 160 170 180 190 200
 50 60 70 80

AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ
 ::: . . : :
 gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
 210 220 230 240

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen Phi p I
 (262 aa)
 initn: 44 initl: 44 opt: 62 Z-score: 85.7 bits: 21.8 E(): 8.4
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (15-74:206-259)

AAD-12 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
 : : : : :
 gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
 180 190 200 210 220 230

AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ
 ::: . . : :
 gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
 240 250 260

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)
 initn: 52 initl: 52 opt: 57 Z-score: 84.9 bits: 20.5 E(): 9.4
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (17-72:29-82)

AAD-12 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
 : : : :
 gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
 10 20 30 40 50 60

AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ
 .. : : : : : : : : : :
 gi+AHw-117 EHGSDWEVAMTKGEGG--VWTFDSEEP LQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
 II) (122 aa)
 initn: 52 initl: 52 opt: 57 Z-score: 84.9 bits: 20.5 E(): 9.4
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (17-72:29-82)

AAD-12 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
 : : : :
 gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
 10 20 30 40 50 60

50 60 70 80

AAAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ

```

...  ::  :  :  :  .:  ::
gi+AHw-400 EHGSDSEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70              80              90              100              110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 84.9 bits: 20.5 E(): 9.4
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (17-72:29-82)

```

              10              20              30              40
AAAD-12      QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
              .....  .  .:  .  .  .  ...  .:  .:
gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
              10              20              30              40              50              60

```

```

50          60          70          80
AAAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
...  ::  :  :  :  .:  ::
gi+AHw-400 EHGSDSEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70              80              90              100              110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 84.9 bits: 20.5 E(): 9.4
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (17-72:29-82)

```

              10              20              30              40
AAAD-12      QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
              .....  .  .:  .  .  .  ...  .:  .:
gi+AHw-400 MSMASSSSSLLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
              10              20              30              40              50              60

```

```

50          60          70          80
AAAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
...  ::  :  :  :  .:  ::
gi+AHw-400 EHGSDSEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70              80              90              100              110

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:45 2010 done: Fri Feb 5 12:55:45 2010

Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006


```

64      38      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
66      26      25:+AD0APQA9AD0APQA9AD0APQAq-
68      23      20:+AD0APQA9AD0APQA9ACoAPQ-
70      32      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      14      12:+AD0APQA9ACoAPQ-
74      5       10:+AD0APQ- +ACo-
76      5       7:+AD0APQAq-
78      5       6:+AD0AKg-
80      4       4:+AD0AKg-
82      1       3:+ACo-
84      6       3:+ACoAPQ-
86      3       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:           +ACo-
104     0       0:           +ACo-
106     0       0:           +ACo-
108     0       0:           +ACo-
110     0       0:           +ACo-
112     0       0:           +ACo-
114     0       0:           +ACo-
116     0       0:           +ACo-
118     0       0:           +ACo-
+AD4-120  0       0:           +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.78320.00373+ADs- mu+AD0- 4.0331
0.193
mean+AF8-var+AD0-51.895314.562, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.178037
Kolmogorov-Smirnov statistic: 0.0333 (N+AD0-28) at 36

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 23.1 1.2

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 22.6 1.8

gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI (263)
63 22.1 7.1

gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc (240)
62 21.8 7.7

gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I (262)
62 21.8 8.4

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
(122) 57 20.6 9.3

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 57 20.6 9.3
 gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
 57 20.6 9.3
 gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 57 20.6 9.3
 gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219)
 60 21.3 10

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 67 Z-score: 100.7 bits: 23.1 E(): 1.2
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (42-71:30-56)

	20	30	40	50	60	70
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS					
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS					
	10	20	30	40	50	

80
 AAD-12 TYMPVMAQG

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 98.0 bits: 22.6 E(): 1.8
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (42-72:30-57)

	20	30	40	50	60	70
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS					
gi+AHw-144	VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKS					
	10	20	30	40	50	

80
 AAD-12 TYMPVMAQG

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
 60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
 +AFs-Phl (263 aa)
 initn: 44 initl: 44 opt: 63 Z-score: 87.1 bits: 22.1 E(): 7.1
 Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (14-73:207-260)

	10	20	30	40
AAD-12	HALLIFPGQHLSDNDQQITFAKRFGAIERIGGGDIVAISNVKAD			

gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
 180 190 200 210 220 230

50 60 70 80
 AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 ::: . . : :
 gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
 240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
 product +AFs-P (240 aa)
 initn: 44 initl: 44 opt: 62 Z-score: 86.5 bits: 21.8 E(): 7.7
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
 in 60 aa overlap (14-73:184-237)

10 20 30 40
 AAD-12 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
 : :
 gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
 160 170 180 190 200

50 60 70 80
 AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 ::: . . : :
 gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
 210 220 230 240

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
 (262 aa)
 initn: 44 initl: 44 opt: 62 Z-score: 85.8 bits: 21.8 E(): 8.4
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (14-73:206-259)

10 20 30 40
 AAD-12 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
 : :
 gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
 180 190 200 210 220 230

50 60 70 80
 AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 ::: . . : :
 gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
 240 250 260

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)
 initn: 52 initl: 52 opt: 57 Z-score: 85.0 bits: 20.6 E(): 9.3
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (16-71:29-82)

10 20 30 40
 AAD-12 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
 : : : :

gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
 10 20 30 40 50 60

50 60 70 80
 AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 ... :: : : : .: ::

gi+AHw-117 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.0 bits: 20.6 E(): 9.3
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (16-71:29-82)

10 20 30 40
 AAD-12 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
 :. :. :. :.
 gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
 10 20 30 40 50 60

50 60 70 80
 AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 ... :: : : : .: ::

gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.0 bits: 20.6 E(): 9.3
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (16-71:29-82)

10 20 30 40
 AAD-12 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
 :. :. :. :.
 gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
 10 20 30 40 50 60

50 60 70 80
 AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 ... :: : : : .: ::

gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.0 bits: 20.6 E(): 9.3
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (16-71:29-82)

10 20 30 40
 AAD-12 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
 :. :. :. :.

```
gi+AHw-400 MSMASSSSSLLAMAVLALFAGAWCVPKVFTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                10          20          30          40          50          60
```

```
50          60          70          80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
      ...  ::  :  :  :  .:  ::
```

```
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDVVPEKYTIGATY
                70          80          90          100          110
```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 84.4 bits: 21.3 E(): 10
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (6-37:133-160)

```
10          20          30
AAD-12 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                :  ::  :...:  .  :  ...  :...
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRRRFQGDQSQQQQDSHQK----VHRFDEGDLI
                110          120          130          140          150
```

```
40          50          60          70          80
AAD-12 AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
      ..
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                160          170          180          190          200          210
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:45 2010 done: Fri Feb 5 12:55:45 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 43 - 122 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```
opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
```



```

  92      0      1:+ACo-      :+ACo-
  94      0      1:+ACo-      :+ACo-
  96      0      1:+ACo-      :+ACo-
  98      1      0:+AD0-      +ACoAPQ-
 100     1      0:+AD0-      +ACoAPQ-
 102     0      0:          +ACo-
 104     0      0:          +ACo-
 106     0      0:          +ACo-
 108     0      0:          +ACo-
 110     0      0:          +ACo-
 112     0      0:          +ACo-
 114     0      0:          +ACo-
 116     0      0:          +ACo-
 118     0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.80130.00371+ADs- mu+AD0- 3.7601
0.192
mean+AF8-var+AD0-51.499514.551, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.178720
Kolmogorov-Smirnov statistic: 0.0305 (N+AD0-29) at 36

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.2      1.2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.7      1.7
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.1      6.7
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.9      7.3
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.9      8
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.6      8.9
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.6      8.9
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.6      8.9
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.6      8.9
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 21.4      9.5

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 init1: 59 opt: 67 Z-score: 101.1 bits: 23.2 E(): 1.2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (41-70:30-56)

```

```

                20          30          40          50          60          70
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS
                ..  .::::.  :::  :  :  :  :  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
                10          20          30          40          50

```

```

                80
AAD-12  TYMPVMAQGA

gi+AHw-126  AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60          70          80          90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 98.4 bits: 22.7 E(): 1.7
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (41-71:30-57)

```

                20          30          40          50          60          70
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS
                ..  .::::.  :::  .  :  :  :  :  :
gi+AHw-144  VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
                10          20          30          40          50

```

```

                80
AAD-12  TYMPVMAQGA

gi+AHw-144  SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                60          70          80          90

```

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 87.5 bits: 22.1 E(): 6.7
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (13-72:207-260)

```

                10          20          30          40
AAD-12  ALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                ..  ...  .  .::::  ::  ...  :
gi+AHw-390  GSNPNYLALLVKFVAGDGDVVAVDIKEKKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                180          190          200          210          220          230

```

```

                50          60          70          80
AAD-12  GTVRQHSPEAWDDMMKVIVGNMAWHADSTYMPVMAQGA
                :::  .  .  :  .  .  .  .:::::
gi+AHw-390  FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
                240          250          260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.9 bits: 21.9 E(): 7.3
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (13-72:184-237)


```

                10         20         30         40
AAD-12          ALLIFPGQHLSDQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..... :. :. . . . . :. :.
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE
                10         20         30         40         50         60

```

```

                50         60         70         80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
                ... :: : : : .: ::
gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDV
                70         80         90         100        110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.4 bits: 20.6 E(): 8.9
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (15-70:29-82)

```

                10         20         30         40
AAD-12          ALLIFPGQHLSDQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..... :. :. . . . . :. :.
gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE
                10         20         30         40         50         60

```

```

                50         60         70         80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
                ... :: : : : .: ::
gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDV
                70         80         90         100        110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.4 bits: 20.6 E(): 8.9
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (15-70:29-82)

```

                10         20         30         40
AAD-12          ALLIFPGQHLSDQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..... :. :. . . . . :. :.
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE
                10         20         30         40         50         60

```

```

                50         60         70         80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
                ... :: : : : .: ::
gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDV
                70         80         90         100        110

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 init1: 43 opt: 60 Z-score: 84.8 bits: 21.4 E(): 9.5
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (5-36:133-160)

```

                                10      20      30
AAD-12      ALLIFPGQHLSDQITFAKRFGAIERIGGGDIV
                                :  :  :...:  .  :  :...  :...
gi+AHw-221  FGLIFPGCPSTYEEPAQQGRRHQSRPPRRFQGDQSQQQQDSHQK----VHRFDEGDLI
                                110      120      130      140      150

                                40      50      60      70      80
AAD-12      AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
                                :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                                160      170      180      190      200      210

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:45 2010 done: Fri Feb 5 12:55:45 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 44 - 123 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      2      0:+AD0-
      30      1      2:+ACo-
      32      8      8:+AD0APQAq-
      34      30     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36      82
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0-
      38      70
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
      40      87
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ-      +ACo-

```


+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 98.5 bits: 22.7 E(): 1.6
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (40-70:30-57)

```

      10      20      30      40      50      60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
      .. .:..: .:..: .:..: .:..: .:..:
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEP LTKK--GNL-WEVKS
      10      20      30      40      50

```

```

      70      80
AAD-12 TYMPVMAQGAV
      .
gi+AHw-144 SKPLTGPFNFRFMSKGMNRNVFDEVIPTAFKIGTTTYTPEE
      60      70      80      90

```

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 87.4 bits: 22.1 E(): 6.8
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (12-71:207-260)

```

      10      20      30      40
AAD-12 LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      .. ... .:..: .:..: .:..: .:..:
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      180      190      200      210      220      230

```

```

      50      60      70      80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
      ::: . . : .. . :..: .:..: .:..:
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
      240      250      260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.8 bits: 21.9 E(): 7.4
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (12-71:184-237)

```

      10      20      30      40
AAD-12 LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      .. ... .:..: .:..: .:..: .:..:
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      160      170      180      190      200

```

```

      50      60      70      80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
      ::: . . : .. . :..: .:..: .:..:
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
      210      220      230      240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen Phi p I
(262 aa)

initn: 44 init1: 44 opt: 62 Z-score: 86.1 bits: 21.9 E(): 8.1
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (12-71:206-259)

```

                                10      20      30      40
AAD-12      LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                :. :.. . :.:: :. :. :.
gi+AHw-158  KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
              180      190      200      210      220      230

```

```

                    50      60      70      80
AAD-12  GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
          ::: . . : .. . :.:::..:
gi+AHw-158  FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
              240      250      260

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.4 bits: 20.6 E(): 8.8
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (14-69:29-82)

```

                                10      20      30      40
AAD-12      LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... :. :. . . ... :. :.
gi+AHw-117  MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELR
              10      20      30      40      50      60

```

```

                    50      60      70      80
AAD-12  QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
          :. :. : : : :. :. :.
gi+AHw-117  EHGSDSEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70      80      90      100      110

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.4 bits: 20.6 E(): 8.8
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (14-69:29-82)

```

                                10      20      30      40
AAD-12      LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... :. :. . . ... :. :.
gi+AHw-400  MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELR
              10      20      30      40      50      60

```

```

                    50      60      70      80
AAD-12  QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
          :. :. : : : :. :. :.
gi+AHw-400  EHGSDSEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70      80      90      100      110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.4 bits: 20.6 E(): 8.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (14-69:29-82)

```

                                10      20      30      40
AAD-12      LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... :. :. . . ... :. :.
gi+AHw-400  MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELR
                                10      20      30      40      50      60

                                50      60      70      80
AAD-12  QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
        ... :: : : : .: ::
gi+AHw-400  EHGSDEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                                70      80      90      100     110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.4 bits: 20.6 E(): 8.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (14-69:29-82)

```

                                10      20      30      40
AAD-12      LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... :. :. . . ... :. :.
gi+AHw-400  MSMASSSSSLLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELR
                                10      20      30      40      50      60

                                50      60      70      80
AAD-12  QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
        ... :: : : : .: ::
gi+AHw-400  EHGSDEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                                70      80      90      100     110

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 init1: 43 opt: 60 Z-score: 84.7 bits: 21.4 E(): 9.6
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (4-35:133-160)

```

                                10      20      30
AAD-12      LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                                : :: :...: . : ...: :...
gi+AHw-221  FGLIFPGCPSTYEEPAQQGRRHQSQRPFRFQGGDQSQQQQDSHQK----VHRFDEGLI
                                110     120     130     140     150

                                40      50      60      70      80
AAD-12  AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
        :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                                160     170     180     190     200     210

```



```

 98      1      0:+AD0-      +ACoAPQ-
100      1      0:+AD0-      +ACoAPQ-
102      0      0:          +ACo-
104      0      0:          +ACo-
106      0      0:          +ACo-
108      0      0:          +ACo-
110      0      0:          +ACo-
112      0      0:          +ACo-
114      0      0:          +ACo-
116      0      0:          +ACo-
118      0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.05830.00364+ADs- mu+AD0- 2.4473
0.188
mean+AF8-var+AD0-52.644514.782, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.176766
Kolmogorov-Smirnov statistic: 0.0366 (N+AD0-28) at 38

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 23.1 1.2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.6 1.7
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0 7.2
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.8 7.8
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.8 8.6
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 57 20.6 9.2
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.6 9.2
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.6 9.2
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.6 9.2

```

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 init1: 59 opt: 67 Z-score: 100.8 bits: 23.1 E(): 1.2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (38-67:30-56)

```

```

      10      20      30      40      50      60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS
      ..  .:.:.  .:.  :  :  .:.  .:.  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVK
      10      20      30      40      50

```

70 80
AAD-12 TYMPVMAQGAVFS

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 98.1 bits: 22.6 E(): 1.7
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (38-68:30-57)

10 20 30 40 50 60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADS
.: .: .: .: .: .:
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEP LTKK--GNL-WEVK S
10 20 30 40 50

70 80
AAD-12 TYMPVMAQGAVFS

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 86.9 bits: 22.0 E(): 7.2
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (10-69:207-260)

10 20 30
AAD-12 IFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
.: .: .: .: .:
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
180 190 200 210 220 230

40 50 60 70 80
AAD-12 GTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
.: .: .: .: .:
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.3 bits: 21.8 E(): 7.8
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (10-69:184-237)

10 20 30
AAD-12 IFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
.: .: .: .: .:
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
160 170 180 190 200


```

          50          60          70          80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
      ...  ::  :  :  :  .:  ::
gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
          70          80          90          100          110
    
```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.1 bits: 20.6 E(): 9.2
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (12-67:29-82)

```

          10          20          30          40
AAD-12          IFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
      .....  .  .:  .  .  .  ...  .:  .:
gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
          10          20          30          40          50          60
    
```

```

          50          60          70          80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
      ...  ::  :  :  :  .:  ::
gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
          70          80          90          100          110
    
```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.1 bits: 20.6 E(): 9.2
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (12-67:29-82)

```

          10          20          30          40
AAD-12          IFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
      .....  .  .:  .  .  .  ...  .:  .:
gi+AHw-400 MSMASSSSSLLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
          10          20          30          40          50          60
    
```

```

          50          60          70          80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
      ...  ::  :  :  :  .:  ::
gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
          70          80          90          100          110
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:45 2010 done: Fri Feb 5 12:55:45 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 47 - 126 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	1	0:+AD0-	
30	3	2:+ACo-	
32	7	8:+AD0APQAq-	
34	20	21:+AD0APQA9AD0APQA9ACo-	
36	72		
44:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-		
38	92		
72:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ		
A9AD0APQA9AD0-			
40	83		
101:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP		
QA9AD0-	+ACo-		
42	118		
123:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP		
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-			
44	142	136:+AD0APQA9AD0APQA9-	
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A			
D0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-			
46	135		
138:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP		
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-			
48	104		
132:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP		
QA9AD0APQA9AD0APQA9AD0APQ-	+ACo-		
50	120		
121:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP		
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-			
52	102	106:+AD0APQA9AD0APQA9AD0-	
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-			
+ACo-			
54	62		
91:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-		
+ACo-			
56	63		
76:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-		+ACo-

gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen Phi p I (262)
 62 21.8 8.6
 gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
 (122) 57 20.6 9.1
 gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 57 20.6 9.1
 gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
 57 20.6 9.1
 gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 57 20.6 9.1

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 100.9 bits: 23.2 E(): 1.2
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (37-66:30-56)

	10	20	30	40	50	60
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS					
				::: . . : ::: ... :
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS					
	10	20	30	40	50	

	70	80
AAD-12	TYMPVMAQGAVFSA	

gi+AHw-126	AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
	60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 65 Z-score: 98.2 bits: 22.7 E(): 1.7
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (37-67:30-57)

	10	20	30	40	50	60
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS					
				::: . . : ::: ... :
gi+AHw-144	VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKS					
	10	20	30	40	50	

	70	80
AAD-12	TYMPVMAQGAVFSA	

gi+AHw-144	SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
	60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phi p I
 +AFs-Phi (263 aa)
 initn: 44 init1: 44 opt: 63 Z-score: 87.0 bits: 22.0 E(): 7.2
 Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (9-68:207-260)

```

AAD-12                      FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                               .. ... . .::: :: ... ..
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
           180          190          200          210          220          230

```

```

           40          50          60          70          80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
           ::: . . . : .. . .::: . . .
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
           240          250          260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein product +AFs-P (240 aa)
 initn: 44 initl: 44 opt: 62 Z-score: 86.3 bits: 21.8 E(): 7.8
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
 in 60 aa overlap (9-68:184-237)

```

                               10          20          30
AAD-12                      FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                               .. ... . .::: :: ... ..
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
           160          170          180          190          200

```

```

           40          50          60          70          80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
           ::: . . . : .. . .::: . . .
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
           210          220          230          240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I (262 aa)
 initn: 44 initl: 44 opt: 62 Z-score: 85.6 bits: 21.8 E(): 8.6
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (9-68:206-259)

```

                               10          20          30
AAD-12                      FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                               .. ... . .::: :: ... ..
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
           180          190          200          210          220          230

```

```

           40          50          60          70          80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
           ::: . . . : .. . .::: . . .
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
           240          250          260

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-Polle (122 aa)
 initn: 52 initl: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (11-66:29-82)

```

AAD-12                      FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                               ..... :. :. . . . . :. :.
gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
              10          20          30          40          50          60

```

```

AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
       ... :. :. :. :. :. :.
gi+AHw-117 EHGSDewVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70          80          90          100          110

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (11-66:29-82)

```

AAD-12                      10          20          30          40
                               FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                               ..... :. :. . . . . :. :.
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
              10          20          30          40          50          60

```

```

AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
       ... :. :. :. :. :. :.
gi+AHw-400 EHGSDewVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70          80          90          100          110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (11-66:29-82)

```

AAD-12                      10          20          30          40
                               FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                               ..... :. :. . . . . :. :.
gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
              10          20          30          40          50          60

```

```

AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
       ... :. :. :. :. :. :.
gi+AHw-400 EHGSDewVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70          80          90          100          110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (11-66:29-82)

10 20 30 40

```

AAD-12                      FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                               ..... :. :. . . . . :. :.
gi+AHw-400 MSMASSSSSLLAMAVLALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                10          20          30          40          50          60

                50          60          70          80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
           ... :: : : : .: ::
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                70          80          90          100          110

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:45 2010 done: Fri Feb 5 12:55:45 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 48 - 127 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      2      0:+AD0-
      30      4      2:+ACoAPQ-
      32      5      8:+AD0APQAq-
      34      22     21:+AD0APQA9AD0APQA9ACoAPQ-
      36      91
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9AD0-
      38      74
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
      40      86
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ- +ACo-
      42      113
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-

```


331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 5.94380.00378+ADs- mu+AD0- 2.9290
0.195

mean+AF8-var+AD0-52.573514.616, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42

Lambda+AD0- 0.176885

Kolmogorov-Smirnov statistic: 0.0345 (N+AD0-28) at 38

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 23.2 1.2

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 22.7 1.7

gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI (263)
63 22.1 7

gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc (240)
62 21.8 7.6

gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I (262)
62 21.8 8.3

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
(122) 57 20.6 9.1

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
57 20.6 9.1

gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
57 20.6 9.1

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
57 20.6 9.1

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 67 Z-score: 100.9 bits: 23.2 E(): 1.2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (36-65:30-56)

```

      10      20      30      40      50      60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
      ..  ....  ...  :  :  :  :  :  :  :  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVK
      10      20      30      40      50

```

```

      70      80
AAD-12 TYMPVMAQGAVFSAE

```

```

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)

initn: 55 init1: 55 opt: 65 Z-score: 98.2 bits: 22.7 E(): 1.7
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (36-66:30-57)

```

      10      20      30      40      50      60
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
      ..  .:.:.  .:.  .  :  .:.  .:.  :
gi+AHw-144  VKVTFKVEKGSDPKKLVLVDIKYTRPGDTLAEVELRQHGSEEWELTKK--GNL-WEVKS
      10      20      30      40      50

```

```

      70      80
AAD-12  TYMPVMAQGAVFSAE
      .
gi+AHw-144  SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPPEE
      60      70      80      90

```

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl p I
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 87.2 bits: 22.1 E(): 7
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (8-67:207-260)

```

      10      20      30
AAD-12  PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      ..  .:.  .  .:.:.  ::  ...  :.
gi+AHw-390  GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      180      190      200      210      220      230

```

```

      40      50      60      70      80
AAD-12  GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
      :::  .  .  :  .  .  .:.:.:.  :
gi+AHw-390  FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
      240      250      260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.5 bits: 21.8 E(): 7.6
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (8-67:184-237)

```

      10      20      30
AAD-12  PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      ..  .:.  .  .:.:.  ::  ...  :.
gi+AHw-458  GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      160      170      180      190      200

```

```

      40      50      60      70      80
AAD-12  GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
      :::  .  .  :  .  .  .:.:.:.  :
gi+AHw-458  FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
      210      220      230      240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.8 bits: 21.8 E(): 8.3
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (8-67:206-259)

```

                                10      20      30
AAD-12      PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                :. :. . . :. :. :. :. :. :. :.
gi+AHw-158  KGSNPNYLALLVKFSGDGDVVAVDIKEKGGKDKWIALKESWGAIWRIDTPEVL-----KGP
                                180      190      200      210      220      230

```

```

                                40      50      60      70      80
AAD-12  GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
                                ::: . . : .. . :. :. :. :. :. :. :.
gi+AHw-158  FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
                                240      250      260

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (10-65:29-82)

```

                                10      20      30      40
AAD-12      PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... :. :. . . . . :. :. :. :.
gi+AHw-117  MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                                10      20      30      40      50      60

```

```

                                50      60      70      80
AAD-12  QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
                                .. :: : : : : : :
gi+AHw-117  EHGSDSEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                                70      80      90      100      110

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (10-65:29-82)

```

                                10      20      30      40
AAD-12      PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... :. :. . . . . :. :. :. :.
gi+AHw-400  MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                                10      20      30      40      50      60

```

```

                                50      60      70      80
AAD-12  QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
                                .. :: : : : : : :
gi+AHw-400  EHGSDSEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                                70      80      90      100      110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (10-65:29-82)

```

                10         20         30         40
AAD-12          PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..... :. :. . . . . :. :.
gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                10         20         30         40         50         60

```

```

                50         60         70         80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
                ... :: : : : .: ::
gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                70         80         90         100        110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 initl: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (10-65:29-82)

```

                10         20         30         40
AAD-12          PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..... :. :. . . . . :. :.
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                10         20         30         40         50         60

```

```

                50         60         70         80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
                ... :: : : : .: ::
gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                70         80         90         100        110

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:45 2010 done: Fri Feb 5 12:55:46 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 49 - 128 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

80      2      4:+AD0AKg-
82      1      3:+ACo-
84      5      3:+ACoAPQ-
86      2      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.12710.00376+ADs- mu+AD0- 2.0908
0.194
mean+AF8-var+AD0-53.630514.904, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.175133
Kolmogorov-Smirnov statistic: 0.0516 (N+AD0-28) at 38

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.1      1.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.6      1.8
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0      7.6
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.7      8.2
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.7      9
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.5      9.5
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.5      9.5
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.5      9.5
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.5      9.5

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

```


gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
 (97) 67 23.0 1.4
 gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
 (96) 65 22.5 1.9
 gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI (263)
 63 21.9 8
 gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc (240)
 62 21.6 8.6
 gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I (262)
 62 21.6 9.4

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 67 Z-score: 99.8 bits: 23.0 E(): 1.4
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (34-63:30-56)

```

                10         20         30         40         50         60
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS
                ..  .::::  :::  :  :  ::  ...  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
                10         20         30         40         50
    
```

```

                70         80
AAD-12  TYMPVMAQGAVFSAEVV
    
```

```

gi+AHw-126  AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60         70         80         90
    
```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 97.2 bits: 22.5 E(): 1.9
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (34-64:30-57)

```

                10         20         30         40         50         60
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS
                ..  .::::  :::  .  :  ::  ...  :
gi+AHw-144  VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKS
                10         20         30         40         50
    
```

```

                70         80
AAD-12  TYMPVMAQGAVFSAEVV
    
```

```

gi+AHw-144  SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                60         70         80         90
    
```

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
 +AFs-Phl (263 aa)
 initn: 44 initl: 44 opt: 63 Z-score: 86.2 bits: 21.9 E(): 8
 Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (6-65:207-260)

```

AAD-12                      QHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                               .. ... . .::: ::  ...  ..
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEK GKDKWIALKESWGAIWRIDTPEVL-----KGP
          180          190          200          210          220          230

```

```

          40          50          60          70          80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV
          :::  . .          : .. . .::: . . . :
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
          240          250          260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein product +AFs-P (240 aa)
 initn: 44 initl: 44 opt: 62 Z-score: 85.6 bits: 21.6 E(): 8.6
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
 in 60 aa overlap (6-65:184-237)

```

                               10          20          30
AAD-12                      QHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                               .. ... . .::: ::  ...  ..
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEK GKDKWIALKESWGAIWRIDTPEVL-----KGP
          160          170          180          190          200

```

```

          40          50          60          70          80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV
          :::  . .          : .. . .::: . . . :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
          210          220          230          240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen Phi p I (262 aa)
 initn: 44 initl: 44 opt: 62 Z-score: 84.9 bits: 21.6 E(): 9.4
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (6-65:206-259)

```

                               10          20          30
AAD-12                      QHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                               .. ... . .::: ::  ...  ..
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEK GKDKWIALKESWGAIWRIDTPEVL-----KGP
          180          190          200          210          220          230

```

```

          40          50          60          70          80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV
          :::  . .          : .. . .::: . . . :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
          240          250          260

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:46 2010 done: Fri Feb 5 12:55:46 2010
 Total Scan time: 0.090 Total Display time: 0.000


```

56      43      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
58      79
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9-
60      55      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      42      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      50      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
66      24      25:+AD0APQA9AD0APQA9AD0APQAq-
68      19      20:+AD0APQA9AD0APQA9ACo-
70      30      16:+AD0APQA9AD0APQAqAD0APQA9AD0-
72      10      12:+AD0APQA9ACo-
74      9       10:+AD0APQA9ACo-
76      7       7:+AD0APQAq-
78      4       6:+AD0AKg-
80      2       4:+AD0AKg-
82      1       3:+ACo-
84      6       3:+ACoAPQ-
86      1       2:+ACo-
88      0       2:+ACo-      inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-      :+ACo-
94      0       1:+ACo-      :+ACo-
96      1       1:+ACo-      :+ACo-
98      1       0:+AD0-      +ACoAPQ-
100     0       0:      +ACo-
102     0       0:      +ACo-
104     0       0:      +ACo-
106     0       0:      +ACo-
108     0       0:      +ACo-
110     0       0:      +ACo-
112     0       0:      +ACo-
114     0       0:      +ACo-
116     0       0:      +ACo-
118     0       0:      +ACo-
+AD4-120 0 0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.92320.00367+ADs- mu+AD0- 3.2489
0.190
mean+AF8-var+AD0-55.187515.506, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.172645
Kolmogorov-Smirnov statistic: 0.0550 (N+AD0-28) at 38

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 22.9 1.5
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.4 2.1
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 21.9 8.2

```

gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc (240)
 62 21.6 8.8
 gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen Phi p I (262)
 62 21.6 9.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 67 Z-score: 99.3 bits: 22.9 E(): 1.5
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (33-62:30-56)

```

                10         20         30         40         50         60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
                ..  .:..:  .:..:  .:  .:  .:..:  .:..:  .:
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
                10         20         30         40         50

```

```

                70         80
AAD-12 TYMPVMAQGAVFSAEVVP

```

```

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPPEYN
                60         70         80         90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 96.7 bits: 22.4 E(): 2.1
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (33-63:30-57)

```

                10         20         30         40         50         60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
                ..  .:..:  .:..:  .:  .:  .:..:  .:..:  .:
gi+AHw-144 VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
                10         20         30         40         50

```

```

                70         80
AAD-12 TYMPVMAQGAVFSAEVVP

```

```

.
gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                60         70         80         90

```

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phi p I
 +AFs-Phi (263 aa)
 initn: 44 initl: 44 opt: 63 Z-score: 86.0 bits: 21.9 E(): 8.2
 Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (5-64:207-260)

```

                10         20         30
AAD-12                HLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                ..  .:..:  .:..:  .:  .:  .:..:  .:..:  .:
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGDVVAVDIKEKGDVVAVDIKEKGDVVAVDI
                180         190         200         210         220         230
                40         50         60         70         80

```



```

62 43 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
64 42 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66 29 25:+AD0APQA9AD0APQA9AD0APQAqAD0-
68 21 20:+AD0APQA9AD0APQA9ACo-
70 30 16:+AD0APQA9AD0APQAqAD0APQA9AD0-
72 11 12:+AD0APQA9ACo-
74 9 10:+AD0APQA9ACo-
76 8 7:+AD0APQAq-
78 3 6:+AD0AKg-
80 3 4:+AD0AKg-
82 1 3:+ACo-
84 5 3:+ACoAPQ-
86 2 2:+ACo-
88 0 2:+ACo- inset +AD0- represents 1 library sequences
90 0 1:+ACo-
92 0 1:+ACo- :+ACo-
94 0 1:+ACo- :+ACo-
96 1 1:+ACo- :+ACo-
98 0 0: +ACo-
100 1 0:+AD0- +ACoAPQ-
102 0 0: +ACo-
104 0 0: +ACo-
106 0 0: +ACo-
108 0 0: +ACo-
110 0 0: +ACo-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.81550.00372+ADs- mu+AD0- 3.7393
0.192
mean+AF8-var+AD0-53.665915.199, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.175075
Kolmogorov-Smirnov statistic: 0.0414 (N+AD0-28) at 38

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 23.0 1.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.5 1.9
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0 7.5
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.7 8.1
gi+AHw-1582250+AHw-prf+AHwAfa-2118271A allergen PhI p I ( 262)
62 21.7 8.9
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 57 20.5 9.8

```

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 57 20.5 9.8
 gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
 57 20.5 9.8
 gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 57 20.5 9.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 100.0 bits: 23.0 E(): 1.3
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (32-61:30-56)

	10	20	30	40	50	60
AAAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS					
				::: . : : ::: ... :
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS					
	10	20	30	40	50	

	70	80
AAAD-12	TYMPVMAQGAVFSAEVVPA	

gi+AHw-126	AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN			
	60	70	80	90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 65 Z-score: 97.4 bits: 22.5 E(): 1.9
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (32-62:30-57)

	10	20	30	40	50	60
AAAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS					
				::: . : : ::: ... :
gi+AHw-144	VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS					
	10	20	30	40	50	

	70	80
AAAD-12	TYMPVMAQGAVFSAEVVPA	

gi+AHw-144	SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE			
	60	70	80	90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
 +AFs-Phl (263 aa)
 initn: 44 init1: 44 opt: 63 Z-score: 86.7 bits: 22.0 E(): 7.5
 Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (4-63:207-260)

		10	20	30
AAAD-12	LSNDQQITFAKRFGAIERIGGGDIVAISNVKAD			
		::: ... :
gi+AHw-390	GSPNYLALLVKFVAGDGDVVAVDIKEKGDKDWIALKESWGAIWRIDTPEVL-----KGP			
	180	190	200	210 220 230

```

          40          50          60          70          80
AAD-12  GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPA
          ::: . . . : . . . . . : . . . . . :
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
          240          250          260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein product +AFs-P (240 aa)
 initn: 44 init1: 44 opt: 62 Z-score: 86.0 bits: 21.7 E(): 8.1
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
 in 60 aa overlap (4-63:184-237)

```

                                10          20          30
AAD-12                                LSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. ... . .::: :: ... ..
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEK GKDKWIALKESWGAIWRIDTPEVL-----KGP
          160          170          180          190          200

```

```

          40          50          60          70          80
AAD-12  GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPA
          ::: . . . : . . . . . : . . . . . :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
          210          220          230          240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I (262 aa)
 initn: 44 init1: 44 opt: 62 Z-score: 85.3 bits: 21.7 E(): 8.9
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (4-63:206-259)

```

                                10          20          30
AAD-12                                LSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. ... . .::: :: ... ..
gi+AHw-158 KGNPNYLALLVKFSGDGDVVAVDIKEK GKDKWIALKESWGAIWRIDTPEVL-----KGP
          180          190          200          210          220          230

```

```

          40          50          60          70          80
AAD-12  GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPA
          ::: . . . : . . . . . : . . . . . :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
          240          250          260

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-Polle (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 84.6 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (6-61:29-82)

```

                                10          20          30
AAD-12                                LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... . .: . . . . . . . . . . . :
gi+AHw-117 MSMASSSSSSLAMAVLAALFAGAWCVPKVTFVTKGSNEKHLAVLVKYEGDTMAEVELR
          10          20          30          40          50          60

```

```

      40          50          60          70          80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPA
      ...  ::  :  :  :  .:  ::

```

```

gi+AHw-117 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70              80              90              100              110

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 84.6 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (6-61:29-82)

```

                                10          20          30
AAD-12                          LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                .....  .  .:  .  .  .  ...  .:  .:
gi+AHw-400 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
              10              20              30              40              50              60

```

```

      40          50          60          70          80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPA
      ...  ::  :  :  :  .:  ::

```

```

gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70              80              90              100              110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 84.6 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (6-61:29-82)

```

                                10          20          30
AAD-12                          LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                .....  .  .:  .  .  .  ...  .:  .:
gi+AHw-400 MSMASSSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
              10              20              30              40              50              60

```

```

      40          50          60          70          80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPA
      ...  ::  :  :  :  .:  ::

```

```

gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70              80              90              100              110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 84.6 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (6-61:29-82)

```

                                10          20          30
AAD-12                          LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                .....  .  .:  .  .  .  ...  .:  .:
gi+AHw-400 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
              10              20              30              40              50              60

```

```
      40          50          60          70          80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEYVPA
      ...  ::  :  :  :  .:  ::
gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70              80              90              100              110
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:46 2010 done: Fri Feb 5 12:55:46 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 53 - 132 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```
      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      5      2:+ACoAPQ-
      32      7      8:+AD0APQAq-
      34      28     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36      83
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0-
      38      72
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
      40      87     101:+AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      42     120
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
      44     136
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
```


Lambda+AD0- 0.175078

Kolmogorov-Smirnov statistic: 0.0333 (N+AD0-28) at 36

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po (97) 67 23.0 1.3

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0- (96) 65 22.5 1.9

gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen PhI pI (263) 63 22.0 7.4

gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc (240) 62 21.8 8

gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I (262) 62 21.8 8.7

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P (122) 57 20.5 9.7

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122) 57 20.5 9.7

gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122) 57 20.5 9.7

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122) 57 20.5 9.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)

initn: 59 initl: 59 opt: 67 Z-score: 100.1 bits: 23.0 E(): 1.3
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (31-60:30-56)

```

                10         20         30         40         50         60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS
                ..  .:.:.  .:.  .  .  .:.  .:.  .
gi+AHw-126  TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVK
                10         20         30         40         50

```

```

                70         80
AAD-12 TYMPVMAQQGAVFSAEVPVAV

```

```

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60         70         80         90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 97.5 bits: 22.5 E(): 1.9
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (31-61:30-57)

```

                10         20         30         40         50         60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEAWDDMMKVIVGNMAWHADS
                ..  .:.:.  .:.  .  .  .:.  .:.  .

```


gi+AHw-400 MSMASSSSSGLLAMAVLALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
10 20 30 40 50 60

40 50 60 70 80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAV
... :: : : : .: ::

gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGPFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.7
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (5-60:29-82)

AAD-12 10 20 30
SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
...: . :. :. :. :.

gi+AHw-400 MSMASSSSSSLLAMAVLALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
10 20 30 40 50 60

40 50 60 70 80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAV
... :: : : : .: ::

gi+AHw-400 EHGSDIEWVAMTKGEGG--VWTFDSEEPLQGPFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:46 2010 done: Fri Feb 5 12:55:46 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 54 - 133 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

opt E()
+ADw- 20 2 0:+AD0-
22 0 0: one +AD0- represents 3 library sequences
24 0 0:


```

90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      1      0:+AD0-      +ACoAPQ-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.86120.00374+ADs- mu+AD0- 3.6807
0.194
mean+AF8-var+AD0-54.053015.372, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.174447
Kolmogorov-Smirnov statistic: 0.0414 (N+AD0-28) at 38

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 22.9 1.4
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.4 2
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 21.9 7.9
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.7 8.6
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen Phi p I ( 262)
62 21.7 9.4

```

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 99.7 bits: 22.9 E(): 1.4
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (30-59:30-56)

```

```

          10          20          30          40          50          60
AAD-12 NDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPPAEWDDMMKVIVGNMAWHADST
          ..  .:.:.  .:. : :  .:. :. :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
          10          20          30          40          50
          70          80
AAD-12 YMPVMAQGAVFSAEVVPAVG

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 97.0 bits: 22.4 E(): 2
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (30-60:30-57)

10 20 30 40 50 60
 AAD-12 NDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
 .. .:.. :. . : :. :. :.
 gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWELTKK--GNL-WEVKSS
 10 20 30 40 50

70 80
 AAD-12 YMPVMAQGAVFSAEVVPAVG

gi+AHw-144 KPLTGFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
 60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
 +AFs-Phl (263 aa)

initn: 44 initl: 44 opt: 63 Z-score: 86.3 bits: 21.9 E(): 7.9
 Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (2-61:207-260)

10 20 30
 AAD-12 NDQQITFAKRFGAIERIGGGDIVAISNVKAD
 .. .:.. :. . :.
 gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKKGDKWIALKESWGAIWRIDTPEVL-----KGP
 180 190 200 210 220 230

40 50 60 70 80
 AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG
 ::: . . : . . .:~:~:~:
 gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
 240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
 product +AFs-P (240 aa)

initn: 44 initl: 44 opt: 62 Z-score: 85.6 bits: 21.7 E(): 8.6
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
 in 60 aa overlap (2-61:184-237)

10 20 30
 AAD-12 NDQQITFAKRFGAIERIGGGDIVAISNVKAD
 .. .:.. :. . :.
 gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKKGDKWIALKESWGAIWRIDTPEVL-----KGP
 160 170 180 190 200

40 50 60 70 80
 AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG
 ::: . . : . . .:~:~:~:

gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
 210 220 230 240

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen Phi p I
 (262 aa)

initn: 44 init1: 44 opt: 62 Z-score: 84.9 bits: 21.7 E(): 9.4
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (2-61:206-259)

```

                                10      20      30
AAD-12                        NDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                :. :... . :... :.
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGDKWIALKESWGAIWRIDTPEVL-----KGP
                                180      190      200      210      220      230
    
```

```

                                40      50      60      70      80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG
                                ::: . . : . . :...:
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
                                240      250      260
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:46 2010 done: Fri Feb 5 12:55:46 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 55 - 134 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
	22	0	0: one +AD0- represents 3 library sequences
	24	0	0:
	26	0	0:
	28	2	0:+AD0-
	30	7	2:+ACoAPQA9-
	32	11	8:+AD0APQAqAD0-
	34	37	21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-


```

 96      1      1:+ACo-          :+ACo-
 98      0      0:              +ACo-
100      0      0:              +ACo-
102      0      0:              +ACo-
104      0      0:              +ACo-
106      0      0:              +ACo-
108      0      0:              +ACo-
110      0      0:              +ACo-
112      0      0:              +ACo-
114      0      0:              +ACo-
116      0      0:              +ACo-
118      0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.09890.00385+ADs- mu+AD0- 3.1493
0.199
mean+AF8-var+AD0-60.104217.939, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.165433
Kolmogorov-Smirnov statistic: 0.0623 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 22.3      2.2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 21.9      3

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 init1: 59 opt: 67 Z-score: 96.4 bits: 22.3 E(): 2.2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (29-58:30-56)

          10          20          30          40          50
AAD-12  DQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST
          . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
          10          20          30          40          50

          60          70          80
AAD-12  YMPVMAQQGAVFSAEVVPAVGG

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
          60          70          80          90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 init1: 55 opt: 65 Z-score: 93.9 bits: 21.9 E(): 3
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (29-59:30-57)

```


116 0 0: +ACo-
 118 0 0: +ACo-
 +AD4-120 0 0: +ACo-
 331323 residues in 1471 sequences
 Expectation+AF8-n fit: rho(ln(x))+AD0- 5.72280.00378+ADs- mu+AD0- 4.9785
 0.196
 mean+AF8-var+AD0-57.859817.442, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
 Lambda+AD0- 0.168611
 Kolmogorov-Smirnov statistic: 0.0729 (N+AD0-26) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)
 gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
 (97) 67 22.5 2
 gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
 (96) 65 22.0 2.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 97.1 bits: 22.5 E(): 2
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (28-57:30-56)

	10	20	30	40	50
AAD-12	QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS	PAEWDDMMKVIVGNMAWHADST			
			::: . : ::. . . :
gi+AHw-126	TKVDLTVEKGS	DAKTLVLN	IKYTRPGD	TLAEVELRQHG	SEEWEPMTK--KGNL-WEVKSA
	10	20	30	40	50

	60	70	80
AAD-12	YMPVMAQGA	VFSAEVVP	PAVGGR

gi+AHw-126	KPLTGPMNFR	FLSKGGMKN	VFDEVIPTAFTV	GKTYTPEYN
	60	70	80	90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 65 Z-score: 94.6 bits: 22.0 E(): 2.7
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (28-58:30-57)

	10	20	30	40	50
AAD-12	QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS	PAEWDDMMKVIVGNMAWHADST			
			::: . : ::. . . . :
gi+AHw-144	VKVTFKVEKGS	DPKKLVLDI	KYTRPGD	TLAEVELRQHG	SEEWEPMTK--GNL-WEVKSS
	10	20	30	40	50

	60	70	80
AAD-12	YMPVMAQGA	VFSAEVVP	PAVGGR

gi+AHw-144	KPLTGPFNFR	FMSKGGMRN	VFDEVIPTAFKIG	TTYTPEE
------------	------------	-----------	---------------	---------

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po

(97) 67 22.4 2

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-

(96) 65 21.9 2.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:

Full+AD0-Pollen (97 aa)

initn: 59 initl: 59 opt: 67 Z-score: 96.8 bits: 22.4 E(): 2

Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)

in 30 aa overlap (27-56:30-56)

	10	20	30	40	50
AAD-12	QITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST				
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA				
	10	20	30	40	50

	60	70	80
AAD-12	YMPVMAQGAVFSAEVVPAVGGRT		

gi+AHw-126	KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN			
	60	70	80	90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:

Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 94.3 bits: 21.9 E(): 2.8

Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)

in 31 aa overlap (27-57:30-57)

	10	20	30	40	50
AAD-12	QITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST				
gi+AHw-144	VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS				
	10	20	30	40	50

	60	70	80
AAD-12	YMPVMAQGAVFSAEVVPAVGGRT		

gi+AHw-144	KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE			
	60	70	80	90

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:47 2010 done: Fri Feb 5 12:55:47 2010

Total Scan time: 0.090 Total Display time: 0.000


```

56      51      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
58      90
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9AD0APQA9-
60      44      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
62      58      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
64      54      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
66      30      25:+AD0APQA9AD0APQA9AD0APQAqAD0-
68      19      20:+AD0APQA9AD0APQA9ACo-
70      16      16:+AD0APQA9AD0APQAq-
72      5       12:+AD0APQ- +ACo-
74      15      10:+AD0APQA9ACoAPQ-
76      4       7:+AD0APQAq-
78      5       6:+AD0AKg-
80      7       4:+AD0AKgA9-
82      0       3:+ACo-
84      0       3:+ACo-
86      0       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      1       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120  0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.25130.00364+ADs- mu+AD0- 7.6333
0.189
mean+AF8-var+AD0-55.200316.529, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.172625
Kolmogorov-Smirnov statistic: 0.0791 (N+AD0-25) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 22.6 1.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.1 2.6

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 97.6 bits: 22.6 E(): 1.9
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (26-55:30-56)

```

                10         20         30         40         50
AAD-12      ITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST
                ..  .:..:  :..  :  :  :..  :..  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                10         20         30         40         50

```

```

        60         70         80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTC

```

```

gi+AHw-126  KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
        60         70         80         90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 65 Z-score: 95.0 bits: 22.1 E(): 2.6
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (26-56:30-57)

```

                10         20         30         40         50
AAD-12      ITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST
                ..  .:..:  :..  :  :  :..  :..  :
gi+AHw-144  VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSS
                10         20         30         40         50

```

```

        60         70         80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTC

```

```

gi+AHw-144  KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
        60         70         80         90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:47 2010 done: Fri Feb 5 12:55:47 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

70    16    16:+AD0APQA9AD0APQAq-
72     9    12:+AD0APQA9ACo-
74    17    10:+AD0APQA9ACoAPQA9-
76     3     7:+AD0- +ACo-
78     5     6:+AD0AKg-
80     3     4:+AD0AKg-
82     0     3:+ACo-
84     0     3:+ACo-
86     0     2:+ACo-
88     0     2:+ACo-          inset +AD0- represents 1 library sequences
90     0     1:+ACo-
92     0     1:+ACo-          :+ACo-
94     1     1:+ACo-          :+ACo-
96     1     1:+ACo-          :+ACo-
98     0     0:              +ACo-
100    0     0:              +ACo-
102    0     0:              +ACo-
104    0     0:              +ACo-
106    0     0:              +ACo-
108    0     0:              +ACo-
110    0     0:              +ACo-
112    0     0:              +ACo-
114    0     0:              +ACo-
116    0     0:              +ACo-
118    0     0:              +ACo-

```

```

+AD4-120    0    0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.27160.00364+ADs- mu+AD0- 7.6296
0.189
mean+AF8-var+AD0-55.037316.386, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.172880
Kolmogorov-Smirnov statistic: 0.0872 (N+AD0-25) at 42

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

```

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

```

```

The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 22.5    1.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.0    2.6

```

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 init1: 59 opt: 67 Z-score: 97.5 bits: 22.5 E(): 1.9
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (25-54:30-56)

```

```

                10          20          30          40          50
AAD-12          TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST
                ..  .....  ...  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                10          20          30          40          50

```


30 9 2:+ACoAPQA9-
 32 24 8:+AD0APQAqAD0APQA9AD0APQ-
 34 30 21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
 36 72
 44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-
 38 77
 72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
 -
 40 111
 101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9ACoAPQA9AD0-
 42 178
 123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA
 9AD0APQA9AD0APQA9-
 44 125
 136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 46 126
 138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 48 95
 132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQ- +ACo-
 50 75
 121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
 +ACo-
 52 76
 106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 Q- +ACo-
 54 60 91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
 +ACo-
 56 76
 76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
 -
 58 76
 62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
 -
 60 51 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
 62 56 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
 64 40 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
 66 35 25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
 68 20 20:+AD0APQA9AD0APQA9ACo-
 70 15 16:+AD0APQA9AD0APQAq-
 72 14 12:+AD0APQA9ACoAPQ-
 74 13 10:+AD0APQA9ACoAPQ-
 76 3 7:+AD0- +ACo-
 78 5 6:+AD0AKg-
 80 2 4:+AD0AKg-
 82 0 3:+ACo-
 84 0 3:+ACo-
 86 0 2:+ACo-
 88 0 2:+ACo- inset +AD0- represents 1 library sequences
 90 0 1:+ACo-

```

92      0      1:+ACo-      :+ACo-
94      1      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120 0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.39000.00367+ADs- mu+AD0- 7.0780
0.190
mean+AF8-var+AD0-55.449216.399, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.172237
Kolmogorov-Smirnov statistic: 0.0906 (N+AD0-25) at 42

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080

The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 22.5 1.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 22.0 2.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 init1: 59 opt: 67 Z-score: 97.4 bits: 22.5 E(): 1.9
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (24-53:30-56)

```

                10      20      30      40      50
AAD-12          FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST
                ..  .:.:.  .:. : :  .:. :. :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                10      20      30      40      50

```

```

                60      70      80
AAD-12 YMPVMAQQGAVFSAEVVPAVGGRTCFA

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 init1: 55 opt: 65 Z-score: 94.7 bits: 22.0 E(): 2.7

Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (24-54:30-57)

```

                10      20      30      40      50
AAD-12      FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
                ..  .:..:  :..  . :  :..  :..  :.
gi+AHw-144  VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEP LTKK--GNL-WEVKSS
                10      20      30      40      50

                60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFA

gi+AHw-144  KPLTGFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                60      70      80      90
    
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:47 2010 done: Fri Feb 5 12:55:47 2010
Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 61 - 140 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      0      0:
      28      4      0:+AD0APQ-
      30      7      2:+ACoAPQA9-
      32      25     8:+AD0APQAqAD0APQA9AD0APQA9-
      34      29    21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36      75
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
      38      77
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
    
```



```

110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.39400.00368+ADs- mu+AD0- 7.1676
0.190
mean+AF8-var+AD0-56.738116.423, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.170270
Kolmogorov-Smirnov statistic: 0.0866 (N+AD0-26) at 42

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 22.4 2.1
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 21.9 2.9

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 67 Z-score: 96.7 bits: 22.4 E(): 2.1
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (23-52:30-56)

```

                10      20      30      40      50
AAD-12      AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
                ..  ..:..  :.  :  :  :.  :.  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                10      20      30      40      50

                60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFAD

gi+AHw-126  KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)

initn: 55 init1: 55 opt: 65 Z-score: 94.1 bits: 21.9 E(): 2.9
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (23-53:30-57)

```

                10      20      30      40      50
AAD-12      AKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
                ..  ..:..  :.  :  :  :.  :.  :
gi+AHw-144  VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS
                10      20      30      40      50

                60      70      80

```


Lambda+AD0- 0.169336

Kolmogorov-Smirnov statistic: 0.0893 (N+AD0-26) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 22.3 2.2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 21.8 3

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 67 Z-score: 96.3 bits: 22.3 E(): 2.2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (22-51:30-56)

	10	20	30	40	50
AAD-12	KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST				
		 : : .. :.. :
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA				
	10	20	30	40	50

	60	70	80
AAD-12	YMPVMAQGAVFSAEVVPAVGGRTCFADM		

gi+AHw-126	60	70	80	90
KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN				

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)

initn: 55 init1: 55 opt: 65 Z-score: 93.7 bits: 21.8 E(): 3
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (22-52:30-57)

	10	20	30	40	50
AAD-12	KRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST				
		 : : .. :.. :..
gi+AHw-144	VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS				
	10	20	30	40	50

	60	70	80
AAD-12	YMPVMAQGAVFSAEVVPAVGGRTCFADM		

gi+AHw-144	60	70	80	90
KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE				

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:47 2010 done: Fri Feb 5 12:55:47 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 63 - 142 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	1	0:+AD0-	
26	0	0:	
28	3	0:+AD0-	
30	5	2:+ACoAPQ-	
32	28	8:+AD0APQAqAD0APQA9AD0APQA9AD0-	
34	27	21:+AD0APQA9AD0APQA9ACoAPQA9-	
36	71		
44:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-
38	84		
72:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9AD0-			
40	112		
101:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-			
42	171		
123:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA			
9AD0APQA9-			
44	131		
136:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-			
46	133		
138:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-			
48	108		
132:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-			
50	75		
121:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-			
52	76		
106:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
Q-			+ACo-

```

54      57      91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56      88
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0APQA9-
58      59
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
60      45      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
62      50      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
64      38      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
66      29      25:+AD0APQA9AD0APQA9AD0APQAqAD0-
68      25      20:+AD0APQA9AD0APQA9ACoAPQA9-
70      10      16:+AD0APQA9AD0- +ACo-
72      19      12:+AD0APQA9ACoAPQA9AD0-
74      5       10:+AD0APQ- +ACo-
76      3       7:+AD0- +ACo-
78      5       6:+AD0AKg-
80      3       4:+AD0AKg-
82      6       3:+ACoAPQ-
84      0       3:+ACo-
86      0       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      1       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.01420.0036+ADs- mu+AD0- 9.0770
0.186
mean+AF8-var+AD0-56.567716.446, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.170526
Kolmogorov-Smirnov statistic: 0.0893 (N+AD0-26) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.100
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 22.4 2.1
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 21.9 3

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 96.5 bits: 22.4 E(): 2.1
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (21-50:30-56)

```

                10         20         30         40         50
AAD-12          RFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST
                ..  .:..:  :..  :  :  :..  :..  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                10         20         30         40         50

                60         70         80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMR

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60         70         80         90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 65 Z-score: 93.9 bits: 21.9 E(): 3
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (21-51:30-57)

```

                10         20         30         40         50
AAD-12          RFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST
                ..  .:..:  :..  :  :  :..  :..  :
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSS
                10         20         30         40         50

                60         70         80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMR

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                60         70         80         90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:47 2010 done: Fri Feb 5 12:55:48 2010
 Total Scan time: 0.100 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 64 - 143 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	1	0:+AD0-	
26	1	0:+AD0-	
28	2	0:+AD0-	
30	4	2:+ACoAPQ-	
32	27	8:+AD0APQAqAD0APQA9AD0APQA9-	
34	28	21:+AD0APQA9AD0APQA9ACoAPQA9AD0-	
36	69		
44:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
38	88		
72:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9AD0APQA9-			
40	114		
101:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
Q-			+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
42	167		
123:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA			
9AD0APQ-			
44	133		
136:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-			
46	130		
138:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-			
48	106	132:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-			+ACo-
50	75		
121:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-			
52	77		
106:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
Q-			+ACo-
54	57	91:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-			
56	90		
76:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0APQA9-			
58	59		
62:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
60	41	50:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
62	51	40:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
64	39	32:	+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
66	33	25:	+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
68	25	20:	+AD0APQA9AD0APQA9ACoAPQA9-


```

                60          70          80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVVGKTYTPEYN
           60          70          80          90

```

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
  initn: 55 initl: 55 opt: 65 Z-score: 93.8 bits: 21.9 E(): 3
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (20-50:30-57)

```

```

                10          20          30          40          50
AAD-12          FGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
                                .. .:::. :. . :  :: .:. :.
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEP LTKK--GNL-WEVKSS
           10          20          30          40          50

```

```

                60          70          80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
           60          70          80          90

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:48 2010 done: Fri Feb 5 12:55:48 2010
Total Scan time: 0.090 Total Display time: 0.010

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

1+AD4APgA+-AAD-12: 65 - 144 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 4 library sequences
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      3      0:+AD0-

```



```

110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.06520.00358+ADs- mu+AD0- 8.7658
0.185
mean+AF8-var+AD0-56.579316.473, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.170508
Kolmogorov-Smirnov statistic: 0.0920 (N+AD0-26) at 42

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 22.4 2.1
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 21.9 2.9

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 67 Z-score: 96.6 bits: 22.4 E(): 2.1
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (19-48:30-56)

```

                10      20      30      40
AAD-12          GAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
                ..  .:.:.  .:. : :  .:. :. :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                10      20      30      40      50

                50      60      70      80
AAD-12 YMPVMAQGAVFSAEVPVAVGGRTCFADMRAA

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)

initn: 55 init1: 55 opt: 65 Z-score: 94.0 bits: 21.9 E(): 2.9
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (19-49:30-57)

```

                10      20      30      40
AAD-12          GAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
                ..  .:.:.  .:. . :  .:. :. :.
gi+AHw-144 VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS
                10      20      30      40      50

                50      60      70      80

```


gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
 (97) 67 22.4 2.1
 gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
 (96) 65 21.9 2.9

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 67 Z-score: 96.6 bits: 22.4 E(): 2.1
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (18-47:30-56)

```

                                10      20      30      40
AAD-12      AIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
                                ..  .::::.  :::  :  :  :::  ...  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                                10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY

```

```

gi+AHw-126  KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                    60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 94.0 bits: 21.9 E(): 2.9
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (18-48:30-57)

```

                                10      20      30      40
AAD-12      AIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
                                ..  .::::.  :::  .  :  :::  ...  ..
gi+AHw-144  VKVTFKVEKGSDPKKLVLVDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSS
                                10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY

```

```

gi+AHw-144  KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                    60      70      80      90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:48 2010 done: Fri Feb 5 12:55:48 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 67 - 146 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 4 library sequences
24	0	0:	
26	1	0:+AD0-	
28	3	0:+AD0-	
30	3	2:+ACo-	
32	20	8:+AD0AKgA9AD0APQ-	
34	30	21:+AD0APQA9AD0APQAqAD0APQ-	
36	69	44:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-	
38	80	72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-	
40	120		
101:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
42	187		
123:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
44	134		
136:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
46	132		
138:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
48	110		
132:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
50	72	121:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-			
52	64	106:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-			
54	61	91:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
56	79	76:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-
58	66	62:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-
60	36	50:	+AD0APQA9AD0APQA9AD0APQA9- +ACo-
62	47	40:	+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
64	43	32:	+AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66	34	25:	+AD0APQA9AD0APQA9ACoAPQA9-
68	21	20:	+AD0APQA9AD0AKgA9-
70	13	16:	+AD0APQA9ACo-
72	18	12:	+AD0APQAqAD0APQ-
74	6	10:	+AD0APQAq-
76	4	7:	+AD0AKg-
78	5	6:	+AD0AKg-
80	3	4:	+ACo-

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 94.3 bits: 21.9 E(): 2.8
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (17-47:30-57)

```

                                10      20      30      40
AAD-12      IERIGGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADST
                                :.  .:..:  :.  . :  :.  .:..:
gi+AHw-144  VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEWEPLTKK--GNL-WEVKSS
                                10      20      30      40      50

                                50      60      70      80
AAD-12  YMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYD

gi+AHw-144  KPLTGFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                                60      70      80      90
  
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:48 2010 done: Fri Feb 5 12:55:48 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 68 - 147 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	4	0:+AD0APQ-	
30	3	2:+ACo-	
32	18	8:+AD0APQAqAD0APQA9-	
34	35	21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-	
36	59	44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-	


```

106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.06700.00358+ADs- mu+AD0- 8.7638
0.185
mean+AF8-var+AD0-54.967716.356, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.172990
Kolmogorov-Smirnov statistic: 0.0997 (N+AD0-27) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080

The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 22.5 1.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 22.0 2.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 init1: 59 opt: 67 Z-score: 97.3 bits: 22.5 E(): 1.9
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (16-45:30-56)

```

                10          20          30          40
AAD-12          ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
                ..  ..:::  ::.  :  :  ::.  ..  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                10          20          30          40          50

                50          60          70          80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDA

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60          70          80          90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 init1: 55 opt: 65 Z-score: 94.7 bits: 22.0 E(): 2.7
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (16-46:30-57)

```

                10          20          30          40
AAD-12          ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
                ..  ..:::  ::.  .  :  ::.  ..  :
gi+AHw-144 VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS
                10          20          30          40          50

```

```
      50      60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDA

gi+AHw-144 KPLTGFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPPEE
      60      70      80      90
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:48 2010 done: Fri Feb 5 12:55:48 2010
Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 69 - 148 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```
      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      3      0:+AD0-
      30      4      2:+ACoAPQ-
      32      19     8:+AD0APQAqAD0APQA9AD0-
      34      32     21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
      36      66
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0-
      38      81
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9-
      40     126
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
      42     174     123:+AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
      44     139
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-
```


Lambda+AD0- 0.174182

Kolmogorov-Smirnov statistic: 0.0969 (N+AD0-27) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 22.5 1.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 22.0 2.6

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 init1: 59 opt: 67 Z-score: 97.5 bits: 22.5 E(): 1.9
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (15-44:30-56)

	10	20	30	40
AAD-12	RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST			
gi+AHw-126	TKVDLTVEKGS	DAKTLVLN	IKYTRPGD	TLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
	10	20	30	40
				50

	50	60	70	80
AAD-12	YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL			

gi+AHw-126	KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
	60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 init1: 55 opt: 65 Z-score: 94.9 bits: 22.0 E(): 2.6
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (15-45:30-57)

	10	20	30	40
AAD-12	RIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST			
gi+AHw-144	VKVTFKVEKGS	DPKKLVLD	IKYTRPGD	TLAEVELRQHGSEEWEPMTK--KGNL-WEVKSS
	10	20	30	40
				50

	50	60	70	80
AAD-12	YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL			

gi+AHw-144	KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
	60 70 80 90

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-


```

54      55      91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56      82
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0-
58      57      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-+AD0APQA9AD0APQA9-
+ACo-
60      47      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
62      42      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      40      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      33      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
68      23      20:+AD0APQA9AD0APQA9ACoAPQ-
70      12      16:+AD0APQA9AD0- +ACo-
72      14      12:+AD0APQA9ACoAPQ-
74      10      10:+AD0APQA9ACo-
76      6       7:+AD0APQAq-
78      2       6:+AD0AKg-
80      2       4:+AD0AKg-
82      5       3:+ACoAPQ-
84      3       3:+ACo-
86      0       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      1       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-

```

```

+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.85670.0036+ADs- mu+AD0- 9.9306
0.186
mean+AF8-var+AD0-54.351216.130, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.173968
Kolmogorov-Smirnov statistic: 0.1031 (N+AD0-27) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 22.5 1.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 22.0 2.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 97.3 bits: 22.5 E(): 1.9
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (14-43:30-56)

```

                                10      20      30      40
AAD-12          IGGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                ..  .: : :  : :  : :  :
gi+AHw-126  TKVDLTVEKGS DAKTLV LNIKYTRPGDTLAEVELRQH GSEEWEPMTK--KGNL-WEVKSA
                                10      20      30      40      50

                                50      60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD

gi+AHw-126  KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                                60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 65 Z-score: 94.6 bits: 22.0 E(): 2.7
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (14-44:30-57)

```

                                10      20      30      40
AAD-12          IGGGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                ..  .: : :  : :  : :  :
gi+AHw-144  VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEEWEP LTKK--GNL-WEVKSS
                                10      20      30      40      50

                                50      60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD

gi+AHw-144  KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                                60      70      80      90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:48 2010 done: Fri Feb 5 12:55:48 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

70      15      16:+AD0APQA9AD0APQAq-
72      6      12:+AD0APQ- +ACo-
74      21      10:+AD0APQ-+AD0AKgA9AD0APQ-
76      4      7:+AD0APQAq-
78      3      6:+AD0AKg-
80      3      4:+AD0AKg-
82      2      3:+ACo-
84      6      3:+ACoAPQ-
86      0      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120  0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.52430.00364+ADs- mu+AD0- 6.0564
0.187
mean+AF8-var+AD0-53.128716.237, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.175958
Kolmogorov-Smirnov statistic: 0.0786 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 22.8      1.6
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.3      2.2
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97)  57 20.3      9
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 20.5      9.5
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  58 20.5      9.5
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
58 20.5      9.5
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
58 20.5      9.5

```


+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 init1: 46 opt: 58 Z-score: 84.9 bits: 20.5 E(): 9.5
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (13-71:55-107)

```

                                10      20      30      40
AAD-12                        GGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :
gi+AHw-400 WCVPKVFTFTVEKGSNEKHLAVLVKYEgDTMAEVELREHGSDewVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

                                50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE
                                :.  ::  :.  .  :  ..  :  :.
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:48 2010 done: Fri Feb 5 12:55:49 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 72 - 151 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

    opt      E()
+ADw- 20    2      0:+AD0-
    22      0      0:      one +AD0- represents 4 library sequences
    24      0      0:
    26      0      0:
    28      3      0:+AD0-
    30      2      2:+ACo-
    32     18      8:+AD0AKgA9AD0APQ-
    34     25     21:+AD0APQA9AD0APQAqAD0-
    36     63     44:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
    38     77     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
    40     94    101:+AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
    
```


Expectation+AF8-n fit: rho(ln(x))+AD0- 5.11310.00346+ADs- mu+AD0- 7.8912
0.179

mean+AF8-var+AD0-49.594015.603, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42

Lambda+AD0- 0.182121

Kolmogorov-Smirnov statistic: 0.0689 (N+AD0-28) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 23.1 1.2

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 22.6 1.8

gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
(97) 57 20.5 7.6

gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
58 20.8 7.9

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
(122) 58 20.8 7.9

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
58 20.8 7.9

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
58 20.8 7.9

gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (419)
64 22.5 8.3

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 67 Z-score: 100.7 bits: 23.1 E(): 1.2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (12-41:30-56)

		10	20	30	40
AAAD-12		GGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST			
			::. : :
gi+AHw-126	TKVDLTVEKGS	DAKTLVLN	IKYTRPGD	TLAEVELRQ	HGSEEWEPMTK--KGNL-WEVKSA
	10	20	30	40	50

	50	60	70	80
AAAD-12	YMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEA			

gi+AHw-126	KPLTGPMNFR	FLSKGGMKN	VFDEVIPTA	FTVGKTYTPEYN
	60	70	80	90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)

initn: 55 init1: 55 opt: 65 Z-score: 98.0 bits: 22.6 E(): 1.8
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (12-42:30-57)

		10	20	30	40
AAAD-12		GGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST			

```

gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEEW EPLTKK--GNL-WEVKSS
              10          20          30          40          50

```

```

AAD-12 YMPVMAQQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA

```

```

gi+AHw-144 KPLTGFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
              60          70          80          90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 init1: 36 opt: 57 Z-score: 86.5 bits: 20.5 E(): 7.6
Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (12-73:31-86)

```

AAD-12 GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
              10          20          30          40
gi+AHw-126 AAPVEFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
              10          20          30          40          50

```

```

AAD-12 TYMPVMAQQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA

```

```

gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTTYKPE
              60          70          80          90

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 86.3 bits: 20.8 E(): 7.9
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (12-70:55-107)

```

AAD-12 GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
              10          20          30          40
gi+AHw-400 WCVPKVFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
              30          40          50          60          70          80

```

```

AAD-12 TYMPVMAQQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA

```

```

gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVVP EKYTIGATYAPEE
              90          100          110          120

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 86.3 bits: 20.8 E(): 7.9
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (12-70:55-107)

```

AAD-12 GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
              10          20          30          40

```

```

                                ..  ....  ::  :  :  :  :  :
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                30          40          50          60          70          80

```

```

                50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA
                ..  ::  :.  .  .  :  .  :  :.

```

```

gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                90          100          110          120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 86.3 bits: 20.8 E(): 7.9
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (12-70:55-107)

```

                                10          20          30          40
AAD-12  GGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                30          40          50          60          70          80

```

```

                50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA
                ..  ::  :.  .  .  :  .  :  :.

```

```

gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                90          100          110          120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 86.3 bits: 20.8 E(): 7.9
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (12-70:55-107)

```

                                10          20          30          40
AAD-12  GGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                30          40          50          60          70          80

```

```

                50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA
                ..  ::  :.  .  .  :  .  :  :.

```

```

gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                90          100          110          120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)

initn: 39 init1: 39 opt: 64 Z-score: 85.8 bits: 22.5 E(): 8.3
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (11-69:89-149)

```

                                10          20          30
AAD-12  GGDIVAISNVKADGT-VRQHS PAEWDDMMKVIVGNMAWHA

```


FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 25.4 0.25
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 24.8 0.38
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
(97) 57 22.4 2
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
58 22.6 2.2
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
(122) 58 22.6 2.2
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
58 22.6 2.2
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
58 22.6 2.2
gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (419)
64 24.1 2.7
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
59 22.8 3.1
gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOb RecName: Full+AD0-
(514) 64 24.1 3.5
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
57 22.3 3.7
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
(379) 61 23.2 4.5
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
56 22.0 4.6
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
(158) 55 21.7 5.6
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
54 21.4 7
gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor (279)
57 22.1 7.2
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144)
53 21.1 7.6
gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34
(379) 58 22.3 8.4
gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
58 22.3 8.4
gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosu (386)
58 22.3 8.6

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 67 Z-score: 113.1 bits: 25.4 E(): 0.25

Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (11-40:30-56)

AAAD-12

10 20 30 40
GDIVAISNVKADGTVRQHSPPAEWDDMMKVIVGNMAWHADST

```

                ..  .:..  :.  :  :  :.  :.  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT

```

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 init1: 55 opt: 65 Z-score: 109.9 bits: 24.8 E(): 0.38
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (11-41:30-57)

```

                10      20      30      40
AAD-12          GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                ..  .:..  :.  :  :  :.  :.  :
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEW EPLTKK--GNL-WEVKSS
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT

```

```

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                60      70      80      90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 init1: 36 opt: 57 Z-score: 96.8 bits: 22.4 E(): 2
Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (11-72:31-86)

```

                10      20      30      40
AAD-12          GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                ..  .:..  :.  :  :  :.  :.  :
gi+AHw-126 AAPVEFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT

```

```

                :.  .:  :.  .  :  :  :.  :.  :
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTTYKPE
                60      70      80      90

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 96.3 bits: 22.6 E(): 2.2
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (11-69:55-107)

```

                10      20      30      40
AAD-12          GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS

```

```
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE... .. : : : : : : : :  
30 40 50 60 70 80
```

```
50 60 70 80  
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
```

```
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE  
90 100 110 120
```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 96.3 bits: 22.6 E(): 2.2
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (11-69:55-107)

```
AAD-12 10 20 30 40  
GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS  
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYE... .. : : : : : : : :  
30 40 50 60 70 80
```

```
50 60 70 80  
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
```

```
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE  
90 100 110 120
```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 96.3 bits: 22.6 E(): 2.2
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (11-69:55-107)

```
AAD-12 10 20 30 40  
GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS  
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE... .. : : : : : : : :  
30 40 50 60 70 80
```

```
50 60 70 80  
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
```

```
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE  
90 100 110 120
```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 96.3 bits: 22.6 E(): 2.2
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (11-69:55-107)

```
AAD-12 10 20 30 40  
GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
```

```

                                ..  ....  ::  :  :  :  :  ::
gi+AHw-400 WCVPKVFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                30          40          50          60          70          80

```

```

                50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
                ..  ::  ..  .  :  ..  :  ::

```

```

gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVVPPEKYTIGATYAPEE
                90          100          110          120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-
Chamaecy (419 aa)
initn: 39 initl: 39 opt: 64 Z-score: 94.6 bits: 24.1 E(): 2.7
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (10-68:89-149)

```

                                10          20          30
AAD-12                                GDIVAISNVKADGT-VRQHSPAEWDDMMKVIVGNMAWHA
                                .....  :  :  .....  .  ..  .  .  :  .
gi+AHw-114 ASAVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                60          70          80          90          100          110

```

```

                40          50          60          70          80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
                :  .  :  .  .  :  .  :  .  :  :  :  :  :
gi+AHw-114 DFNLMGTGVIDGQQQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                120          130          140          150          160          170

```

```

gi+AHw-114 FHLVFGEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
                180          190          200          210          220          230

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfa-2103117A allergen Dac g II
(196 aa)
initn: 36 initl: 36 opt: 59 Z-score: 93.5 bits: 22.8 E(): 3.1
Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
in 62 aa overlap (11-72:31-86)

```

                                10          20          30          40
AAD-12                                GDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAHADS
                                ..  ....  ::  .  :  :  .  .  :
gi+AHw-109 EAPVFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
                ..  ::  ..  .  :  ..  :  .....  :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGMNRNVFDVVPADFKVGTTYKPEEAAAASARRRSSEVFQF
                60          70          80          90          100          110

```

```

gi+AHw-109 LILSCQGRIVNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIYKIFKMMFQ
                120          130          140          150          160          170

```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName:
Full+AD0-Poly (514 aa)

initn: 39 initl: 39 opt: 64 Z-score: 92.7 bits: 24.1 E(): 3.5
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (10-68:119-179)

```

                                10          20          30
AAD-12          GDIVAI SNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                : : : : : : : : : : : :
gi+AHw-476 ASAVLLVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
          90          100          110          120          130          140
    
```

```

          40          50          60          70          80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
          : . : . . : : . : . : : : : : :
gi+AHw-476 DFNLMGTGVIDGQGGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
          150          160          170          180          190          200
    
```

```

gi+AHw-476 FHLVFGECEGVKIQGLKIKAPRDS PNTDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
          210          220          230          240          250          260
    
```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)

initn: 55 initl: 55 opt: 57 Z-score: 92.1 bits: 22.3 E(): 3.7
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (34-62:23-50)

```

          10          20          30          40          50          60
AAD-12 VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA DSTYMPVMAQGAVFSAEVVPAVGGR
                                .. : : : : : : : : : : : :
gi+AHw-444          MGVF TYADESTSVIP PRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGV
          10          20          30          40          50
    
```

```

          70          80
AAD-12 TCFADMRAAYDALDEAT
          : : : : : : : : : : : :
gi+AHw-444 GTIKKISFGEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADG
          60          70          80          90          100          110
    
```

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0- (379 aa)

initn: 49 initl: 49 opt: 61 Z-score: 90.6 bits: 23.2 E(): 4.5
 Smith-Waterman score: 61+ADs- 20.779+ACU- identity (61.039+ACU- similar)
 in 77 aa overlap (4-79:120-194)

```

                                10          20          30
AAD-12          GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGN
                                : : : : : : : : : : : :
gi+AHw-309 LGLNKFADITPQEF SSKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKGVITQ
          90          100          110          120          130          140
    
```

```

          40          50          60          70          80
AAD-12 MAWHA D-STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
          . . . . . : : : . : : : : : : : : : :
gi+AHw-309 VKYQGGCGSGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFE
          150          160          170          180          190          200
    
```



```

      . . . . .      : ::. .: . . . . . : : . . . . . : : . . . . .
gi+AHw-129 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
      150          160          170          180          190          200

```

```

gi+AHw-129 WVLEHGGIATDDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
      210          220          230          240          250          260

```

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vacuola (379 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 85.7 bits: 22.3 E(): 8.4
 Smith-Waterman score: 58+ADs- 20.779+ACU- identity (58.442+ACU- similar)
 in 77 aa overlap (4-79:120-194)

```

                                10          20          30
AAD-12                          GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGN
                                .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-119 LGLNKFADITPQEF SKKYLQAPKDV SQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQ
      90          100          110          120          130          140

```

```

      40          50          60          70          80
AAD-12 MAWHADSTY-MPVMAQ GAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
      . . . . .      : ::. .: . . . . . : : . . . . . : : . . . . .
gi+AHw-119 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
      150          160          170          180          190          200

```

```

gi+AHw-119 WVLEHGGIATDDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
      210          220          230          240          250          260

```

+AD4APg-gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosum+AF0- (386 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 85.6 bits: 22.3 E(): 8.6
 Smith-Waterman score: 58+ADs- 25.000+ACU- identity (58.333+ACU- similar)
 in 48 aa overlap (7-54:262-309)

```

                                10          20          30
AAD-12                          GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAW
                                .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-169 ATRLAQEDPAFSSIKSLDYKQMLLSLGTGTNSEFDKTYTAQEAAKWGPLRWMLAIQQMT
      240          250          260          270          280          290

```

```

      40          50          60          70          80
AAD-12 HADSTYMPVMAQ GAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-169 NAASSYMTDYYISTV FQARHSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLK
      300          310          320          330          340          350

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:49 2010 done: Fri Feb 5 12:55:49 2010
 Total Scan time: 0.090 Total Display time: 0.010


```

60      45      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
62      43      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
64      70
32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
66      31      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
68      30      20:+AD0APQA9AD0APQA9ACoAPQA9AD0-
70      38      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0-
72      21      12:+AD0APQA9ACoAPQA9AD0-
74      17      10:+AD0APQA9ACoAPQA9-
76      19      7:+AD0APQAqAD0APQA9AD0-
78      11      6:+AD0AKgA9AD0-
80      6       4:+AD0AKg-
82      5       3:+ACoAPQ-
84      14      3:+ACoAPQA9AD0APQ-
86      5       2:+ACoAPQ-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      3       1:+ACo-
92      2       1:+ACo-          :+ACoAPQ-
94      2       1:+ACo-          :+ACoAPQ-
96      5       1:+ACoAPQ-          :+ACoAPQA9AD0APQ-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     1       0:+AD0-          +ACoAPQ-
112     1       0:+AD0-          +ACoAPQ-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.55780.00328+ADs- mu+AD0- 2.9452
0.169
mean+AF8-var+AD0-37.2076 9.431, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
Lambda+AD0- 0.210261
Kolmogorov-Smirnov statistic: 0.0944 (N+AD0-29) at 60

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 25.5 0.25
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 24.9 0.37
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 57 22.4 2
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 22.7 2.1
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 58 22.7 2.1

```

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 58 22.7 2.1
 gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 58 22.7 2.1
 gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (419)
 64 24.2 2.5
 gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
 59 22.9 3
 gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOb RecName: Full+AD0- (514)
 64 24.2 3.2
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 22.3 3.6
 gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0- (379)
 61 23.3 4.3
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
 56 22.0 4.4
 gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl (158)
 55 21.7 5.4
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.4 6.8
 gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor (279)
 57 22.2 6.9
 gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144)
 53 21.1 7.4
 gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34 (379)
 58 22.4 8
 gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
 58 22.4 8
 gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosu (386)
 58 22.4 8.2

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 113.3 bits: 25.5 E(): 0.25
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (10-39:30-56)

		10	20	30	40
AAD-12		DIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST			
			:	:	:
gi+AHw-126	TKVDLTVEKGS	DAKTLVLN	IKYTRPGD	TAEVELRQ	HGSEEWEPMTK--KGNL-WEVKSA
	10	20	30	40	50
	50	60	70	80	
AAD-12	YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR				
gi+AHw-126	KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN				
	60	70	80	90	

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 65 Z-score: 110.1 bits: 24.9 E(): 0.37
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (10-40:30-57)

```

                10         20         30         40
AAD-12          DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADST
                ..  ....  ...  .  :  ...  ...  ..
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEEW EPLTKK--GNL-WEVKSS
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12 YMPVMAQQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR

gi+AHw-144 KPLTGFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                60         70         80         90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 init1: 36 opt: 57 Z-score: 96.9 bits: 22.4 E(): 2
Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (10-71:31-86)

```

                10         20         30
AAD-12          DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                ..  ....  ...  .  :  ...  ...  ..
gi+AHw-126 AAPVEFTVEKGSDEKLNLSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                10         20         30         40         50

```

```

                40         50         60         70         80
AAD-12 TYMPVMAQQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
                ..  .:  ..  .  :  :  :  :  :  :
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTTYKPE
                60         70         80         90

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 96.5 bits: 22.7 E(): 2.1
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (10-68:55-107)

```

                10         20         30
AAD-12          DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                ..  ....  ...  :  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                30         40         50         60         70         80

```

```

                40         50         60         70         80
AAD-12 TYMPVMAQQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVVPPEKYTIGATYAPEE
                90         100         110         120

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 96.5 bits: 22.7 E(): 2.1
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (10-68:55-107)

```

                                10         20         30
AAD-12          DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                30         40         50         60         70         80

```

```

        40         50         60         70         80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
        ..  ::  ..  .  .  :  ..  :  :
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                90         100        110        120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 init1: 46 opt: 58 Z-score: 96.5 bits: 22.7 E(): 2.1
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (10-68:55-107)

```

                                10         20         30
AAD-12          DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                30         40         50         60         70         80

```

```

        40         50         60         70         80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
        ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                90         100        110        120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 init1: 46 opt: 58 Z-score: 96.5 bits: 22.7 E(): 2.1
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (10-68:55-107)

```

                                10         20         30
AAD-12          DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                30         40         50         60         70         80

```

```

        40         50         60         70         80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
        ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                90         100        110        120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)
 initn: 39 init1: 39 opt: 64 Z-score: 95.1 bits: 24.2 E(): 2.5
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (9-67:89-149)

```

                                10      20      30
AAD-12          DIVAISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                : : : : : : : : : :
gi+AHw-114 ASAVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
              60      70      80      90      100     110
    
```

```

              40      50      60      70      80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
              : . : . . : . : . : : : : :
gi+AHw-114 DFNLMGTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
              120     130     140     150     160     170
    
```

```

gi+AHw-114 FHLVFGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
              180     190     200     210     220     230
    
```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
 (196 aa)
 initn: 36 init1: 36 opt: 59 Z-score: 93.8 bits: 22.9 E(): 3
 Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
 in 62 aa overlap (10-71:31-86)

```

                                10      20      30
AAD-12          DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                : . . . : : : . : : . : :
gi+AHw-109 EAPVTFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
              10      20      30      40      50
    
```

```

              40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
              : . . : : . : : : : : :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGTTYKPEEAAAASASRRRSSEVFQF
              60      70      80      90      100     110
    
```

```

gi+AHw-109 LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIIYKIFKMMFQ
              120     130     140     150     160     170
    
```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOb RecName:
 Full+AD0-Poly (514 aa)
 initn: 39 init1: 39 opt: 64 Z-score: 93.2 bits: 24.2 E(): 3.2
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (9-67:119-179)

```

                                10      20      30
AAD-12          DIVAISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                : : : : : : : : : :
gi+AHw-476 ASAVLLVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
              90      100     110     120     130     140
    
```

```

              40      50      60      70      80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
              : . : . . : . : . : : : : :
gi+AHw-476 DFNLMGTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
              150     160     170     180     190     200
    
```

gi+AHw-476 FHLVFGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
 210 220 230 240 250 260

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 55 init1: 55 opt: 57 Z-score: 92.4 bits: 22.3 E(): 3.6
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (33-61:23-50)

10 20 30 40 50 60
 AAD-12 VAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGR
 .. .:: : .: .: .: :::: . ::

gi+AHw-444 MGVFTYADESTSVIPPPRLFALVLEAD-TLIPKIA PQSVKSAEIVEGDGGV
 10 20 30 40 50

70 80
 AAD-12 TCFADMRAAYDALDEATR

gi+AHw-444 GTIKKISFGEESHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADG
 60 70 80 90 100 110

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
 max+AF0- (379 aa)

initn: 49 init1: 49 opt: 61 Z-score: 91.1 bits: 23.3 E(): 4.3
 Smith-Waterman score: 61+ADs- 20.779+ACU- identity (61.039+ACU- similar)
 in 77 aa overlap (3-78:120-194)

10 20 30
 AAD-12 DIVAISNVKADGTVRQHSPAEDDMMKVIVGN
 .: .:: . : : : : : . . .

gi+AHw-309 LGLNKFADITPQEFSSKYLQAPKDVSQQIKMANKMKKEQYSCDHPPASWDWRKKGVITQ
 90 100 110 120 130 140

40 50 60 70 80
 AAD-12 MAWHAD-STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
 : : : : : :

gi+AHw-309 VKYQGGCGSGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFE
 150 160 170 180 190 200

gi+AHw-309 WVLEHGGIATDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
 210 220 230 240 250 260

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
 sativa+AF0- (160 aa)

initn: 55 init1: 55 opt: 56 Z-score: 90.7 bits: 22.0 E(): 4.4
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (37-61:27-50)

10 20 30 40 50 60
 AAD-12 NVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFA
 : : .: .: .: .: : : : . : :

gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFLVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIK
 10 20 30 40 50


```

      40      50      60      70      80
AAD-12 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
      .   :   .   .   :   .   .   .   .
gi+AHw-106 NVYVPPYCSTIRAPFASIVAGIGGQ
      260      270

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 53 initl: 53 opt: 53 Z-score: 86.8 bits: 21.1 E(): 7.4
Smith-Waterman score: 53+ADs- 26.667+ACU- identity (66.667+ACU- similar)
in 30 aa overlap (39-68:5-34)

```

      10      20      30      40      50      60
AAD-12 KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
      .   .   .   .   .   .   .   .   .   .   .   .   .   .
gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGM
      10      20      30

```

```

      70      80
AAD-12 RAAVDALDEATR

```

```

gi+AHw-189 GLPSNPLEGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHRCRCRVRYFIG
      40      50      60      70      80      90

```

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
Full+AD0-P34 prob (379 aa)
initn: 49 initl: 49 opt: 58 Z-score: 86.2 bits: 22.4 E(): 8
Smith-Waterman score: 58+ADs- 20.779+ACU- identity (58.442+ACU- similar)
in 77 aa overlap (3-78:120-194)

```

      10      20      30
AAD-12 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGN
      .   .   .   .   .   .   .   .   .   .   .   .
gi+AHw-129 LGLNKFADITPQEFSSKKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKGVITQ
      90      100      110      120      130      140

```

```

      40      50      60      70      80
AAD-12 MAWHADSTY-MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
      .   .   .   .   .   .   .   .   .   .   .   .
gi+AHw-129 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
      150      160      170      180      190      200

```

```

gi+AHw-129 WVLEHGGIATDDDYPIRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
      210      220      230      240      250      260

```

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
vacuola (379 aa)
initn: 49 initl: 49 opt: 58 Z-score: 86.2 bits: 22.4 E(): 8
Smith-Waterman score: 58+ADs- 20.779+ACU- identity (58.442+ACU- similar)
in 77 aa overlap (3-78:120-194)

```

      10      20      30
AAD-12 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGN

```

```

gi+AHw-119 LGLNKFADITPQEFSSKKYLQAPKDVSQQIKMANKKMKKKEQYSCDHPPASWDWRKKGVITQ
          90          100          110          120          130          140
          40          50          60          70          80
AAD-12 MAWHADSTY-MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
      . . . . . : : : . . . . . : : . . . . . : : : :
gi+AHw-119 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
          150          160          170          180          190          200
gi+AHw-119 WVLEHGGIATDDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
          210          220          230          240          250          260

```

+AD4APg-gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosum+AF0- (386 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 86.0 bits: 22.4 E(): 8.2
 Smith-Waterman score: 58+ADs- 25.000+ACU- identity (58.333+ACU- similar)
 in 48 aa overlap (6-53:262-309)

```

AAD-12          10          20          30
          DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
          . : . : . : . : : . . . . .
gi+AHw-169 ATRLAQEDPAFSSIKSLDYKQMLLSLGTGTNSEFDKTYTAQEAAKWGPLRWMLAIQQMT
          240          250          260          270          280          290
          40          50          60          70          80
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
      . : : : . . . . .
gi+AHw-169 NAASSYMTDYIISTVVFQARHSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLK
          300          310          320          330          340          350

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:49 2010 done: Fri Feb 5 12:55:49 2010
 Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 75 - 154 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      1      0:+AD0-      +ACoAPQ-
110      0      0:      +ACo-
112      1      0:+AD0-      +ACoAPQ-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.61550.00328+ADs- mu+AD0- 2.7599
0.170
mean+AF8-var+AD0-38.0417 9.711, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
Lambda+AD0- 0.207943
Kolmogorov-Smirnov statistic: 0.0991 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 25.3 0.27
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 24.7 0.41
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 57 22.3 2.2
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 58 22.6 2.3
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (
419) 64 24.1 2.8
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II ( 196)
59 22.7 3.3
gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0-
( 514) 64 24.0 3.6
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.2 3.9
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379) 61 23.2 4.7
gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosu (
386) 61 23.2 4.8
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 21.9 4.8
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-G1
( 158) 55 21.6 5.8
gi+AHw-21510+AHw-emb+AHw-CAA31575.1+AHw- unnamed protein product +AFs- (
386) 60 22.9 5.9

```


Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (9-70:31-86)

```

                                10      20      30
AAD-12                          IVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  ..  ...  :
gi+AHw-126 AAPVEFTVEKGSDEKLNLSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                ..  ..  ..  .  :  :  :  :  :
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTTYKPE
                                60      70      80      90

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 95.8 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (9-67:55-107)

```

                                10      20      30
AAD-12                          IVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                ..  ::  ..  .  :  :  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100      110      120

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-Polle (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 95.8 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (9-67:55-107)

```

                                10      20      30
AAD-12                          IVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                ..  ::  ..  .  :  :  :  :
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100      110      120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 95.8 bits: 22.6 E(): 2.3

Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (9-67:55-107)

```

                                10      20      30
AAD-12                        IVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFVTEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                :.  ::  :.  .  .  :  ..  :  :.
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 initl: 46 opt: 58 Z-score: 95.8 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (9-67:55-107)

```

                                10      20      30
AAD-12                        IVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFVTEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                :.  ::  :.  .  .  :  ..  :  :.
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs- Chamaecy (419 aa)

initn: 39 initl: 39 opt: 64 Z-score: 94.3 bits: 24.1 E(): 2.8
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (8-66:89-149)

```

                                10      20      30
AAD-12                        IVAISNVKADGT-VRQHS PAEWDDMMKVIVGNMAWHA
                                :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-114 ASAVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                60      70      80      90      100     110

                                40      50      60      70      80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                :  .  :  .  :.  :  :  :.  :.  :.  :.
gi+AHw-114 DFNLMGTGVIDGQGQWVAGQCKVNVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                120     130     140     150     160     170

gi+AHw-114 FHLVFGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
                                180     190     200     210     220     230

```


70 80
AAD-12 TCFADMRAAYDALDEATRA

gi+AHw-444 GTIKKISFGEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADG
60 70 80 90 100 110

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
max+AF0- (379 aa)
initn: 49 initl: 49 opt: 61 Z-score: 90.4 bits: 23.2 E(): 4.7
Smith-Waterman score: 61+ADs- 20.779+ACU- identity (61.039+ACU- similar)
in 77 aa overlap (2-77:120-194)

10 20 30
AAD-12 IVAISNVKADGTVRQHSPAEWDDMMKVIVGN
.: .:. . :. :. :. :. :.
gi+AHw-309 LGLNKFADITPQEFSSKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQ
90 100 110 120 130 140

40 50 60 70 80
AAD-12 MAWHAD-STYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRA
. : :. :. . . . : :.
gi+AHw-309 VKYQGGCGSGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFE
150 160 170 180 190 200

gi+AHw-309 WVLEHGGIATDDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
210 220 230 240 250 260

+AD4APg-gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum
tuberosum+AF0- (386 aa)
initn: 61 initl: 61 opt: 61 Z-score: 90.2 bits: 23.2 E(): 4.8
Smith-Waterman score: 61+ADs- 21.053+ACU- identity (53.947+ACU- similar)
in 76 aa overlap (5-80:262-337)

10 20 30
AAD-12 IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
.: . : : . :. :
gi+AHw-169 ATRLAQEDPAFSSIKSLDYKQMLLSLGTGTNSEFDKTYTAQEAAKWGPLRWMLAIQQMT
240 250 260 270 280 290

40 50 60 70 80
AAD-12 HADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRA
. : :. :. . :. :. :. :. :.
gi+AHw-169 NAASSYMTDYYISTVFQARHSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLK
300 310 320 330 340 350

gi+AHw-169 KPVS KDSPET YEEALKRF AKLLSDRKKLRANKASY
360 370 380

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 initl: 55 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (36-60:27-50)

gi+AHw-444 GTIKKISFGEESHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADG
60 70 80 90 100 110

+AD4APg-gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor
+AFs-Tr (279 aa)
initn: 57 initl: 57 opt: 57 Z-score: 86.7 bits: 22.1 E(): 7.5
Smith-Waterman score: 57+ADs- 18.182+ACU- identity (58.182+ACU- similar)
in 55 aa overlap (7-61:225-279)

AAD-12 IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHA
:
gi+AHw-106 IMQEQEQEQRQGVQILVPLSQQQVQGGTLVQGGQIIQPQQPAQLE VIRSSVLQTLATMC
200 210 220 230 240 250

AAD-12 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
. : . . : . :
gi+AHw-106 NVYVPPYCSTIRAPFASIVAGIGGQ
260 270

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 53 initl: 53 opt: 53 Z-score: 86.2 bits: 21.0 E(): 7.9
Smith-Waterman score: 53+ADs- 26.667+ACU- identity (66.667+ACU- similar)
in 30 aa overlap (38-67:5-34)

AAD-12 KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
:
gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGM
10 20 30

AAD-12 RAAVDALDEATRA

gi+AHw-189 GLPSNPLEGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHRCRVRVYFIG
40 50 60 70 80 90

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
vacuola (379 aa)
initn: 49 initl: 49 opt: 58 Z-score: 85.5 bits: 22.3 E(): 8.7
Smith-Waterman score: 58+ADs- 20.779+ACU- identity (58.442+ACU- similar)
in 77 aa overlap (2-77:120-194)

AAD-12 IVAISNVKADGTVRQHSPAEWDDMMKVIVGN
:
gi+AHw-119 LGLNKFADITPQEFSSKKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKGVITQ
90 100 110 120 130 140

AAD-12 MAWHADSTY-MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
.

gi+AHw-119 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
150 160 170 180 190 200

gi+AHw-119 WVLEHGGIATDDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
210 220 230 240 250 260

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
Full+AD0-P34 prob (379 aa)
initn: 49 initl: 49 opt: 58 Z-score: 85.5 bits: 22.3 E(): 8.7
Smith-Waterman score: 58+ADs- 20.779+ACU- identity (58.442+ACU- similar)
in 77 aa overlap (2-77:120-194)

AAAD-12 IVAIISNVKADGTVRQHSPAEDDDMMKVIVGN
.: .:.: . :. :. :. :. :.
gi+AHw-129 LGLNKFADITPQEFSSKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQ
90 100 110 120 130 140

AAAD-12 MAWHADSTY-MPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRA
. . . : :. :. . . :. :. :. :. :. :.
gi+AHw-129 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
150 160 170 180 190 200

gi+AHw-129 WVLEHGGIATDDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
210 220 230 240 250 260

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:49 2010 done: Fri Feb 5 12:55:49 2010
Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 76 - 155 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

opt E()
+ADw- 20 2 0:+AD0-
22 0 0: one +AD0- represents 4 library sequences
24 1 0:+AD0-


```

108      1      0:+AD0-      +ACoAPQ-
110      0      0:      +ACo-
112      1      0:+AD0-      +ACoAPQ-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.71290.00328+ADs- mu+AD0- 2.2319
0.169
mean+AF8-var+AD0-37.9027 9.671, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
Lambda+AD0- 0.208324
Kolmogorov-Smirnov statistic: 0.0997 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 25.4 0.26
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 24.8 0.4
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 57 22.4 2.1
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 58 22.6 2.3
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (
419) 64 24.1 2.8
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II ( 196)
59 22.8 3.2
gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0-
( 514) 64 24.0 3.6
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.2 3.8
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379) 61 23.2 4.7
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 21.9 4.7
gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosu (
386) 61 23.2 4.8
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
( 158) 55 21.6 5.7
gi+AHw-21510+AHw-emb+AHw-CAA31575.1+AHw- unnamed protein product +AFs- (
386) 60 22.9 5.9
gi+AHw-21514+AHw-emb+AHw-CAA27588.1+AHw- patatin +AFs-Solanum tuberosu (
386) 60 22.9 5.9

```

gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.3 7.2
 gi+AHw-158517845+AHw-sp+AHw-P15476.2+AHw-PATB1+AF8-SOLTU RecName: Full (386)
 59 22.6 7.2
 gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor (279)
 57 22.1 7.5
 gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144)
 53 21.0 7.8
 gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
 58 22.3 8.7
 gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34 (379)
 58 22.3 8.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 112.8 bits: 25.4 E(): 0.26
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (8-37:30-56)

		10	20	30	
AAD-12		VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST			
			:	:	:
		:	:	:	:
gi+AHw-126	TKVDLTVEKGS	DAKTLV	LNIKYTR	PGD	TLAEVELRQH
	10	20	30	40	50
	40	50	60	70	80
AAD-12	YMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRAL				
gi+AHw-126	KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN				
	60	70	80	90	

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 65 Z-score: 109.6 bits: 24.8 E(): 0.4
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (8-38:30-57)

		10	20	30	
AAD-12		VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST			
			:	:	:
		:	:	:	:
gi+AHw-144	VKVTFKVEKGS	DPKKLV	LDIKYTR	PGD	TLAEVELRQH
	10	20	30	40	50
	40	50	60	70	80
AAD-12	YMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRAL				
gi+AHw-144	KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE				
	60	70	80	90	

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 36 init1: 36 opt: 57 Z-score: 96.5 bits: 22.4 E(): 2.1
 Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
 in 62 aa overlap (8-69:31-86)

```

                                10      20      30
AAD-12      VAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  ..  ...  :
gi+AHw-126  AAPVEFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR AL
                                ..  .:  :.  .  :  :  :.  :.  :
gi+AHw-126  DK-PL--KGP-FNFRFVSEKGM RNVFDDVVPADFKVGT TYKPE
                                60      70      80      90

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (8-66:55-107)

```

                                10      20      30
AAD-12      VAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :.  ::
gi+AHw-400  WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR AL
                                ..  ::  :.  .  .  :  ..  :  :.
gi+AHw-400  EE-PL--QGP-FNFRFLTEKGMKNV FDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-Polle (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (8-66:55-107)

```

                                10      20      30
AAD-12      VAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :.  ::
gi+AHw-117  WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR AL
                                ..  ::  :.  .  .  :  ..  :  :.
gi+AHw-117  EE-PL--QGP-FNFRFLTEKGMKNV FDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (8-66:55-107)

```

                                10      20      30
AAD-12      VAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  .:  ::
gi+AHw-400  WCVPKVTFVTEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                                :.  ::  :.  .  .  :  ..  :  ::
gi+AHw-400  EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 initl: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (8-66:55-107)

```

                                10      20      30
AAD-12      VAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  .:  ::
gi+AHw-400  WCVPKVTFVTEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                                :.  ::  :.  .  .  :  ..  :  ::
gi+AHw-400  EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)
 initn: 39 initl: 39 opt: 64 Z-score: 94.3 bits: 24.1 E(): 2.8
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (7-65:89-149)

```

                                10      20      30
AAD-12      VAISNVKADGT-VRQHS PAEWDDMMKVIVGNMAWHA
                                :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-114  ASAVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                60      70      80      90      100     110

```

```

                                40      50      60      70      80
AAD-12  DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                                :  .  :  .  :.  :.  :.  :.  :.  :.  :.
gi+AHw-114  DFNLMGTGVIDGQGQWVAGQCKVNVGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                120     130     140     150     160     170

```

```

                                180     190     200     210     220     230
gi+AHw-114  FHLVFGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196 aa)

initn: 36 init1: 36 opt: 59 Z-score: 93.2 bits: 22.8 E(): 3.2
 Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
 in 62 aa overlap (8-69:31-86)

```

                                10      20      30
AAD-12      VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  . :  ..  ...  :
gi+AHw-109  EAPVTFTEVEKGSDEKLNLSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12      TYMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRAL
                                .:  .:  .:  . :  : :.  :...  :
gi+AHw-109  DK-PL--KGP-FNFRFVSEKGM RNVFVDVVPADFKVGT TYKPEEAAAASASRRRSSEVFQF
                                60      70      80      90      100     110

gi+AHw-109  LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEI IYKIFKMMFQ
                                120     130     140     150     160     170
    
```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHA OB RecName:
 Full+AD0-Poly (514 aa)

initn: 39 init1: 39 opt: 64 Z-score: 92.4 bits: 24.0 E(): 3.6
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (7-65:119-179)

```

                                10      20      30
AAD-12      VAISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                ::::  : :  ::::  .  .:  . . . :  .
gi+AHw-476  ASAVLLVPANKKFFVNNL VFRGPCPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                90      100     110     120     130     140

                                40      50      60      70      80
AAD-12      DSTYMP---VMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRAL
                                : . :  . . : :  . :  . : : : :  :
gi+AHw-476  DFNLMGTGVIDGQQQW WAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKEL TLMNSPE
                                150     160     170     180     190     200

gi+AHw-476  FHLVFGECEGVKIQGLK IKA PRDSPNTDGIDIFASKRFHIEKCVIGTGD DDCIAIGTGSSN
                                210     220     230     240     250     260
    
```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 55 init1: 55 opt: 57 Z-score: 91.9 bits: 22.2 E(): 3.8
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (31-59:23-50)

```

                                10      20      30      40      50      60
AAD-12      VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPAVGGR
                                ..  :: :  .:  .:  .:  ::::  .  ::
gi+AHw-444      MGVFTYADESTSVIP PRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGV
                                10      20      30      40      50

                                70      80
AAD-12      TCFADMRAAYDALDEATRAL
    
```


+AD4APg-gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor
 +AFs-Tr (279 aa)
 initn: 57 initl: 57 opt: 57 Z-score: 86.7 bits: 22.1 E(): 7.5
 Smith-Waterman score: 57+ADs- 18.182+ACU- identity (58.182+ACU- similar)
 in 55 aa overlap (6-60:225-279)

```

                                10      20      30
AAD-12                          VAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHA
                                :...: .. :...: . . . . . :
gi+AHw-106 IMQQEQQEQRQGVQILVPLSQQQVGGTLVQGGI IQPQQPAQLE VIRSSVLQTLATMC
                200      210      220      230      240      250
  
```

```

                40      50      60      70      80
AAD-12 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                .   :   .   .   :   .:   .:   .:
gi+AHw-106 NVYVPPYCSTIRAPFASIVAGIGGQ
                260      270
  
```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 53 initl: 53 opt: 53 Z-score: 86.3 bits: 21.0 E(): 7.8
 Smith-Waterman score: 53+ADs- 26.667+ACU- identity (66.667+ACU- similar)
 in 30 aa overlap (37-66:5-34)

```

                10      20      30      40      50      60
AAD-12 KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
                                ..  :..  ...  :.  .  :.  :.  :.  :
gi+AHw-189                          MASKSSITPLLLAAVLASVFAAAAATGQYCYAGM
                                10      20      30
  
```

```

                70      80
AAD-12 RAAVDALDEATRAL
gi+AHw-189 GLPSNPLEGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHRCRVRVYFIG
                40      50      60      70      80      90
  
```

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
 vacuola (379 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 85.5 bits: 22.3 E(): 8.7
 Smith-Waterman score: 58+ADs- 20.779+ACU- identity (58.442+ACU- similar)
 in 77 aa overlap (1-76:120-194)

```

                                10      20      30
AAD-12                          VAISNVKADGTVRQHSPAEWDDMMKVIVGN
                                .:  :...: .  :.  :.  :.  :.  :.  :
gi+AHw-119 LGLNKFADITPQEFSSKKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKGVITQ
                90      100      110      120      130      140
  
```

```

                40      50      60      70      80
AAD-12 MAWHADSTY-MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                .  ...  :  :..  :...  :.  :.  :.  :.  :.  :
gi+AHw-119 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
                150      160      170      180      190      200
  
```

```
gi+AHw-119 WVLEHGGIATDDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
          210          220          230          240          250          260
```

```
+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
Full+AD0-P34 prob (379 aa)
  initn: 49 initl: 49 opt: 58 Z-score: 85.5 bits: 22.3 E(): 8.7
Smith-Waterman score: 58+ADs- 20.779+ACU- identity (58.442+ACU- similar)
in 77 aa overlap (1-76:120-194)
```

```

                                10          20          30
AAD-12                          VAISNVKADGTVRQHSPAEWDDMMKVIVGN
                                .: .:.: . .: :. :. : . . .
gi+AHw-129 LGLNKFADITPQEFSSKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQ
          90          100          110          120          130          140
```

```

                                40          50          60          70          80
AAD-12 MAWHADSTY-MPVMAQGVFSAEVPVAVGGRTCFADMRAAYDALDEATRAL
          . . . . . : :. .: . . . . : . . . . . : . . . .
gi+AHw-129 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
          150          160          170          180          190          200
```

```
gi+AHw-129 WVLEHGGIATDDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
          210          220          230          240          250          260
```

```
80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:49 2010 done: Fri Feb 5 12:55:49 2010
Total Scan time: 0.090 Total Display time: 0.010
```

```
Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
```

```
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448
```

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 77 - 156 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 4 library sequences
      24      1      0:+AD0-
      26      0      0:
      28      1      0:+AD0-
```



```

112      1      0:+AD0-      +ACoAPQ-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.79730.0033+ADs- mu+AD0- 1.8060
0.170
mean+AF8-var+AD0-37.9943 9.688, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
Lambda+AD0- 0.208073
Kolmogorov-Smirnov statistic: 0.1025 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 25.4 0.26
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 24.8 0.4
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 57 22.4 2.1
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 58 22.6 2.3
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (
419) 64 24.0 2.9
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II ( 196)
59 22.8 3.3
gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOb RecName: Full+AD0-
( 514) 64 24.0 3.7
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.2 3.9
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 21.9 4.8
gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosu (
386) 61 23.2 4.9
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
( 158) 55 21.6 5.8
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379) 60 22.9 5.9
gi+AHw-21510+AHw-emb+AHw-CAA31575.1+AHw- unnamed protein product +AFs- (
386) 60 22.9 6
gi+AHw-21514+AHw-emb+AHw-CAA27588.1+AHw- patatin +AFs-Solanum tuberosu (
386) 60 22.9 6
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 54 21.3 6.4

```


gi+AHw-126 AAPVEFTVEKGSDEKLNLSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
10 20 30 40 50

40 50 60 70 80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
:. .: .: .: : : : : : :

gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMKNVFDVVPADFKVGTTYKPE
60 70 80 90

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (7-65:55-107)

AAD-12 AISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
:. .: .: .: : : : : : : : :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
30 40 50 60 70 80

40 50 60 70 80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
:. .: .: .: : : : : : : : :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVVP EKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-Polle (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (7-65:55-107)

AAD-12 AISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
:. .: .: .: : : : : : : : :
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
30 40 50 60 70 80

40 50 60 70 80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
:. .: .: .: : : : : : : : :
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDVVP EKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (7-65:55-107)

AAD-12 AISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
:. .: .: .: : : : : : : : :

gi+AHw-400 WCVPKVFTFTVEKGSNEKHLAVLVKYEKDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
 30 40 50 60 70 80

40 50 60 70 80
 AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR_{LV}
 :. :: :. . . : .. : :.

gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
 90 100 110 120

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (7-65:55-107)

10 20 30
 AAD-12 AISNVKADGTVRQHS_{PAEWDDMMKVIVGNMAWHADS}
 :. :. :. :. :. :. :. :.
 gi+AHw-400 WCVPKVFTFTVEKGSNEKHLAVLVKYEKDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
 30 40 50 60 70 80

40 50 60 70 80
 AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR_{LV}
 :. :: :. . . : .. : :.

gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
 90 100 110 120

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)

initn: 39 init1: 39 opt: 64 Z-score: 94.1 bits: 24.0 E(): 2.9
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (6-64:89-149)

10 20 30
 AAD-12 AISNVKADGT-VRQHS_{PAEWDDMMKVIVGNMAWHA}
 :. :. :. :. :. :. :. :.
 gi+AHw-114 ASAVLVVPANKKFFVNNL_{VFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT}
 60 70 80 90 100 110

40 50 60 70 80
 AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR_{LV}
 :. :. :. :. :. :. :. :.

gi+AHw-114 DFNLMGTGVIDGQ_{QWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE}
 120 130 140 150 160 170

gi+AHw-114 FHLVFGEGEVKIQGLKIKAPR_{DSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN}
 180 190 200 210 220 230

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196 aa)

initn: 36 init1: 36 opt: 59 Z-score: 93.1 bits: 22.8 E(): 3.3
 Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
 in 62 aa overlap (7-68:31-86)

```

                                10      20      30
AAD-12      AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                :.  ....  ::  .  :  ..  ...  :
gi+AHw-109  EAPVTFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12      TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
                                :.  .:  .:  .:  .:  :  ::  ....  :
gi+AHw-109  DK-PL--KGP-FNFRFVSEKMRNVFVDVVPADFKVGTTYKPEEAAAASASRRRSSEVFQF
                                60      70      80      90      100     110

```

```

gi+AHw-109  LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEI IYKIFKMMFQ
                                120     130     140     150     160     170

```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0-Poly (514 aa)
 initn: 39 init1: 39 opt: 64 Z-score: 92.2 bits: 24.0 E(): 3.7
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (6-64:119-179)

```

                                10      20      30
AAD-12      AISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                ::::  :  :  ::::  .  .  .  .  :  .
gi+AHw-476  ASAVLLVPANKKFFVNNLVFRGPCPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                90      100     110     120     130     140

```

```

                                40      50      60      70      80
AAD-12      DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
                                :  .  :  .  :  .  :  .:  :  :  :  :  :
gi+AHw-476  DFNLMGTGVIDGQQQWWAGQCKVNVGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                150     160     170     180     190     200

```

```

gi+AHw-476  FHLVFGECEGVKIQGLKIKAPRDS PNTDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
                                210     220     230     240     250     260

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 init1: 55 opt: 57 Z-score: 91.8 bits: 22.2 E(): 3.9
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (30-58:23-50)

```

                                10      20      30      40      50      60
AAD-12      AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRT
                                ..  .:  :  .:  .:  .:  ::::  .  :  :
gi+AHw-444      MGVFTYADESTSVIPPPRLFALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVG
                                10      20      30      40      50

```

```

                                70      80
AAD-12      CFADMRAAYDALDEATRALV
gi+AHw-444  TIKKISFGEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGG
                                60      70      80      90      100     110

```


gi+AHw-215 ATRLAQDDPAFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAEAAKWGPLRWMLAIQQMT
 240 250 260 270 280 290

40 50 60 70 80
 AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
 .: :.:. . .:..: .: . . .:..:.

gi+AHw-215 NAASSYMTDYIISTVVFQARHSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLK
 300 310 320 330 340 350

gi+AHw-215 KPVS KDSPET YEEALKRFAKLLSDRKKLRANKASH
 360 370 380

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 53 initl: 53 opt: 54 Z-score: 87.9 bits: 21.3 E(): 6.4
 Smith-Waterman score: 54+ADs- 26.667+ACU- identity (57.778+ACU- similar)
 in 45 aa overlap (36-80:5-48)

10 20 30 40 50 60
 AAD-12 KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
 .: :.:. . .:..: .: . . .:..:.
 gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGM
 10 20 30

70 80
 AAD-12 RAA YDALDEATRALV
 . : : . :
 gi+AHw-189 GLPSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCR CRVRYFI
 40 50 60 70 80 90

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
 Lolium per (301 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 87.5 bits: 22.3 E(): 6.7
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (31-80:23-71)

10 20 30 40 50 60
 AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRT
 .: :.:. . .:..: .: . . .:..:.
 gi+AHw-663 MAVQKYTVLALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGK
 10 20 30 40 50

70 80
 AAD-12 CFADMRAAYDALDEATRALV
 .: . . .:..: .: :
 gi+AHw-663 ATTDEQKLLLEDVNAGFKAAVAADANAPPADKFKIFEAAFS ESCKGLLATSDAKAPGLILK
 60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 52 initl: 52 opt: 54 Z-score: 86.9 bits: 21.3 E(): 7.2
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (30-58:23-50)

```

      10      20      30      40      50      60
AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ GAVFSAEVVPAVGGRT
      . . . . .
gi+AHw-444      MGVTYSDESTSVIPPPRLFKALVLEAD-TLIPK IAPQSVKTA EIVEGDGGVG
      10      20      30      40      50

```

```

      70      80
AAD-12 CFADMRAAYDALDEATRALV
      . . . . .
gi+AHw-444 TIKKISFGEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGG
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-158517845+AHw-sp+AHw-P15476.2+AHw-PATB1+AF8-SOLTU RecName: Full+AD0-Pat (386 aa)
 initn: 59 initl: 59 opt: 59 Z-score: 86.8 bits: 22.6 E(): 7.4
 Smith-Waterman score: 59+ADs- 21.053+ACU- identity (53.947+ACU- similar)
 in 76 aa overlap (3-78:262-337)

```

      10      20      30
AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
      . . . . .
gi+AHw-158 ATRLAQEDPAFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAE EAAKWGPLRWMLAIQQLT
      240      250      260      270      280      290

```

```

      40      50      60      70      80
AAD-12 HADSTYMPVMAQ GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
      . . . . .
gi+AHw-158 NAASSYMTDYIISTV FQARHSQNNYL RVQENALTGTTTEMDDASEANMELLVQVGETLLK
      300      310      320      330      340      350

```

```

gi+AHw-158 KPVS KDSPET YEEALKRF AKLLSNRKKLRANKASY
      360      370      380

```

+AD4APg-gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor +AFs-Tr (279 aa)
 initn: 57 initl: 57 opt: 57 Z-score: 86.6 bits: 22.0 E(): 7.6
 Smith-Waterman score: 57+ADs- 18.182+ACU- identity (58.182+ACU- similar)
 in 55 aa overlap (5-59:225-279)

```

      10      20      30
AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA
      . . . . .
gi+AHw-106 IMQQEQQEQRQGVQILVPLSQQQVQGGLVQGGGI IQPQQPAQLE VIRSSVLQTLATMC
      200      210      220      230      240      250

```

```

      40      50      60      70      80
AAD-12 DSTYMPVMAQ GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
      . . . . .
gi+AHw-106 NVYVPPYCSTIRAPFASIVAGIGGQ
      260      270

```

80 residues in 1 query sequences


```

60 50 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62 44 40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQ-
64 67 32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
66 45 25:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
68 20 20:+AD0APQA9AD0AKg-
70 41 16:+AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
72 17 12:+AD0APQAqAD0APQ-
74 20 10:+AD0APQAqAD0APQ-
76 17 7:+AD0AKgA9AD0APQ-
78 7 6:+AD0AKg-
80 4 4:+ACo-
82 13 3:+ACoAPQA9AD0-
84 7 3:+ACoAPQ-
86 4 2:+ACo-
88 5 2:+ACoAPQ- inset +AD0- represents 1 library
sequences
90 2 1:+ACo-
92 3 1:+ACo- :+ACoAPQA9-
94 1 1:+ACo- :+ACo-
96 5 1:+ACoAPQ- :+ACoAPQA9AD0APQ-
98 0 0: +ACo-
100 0 0: +ACo-
102 0 0: +ACo-
104 0 0: +ACo-
106 0 0: +ACo-
108 1 0:+AD0- +ACoAPQ-
110 0 0: +ACo-
112 1 0:+AD0- +ACoAPQ-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.86300.00331+ADs- mu+AD0- 1.4079
0.171
mean+AF8-var+AD0-38.2664 9.716, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
Lambda+AD0- 0.207332
Kolmogorov-Smirnov statistic: 0.1018 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 25.4 0.27
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 24.8 0.4
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 57 22.4 2.1
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 58 22.6 2.3

```

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 58 22.6 2.3
 gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 58 22.6 2.3
 gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (419)
 64 24.0 2.9
 gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
 59 22.7 3.3
 gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOb RecName: Full+AD0- (514)
 64 23.9 3.8
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 22.2 3.9
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
 56 21.9 4.8
 gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosu (386)
 61 23.1 5
 gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-G1 (158)
 55 21.6 5.8
 gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0- (379)
 60 22.8 6
 gi+AHw-21510+AHw-emb+AHw-CAA31575.1+AHw- unnamed protein product +AFs- (386)
 60 22.8 6.1
 gi+AHw-21514+AHw-emb+AHw-CAA27588.1+AHw- patatin +AFs-Solanum tuberosu (386)
 60 22.8 6.1
 gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144)
 54 21.3 6.4
 gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
 58 22.3 6.8
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.3 7.3
 gi+AHw-158517845+AHw-sp+AHw-P15476.2+AHw-PATB1+AF8-SOLTU RecName: Full (386)
 59 22.5 7.5
 gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor (279)
 57 22.0 7.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 112.7 bits: 25.4 E(): 0.27
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (6-35:30-56)

			10	20	30
AAD-12			ISNVKADGTVRQHS	PAEWDDMMKVIVGNMA	WHADST
			::: : : ::: ... :
gi+AHw-126	TKVDLTVEKGS	DAKTLVLN	IKYTRPGD	TLAEVELRQHG	SEEWEPMTK--KGNL-WEVKSA
	10	20	30	40	50
	40	50	60	70	80
AAD-12	YMPVMAQGA	VFSAEV	VPVAVGG	RTCFADMRA	AYDALDEATRALVH
	60	70	80	90	
gi+AHw-126	KPLTGPMN	FRFLSK	GGMKNV	FDEVIPTA	FTVGKTYTPEYN
	60	70	80	90	

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)
 initn: 39 init1: 39 opt: 64 Z-score: 94.0 bits: 24.0 E(): 2.9
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (5-63:89-149)

```

                                10      20      30
AAD-12                        ISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                :.:.:. : : :.:.:. : :.:.:. :
gi+AHw-114 ASAVLVVPANKKFFVNNLVFRGPCPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                60      70      80      90      100     110
  
```

```

                                40      50      60      70      80
AAD-12 DSTYMP--VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
                :. : . :. : . : :. :. :. :
gi+AHw-114 DFNLMGTGVIDGQGGQWWAGQCKVNVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                120     130     140     150     160     170
  
```

```

gi+AHw-114 FHLVFGEGVVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
                180     190     200     210     220     230
  
```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196 aa)
 initn: 36 init1: 36 opt: 59 Z-score: 93.1 bits: 22.7 E(): 3.3
 Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
 in 62 aa overlap (6-67:31-86)

```

                                10      20      30
AAD-12                        ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                :. :. :. :. :. :. :. :. :
gi+AHw-109 EAPVTFTEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                10      20      30      40      50
  
```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
                :. :. :. :. :. :. :. :. :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGTTYKPEEAAAASARRRSSEVFQF
                60      70      80      90      100     110
  
```

```

gi+AHw-109 LILSCQGRIVNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIIYKIFKMMFQ
                120     130     140     150     160     170
  
```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHA OB RecName: Full+AD0-Poly (514 aa)
 initn: 39 init1: 39 opt: 64 Z-score: 92.0 bits: 23.9 E(): 3.8
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (5-63:119-179)

```

                                10      20      30
AAD-12                        ISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                :.:.:. : : :.:.:. : :.:.:. :
gi+AHw-476 ASAVLLVPANKKFFVNNLVFRGPCPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                90      100     110     120     130     140
  
```

```

                40          50          60          70          80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
      : . : . . : . : . : . : . : . : . : . : . : . : . :
gi+AHw-476 DFNLMGTGVIDGQGQWWAGQCKVVGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
      150          160          170          180          190          200

```

```

gi+AHw-476 FHLVFGECEGVKIQGLKIKAPRDSPTNDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
      210          220          230          240          250          260

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)

initn: 55 initl: 55 opt: 57 Z-score: 91.8 bits: 22.2 E(): 3.9
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (29-57:23-50)

```

                10          20          30          40          50          60
AAD-12 ISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTC
      .. . : : . : . : . : . : . : . : . :
gi+AHw-444      MGVFTYADESTSVIPPPRLFALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGT
      10          20          30          40          50

```

```

                70          80
AAD-12 FADMRAAYDALDEATRALVH

```

```

gi+AHw-444 IKKISFGEESHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLIVASADGGS
      60          70          80          90          100          110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)

initn: 55 initl: 55 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (33-57:27-50)

```

                10          20          30          40          50          60
AAD-12 NVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCF
      : . : . : . : . : . : . : . : . : . : . :
gi+AHw-165      MGVFTHENEITSAIPPGRLFKAFLVDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIK
      10          20          30          40          50

```

```

                70          80
AAD-12 DMRAAYDALDEATRALVH

```

```

gi+AHw-165 KITFGEQSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSIL
      60          70          80          90          100          110

```

+AD4APg-gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosum+AF0- (386 aa)

initn: 61 initl: 61 opt: 61 Z-score: 89.9 bits: 23.1 E(): 5
 Smith-Waterman score: 61+ADs- 21.053+ACU- identity (53.947+ACU- similar)
 in 76 aa overlap (2-77:262-337)

```

                10          20          30
AAD-12      ISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
      . : . : . : . : . : . : . : . : . : . :

```


gi+AHw-189 GLPSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFI
40 50 60 70 80 90

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)

initn: 49 initl: 49 opt: 58 Z-score: 87.4 bits: 22.3 E(): 6.8
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (30-79:23-71)

10 20 30 40 50 60
AAD-12 ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTC
.. :. : :. : . ::
gi+AHw-663 MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKA
10 20 30 40 50

70 80
AAD-12 FADMRAAYDALDEATRALVH
.: : :
gi+AHw-663 TTDEQKLLLEDVNAGFKAAVAADANAPPADKFKIFEAAFSSECKGLLATSDAKAPGLILKL
60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 86.9 bits: 21.3 E(): 7.3
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (29-57:23-50)

10 20 30 40 50 60
AAD-12 ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTC
.. :. : :. : . ::
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTAEIVEGDDGGVGT
10 20 30 40 50

70 80
AAD-12 FADMRAAYDALDEATRALVH
gi+AHw-444 IKKISFGEESHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGS
60 70 80 90 100 110

+AD4APg-gi+AHw-158517845+AHw-sp+AHw-P15476.2+AHw-PATB1+AF8-SOLTU RecName:
Full+AD0-Pat (386 aa)

initn: 59 initl: 59 opt: 59 Z-score: 86.7 bits: 22.5 E(): 7.5
Smith-Waterman score: 59+ADs- 21.053+ACU- identity (53.947+ACU- similar)
in 76 aa overlap (2-77:262-337)

10 20 30
AAD-12 ISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
.: . : : . :. :
gi+AHw-158 ATRLAQEDPAFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAEAAKWGPLRWMLAIQQLT
240 250 260 270 280 290

40 50 60 70 80
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
.: :. : . . :. :

gi+AHw-158 NAASSYMTDYYIISTVFQARHSQNNYLVRVQENALTGTTTEMDDASEANMELLVQVGETLLK
300 310 320 330 340 350

gi+AHw-158 KPVS KDSPET YEEALKRFAKLLSNRKKLRANKASY
360 370 380

+AD4APg-gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor
+AFs-Tr (279 aa)
initn: 57 initl: 57 opt: 57 Z-score: 86.5 bits: 22.0 E(): 7.7
Smith-Waterman score: 57+ADs- 18.182+ACU- identity (58.182+ACU- similar)
in 55 aa overlap (4-58:225-279)

AAD-12 ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA
:
gi+AHw-106 IMQQEQQEQRQGVQILVPLSQQQVGGTLVQGGQGI IQPQQPAQLE VIRSSVLQTLATMC
200 210 220 230 240 250

AAD-12 DSTYMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVH
. : . . : . :
gi+AHw-106 NVYVPPYCSTIRAPFASIVAGIGGQ
260 270

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:50 2010 done: Fri Feb 5 12:55:50 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 79 - 158 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

opt E()
+ADw- 20 2 0:+AD0-
22 0 0: one +AD0- represents 4 library sequences
24 1 0:+AD0-
26 0 0:
28 1 0:+AD0-
30 6 2:+ACoAPQ-

```

32      6      8:+AD0AKg-
34     12     21:+AD0APQA9- +ACo-
36     43     44:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
38     74     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
40     69     101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42     129    123:+AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqA
D0APQ-
44     170
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0-
46     202
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
48     124
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0- +ACo-
50     98
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0-      +ACo-
52     81
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
54     60     91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
56     57     76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
58     54     62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
60     71     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
62     50     40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
64     19     32:+AD0APQA9AD0APQ- +ACo-
66     37     25:+AD0APQA9AD0APQA9ACoAPQA9AD0-
68     26     20:+AD0APQA9AD0AKgA9AD0-
70     22     16:+AD0APQA9ACoAPQA9-
72     9      12:+AD0APQAq-
74     4      10:+AD0- +ACo-
76     14     7:+AD0AKgA9AD0-
78     7      6:+AD0AKg-
80     7      4:+ACoAPQ-
82     3      3:+ACo-
84     3      3:+ACo-
86     2      2:+ACo-
88     6      2:+ACoAPQ-      inset +AD0- represents 1 library
sequences
90     0      1:+ACo-
92     0      1:+ACo-      :+ACo-
94     0      1:+ACo-      :+ACo-
96     0      1:+ACo-      :+ACo-
98     0      0:      +ACo-
100    1      0:+AD0-      +ACoAPQ-
102    1      0:+AD0-      +ACoAPQ-
104    0      0:      +ACo-
106    0      0:      +ACo-
108    0      0:      +ACo-
110    0      0:      +ACo-
112    0      0:      +ACo-

```


AAAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQ

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 100.7 bits: 23.1 E(): 1.2
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (5-35:30-57)

AAAD-12 SNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADST
::: . : ::. :. :.
 gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEW EPLTKK--GNL-WEVKSS
 10 20 30 40 50

AAAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQ

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
 60 70 80 90

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 89.1 bits: 21.0 E(): 5.5
 Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
 in 62 aa overlap (5-66:31-86)

AAAD-12 SNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
::: . : ::. :. :.
 gi+AHw-126 AAPVEFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
 10 20 30 40 50

AAAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQ

gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTTYKPE
 60 70 80 90

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 59 Z-score: 88.6 bits: 21.5 E(): 5.8
 Smith-Waterman score: 59+ADs- 27.660+ACU- identity (57.447+ACU- similar)
 in 47 aa overlap (34-80:5-50)

AAAD-12 KADGTVRQHS PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
 .. :.. ... :. . :. :. :.
 gi+AHw-189 MASKSSITPLLLAAV LASVF AAAAATGQYCYAGM
 10 20 30

70 80

AAD-12 RAAVDALDEATRVLVHQ

. : . : . : . :

gi+AHw-189 GLPSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFI
 40 50 60 70 80 90

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (5-63:55-107)

AAD-12 SNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
 :. :: : : : .: ::
 gi+AHw-117 WCVPKVTFTEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
 30 40 50 60 70 80

AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQ
 :. :: . . . : . : . : .
 gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
 90 100 110 120

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
 II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (5-63:55-107)

AAD-12 SNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
 :. :: : : : .: ::
 gi+AHw-400 WCVPKVTFTEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
 30 40 50 60 70 80

AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQ
 :. :: . . . : . : . : .
 gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
 90 100 110 120

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
 II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (5-63:55-107)

AAD-12 SNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
 :. :: : : : .: ::
 gi+AHw-400 WCVPKVTFTEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
 30 40 50 60 70 80

40 50 60 70 80


```

                10          20          30          40          50
      40          50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ
      :.  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGTITYKPEEAAAASASRRRSSEVFQF
      60          70          80          90          100          110

gi+AHw-109 LILSCQGRIVNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIYYKIFKMMFQ
      120          130          140          150          160          170

```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOb RecName:
Full+AD0-Poly (514 aa)
initn: 39 initl: 39 opt: 64 Z-score: 85.1 bits: 22.6 E(): 9.2
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (4-62:119-179)

```

                                10          20          30
AAD-12                                SNVKADGT-VRQHSPAEWDDMMKVIVGNMAWAH
                                :.:.:.:  :  :  :.:.:.:  .  .  .  .:  .
gi+AHw-476 ASAVLLVPANKKFFVNNLVFRGPCPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
      90          100          110          120          130          140

```

```

                40          50          60          70          80
AAD-12  DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ
      :  .  :  .  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-476 DFNLMGTGVIDGQQQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
      150          160          170          180          190          200

gi+AHw-476 FHLVFGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
      210          220          230          240          250          260

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 initl: 55 opt: 57 Z-score: 84.9 bits: 20.9 E(): 9.4
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (28-56:23-50)

```

                10          20          30          40          50          60
AAD-12  SNVKADGTVRQHSPAEWDDMMKVIVGNMAWAHADSTYMPVMAQGAVFSAEVVPAVGGRTCF
                                ..  .:  :  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-444  MGVFTYADESTSVIPPPRLFALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTI
                                10          20          30          40          50

```

```

                70          80
AAD-12  ADMRAAYDALDEATRALVHQ

gi+AHw-444 KKISFGEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSI
      60          70          80          90          100          110

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences


```

64    15    32:+AD0APQA9AD0-   +ACo-
66    39    25:+AD0APQA9AD0APQA9ACoAPQA9AD0-
68    25    20:+AD0APQA9AD0AKgA9AD0-
70    23    16:+AD0APQA9ACoAPQA9-
72    10    12:+AD0APQAq-
74     3    10:+AD0- +ACo-
76    14    7:+AD0AKgA9AD0-
78    10    6:+AD0AKgA9-
80     4    4:+ACo-
82     3    3:+ACo-
84     3    3:+ACo-
86     2    2:+ACo-
88     5    2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90     1    1:+ACo-
92     0    1:+ACo-          :+ACo-
94     0    1:+ACo-          :+ACo-
96     0    1:+ACo-          :+ACo-
98     0    0:              +ACo-
100    1    0:+AD0-          +ACoAPQ-
102    1    0:+AD0-          +ACoAPQ-
104    0    0:              +ACo-
106    0    0:              +ACo-
108    0    0:              +ACo-
110    0    0:              +ACo-
112    0    0:              +ACo-
114    0    0:              +ACo-
116    0    0:              +ACo-
118    0    0:              +ACo-
+AD4-120    0    0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.83440.0033+ADs- mu+AD0- 3.1543
0.170
mean+AF8-var+AD0-48.265516.785, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.184610
Kolmogorov-Smirnov statistic: 0.0479 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.7    0.87
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 23.1    1.2
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)  60 21.7    4.8
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97)  57 21.0    5.5
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 58 21.2    5.8
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 21.2    5.8

```

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 58 21.2 5.8
 gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 58 21.2 5.8
 gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (419)
 64 22.7 7.3
 gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
 59 21.4 8.1
 gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOb RecName: Full+AD0- (514)
 64 22.7 9.1
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 20.9 9.4

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 103.5 bits: 23.7 E(): 0.87
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (4-33:30-56)

```

                                10      20      30
AAD-12                        NVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
                                ..  ....  ...  :  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQR

```

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                                60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 65 Z-score: 100.7 bits: 23.1 E(): 1.2
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (4-34:30-57)

```

                                10      20      30
AAD-12                        NVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
                                ..  ....  ...  :  :  ...  ...  ..
gi+AHw-144 VKVTFKVEKGSDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQR

```

```

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                                60      70      80      90

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
 initn: 55 init1: 55 opt: 60 Z-score: 90.1 bits: 21.7 E(): 4.8
 Smith-Waterman score: 60+ADs- 27.083+ACU- identity (58.333+ACU- similar)
 in 48 aa overlap (33-80:5-51)

```

                10         20         30         40         50         60
AAD-12  KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
                ..  ...  ...  ..  ..  ..  ..  ..  ..
gi+AHw-189  MASKSSITPLLLAAVLASVF AAAAATGQYCYAGM
                10         20         30

```

```

                70         80
AAD-12  RAAVDALDEATR ALVHQR
                .  :  :  :  :  :  :
gi+AHw-189  GLPSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCR CRVRYFI
                40         50         60         70         80         90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 initl: 36 opt: 57 Z-score: 89.1 bits: 21.0 E(): 5.5
Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (4-65:31-86)

```

                                10         20         30
AAD-12  NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  :  ...  :
gi+AHw-126  AAPVEFTVEKGSDEK NLALS IKYNKEGDSMAEVELKEHGSNEWLAL KKN--GDGVWEIKS
                10         20         30         40         50

```

```

                40         50         60         70         80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQR
                ..  .:  :  .  :  :  :  :  :  :
gi+AHw-126  DK-PL--KGP-FNFRFVSEKGM RNVFDDVVPADFKVGT TYKPE
                60         70         80         90

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 46 initl: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (4-62:55-107)

```

                                10         20         30
AAD-12  NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-117  WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                30         40         50         60         70         80

```

```

                40         50         60         70         80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQR
                ..  ::  :  .  .  :  :  :  :
gi+AHw-117  EE-PL--QGP-FNFRFLTEKGMKNV FDDVVPEKYTIGAT YAPEE
                90         100        110        120

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II)
(122 aa)
initn: 46 initl: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (4-62:55-107)

```

                                10      20      30
AAD-12                          NVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQR
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 init1: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (4-62:55-107)

```

                                10      20      30
AAD-12                          NVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQR
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 init1: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (4-62:55-107)

```

                                10      20      30
AAD-12                          NVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQR
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)
 initn: 39 init1: 39 opt: 64 Z-score: 86.9 bits: 22.7 E(): 7.3
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (3-61:89-149)

```

                                10      20      30
AAD-12                          NVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                : : : : : : : : : : : :
gi+AHw-114 ASAVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                60      70      80      90      100     110

```

```

                                40      50      60      70      80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQR
                                : . : . : : : : : : : :
gi+AHw-114 DFNLMGTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                120     130     140     150     160     170

```

```

gi+AHw-114 FHLVFGEGEVKIQGLKIKAPRDS PNTDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
                                180     190     200     210     220     230

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
(196 aa)
initn: 36 init1: 36 opt: 59 Z-score: 86.1 bits: 21.4 E(): 8.1
Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
in 62 aa overlap (4-65:31-86)

```

                                10      20      30
AAD-12                          NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                : : : : : : : : : : :
gi+AHw-109 EAPVTFTEKGSDEKNLALS I KYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQR
                                : . : : : : : : : :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGM RNVFVDVVPADFKVGT TYKPEEAAA SASRRRSSEVFQF
                                60      70      80      90      100     110

```

```

gi+AHw-109 LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIIYKIFKMMFQ
                                120     130     140     150     160     170

```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHA OB RecName:
Full+AD0-Poly (514 aa)
initn: 39 init1: 39 opt: 64 Z-score: 85.2 bits: 22.7 E(): 9.1
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (3-61:119-179)

```

                                10      20      30
AAD-12                          NVKADGTVRQHSPA EWDDMMKVIVGNMAWHA
                                : : : : : : : : : : :
gi+AHw-476 ASAVLLVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                90      100     110     120     130     140

```

```

                                40      50      60      70      80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQR
                                : . : . : : : : : : :
gi+AHw-476 DFNLMGTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                150     160     170     180     190     200

```

gi+AHw-476 FHLVFGEGEVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
 210 220 230 240 250 260

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 55 init1: 55 opt: 57 Z-score: 84.9 bits: 20.9 E(): 9.4
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (27-55:23-50)

10 20 30 40 50 60
 AAD-12 NVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFA
 .. .:: : .: .: .: :::: . ::
 gi+AHw-444 MGVFTYADESTSVIPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTIK
 10 20 30 40 50

70 80
 AAD-12 DMRAAYDALDEATRALVHQR

gi+AHw-444 KISFEGEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSII
 60 70 80 90 100 110

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:50 2010 done: Fri Feb 5 12:55:50 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 81 - 160 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
	22	0	0: one +AD0- represents 4 library sequences
	24	1	0:+AD0-
	26	0	0:
	28	1	0:+AD0-
	30	8	2:+ACo-+AD0-
	32	6	8:+AD0AKg-
	34	18	21:+AD0APQA9AD0APQAq-

118 0 0: +ACo-
 +AD4-120 0 0: +ACo-
 331323 residues in 1471 sequences
 Expectation+AF8-n fit: rho(ln(x))+AD0- 5.92730.00322+ADs- mu+AD0- 2.6387
 0.166
 mean+AF8-var+AD0-48.786316.943, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
 Lambda+AD0- 0.183622
 Kolmogorov-Smirnov statistic: 0.0506 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
 Scan time: 0.090

The best scores are: opt bits E(1471)
 gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
 (97) 67 23.6 0.88
 gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
 (96) 65 23.1 1.3
 gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144)
 62 22.2 3.4
 gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
 (97) 57 21.0 5.5
 gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
 (122) 58 21.2 5.9
 gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
 58 21.2 5.9
 gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 58 21.2 5.9
 gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 58 21.2 5.9
 gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (419)
 64 22.6 7.5
 gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
 59 21.4 8.3
 gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145)
 57 20.9 8.6
 gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0-
 (514) 64 22.6 9.4
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 20.9 9.6

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 67 Z-score: 103.3 bits: 23.6 E(): 0.88
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (3-32:30-56)

			10	20	30	
AAD-12			VKADGTVRQHSPA	EWDDMMKVIVGNMA	WHADST	
		 : :	... : :
gi+AHw-126	TKVDLTVEKGS	DAKTLVLN	IKYTRPGD	TLAEVELRQH	GSEEWEPMTK--	KGNL-WEVKSA
	10	20	30	40	50	
	40	50	60	70	80	

AAAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRS

```

      ..  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMARNVFDVVPADFKVGTTYKPE
      60          70          80          90

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 88.5 bits: 21.2 E(): 5.9
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (3-61:55-107)

```

      10          20          30
AAAD-12          VKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
      ..  .:  .:  .:  .:  .:  .:  .:
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
      30          40          50          60          70          80

```

```

      40          50          60          70          80
AAAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRS
      ..  .:  .:  .:  .:  .:  .:  .:
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDVVPPEKYTIGATYAPEE
      90          100          110          120

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 88.5 bits: 21.2 E(): 5.9
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (3-61:55-107)

```

      10          20          30
AAAD-12          VKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
      ..  .:  .:  .:  .:  .:  .:  .:
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
      30          40          50          60          70          80

```

```

      40          50          60          70          80
AAAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRS
      ..  .:  .:  .:  .:  .:  .:  .:
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVVPPEKYTIGATYAPEE
      90          100          110          120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 88.5 bits: 21.2 E(): 5.9
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (3-61:55-107)

```

      10          20          30
AAAD-12          VKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
      ..  .:  .:  .:  .:  .:  .:  .:
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
      30          40          50          60          70          80

```

```

      40          50          60          70          80

```

AAAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAlVHQRS

:. :: :. . . : .. : ..

gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 88.5 bits: 21.2 E(): 5.9
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (3-61:55-107)

AAAD-12 VKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
:. :: : : : . : :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
30 40 50 60 70 80

AAAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAlVHQRS
:. :: :. . . : .. : ..
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)

initn: 39 init1: 39 opt: 64 Z-score: 86.6 bits: 22.6 E(): 7.5
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (2-60:89-149)

AAAD-12 VKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
:. : : :
gi+AHw-114 ASAVLVVPANKKFFVNNLVRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
60 70 80 90 100 110

AAAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAlVHQRS
: . : . . : : . : . : : : :
gi+AHw-114 DFNLMGTGVIDGQQQWAGQCKV VNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
120 130 140 150 160 170

gi+AHw-114 FHLVFGECEGVKIQGLKIKAPRDS PNTDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
180 190 200 210 220 230

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196 aa)

initn: 36 init1: 36 opt: 59 Z-score: 85.9 bits: 21.4 E(): 8.3
Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
in 62 aa overlap (3-64:31-86)

AAAD-12 VKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
:. :: : : : . : : :
gi+AHw-109 EAPVTFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS

```

                10          20          30          40          50
          40          50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRLVHQRS
      . . . . . : : : : :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGMRNVFDVVPADFKVGTTYKPEEAAASASRRRSSEVFQF
          60          70          80          90          100          110

```

```

gi+AHw-109 LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIIYKIFKMMFQ
          120          130          140          150          160          170

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 85.6 bits: 20.9 E(): 8.6
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (32-80:5-52)

```

                10          20          30          40          50          60
AAD-12  KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
      . . . . . : . . . . . : : : :
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGM
          10          20          30

```

```

          70          80
AAD-12  RAAYDALDEATRLVHQRS
      . : : : : : : :
gi+AHw-439 GLPSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYF
          40          50          60          70          80          90

```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHA_OB RecName: Full+AD0-Poly (514 aa)
 initn: 39 initl: 39 opt: 64 Z-score: 84.9 bits: 22.6 E(): 9.4
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (2-60:119-179)

```

                                10          20          30
AAD-12                                VKADGT-VRQHSPAEWDDMMKVIVGNMAWHA
      . : : : : : : : : : : :
gi+AHw-476 ASAVLLVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
          90          100          110          120          130          140

```

```

          40          50          60          70          80
AAD-12  DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRLVHQRS
      . . : . . : : : : : :
gi+AHw-476 DFNLMGTGVIDGQGQWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
          150          160          170          180          190          200

```

```

gi+AHw-476 FHLVFGECEGVKIQGLKIKAPRDSPNTDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
          210          220          230          240          250          260

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 84.8 bits: 20.9 E(): 9.6

Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (26-54:23-50)

```

                10         20         30         40         50         60
AAD-12 VKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFAD
                .. .:: : .: .: .: ::::: . ::
gi+AHw-444   MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTIKK
                10         20         30         40         50

                70         80
AAD-12 MRAAYDALDEATRALLVHQRS

gi+AHw-444 ISFGEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIK
                60         70         80         90         100        110

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:51 2010 done: Fri Feb 5 12:55:51 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 82 - 161 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 4 library sequences
      24      1      0:+AD0-
      26      0      0:
      28      1      0:+AD0-
      30      4      2:+ACo-
      32      6      8:+AD0AKg-
      34     10     21:+AD0APQA9- +ACo-
      36     31     44:+AD0APQA9AD0APQA9AD0APQ- +ACo-
      38     32     72:+AD0APQA9AD0APQA9AD0APQ- +ACo-
      40     72    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      42     76    123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-

```


Lambda+AD0- 0.207433

Kolmogorov-Smirnov statistic: 0.1025 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 25.4 0.26

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 24.8 0.39

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 23.8 1.2

gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
(97) 57 22.4 2.1

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
(122) 58 22.6 2.3

gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
58 22.6 2.3

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
58 22.6 2.3

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
58 22.6 2.3

gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (
419) 64 24.0 2.9

gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
59 22.8 3.2

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145)
57 22.3 3.4

gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0-
(514) 64 24.0 3.7

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
57 22.2 3.8

gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 21.9 4.7

gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
(158) 55 21.6 5.7

gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
(379) 60 22.9 5.8

gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.3 6.7

gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
54 21.3 7.2

gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.1 7.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 67 Z-score: 112.8 bits: 25.4 E(): 0.26

Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (2-31:30-56)

```

AAD-12                                KADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                ..  ....  ...  :  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGS DAKTLV LNIKYTRPGD TLA EVELRQH GSEEWEPMTK--KGNL-WEVKSA
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 YMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSA

```

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTV GKTYTPEYN
                                60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 109.6 bits: 24.8 E(): 0.39
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (2-32:30-57)

```

                                10      20      30
AAD-12                                KADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                ..  ....  ...  .  :  ...  ...  ..
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGD TLA EVELRQH GSEEWEP LTKK--GNL-WEVKSS
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 YMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSA

```

```

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGT TYTPEE
                                60      70      80      90

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 100.9 bits: 23.8 E(): 1.2
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (31-79:5-52)

```

                                10      20      30      40      50      60
AAD-12 KADGTVRQHSPA EWDDMMKVIVGNMAWHADST YMPVMAQGAVFSAE VVPAVGGRTCFADM
                                ..  ...  ...  :  .  .  :  .  :  :
gi+AHw-189                                MASKSSITPLLLAAV LASVFAAAAATGQYCYAGM
                                10      20      30

```

```

                                70      80
AAD-12 RAA YDALDEATRALVHQRSA
                                .  :  :  :  :  :  :
gi+AHw-189 GLPSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCR CRVRYFI
                                40      50      60      70      80      90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 96.6 bits: 22.4 E(): 2.1
 Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
 in 62 aa overlap (2-63:31-86)

```

AAD-12                                KADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-126 AAPVEFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSA
                                ..  ::  :.  .  :  :  :  :  :
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGM RNVFDDVVPADFKVGT TYKPE
                                60      70      80      90

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-Polle (122 aa)
 initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (2-60:55-107)

```

                                10      20      30
AAD-12                                KADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSA
                                ..  ::  :.  .  :  :  :  :
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNV FDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (2-60:55-107)

```

                                10      20      30
AAD-12                                KADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSA
                                ..  ::  :.  .  :  :  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNV FDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (2-60:55-107)

```

AAD-12                                KADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTEVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSA
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (2-60:55-107)

```

                                10      20      30
AAD-12                                KADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTEVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSA
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)
 initn: 39 init1: 39 opt: 64 Z-score: 94.1 bits: 24.0 E(): 2.9
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (1-59:89-149)

```

                                10      20
AAD-12                                KADGT-VRQHS PAEWDDMMKVIVGNMAWHA
                                :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-114 ASAVLVVPANKKFFVN NLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                60      70      80      90      100     110

```

```

                                30      40      50      60      70      80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSA
                                :  .  :  .  :  :  :  :  :  :
gi+AHw-114 DFNLMGTGVIDGQGGQW WAGQCKV VNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                120     130     140     150     160     170

```

```

gi+AHw-114 FHLVFGECEGVKIQGLKIKAPRDS PNTDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
                                180     190     200     210     220     230

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196 aa)
 initn: 36 init1: 36 opt: 59 Z-score: 93.2 bits: 22.8 E(): 3.2

gi+AHw-250 APVLDFVVFSTLKNEL
150

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
max+AF0- (379 aa)
initn: 48 init1: 48 opt: 60 Z-score: 88.6 bits: 22.9 E(): 5.8
Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
in 63 aa overlap (9-70:134-194)

```

                                10      20      30
AAD-12      KADGTVRQHSPA EWDDMMKVIVGNMAWHAD-STYMPVM
              :  ::  ::  :  ..  ..  ..  ..
gi+AHw-309  SKKYLQAPKDV SQQIKMANKKMKKEQYSCDHPPASWDWRKKG VITQVKYQGGCGSGWAFS
              110      120      130      140      150      160
    
```

```

                40      50      60      70      80
AAD-12  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSA
              :  ::  ..  ..  ::  .  ..  ..  .  :  ..  ::
gi+AHw-309  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSF EWVLEHGGIATDDDDY
              170      180      190      200      210      220
    
```

```

gi+AHw-309  PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISV SIDAKDFH
              230      240      250      260      270      280
    
```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)
initn: 49 init1: 49 opt: 58 Z-score: 87.5 bits: 22.3 E(): 6.7
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (26-75:23-71)

```

                10      20      30      40      50      60
AAD-12  KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
              ..  ::  :  ::  :  .  :  ..  ::  ::  .:
gi+AHw-663  MAVQKYTV ALFLAVALVAGPADSYAADAGYTPAAAAATPATPA-ATPAAGGGKATTDE
              10      20      30      40      50
    
```

```

                70      80
AAD-12  RAA YDALDEATR ALVHQRSA
              .  .  .  .  .  :  :
gi+AHw-663  QK LLEDVNAGFKAAVAADANAPPADKFKIF EAAFS ESCKGLLATSDAKAPGLILKLD TDY
              60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 52 init1: 52 opt: 54 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (25-53:23-50)

```

                10      20      30      40      50      60
AAD-12  KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
              ..  ::  :  ::  :  .  :  ..  ::  ::
gi+AHw-444  MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTA EIVEGDGGVGTIKKI
              10      20      30      40      50
    
```

```

              70          80
AAD-12 RAAVDALDEATRALVHQRSA

gi+AHw-444 SFGEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKS
              60          70          80          90          100          110

```

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
  initn: 46 initl: 46 opt: 53 Z-score: 86.3 bits: 21.1 E(): 7.8
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (31-79:5-52)

```

```

              10          20          30          40          50          60
AAD-12 KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADM
              ..  ...  ..  ..  ..  ..  :  :::  :
gi+AHw-217 MASKSSISPLLLATVLSVFAAATATGPYCYAGM
              10          20          30

```

```

              70          80
AAD-12 RAAVDALDEATRALVHQRSA
              .  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-217 GLPINPL-EGCREYVAQQTCGISISGSAVSTEPGNTPRDRCCCKELYDASQHCRCCEAVRYF
              40          50          60          70          80          90

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:51 2010 done: Fri Feb 5 12:55:51 2010
Total Scan time: 0.090 Total Display time: 0.000

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

1+AD4APgA+-AAD-12: 83 - 162 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 4 library sequences
      24      1      0:+AD0-
      26      0      0:
      28      1      0:+AD0-
      30      4      2:+ACo-

```


116 0 0: +ACo-
 118 0 0: +ACo-
 +AD4-120 0 0: +ACo-
 331323 residues in 1471 sequences
 Expectation+AF8-n fit: rho(ln(x))+AD0- 5.84990.00316+ADs- mu+AD0- 1.4245
 0.163
 mean+AF8-var+AD0-38.022910.019, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
 Lambda+AD0- 0.207994
 Kolmogorov-Smirnov statistic: 0.1004 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR	RecName: Full+AD0-Po
(97) 67 25.4 0.26	
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL	RecName: Full+AD0-
(96) 65 24.8 0.39	
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-	(
144) 62 23.8 1.2	
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR	RecName: Full+AD0-Po
(97) 57 22.4 2.1	
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR	RecName: Full+AD0-P
(122) 58 22.6 2.2	
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group	(122)
58 22.6 2.2	
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group	(122)
58 22.6 2.2	
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group	(122)
58 22.6 2.2	
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II	(196)
59 22.8 3.2	
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram	(145)
57 22.3 3.4	
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P	(160)
57 22.2 3.8	
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa	(
160) 56 21.9 4.7	
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH	RecName: Full+AD0-Gl
(158) 55 21.6 5.7	
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-	
(379) 60 22.9 5.8	
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium	(
301) 58 22.3 6.6	
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P	(160)
54 21.3 7.1	
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs-	(
145) 53 21.1 7.7	
gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham	(
419) 58 22.2 9.9	

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)

initn: 59 initl: 59 opt: 67 Z-score: 112.9 bits: 25.4 E(): 0.26
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (1-30:30-56)

```

                                10      20      30
AAD-12          ADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                   ..  ..:..  :..  :  :  :..  :..  :
gi+AHw-126 TKVDLTVEKGS DAKTLVLNIKYTRPGDTLAEVELRQH GSEEWEPMTK--KGNL-WEVKSA
                   10      20      30      40      50

                   40      50      60      70      80
AAD-12 YMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                   60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 109.8 bits: 24.8 E(): 0.39
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (1-31:30-57)

```

                                10      20      30
AAD-12          ADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                   ..  ..:..  :..  :  :  :..  :..  :
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEEWEPMTK--GNL-WEVKSS
                   10      20      30      40      50

                   40      50      60      70      80
AAD-12 YMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                   60      70      80      90

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)

initn: 55 initl: 55 opt: 62 Z-score: 101.1 bits: 23.8 E(): 1.2
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (30-78:5-52)

```

                   10      20      30      40      50      60
AAD-12 ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPAVGGRTCFADMR
                   ..  :..  ...  :.  .  :.  :.  :..  :
gi+AHw-189          MASKSSITPLLLAAV LASVFAAAAATGQYCYAGMG
                   10      20      30

                   70      80
AAD-12 AAYDALDEATRALVHQRSAR
                   .  :  :.  :  :  :..
gi+AHw-189 LPSNPL-EGCREYVAQQTCGV TIAGSPVSSEPGDTPKDRCCQELDEAPQHCR CRVRYFIG
                   40      50      60      70      80      90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)

initn: 36 init1: 36 opt: 57 Z-score: 96.7 bits: 22.4 E(): 2.1
 Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
 in 62 aa overlap (1-62:31-86)

```

                                10      20      30
AAD-12                        ADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  ..  ..  :
gi+AHw-126 AAPVEFTVEKGSDEKLNLSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSAR
                                ..  ::  :.  .  :  :  ::  :  ::  :
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGM RNVFDDVVPADFKVGT TYKPE
                                60      70      80      90

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)
 initn: 46 init1: 46 opt: 58 Z-score: 96.2 bits: 22.6 E(): 2.2
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (1-59:55-107)

```

                                10      20      30
AAD-12                        ADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  ::  ::
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSAR
                                ..  ::  :.  .  .  :  ..  :  ::
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNV FDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
 II) (122 aa)
 initn: 46 init1: 46 opt: 58 Z-score: 96.2 bits: 22.6 E(): 2.2
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (1-59:55-107)

```

                                10      20      30
AAD-12                        ADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  ::  ::
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSAR
                                ..  ::  :.  .  .  :  ..  :  ::
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNV FDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
 II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 96.2 bits: 22.6 E(): 2.2
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (1-59:55-107)

```

                                10      20      30
AAD-12                        ADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTF TVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                   30      40      50      60      70      80

                   40      50      60      70      80
AAD-12 TYMPVMAQ GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSAR
                   ..  ::  :.  .  .  :  ..  :  :.
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFD DVVPEKYTIGATYAPEE
                   90      100     110     120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 96.2 bits: 22.6 E(): 2.2
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (1-59:55-107)

```

                                10      20      30
AAD-12                        ADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTF TVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                   30      40      50      60      70      80

                   40      50      60      70      80
AAD-12 TYMPVMAQ GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSAR
                   ..  ::  :.  .  .  :  ..  :  :.
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFD DVVPEKYTIGATYAPEE
                   90      100     110     120

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196 aa)

initn: 36 init1: 36 opt: 59 Z-score: 93.3 bits: 22.8 E(): 3.2
 Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
 in 62 aa overlap (1-62:31-86)

```

                                10      20      30
AAD-12                        ADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  :.  .  .  :
gi+AHw-109 EAPVTF TVEKGSDEKLN LALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                   10      20      30      40      50

                   40      50      60      70      80
AAD-12 TYMPVMAQ GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSAR
                   ..  ::  :.  .  :  :  :.  :.  :.  :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGM RNVFDVVPADFKVGT TYKPEEAAA SASRRRSSEVFQF
                   60      70      80      90      100     110

gi+AHw-109 LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIIYKIFKMMFQ
                   120     130     140     150     160     170

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)
 initn: 50 init1: 50 opt: 57 Z-score: 92.9 bits: 22.3 E(): 3.4
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (30-78:5-52)

```

                10      20      30      40      50      60
AAD-12 ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
                ..  ...  ...  ..  ..  ..  ..  ::  :
gi+AHw-439                MASKSSITPLLLAAVLASVFAAATATGQYCYAGMG
                        10      20      30

```

```

                70      80
AAD-12 AAYDALDEATRALLVHQRSAR
                . : : . : : : .
gi+AHw-439 LPSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFI
                40      50      60      70      80      90

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 init1: 55 opt: 57 Z-score: 92.0 bits: 22.2 E(): 3.8
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (24-52:23-50)

```

                10      20      30      40      50      60
AAD-12 ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
                ..  ::  :  :  :  :  ::  ::  :  :
gi+AHw-444  MGVTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKIS
                10      20      30      40      50

```

```

                70      80
AAD-12 AAYDALDEATRALLVHQRSAR
gi+AHw-444 FGEESHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKST
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 init1: 55 opt: 56 Z-score: 90.4 bits: 21.9 E(): 4.7
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (28-52:27-50)

```

                10      20      30      40      50      60
AAD-12 ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
                ::  . :  :  :  :  :  ::  :  :
gi+AHw-165  MGVTTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKIT
                10      20      30      40      50

```

```

                70      80
AAD-12 AAYDALDEATRALLVHQRSAR
gi+AHw-165 FGEQSQFKYVKHRIDEIDQANFTYCYSVIEGDVNNELLEKISYEIKIVASPDGGSILKNT
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
Full+AD0-Globin (158 aa)
initn: 39 initl: 39 opt: 55 Z-score: 88.9 bits: 21.6 E(): 5.7
Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
in 34 aa overlap (9-36:114-147)

```

                                10      20      30
AAD-12      ADGTVRQHSPAEWDDMMKVIV----GNMAWHA--DSTY
                                ::.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-250  EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGGATKWDSSAVESSW
              90      100      110      120      130      140

```

```

              40      50      60      70      80
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSAR
              :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-250  APVLDFVVFSTLKNEL
              150

```

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
max+AF0- (379 aa)
initn: 48 initl: 48 opt: 60 Z-score: 88.7 bits: 22.9 E(): 5.8
Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
in 63 aa overlap (8-69:134-194)

```

                                10      20      30
AAD-12      ADGTVRQHSPAEWDDMMKVIVGNMAWHAD-STYMPVM
                                :  :  :  :  :  :  :  :  :  :  :
gi+AHw-309  SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGSGWAFS
              110      120      130      140      150      160

```

```

              40      50      60      70      80
AAD-12  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSAR
              :  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-309  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFVWVLEHGGIATDDDDY
              170      180      190      200      210      220

```

```

gi+AHw-309  PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
              230      240      250      260      270      280

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)
initn: 49 initl: 49 opt: 58 Z-score: 87.6 bits: 22.3 E(): 6.6
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (25-74:23-71)

```

              10      20      30      40      50      60
AAD-12  ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
              ..  ::.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-663  MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQ
              10      20      30      40      50

```

```

              70      80
AAD-12  AAYDALDEATRALLVHQRSAR

```

```

. . . . . : :
gi+AHw-663 KLEEDVNAGFKAAVAADANAPPADKFKIFEAAFSESCKGLLATSDAKAPGLILKLDTDYD
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 87.1 bits: 21.3 E(): 7.1
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (24-52:23-50)

```

          10          20          30          40          50          60
AAD-12 ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
          .. .:: : .: .: .: .::: . : :
gi+AHw-444 MGVTYSDESTSVIPPRFLKALVLEAD-TLIPKIA PQSVKTA EIVEG DGGVGTIKKIS
          10          20          30          40          50

```

```

          70          80
AAD-12 AAYDALDEATR ALVHQRSAR

```

```

gi+AHw-444 FGE GSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKST
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 86.4 bits: 21.1 E(): 7.7
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (30-78:5-52)

```

          10          20          30          40          50          60
AAD-12 ADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
          .. :.. .: .: .: .: .: .: .: .:
gi+AHw-217 MASKSSISPLLLATV LVS VF AAATATGPYCYAGMG
          10          20          30

```

```

          70          80
AAD-12 AAYDALDEATR ALVHQRSAR

```

```

. : : . : : : . .
gi+AHw-217 LPINPL-EGCREYVAQQTCGISISGSAVSTEPGNTPRDRCCKELYDASQHCRC EAVRYFI
          40          50          60          70          80          90

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)

initn: 39 initl: 39 opt: 58 Z-score: 84.5 bits: 22.2 E(): 9.9
 Smith-Waterman score: 58+ADs- 32.787+ACU- identity (55.738+ACU- similar)
 in 61 aa overlap (2-58:91-149)

```

          10          20          30
AAD-12 ADGT-VRQHSPAEWDDMMKVIVGNMAWHADS
          ::: : : .::: . : . . . : . :
gi+AHw-114 AVLVVPANKKFFVNNL VFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLTDF
          70          80          90          100          110

```

```

          40          50          60          70          80
AAD-12 TYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSAR

```



```

50      98
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
52      103
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QAq-
54      68      91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
56      74      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
58      44      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
60      49      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62      49      40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
64      66      32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-+AD0-
66      33      25:+AD0APQA9AD0APQA9ACoAPQA9-
68      29      20:+AD0APQA9AD0AKgA9AD0APQ-
70      38      16:+AD0APQA9ACoAPQA9AD0APQA9AD0-
72      21      12:+AD0APQAqAD0APQA9-
74      19      10:+AD0APQAqAD0APQ-
76      21      7:+AD0AKgA9AD0APQA9-
78      9       6:+AD0AKgA9-
80      5       4:+ACoAPQ-
82      8       3:+ACoAPQ-
84      14      3:+ACoAPQA9AD0-
86      2       2:+ACo-
88      2       2:+ACo-      inset +AD0- represents 1 library sequences
90      3       1:+ACo-
92      7       1:+ACoAPQ-      :+ACoAPQA9AD0APQA9AD0-
94      0       1:+ACo-      :+ACo-
96      0       1:+ACo-      :+ACo-
98      0       0:      +ACo-
100     0       0:      +ACo-
102     1       0:+AD0-      +ACoAPQ-
104     0       0:      +ACo-
106     1       0:+AD0-      +ACoAPQ-
108     0       0:      +ACo-
110     1       0:+AD0-      +ACoAPQ-
112     0       0:      +ACo-
114     0       0:      +ACo-
116     0       0:      +ACo-
118     0       0:      +ACo-
+AD4-120 0 0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.87230.00303+ADs- mu+AD0- 1.2936
0.157
mean+AF8-var+AD0-37.6036 9.920, 0's: 2 Z-trim: 2 B-trim: 223 in 2/41
Lambda+AD0- 0.209151
Kolmogorov-Smirnov statistic: 0.1052 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)

```

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
 (97) 65 24.9 0.37
 gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
 (96) 63 24.3 0.56
 gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
 144) 62 23.8 1.1
 gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
 (97) 55 21.9 3
 gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
 (122) 56 22.1 3.2
 gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
 56 22.1 3.2
 gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 56 22.1 3.2
 gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 56 22.1 3.2
 gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145)
 57 22.3 3.2
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 22.3 3.7
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
 160) 56 22.0 4.5
 gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
 57 22.2 4.7
 gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
 (158) 55 21.7 5.5
 gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
 (379) 60 22.9 5.6
 gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
 301) 58 22.4 6.5
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.4 6.9
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
 145) 53 21.1 7.5
 gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (
 419) 58 22.3 9.7
 gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
 (91) 49 20.1 9.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 57 init1: 57 opt: 65 Z-score: 110.1 bits: 24.9 E(): 0.37
 Smith-Waterman score: 65+ADs- 42.308+ACU- identity (65.385+ACU- similar)
 in 26 aa overlap (4-29:34-56)

			10	20	30	
AAD-12			DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP			
		 :	... :	
gi+AHw-126	DLTVEKGS	DAKTLVL	NIKYTRP	GDTLAEV	ELRQHG	SEEWEPMTK--KGNL-WEVKS
	10	20	30	40	50	60
	40	50	60	70	80	
AAD-12	VMAQGAVFSAE VVPAVGGRTCFADMR AAYDALDEATRALVHQRSARH					

gi+AHw-126 TGP MNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 53 initl: 53 opt: 63 Z-score: 106.9 bits: 24.3 E(): 0.56
Smith-Waterman score: 63+ADs- 37.037+ACU- identity (66.667+ACU- similar)
in 27 aa overlap (4-30:34-57)

AAD-12 DGT VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
gi+AHw-144 TFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEW EPLTK--KGNL-WEVKSSKPL
10 20 30 40 50 60

AAD-12 VMAQ GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARH

gi+AHw-144 TGPFNFRFMSKGM RNVFDEVIPTAFKIGT TYTPEE
70 80 90

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 initl: 55 opt: 62 Z-score: 101.4 bits: 23.8 E(): 1.1
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (29-77:5-52)

AAD-12 DGT VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQ GAVFSAEVVPAVGGRTCFADMRA
gi+AHw-189 MASKSSITPLLLAAVLASVF AAAAATGQYCYAGMGL
10 20 30

AAD-12 AYDALDEATR ALVHQRSARH
gi+AHw-189 PSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCR CRVRYFIGR
40 50 60 70 80 90

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 initl: 36 opt: 55 Z-score: 93.8 bits: 21.9 E(): 3
Smith-Waterman score: 55+ADs- 27.586+ACU- identity (51.724+ACU- similar)
in 58 aa overlap (4-61:35-86)

AAD-12 DGT VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
gi+AHw-126 EFTVEKGSDEK NLA LSIKYNKEGDSMAEVELKEHGSNEWLAL KKN--GDGVWEIKSDK-P
10 20 30 40 50 60

AAD-12 VMAQ GAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARH

gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
 90 100 110 120

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 44 init1: 44 opt: 56 Z-score: 93.2 bits: 22.1 E(): 3.2
 Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
 in 55 aa overlap (4-58:59-107)

AAD-12 DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
 :: :: : .: :: :
 gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
 30 40 50 60 70 80

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARH
 . :: . . . : .. ::

gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
 90 100 110 120

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)

initn: 50 init1: 50 opt: 57 Z-score: 93.2 bits: 22.3 E(): 3.2
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (29-77:5-52)

AAD-12 DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 : :: :
 gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGL
 10 20 30

AAD-12 AYDALDEATR ALVHQRSARH
 . : :: : : : ..

gi+AHw-439 PSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIG
 40 50 60 70 80 90

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)

initn: 55 init1: 55 opt: 57 Z-score: 92.2 bits: 22.3 E(): 3.7
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (23-51:23-50)

AAD-12 DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. :: : .: .: .: :::: . : :
 gi+AHw-444 MGVFYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTIKKISF
 10 20 30 40 50

AAD-12 AYDALDEATR ALVHQRSARH

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 init1: 55 opt: 56 Z-score: 90.6 bits: 22.0 E(): 4.5
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (27-51:27-50)

10 20 30 40 50 60
AAD-12 DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: .: :::: . :
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
10 20 30 40 50

70 80
AAD-12 AYDALDEATR ALVHQRSARH

gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
60 70 80 90 100 110

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
(196 aa)
initn: 36 init1: 36 opt: 57 Z-score: 90.3 bits: 22.2 E(): 4.7
Smith-Waterman score: 57+ADs- 27.586+ACU- identity (53.448+ACU- similar)
in 58 aa overlap (4-61:35-86)

10 20 30
AAD-12 DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
..... :: . : .: .: :
gi+AHw-109 TFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKSDK-P
10 20 30 40 50 60

40 50 60 70 80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARH
. .: .: .: : .: .: .:
gi+AHw-109 L--KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGTTYKPEEAAAASARRRSSEVFQFLILS
70 80 90 100 110

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
Full+AD0-Globin (158 aa)
initn: 39 init1: 39 opt: 55 Z-score: 89.1 bits: 21.7 E(): 5.5
Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
in 34 aa overlap (8-35:114-147)

10 20 30
AAD-12 DGTVRQHSPA EWDDMMKVIV----GNMAWHA--DSTY
:::: .: .: : .: : .: .:
gi+AHw-250 EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGTKWDSAVESSW
90 100 110 120 130 140

40 50 60 70 80
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARH
:::

gi+AHw-250 APVLDFVVFSTLKNEL
150

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
max+AF0- (379 aa)
initn: 48 init1: 48 opt: 60 Z-score: 88.9 bits: 22.9 E(): 5.6
Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
in 63 aa overlap (7-68:134-194)

```

                                10      20      30
AAD-12      DGTVRQHSPA EWDDMMKVIVGNMAWHAD-STYMPVM
              :  ::  ::  :  ..  ..  ..  ..
gi+AHw-309  SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGSGWAFS
              110      120      130      140      150      160
    
```

```

                40      50      60      70      80
AAD-12  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARH
              :  ::  ..  ..  ::  .  ..  ..  .  :  ..  ::
gi+AHw-309  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSF EWVLEHGGIATDDDDY
              170      180      190      200      210      220
    
```

```

gi+AHw-309  PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISV SIDAKDFH
              230      240      250      260      270      280
    
```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)
initn: 49 init1: 49 opt: 58 Z-score: 87.8 bits: 22.4 E(): 6.5
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (24-73:23-71)

```

                10      20      30      40      50      60
AAD-12  DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ..  ::  :  ::  :  .  :  ..  ::  ::  .  :  .
gi+AHw-663  MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAAATPATPA-ATPAAGGGKATTDEQK
              10      20      30      40      50
    
```

```

                70      80
AAD-12  AYDALDEATR ALVHQRSARH
              .  ..  .  ::  :
gi+AHw-663  LLEDVNAGFKA AVAADANAPPADKFKIFEAAFSE SCKGLLATSDAKAPGLILKLDTDYDV
              60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 52 init1: 52 opt: 54 Z-score: 87.3 bits: 21.4 E(): 6.9
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (23-51:23-50)

```

                10      20      30      40      50      60
AAD-12  DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ..  ::  :  ::  :  .  :  ..  ::  ::
gi+AHw-444  MGVFYTSDESTSVIPPPRLFKALVLEAD-TLIPK IAPQSVKTAEIVEG DGGVGTIKKISF
              10      20      30      40      50
    
```

70 80
AAD-12 AYDALDEATRALVHQRSARH

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 86.7 bits: 21.1 E(): 7.5
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (29-77:5-52)

10 20 30 40 50 60
AAD-12 DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPAVGGRTCFADMRA
gi+AHw-217 MASKSSISPLLLATV LSVVFAAATATGPYCYAGMGL
10 20 30

70 80
AAD-12 AYDALDEATRALVHQRSARH
gi+AHw-217 PINPL-EGCREYVAQQTCGISISGS AVSTEPGNTPRDRCC KELYDASQHCRCEAVRYFIG
40 50 60 70 80 90

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-
Chamaecy (419 aa)
initn: 39 initl: 39 opt: 58 Z-score: 84.7 bits: 22.3 E(): 9.7
Smith-Waterman score: 58+ADs- 32.787+ACU- identity (55.738+ACU- similar)
in 61 aa overlap (1-57:91-149)

10 20
AAD-12 DGT-VRQHSPA EWDDMMKVIVGNMAWHADS
gi+AHw-114 AVLVVPANKKFFVNNLVFRGPCPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLTDF
70 80 90 100 110

30 40 50 60 70 80
AAD-12 TYMP---VMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH
gi+AHw-114 NLMGTGVIDGQGWAGQCKV VNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPEFH
120 130 140 150 160 170

gi+AHw-114 LVFGECEGVKIQGLKIKAPRDS PNTDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSNIT
180 190 200 210 220 230

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 37 initl: 37 opt: 49 Z-score: 84.6 bits: 20.1 E(): 9.8
Smith-Waterman score: 49+ADs- 32.258+ACU- identity (58.065+ACU- similar)
in 31 aa overlap (3-31:35-64)

10 20 30
AAD-12 DGTVRQHSPA E--WDDMMKVIVGNMAWHADST
: : : . : . : :

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 65 25.1 0.31

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 63 24.5 0.47

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.0 0.98

gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
(97) 55 22.1 2.6

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
(122) 56 22.3 2.8

gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
56 22.3 2.8

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
56 22.3 2.8

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
56 22.3 2.8

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145)
57 22.5 2.8

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
57 22.5 3.2

gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.2 4

gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
57 22.4 4.2

gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
(158) 55 21.9 4.8

gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
(379) 60 23.0 5.2

gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.5 5.9

gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
54 21.6 6.1

gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.3 6.6

gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(91) 49 20.3 8.5

gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159)
52 21.0 9.2

gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
52 21.0 9.2

gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
52 21.0 9.2

gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
52 21.0 9.2

gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
52 21.0 9.2

gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
52 21.0 9.2

gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
52 21.0 9.2

gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
52 21.0 9.2

gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9.2
 gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9.2
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.0 9.3
 gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34
 (379) 57 22.1 9.8
 gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
 57 22.1 9.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 57 initl: 57 opt: 65 Z-score: 111.5 bits: 25.1 E(): 0.31
 Smith-Waterman score: 65+ADs- 42.308+ACU- identity (65.385+ACU- similar)
 in 26 aa overlap (3-28:34-56)

			10	20	30
AAD-12			GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP		
		 :	... :
gi+AHw-126	DLTVEKGS	DAKTLVL	NIKYTRP	GDTLAEV	ELRQHG
	10	20	30	40	50
					60

	40	50	60	70	80
AAD-12	VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHS				

gi+AHw-126	TGPMNFR	FLSKGGM	KNVFDEV	IPTAFTV	GKTYTPE
	70	80	90		

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 53 initl: 53 opt: 63 Z-score: 108.3 bits: 24.5 E(): 0.47
 Smith-Waterman score: 63+ADs- 37.037+ACU- identity (66.667+ACU- similar)
 in 27 aa overlap (3-29:34-57)

			10	20	30
AAD-12			GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP		
		 :	... :
gi+AHw-144	TFKVEKGS	DPKKLV	LDIKYTR	PGDTLAE	VELRQHG
	10	20	30	40	50
					60

	40	50	60	70	80
AAD-12	VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHS				

gi+AHw-144	TGPFNFR	FMSKGG	MNRNVF	DEVIPTA	FKIGTT
	70	80	90		

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 102.6 bits: 24.0 E(): 0.98
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (28-76:5-52)

	10	20	30	40	50	60
--	----	----	----	----	----	----


```

AAD-12                               GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                               .....  ::  :  :  :  :  :  :  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSD EWVAMTKGEGG--VWTFDSEE-P
           30          40          50          60          70          80
    
```

```

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHS
.  ::  ..  .  .  :  ..  :  :
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
           90          100         110         120
    
```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 44 init1: 44 opt: 56 Z-score: 94.3 bits: 22.3 E(): 2.8
 Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
 in 55 aa overlap (3-57:59-107)

```

AAD-12                               10          20          30
                               GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                               .....  ::  :  :  :  :  :  :  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSD EWVAMTKGEGG--VWTFDSEE-P
           30          40          50          60          70          80
    
```

```

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHS
.  ::  ..  .  .  :  ..  :  :
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
           90          100         110         120
    
```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 44 init1: 44 opt: 56 Z-score: 94.3 bits: 22.3 E(): 2.8
 Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
 in 55 aa overlap (3-57:59-107)

```

AAD-12                               10          20          30
                               GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                               .....  ::  :  :  :  :  :  :  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSD EWVAMTKGEGG--VWTFDSEE-P
           30          40          50          60          70          80
    
```

```

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHS
.  ::  ..  .  .  :  ..  :  :
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
           90          100         110         120
    
```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)
 initn: 50 init1: 50 opt: 57 Z-score: 94.2 bits: 22.5 E(): 2.8
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (28-76:5-52)

10 20 30 40 50 60


```

AAD-12                               GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                               ..... :: . : .. ... : :
gi+AHw-109 TFTVEKGSDEKLNLSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKSDK-P
            10          20          30          40          50          60

```

```

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHS
. .: .. . : : .. :... :
gi+AHw-109 L--KGP-FNFRFVSEKGM RNVFVDVVPADFKVGT TYKPEEAAAASARRRSSEVFQFLILS
            70          80          90          100         110

```

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Globin (158 aa)
 initn: 39 initl: 39 opt: 55 Z-score: 90.1 bits: 21.9 E(): 4.8
 Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
 in 34 aa overlap (7-34:114-147)

```

AAD-12                               10          20          30
                               GTVRQHSPA EWDDMMKVIV----GNMAWHA--DSTY
                               ::.. ... : : : : . ...
gi+AHw-250 EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLK GATKWDSAVESSW
            90          100         110         120         130         140

```

```

AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHS
::.
gi+AHw-250 APVLDFVFSTLKNEL
            150

```

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0- (379 aa)
 initn: 48 initl: 48 opt: 60 Z-score: 89.5 bits: 23.0 E(): 5.2
 Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
 in 63 aa overlap (6-67:134-194)

```

AAD-12                               10          20          30
                               GTVRQHSPA EWDDMMKVIVGNMAWHAD-STYMPVM
                               : :: :: : .. . ... ..
gi+AHw-309 SKKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGSGWAFS
            110         120         130         140         150         160

```

```

AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHS
: ::. .... ::. . .... . : ...
gi+AHw-309 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSF EWVLEHGGIATDDDDY
            170         180         190         200         210         220

```

```

gi+AHw-309 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISV SIDAKDFH
            230         240         250         260         270         280

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs- Lolium per (301 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 88.6 bits: 22.5 E(): 5.9

Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (23-72:23-71)

```

                10         20         30         40         50         60
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                .. ::: : : : . : .....: : .
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                10         20         30         40         50

```

```

                70         80
AAD-12  YDALDEATRALVHQRSARHS
                . . . . : :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 88.3 bits: 21.6 E(): 6.1
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (22-50:23-50)

```

                10         20         30         40         50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. ::: : : : . : .....: : .
gi+AHw-444 MGVFTYSDESTSVIPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
                10         20         30         40         50

```

```

                60         70         80
AAD-12  AYDALDEATRALVHQRSARHS
                . . . . : :
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 87.6 bits: 21.3 E(): 6.6
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (28-76:5-52)

```

                10         20         30         40         50         60
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                .. ::: : : : . : .....: : .
gi+AHw-217 MASKSSISPLLLATV LVS VFAAATATGPYCYAGMGLP
                10         20         30

```

```

                70         80
AAD-12  YDALDEATRALVHQRSARHS
                . : : : : : : . .
gi+AHw-217 INPL-EGCREYVAQQTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRC EAVRYFIGR
                40         50         60         70         80         90

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-Chiti (91 aa)

initn: 37 initl: 37 opt: 49 Z-score: 85.7 bits: 20.3 E(): 8.5

Smith-Waterman score: 49+ADs- 32.258+ACU- identity (58.065+ACU- similar)
in 31 aa overlap (2-30:35-64)

```

                                10          20
AAD-12          GTVRQHSPAEE--WDDMMKVIVGNMAWHADST
                   : . . . . .  :: . . .  :: : .
gi+AHw-323 QTCAGNICCSQYGYCGTTADYCS PDNNCQATYHYYNPAQNNWD-LRAVSAYCSTWDADKP
                   10          20          30          40          50          60

```

```

          30          40          50          60          70          80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
          :
gi+AHw-323 YSWRYGWTAFCGPAGPRCLRTNAAVTVR
          70          80          90

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10          20          30          40          50
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                   :: . . . . .  :: : . . . . .  ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                   10          20          30          40          50

```

```

          60          70          80
AAD-12 AYDALDEATRALVHQRSARHS

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10          20          30          40          50
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                   :: . . . . .  :: : . . . . .  ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                   10          20          30          40          50

```

```

          60          70          80
AAD-12 AYDALDEATRALVHQRSARHS

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10      20      30      40      50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  ::  :::. .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
          10      20      30      40      50

```

```

        60      70      80
AAD-12  AYDALDEATRALVHQRSARHS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10      20      30      40      50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  ::  :::. .  ::
gi+AHw-279  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
          10      20      30      40      50

```

```

        60      70      80
AAD-12  AYDALDEATRALVHQRSARHS

```

```

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10      20      30      40      50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  ::  :::. .  ::
gi+AHw-131  MGVFN YETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
          10      20      30      40      50

```

```

        60      70      80
AAD-12  AYDALDEATRALVHQRSARHS

```

```

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10      20      30      40      50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  ::  :::. .  ::
gi+AHw-602  MGVTYSEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
          10      20      30      40      50

```

```

        60      70      80
AAD-12  AYDALDEATRALVHQRSARHS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10      20      30      40      50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  ::  :::. .  ::
gi+AHw-602  MGVTYSEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
          10      20      30      40      50

```

```

        60      70      80
AAD-12  AYDALDEATRALVHQRSARHS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10      20      30      40      50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  ::  :::. .  ::
gi+AHw-602  MGVTYSEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
          10      20      30      40      50

```

```

        60      70      80
AAD-12  AYDALDEATRALVHQRSARHS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10          20          30          40          50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  .:  ::  :::. . .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10          20          30          40          50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  .:  ::  :::. . .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 50 init1: 50 opt: 52 Z-score: 85.0 bits: 21.0 E(): 9.3
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (22-50:23-50)

```

          10          20          30          40          50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ..  ::  :  .:  .:  .:  :::. . .  ::
gi+AHw-444  MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIA PQSVKGAEIVEG DGGVGTIKKISF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHS

```

```

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
Full+AD0-P34 prob (379 aa)

initn: 48 init1: 48 opt: 57 Z-score: 84.6 bits: 22.1 E(): 9.8

Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
in 63 aa overlap (6-67:134-194)

```

                                10      20      30
AAD-12      GTVRQHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
                                :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-129  SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
                110      120      130      140      150      160

                40      50      60      70      80
AAD-12  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHS
                :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-129  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSF EWVLEHGGIATDDDDY
                170      180      190      200      210      220

gi+AHw-129  PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTES ETEQAFLSAILEQPISV SIDAKDFH
                230      240      250      260      270      280

```

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
vacuola (379 aa)
initn: 48 initl: 48 opt: 57 Z-score: 84.6 bits: 22.1 E(): 9.8
Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
in 63 aa overlap (6-67:134-194)

```

                                10      20      30
AAD-12      GTVRQHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
                                :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-119  SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
                110      120      130      140      150      160

                40      50      60      70      80
AAD-12  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHS
                :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-119  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSF EWVLEHGGIATDDDDY
                170      180      190      200      210      220

gi+AHw-119  PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTES ETEQAFLSAILEQPISV SIDAKDFH
                230      240      250      260      270      280

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:51 2010 done: Fri Feb 5 12:55:52 2010
Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

82      2      3:+ACo-
84     17     3:+ACoAPQA9AD0APQ-
86      1     2:+ACo-
88      4     2:+ACo-          inset +AD0- represents 1 library sequences
90      2     1:+ACo-
92      2     1:+ACo-          :+ACoAPQ-
94      6     1:+ACoAPQ-        :+ACoAPQA9AD0APQA9-
96      0     1:+ACo-          :+ACo-
98      0     0:              +ACo-
100     0     0:              +ACo-
102     1     0:+AD0-        +ACoAPQ-
104     0     0:              +ACo-
106     0     0:              +ACo-
108     1     0:+AD0-        +ACoAPQ-
110     1     0:+AD0-        +ACoAPQ-
112     0     0:              +ACo-
114     0     0:              +ACo-
116     0     0:              +ACo-
118     0     0:              +ACo-
+AD4-120  0     0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.05020.00293+ADs- mu+AD0- -
0.0733 0.152
mean+AF8-var+AD0-36.8188 9.860, 0's: 2 Z-trim: 2 B-trim: 223 in 2/41
Lambda+AD0- 0.211368
Kolmogorov-Smirnov statistic: 0.1278 (N+AD0-29) at 46

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

```

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  65 25.2    0.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  63 24.6    0.46
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)  62 24.1    0.95
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97)  55 22.1    2.5
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 56 22.3    2.7
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
56 22.3    2.7
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
56 22.3    2.7
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
56 22.3    2.7
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 22.6    2.8
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.5    3.1
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)  56 22.2    3.9

```

gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
 57 22.4 4.1
 gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-G1
 (158) 55 21.9 4.7
 gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
 (379) 60 23.1 5
 gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
 58 22.6 5.7
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.6 5.9
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145)
 53 21.3 6.4
 gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
 (91) 49 20.3 8.3
 gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9
 gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9
 gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9
 gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
 52 21.0 9
 gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
 52 21.0 9
 gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9
 gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9
 gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9
 gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9
 gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.0 9
 gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34
 (379) 57 22.2 9.4
 gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
 57 22.2 9.4

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 57 init1: 57 opt: 65 Z-score: 111.6 bits: 25.2 E(): 0.3
 Smith-Waterman score: 65+ADs- 42.308+ACU- identity (65.385+ACU- similar)
 in 26 aa overlap (2-27:34-56)

			10	20	30	
AAD-12			TVRQHSPA EWDDMMKVIVGNMAWHADSTYMP			
		 : :	... : : :	
gi+AHw-126	DLTVEKGS	DAKTLVL	NIKYTRP	GDTLAE	VELRQH	GSEEWEPMTK--KGNL-WEVKS
	10	20	30	40	50	60
	40	50	60	70	80	

AAAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSL

gi+AHw-126 TGP MNFRFLSKGGMKNVFDEVIPTAFTV GKTYTPEYN
 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 53 initl: 53 opt: 63 Z-score: 108.4 bits: 24.6 E(): 0.46
 Smith-Waterman score: 63+ADs- 37.037+ACU- identity (66.667+ACU- similar)
 in 27 aa overlap (2-28:34-57)

AAAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
 ::. . : ::. ... ::.
 gi+AHw-144 TFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEW EPLTK--KGNL-WEVKSSKPL
 10 20 30 40 50 60

AAAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSL

gi+AHw-144 TGP FNFRFMSKGGMRNVFDEVIPTAFKIGT TYTPEE
 70 80 90

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 102.7 bits: 24.1 E(): 0.95
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (27-75:5-52)

AAAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY
 : . . : . : : :
 gi+AHw-189 MASKSSITPLLLAAVLASVF AAAAAATGQYCYAGMGLPS
 10 20 30

AAAD-12 DALDEATRALLVHQRSARHSL
 . : : : : : : :
 gi+AHw-189 NPL-EGCREYVAQQTCGV TIAGSPVSSEPGDTPKDRCCQELDEAPQHCR CRVRYFIGRRS
 40 50 60 70 80 90

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 36 initl: 36 opt: 55 Z-score: 95.1 bits: 22.1 E(): 2.5
 Smith-Waterman score: 55+ADs- 27.586+ACU- identity (51.724+ACU- similar)
 in 58 aa overlap (2-59:35-86)

AAAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
 ::. . : ::. ... : :
 gi+AHw-126 EFTVEKGSDEKLN LALS IKYNKEGDSMAEVELKEHGSNEWLAL KKN--GDGVWEIKSDK-P
 10 20 30 40 50 60
 40 50 60 70 80

AAAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSL

```

.  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-126 L--KGP-FNFRFVSEKGMKNVFDVDDVVPADFKVGTTYKPE
              70              80              90
    
```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 44 initl: 44 opt: 56 Z-score: 94.5 bits: 22.3 E(): 2.7
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (2-56:59-107)

```

                                10          20          30
AAAD-12                        TVRQHSPAEDDMMKVIVGNMAWHADSTYMP
                                .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-117 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
              30          40          50          60          70          80
    
```

AAAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSL

```

.  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-117 L--QGP-FNFRFLTEKGMKNVFDVDDVPEKYTIGATYAPEE
              90          100          110          120
    
```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
initn: 44 initl: 44 opt: 56 Z-score: 94.5 bits: 22.3 E(): 2.7
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (2-56:59-107)

```

                                10          20          30
AAAD-12                        TVRQHSPAEDDMMKVIVGNMAWHADSTYMP
                                .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
              30          40          50          60          70          80
    
```

AAAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSL

```

.  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDVDDVPEKYTIGATYAPEE
              90          100          110          120
    
```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
initn: 44 initl: 44 opt: 56 Z-score: 94.5 bits: 22.3 E(): 2.7
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (2-56:59-107)

```

                                10          20          30
AAAD-12                        TVRQHSPAEDDMMKVIVGNMAWHADSTYMP
                                .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
              30          40          50          60          70          80
    
```

```

              40          50          60          70          80
    
```

AAAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSL

```

.  ::  ..  .  .  :  ..  :  ::
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
          90          100          110          120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 44 init1: 44 opt: 56 Z-score: 94.5 bits: 22.3 E(): 2.7
 Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
 in 55 aa overlap (2-56:59-107)

```

          10          20          30
AAAD-12 TVRQHSPAEDDDMMKVIVGNMAWHADSTYMP
          .....  ::  :  :  :  :  :  :  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYEGLTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
          30          40          50          60          70          80

```

AAAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSL

```

.  ::  ..  .  .  :  ..  :  ::
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
          90          100          110          120

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)

initn: 50 init1: 50 opt: 57 Z-score: 94.4 bits: 22.6 E(): 2.8
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (27-75:5-52)

```

          10          20          30          40          50          60
AAAD-12 TVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY
          ..  ...  ...  :  .  .  .  :  :  :  :
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPS
          10          20          30

```

AAAD-12 DALDEATRALLVHQRSARHSL

```

.  :  :  :  :  :  :
gi+AHw-439 NPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHRCCEAVRYFIGRR
          40          50          60          70          80          90

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)

initn: 55 init1: 55 opt: 57 Z-score: 93.5 bits: 22.5 E(): 3.1
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (21-49:23-50)

```

          10          20          30          40          50
AAAD-12 TVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ..  ...  :  :  :  :  :  :  :  :
gi+AHw-444 MGVTYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTIKKISF
          10          20          30          40          50

```

```

60          70          80

```



```

                10         20         30         40         50
        60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
        60         70         80         90         100        110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 87.8 bits: 21.3 E(): 6.4
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (27-75:5-52)

```

                10         20         30         40         50         60
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY
                                ..  ...  ..  :.  ..  .  :  ::  :
gi+AHw-217                                MASKSSISPLLLATVIVSVFAAATATGPYCYAGMGLPI
                                10         20         30

```

```

                70         80
AAD-12 DALDEATRALVHQRSARHSL
        .  :  :.  :  :  :..
gi+AHw-217 NPL-EGCREYVAQQTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRC EAVRYFIGRR
        40         50         60         70         80         90

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 37 initl: 37 opt: 49 Z-score: 85.9 bits: 20.3 E(): 8.3
Smith-Waterman score: 49+ADs- 32.258+ACU- identity (58.065+ACU- similar)
in 31 aa overlap (1-29:35-64)

```

                                10         20
AAD-12                                TVRQHSPA E--WDDMMKVIVGNMAWHADST
                                :  .  .  .  .  .  ::  .  :  .  .  :  :.
gi+AHw-323 QTCAGNICCSQYGYCGTTADYCS PDNNCQATYHYYNPAQNNWD-LRAVSAYCSTWDADKP
        10         20         30         40         50         60

```

```

        30         40         50         60         70         80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL
        :
gi+AHw-323 YSWRYGWTAFCGPAGPRCLRTNAAVTVR
        70         80         90

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

```

                10         20         30         40         50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ...  .:  .:  ::  ::  :...  .  ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGGVGTIKKINF

```

```

                10         20         30         40         50
        60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
        60         70         80         90         100        110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (25-49:27-50)

```

                10         20         30         40         50
AAD-12 TVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::. .: .: :: ::::. . ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

        60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (25-49:27-50)

```

                10         20         30         40         50
AAD-12 TVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::. .: .: :: ::::. . ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

        60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
        60         70         80         90         100        110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (25-49:27-50)

```

                10         20         30         40         50
AAD-12 TVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::. .: .: :: ::::. . ::
gi+AHw-279 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF

```

```

                10         20         30         40         50
        60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10         20         30         40         50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: :::. . ::
gi+AHw-131 MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

        60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10         20         30         40         50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: :::. . ::
gi+AHw-602 MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

        60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
        60         70         80         90         100        110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10         20         30         40         50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: :::. . ::
gi+AHw-602 MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
```

```

                10         20         30         40         50
        60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)
  initn: 51 init1: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10         20         30         40         50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-602 MGVF TYESEFTSIIPP AR LFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

        60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
  initn: 51 init1: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10         20         30         40         50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-602 MGVF TYESEFTSVI PP AR LFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

        60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
  initn: 51 init1: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10         20         30         40         50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-602 MGVF TYESEFTSVI PP AR LFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
```

```

                10         20         30         40         50
        60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 50 initl: 50 opt: 52 Z-score: 85.2 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (21-49:23-50)

```

                10         20         30         40         50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGVFSAEVVPAVGGRTCFADMRA
                .. .:: : .: .: .: .::: . :
gi+AHw-444 MGVFYADESTSVITPPRLFALVLEAD-TLIPKIA PQSVKGAEIVEGDGGVGTIKKISF
                10         20         30         40         50

```

```

        60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVSADGGSIKSTS
        60         70         80         90         100        110

```

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34 prob (379 aa)
 initn: 48 initl: 48 opt: 57 Z-score: 84.9 bits: 22.2 E(): 9.4
 Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
 in 63 aa overlap (5-66:134-194)

```

                10         20         30
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
                : :: : : . . . .
gi+AHw-129 SKKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKG VITQVKYQGGCGRGWAFS
        110        120        130        140        150        160

```

```

        40         50         60         70         80
AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL
        : :: . . . . : : . . . . : : :
gi+AHw-129 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSF EWVLEHGGIATDDDDY
        170        180        190        200        210        220

```

```

gi+AHw-129 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISV SIDAKDFH
        230        240        250        260        270        280

```

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vacuola (379 aa)
 initn: 48 initl: 48 opt: 57 Z-score: 84.9 bits: 22.2 E(): 9.4
 Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
 in 63 aa overlap (5-66:134-194)

```

AAD-12 TVRQHSPAEWDDMMKVIVGNMAWHADSTY-MPVM
      :  ::  ::  :  .  .  .  .  .
gi+AHw-119 SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
      110      120      130      140      150      160

      40      50      60      70      80
AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSL
      :  ::  .  .  .  .  .  ::  .  .  .  .  .  :  .  .  .  .
gi+AHw-119 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFVWLEHGGIATDDDDY
      170      180      190      200      210      220

gi+AHw-119 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
      230      240      250      260      270      280

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:52 2010 done: Fri Feb 5 12:55:52 2010
Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 87 - 166 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      4      2:+ACo-
      32      3      8:+AD0AKg-
      34      6      21:+AD0APQ- +ACo-
      36      35      44:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38      39      72:+AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      40      98
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AK
g-
      42      53      123:+AD0APQ-+AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-

```


Lambda+AD0- 0.211971

Kolmogorov-Smirnov statistic: 0.1257 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR	RecName: Full+AD0-Po
(97) 65 25.2 0.29	
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL	RecName: Full+AD0-
(96) 63 24.6 0.44	
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-	(
144) 62 24.1 0.92	
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR	RecName: Full+AD0-Po
(97) 55 22.2 2.5	
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR	RecName: Full+AD0-P
(122) 56 22.4 2.7	
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group	(122)
56 22.4 2.7	
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group	(122)
56 22.4 2.7	
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group	(122)
56 22.4 2.7	
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram	(145)
57 22.6 2.7	
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P	(160)
57 22.6 3	
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa	(
160) 56 22.3 3.8	
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II	(196)
57 22.5 3.9	
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH	RecName: Full+AD0-Gl
(158) 55 22.0 4.6	
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-	
(379) 60 23.1 4.8	
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium	(
301) 58 22.6 5.5	
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P	(160)
54 21.6 5.7	
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs-	(
145) 53 21.4 6.3	
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1	(160)
53 21.3 7.1	
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1	(159)
52 21.0 8.7	
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1.	(159)
52 21.0 8.7	
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.	(159)
52 21.0 8.7	
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.	(159)
52 21.0 8.7	
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.	(159)
52 21.0 8.7	

gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
 52 21.0 8.7
 gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 21.0 8.7
 gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
 52 21.0 8.7
 gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
 52 21.0 8.7
 gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
 52 21.0 8.7
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.0 8.8
 gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34
 (379) 57 22.2 9.1
 gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
 57 22.2 9.1

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 57 init1: 57 opt: 65 Z-score: 111.9 bits: 25.2 E(): 0.29
 Smith-Waterman score: 65+ADs- 42.308+ACU- identity (65.385+ACU- similar)
 in 26 aa overlap (1-26:34-56)

			10	20	30
AAD-12			VRQHSPA EWDDMMKVIVGNMAWHADSTYMP		
		 :. . : : :. . . . :		
gi+AHw-126	DLTVEKGS	DAKTLVL	NIKYTRP	GDTLAEV	ELRQHG
	10	20	30	40	50
					60
	40	50	60	70	80
AAD-12	VMAQGAV	FSAEVVP	AVGGRT	CFADMRA	AYDALDE
					ATRALVH
					QRSARH
					SLV
gi+AHw-126	TGPMNFR	FLSKGG	MKNVF	DEVIPTA	FTVGKTY
	70	80	90		

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 53 init1: 53 opt: 63 Z-score: 108.7 bits: 24.6 E(): 0.44
 Smith-Waterman score: 63+ADs- 37.037+ACU- identity (66.667+ACU- similar)
 in 27 aa overlap (1-27:34-57)

			10	20	30
AAD-12			VRQHSPA EWDDMMKVIVGNMAWHADSTYMP		
		 :. . : : :. . . . :		
gi+AHw-144	TFKVEKGS	DPKLVLD	IKYTRP	GDTLAEV	ELRQHG
	10	20	30	40	50
					60
	40	50	60	70	80
AAD-12	VMAQGAV	FSAEVVP	AVGGRT	CFADMRA	AYDALDE
					ATRALVH
					QRSARH
					SLV
gi+AHw-144	TGPFNFR	FMSKGG	MRNVF	DEVIPTA	FKIGTTY
	70	80	90		

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 init1: 55 opt: 62 Z-score: 103.0 bits: 24.1 E(): 0.92
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (26-74:5-52)

```

                10      20      30      40      50      60
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD
                ..  ...  ...  ..  ..  ..  ..  ..  ..  ..
gi+AHw-189                MASKSSITPLLLAAV LASVF AAAAAATGQYCYAGMGLPSN
                        10      20      30

```

```

                70      80
AAD-12 ALDEATRALVHQRSARHSLV
                :  ..  :  :  ...
gi+AHw-189 PL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCRVRYFIGRRSH
                40      50      60      70      80      90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 36 init1: 36 opt: 55 Z-score: 95.4 bits: 22.2 E(): 2.5
 Smith-Waterman score: 55+ADs- 27.586+ACU- identity (51.724+ACU- similar)
 in 58 aa overlap (1-58:35-86)

```

                                10      20      30
AAD-12                                VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::  .  :  :  ..  :  :
gi+AHw-126 EFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKSDK-P
                10      20      30      40      50      60

```

```

                40      50      60      70      80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
                .  .:  .:  .  :  :  ..  :  :  :
gi+AHw-126 L--KGP-FNFRFVSEKGM RNVFDDVVPADFKVGT TYKPE
                70      80      90

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)
 initn: 44 init1: 44 opt: 56 Z-score: 94.7 bits: 22.4 E(): 2.7
 Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
 in 55 aa overlap (1-55:59-107)

```

                                10      20      30
AAD-12                                VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::  :  :  :  :  :  :
gi+AHw-117 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
                30      40      50      60      70      80

```

```

                40      50      60      70      80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
                .  ::  .:  .  .  :  :  :  :
gi+AHw-117 L--QGP-FNFRFLTEKGMKNV FDDVVPEKYTIGATYAPEE
                90      100      110      120

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
 initn: 44 init1: 44 opt: 56 Z-score: 94.7 bits: 22.4 E(): 2.7
 Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
 in 55 aa overlap (1-55:59-107)

```

                                10      20      30
AAD-12                        VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::  ::  :  .:  ::  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
                30      40      50      60      70      80

                40      50      60      70      80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV
.  ::  .:  .:  :  .:  ::
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 44 init1: 44 opt: 56 Z-score: 94.7 bits: 22.4 E(): 2.7
 Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
 in 55 aa overlap (1-55:59-107)

```

                                10      20      30
AAD-12                        VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::  ::  :  .:  ::  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
                30      40      50      60      70      80

                40      50      60      70      80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV
.  ::  .:  .:  :  .:  ::
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                90      100     110     120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 44 init1: 44 opt: 56 Z-score: 94.7 bits: 22.4 E(): 2.7
 Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
 in 55 aa overlap (1-55:59-107)

```

                                10      20      30
AAD-12                        VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::  ::  :  .:  ::  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
                30      40      50      60      70      80

                40      50      60      70      80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV
.  ::  .:  .:  :  .:  ::
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                90      100     110     120

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)

initn: 50 init1: 50 opt: 57 Z-score: 94.7 bits: 22.6 E(): 2.7
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (26-74:5-52)

```

                10         20         30         40         50         60
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD
                ..  ...  ...  ..  ..  ..  ..  ::  :
gi+AHw-439                MASKSSITPLLLAAVLA SVFAAATATGQYCYAGMGLPSN
                        10         20         30

```

```

                70         80
AAD-12 ALDEATRALVHQRSARHSLV
                :  ::  :  :  :..
gi+AHw-439 PL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRC EAVRYFIGRRS
                40         50         60         70         80         90

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)

initn: 55 init1: 55 opt: 57 Z-score: 93.7 bits: 22.6 E(): 3
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (20-48:23-50)

```

                10         20         30         40         50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  ::  :  :  :  :  ::  ::  :
gi+AHw-444 MGVTYADESTSVIPPR LFKALVLEAD-TLIPK IAPQSVKSAEIVEGDGGVGTIKKISF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLV
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)

initn: 55 init1: 55 opt: 56 Z-score: 92.1 bits: 22.3 E(): 3.8
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

```

                10         20         30         40         50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::  ..  :  :  :  :  ::  :
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHA IKS AEIIEGNGGPGTIKKITF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLV
gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
(196 aa)

initn: 36 init1: 36 opt: 57 Z-score: 91.7 bits: 22.5 E(): 3.9
Smith-Waterman score: 57+ADs- 27.586+ACU- identity (53.448+ACU- similar)
in 58 aa overlap (1-58:35-86)

```

                                10      20      30
AAD-12                        VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::  .  :  :.  ...  :  :
gi+AHw-109 TFTVEKGSDEKLNLSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKSDK-P
                                10      20      30      40      50      60
    
```

```

                                40      50      60      70      80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR LVHQRSARHSLV
                                .  .:  :.  .  :  :  :.  :...  :
gi+AHw-109 L--KGP-FNFRFVSEKGM RNVFVDVVPADFKVGT TTYKPEEAAAASARRRSSEVFQFLILS
                                70      80      90      100     110
    
```

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
Full+AD0-Globin (158 aa)
initn: 39 init1: 39 opt: 55 Z-score: 90.5 bits: 22.0 E(): 4.6
Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
in 34 aa overlap (5-32:114-147)

```

                                10      20
AAD-12                        VRQHSPA EWDDMMKVIV----GNMAWHA--DSTY
                                :...  ...  :  :  :  :  :  :...
gi+AHw-250 EVMDLLGN DANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLK GATKWDSAVESSW
                                90      100     110     120     130     140
    
```

```

                                30      40      50      60      70      80
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR LVHQRSARHSLV
                                :...
gi+AHw-250 APVLDFV FSTLKNEL
                                150
    
```

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
max+AF0- (379 aa)
initn: 48 init1: 48 opt: 60 Z-score: 90.1 bits: 23.1 E(): 4.8
Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
in 63 aa overlap (4-65:134-194)

```

                                10      20      30
AAD-12                        VRQHSPA EWDDMMKVIVGNMAWHAD-STYMPVM
                                :  ::  ::  :  .  .  .  .  .  .
gi+AHw-309 SKKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKG VITQVKYQGGCGSGWAFS
                                110     120     130     140     150     160
    
```

```

                                40      50      60      70      80
AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR LVHQRSARHSLV
                                :  ::  .....  ::  .  .....  .  :  :...
gi+AHw-309 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSF EWVLEHGGIATDDDDY
                                170     180     190     200     210     220
    
```


gi+AHw-217 PL-EGCREYVAQQTTCGISISGSAVSTEPGNTPRDRCCCKELYDASQHCRCCEAVRYFIGRRS
40 50 60 70 80 90

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 87.1 bits: 21.3 E(): 7.1
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (29-80:31-87)

10 20 30 40 50
AAD-12 VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
.: .: .: .: .: .: .: .: .:
gi+AHw-132 MGVFNJETETTSVIPPARLFKRFLVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
10 20 30 40 50

60 70 80
AAD-12 DMRAAYDALDEATRALLVHQR-SARHSLV
: : : : : :
gi+AHw-132 DEGSPFNFIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
60 70 80 90 100 110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
: : .: .: .: : : : : : : : :
gi+AHw-279 MGVFTYESEFTSVIPPARLFNFAVFLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALLVHQRSARHSLV
gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
: : .: .: .: : : : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNFAVFLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALLVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :::: . :
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :::: . :
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :::: . :
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
 +AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (24-48:27-50)

10 20 30 40 50
 AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: ::::. . ::
 gi+AHw-131 MGVFN YETEF TSVIP PARLFN AFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
 1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (24-48:27-50)

10 20 30 40 50
 AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: ::::. . ::
 gi+AHw-602 MGVFTY ESEFTSVIP PARLFN AFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
 1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (24-48:27-50)

10 20 30 40 50
 AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: ::::. . ::
 gi+AHw-602 MGVFTY ESEFTSVIP PARLFN AFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
 1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (24-48:27-50)

10 20 30 40 50
 AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 :: .: .: :: :::: . ::
 gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDDGGVGTIKKINF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
 1.03A (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (24-48:27-50)

10 20 30 40 50
 AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 :: .: .: :: :::: . ::
 gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDDGGVGTIKKINF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 50 init1: 50 opt: 52 Z-score: 85.4 bits: 21.0 E(): 8.8
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (20-48:23-50)

10 20 30 40 50
 AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. :: : .: .: .: :::: . ::
 gi+AHw-444 MGVFYADESTSVITPPRLFKALVLEAD-TLIPKIA PQSVKGAEIVEGDDGGVGTIKKISF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
Full+AD0-P34 prob (379 aa)
initn: 48 initl: 48 opt: 57 Z-score: 85.1 bits: 22.2 E(): 9.1
Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
in 63 aa overlap (4-65:134-194)

AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
: : : : :
gi+AHw-129 SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKG VITQVKYQGGCGRGWAFS
110 120 130 140 150 160

AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV
: : : : : : : : :
gi+AHw-129 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSF EWVLEHGGIATDDDDY
170 180 190 200 210 220

gi+AHw-129 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTES ETEQAFLSAILEQPISV SIDAKDFH
230 240 250 260 270 280

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
vacuola (379 aa)
initn: 48 initl: 48 opt: 57 Z-score: 85.1 bits: 22.2 E(): 9.1
Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
in 63 aa overlap (4-65:134-194)

AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
: : : : :
gi+AHw-119 SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKG VITQVKYQGGCGRGWAFS
110 120 130 140 150 160

AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLV
: : : : : : : : :
gi+AHw-119 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSF EWVLEHGGIATDDDDY
170 180 190 200 210 220

gi+AHw-119 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTES ETEQAFLSAILEQPISV SIDAKDFH
230 240 250 260 270 280

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:52 2010 done: Fri Feb 5 12:55:52 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-


```

68 41 20:+AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
70 19 16:+AD0APQA9ACoAPQ-
72 34 12:+AD0APQAqAD0APQA9AD0APQA9-
74 19 10:+AD0APQAqAD0APQ-
76 26 7:+AD0AKgA9-+AD0APQA9AD0-
78 8 6:+AD0AKg-
80 8 4:+ACoAPQ-
82 1 3:+ACo-
84 17 3:+ACoAPQA9AD0APQ-
86 2 2:+ACo-
88 3 2:+ACo- inset +AD0- represents 1 library sequences
90 3 1:+ACo-
92 6 1:+ACoAPQ- :+ACoAPQA9AD0APQA9-
94 2 1:+ACo- :+ACoAPQ-
96 0 1:+ACo- :+ACo-
98 0 0: +ACo-
100 0 0: +ACo-
102 1 0:+AD0- +ACoAPQ-
104 0 0: +ACo-
106 1 0:+AD0- +ACoAPQ-
108 0 0: +ACo-
110 1 0:+AD0- +ACoAPQ-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.00820.00294+ADs- mu+AD0- 0.1418
0.153
mean+AF8-var+AD0-36.4107 9.920, 0's: 2 Z-trim: 2 B-trim: 223 in 2/41
Lambda+AD0- 0.212549
Kolmogorov-Smirnov statistic: 0.1244 (N+AD0-29) at 46

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po

(97) 64 24.9 0.36

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-

(96) 62 24.3 0.55

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (

144) 62 24.1 0.92

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145)

57 22.6 2.7

gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po

(97) 54 21.8 3

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)

57 22.6 3

gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)

55 22.1 3.3

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
55 22.1 3.3
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
(122) 55 22.1 3.3
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
55 22.1 3.3
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
56 22.3 3.8
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-G1
(158) 55 22.0 4.6
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
(379) 60 23.1 4.8
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
56 22.2 4.9
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
58 22.6 5.5
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
54 21.6 5.8
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145)
53 21.4 6.3
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160)
53 21.3 7.1
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
52 21.0 8.7
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.7
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.7
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.7
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.7
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
52 21.0 8.7
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.7
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.7
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.7
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.7
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
52 21.0 8.8
gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34
(379) 57 22.2 9.2
gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
57 22.2 9.2

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 56 init1: 56 opt: 64 Z-score: 110.3 bits: 24.9 E(): 0.36
Smith-Waterman score: 64+ADs- 44.000+ACU- identity (64.000+ACU- similar)
in 25 aa overlap (1-25:35-56)

```

                                10      20      30
AAD-12                        RQHSPA EWDDMMKVIVGNMAWHADSTYMPV
                                : : : : : : : : :
gi+AHw-126 LTVEKGS DAKTLV LNIKYTRPGDTLAEVELRQH GSEEWEPMTK--KGNL-WEVKSAKPLT
                   10      20      30      40      50      60

```

```

                   40      50      60      70      80
AAD-12 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY

gi+AHw-126 GPMNFRFLSKGGMKNV FDEVIPTAFTV GKTYYTPEYN
                   70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 52 init1: 52 opt: 62 Z-score: 107.1 bits: 24.3 E(): 0.55
 Smith-Waterman score: 62+ADs- 38.462+ACU- identity (65.385+ACU- similar)
 in 26 aa overlap (1-26:35-57)

```

                                10      20      30
AAD-12                        RQHSPA EWDDMMKVIVGNMAWHADSTYMPV
                                : : : : : : : : :
gi+AHw-144 FKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEEWEP LTKK--GNL-WEVKSSKPLT
                   10      20      30      40      50      60

```

```

                   40      50      60      70      80
AAD-12 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY

gi+AHw-144 GPFNFRFMSKGGMRNV FDEVIPTAFKIGT TYTPEE
                   70      80      90

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 init1: 55 opt: 62 Z-score: 103.0 bits: 24.1 E(): 0.92
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (25-73:5-52)

```

                   10      20      30      40      50      60
AAD-12 RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDA
                                :. :.. ... :. .. :. :. :. :
gi+AHw-189                        MASKSSITPLLLAAVLASVF AAAAAATGQYCYAGMGLPSNP
                                10      20      30      40

```

```

                   70      80
AAD-12 LDEATR ALVHQRSARHSLVY
                   : : : : :
gi+AHw-189 L-EGCREYVAQQTCGV TIAGSPVSSEPGDTPKDRCCQELDEAPQHCR CRVRYFIGRRSHP
                   50      60      70      80      90

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)
 initn: 50 init1: 50 opt: 57 Z-score: 94.7 bits: 22.6 E(): 2.7
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (25-73:5-52)


```

                                10      20      30
AAD-12                        RQHSPAEWDDMMKVIVGNMAWHADSTYMPV
                                :...  ::  :  :  :  .:  ::  :.
gi+AHw-400 VTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-PL
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                                ::  :.  .  .  :  .:  ::
gi+AHw-400 --QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 43 init1: 43 opt: 55 Z-score: 93.1 bits: 22.1 E(): 3.3
 Smith-Waterman score: 55+ADs- 31.481+ACU- identity (50.000+ACU- similar)
 in 54 aa overlap (1-54:60-107)

```

                                10      20      30
AAD-12                        RQHSPAEWDDMMKVIVGNMAWHADSTYMPV
                                :...  ::  :  :  :  .:  ::  :.
gi+AHw-400 VTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-PL
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                                ::  :.  .  .  :  .:  ::
gi+AHw-400 --QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-Polle (122 aa)

initn: 43 init1: 43 opt: 55 Z-score: 93.1 bits: 22.1 E(): 3.3
 Smith-Waterman score: 55+ADs- 31.481+ACU- identity (50.000+ACU- similar)
 in 54 aa overlap (1-54:60-107)

```

                                10      20      30
AAD-12                        RQHSPAEWDDMMKVIVGNMAWHADSTYMPV
                                :...  ::  :  :  :  .:  ::  :.
gi+AHw-117 VTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-PL
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 MAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                                ::  :.  .  .  :  .:  ::
gi+AHw-117 --QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 43 init1: 43 opt: 55 Z-score: 93.1 bits: 22.1 E(): 3.3
 Smith-Waterman score: 55+ADs- 31.481+ACU- identity (50.000+ACU- similar)
 in 54 aa overlap (1-54:60-107)

```

                                10      20      30
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPV
                                :.:. :. : : :. :. :. :.
gi+AHw-400  VTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-PL
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12  MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY
                                :: :. . . : .. : ::
gi+AHw-400  --QGP-FNFRFLTEKGMKNVFD DVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 init1: 55 opt: 56 Z-score: 92.0 bits: 22.3 E(): 3.8
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                                10      20      30      40      50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                :.:. :. :. :. :. :. :.
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVL DADNL-IPKLAPHAIKSAEII EGNNGGPGTIKKITF
                                10      20      30      40      50

```

```

                                60      70      80
AAD-12  AYDALDEATR ALVHQRSARHSLVY

```

```

gi+AHw-165  GEGSQFKYVKHRIDEIDQANFTYCY SVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
 Full+AD0-Globin (158 aa)
 initn: 39 init1: 39 opt: 55 Z-score: 90.5 bits: 22.0 E(): 4.6
 Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
 in 34 aa overlap (4-31:114-147)

```

                                10      20
AAD-12      RQHSPA EWDDMMKVIV----GNMAWHA--DSTY
                                :.:. :. :. :. :. :. :.
gi+AHw-250  EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLK GATKWDSAVESSW
                                90      100     110     120     130     140

```

```

                                30      40      50      60      70      80
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVY

```

```

                                :.:.
gi+AHw-250  APVLDFVFSTLKNEL
                                150

```

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0- (379 aa)
 initn: 48 init1: 48 opt: 60 Z-score: 90.1 bits: 23.1 E(): 4.8
 Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
 in 63 aa overlap (3-64:134-194)

```

                                10      20      30
AAD-12      RQHSPAEWDDMMKVIVGNMAWHAD-STYMPVM
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-309  SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGSGWAFS
              110      120      130      140      150      160
    
```

```

                40      50      60      70      80
AAD-12  AQQAVFSAEVVPAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVY
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-309  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFVWLEHGGIATDDDDY
              170      180      190      200      210      220
    
```

```

gi+AHw-309  PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
              230      240      250      260      270      280
    
```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196 aa)
 initn: 35 init1: 35 opt: 56 Z-score: 90.0 bits: 22.2 E(): 4.9
 Smith-Waterman score: 56+ADs- 28.070+ACU- identity (52.632+ACU- similar)
 in 57 aa overlap (1-57:36-86)

```

                                10      20      30
AAD-12      RQHSPAEWDDMMKVIVGNMAWHADSTYMPV
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-109  FTVEKGSDEKLNLSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKSDK-PL
              10      20      30      40      50      60
    
```

```

                40      50      60      70      80
AAD-12  MAQQAVFSAEVVPAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVY
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-109  --KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGTTYKPEEAAAASASRRRSSEVFQFLILSC
              70      80      90      100      110
    
```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium per (301 aa)
 initn: 49 init1: 49 opt: 58 Z-score: 89.1 bits: 22.6 E(): 5.5
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (20-69:23-71)

```

                10      20      30      40      50
AAD-12      RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQQAVFSAEVVPAVGGRTCFADMRAA
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-663  MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
              10      20      30      40      50
    
```

```

                60      70      80
AAD-12  YDALDEATRNLVHQRSARHSLVY
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-663  LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
              60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 88.7 bits: 21.6 E(): 5.8
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (19-47:23-50)

```

                10      20      30      40      50
AAD-12      RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  :::  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFYTSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDDGGVGTIKKISF
                10      20      30      40      50

```

```

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVY

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
 +AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 88.0 bits: 21.4 E(): 6.3
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (25-73:5-52)

```

                10      20      30      40      50      60
AAD-12  RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDA
                ..  ...  ..  :  :  :  :  :  :  :  :  :  :
gi+AHw-217  MASKSSISPLLLLATV LVS VFAAATATGPYCYAGMGLPINP
                10      20      30      40

```

```

                70      80
AAD-12  LDEATRALVHQRSARHSLVY
                :  :  :  :  :  :
gi+AHw-217  L-EGCREYVAQQTCGISISGS AVSTEPGNTPRDRCKELYDASQHCRCEAVRYFIGRRSD
                50      60      70      80      90

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)

initn: 47 initl: 47 opt: 53 Z-score: 87.1 bits: 21.3 E(): 7.1
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (28-79:31-87)

```

                10      20      30      40      50
AAD-12      RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
                ..  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-132  MGVFNYETETTSVIPPARLFKRFVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
                10      20      30      40      50

```

```

                60      70      80
AAD-12  DMRAAYDALDEATRALVHQR-SARHSLVY
                :  .  .  .  .  .  .  :  :  :  :
gi+AHw-132  DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
 +AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::..  .  ::
gi+AHw-279  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

        60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

```

```

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
 1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::..  .  ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

        60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
        60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
 1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::..  .  ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

        60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSNGSGSVIKSTSH
        60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
 1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::..  .  ::
gi+AHw-602  MGVF TYESEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

        60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::..  .  ::
gi+AHw-602  MGVF TYESEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

        60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::..  .  ::
gi+AHw-131  MGVF NYETEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

        60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

```

```

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::..  .  ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

                60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
 1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::..  .  ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

                60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
 1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::..  .  ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

                60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
 1.03A (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  .:  .:  .:  .:  .:  .:  .:
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVL DADNL-IPK IAPQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

        60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 50 init1: 50 opt: 52 Z-score: 85.4 bits: 21.0 E(): 8.8
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (19-47:23-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  .:  .:  .:  .:  .:  .:  .:
gi+AHw-444  MGVF TYADESTSVITP PRLFKALVLEAD-TLIPK IAPQSVKGA EIVEG DGGVGTIKKISF
                10         20         30         40         50

```

```

        60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

```

```

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
        60         70         80         90         100        110

```

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
 Full+AD0-P34 prob (379 aa)

initn: 48 init1: 48 opt: 57 Z-score: 85.1 bits: 22.2 E(): 9.2
 Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
 in 63 aa overlap (3-64:134-194)

```

                                10         20         30
AAD-12                                RQHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
                                :  :  :  :  :  :  :  :
gi+AHw-129  SKKYLQAPKDVSQQIKMANKMKKQEYSCDHPPASWDWRKKG VITQVKYQGGCGRGWAFS
                110        120        130        140        150        160

```

```

        40         50         60         70         80
AAD-12  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
        :  :  :  .:  .:  .:  .:  .:  .:  .:

```

```

gi+AHw-129  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSF EWVLEHGGIATDDDDY
                170        180        190        200        210        220

```

```

gi+AHw-129  PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISV SIDAKDFH
                230        240        250        260        270        280

```

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
 vacuola (379 aa)
 initn: 48 init1: 48 opt: 57 Z-score: 85.1 bits: 22.2 E(): 9.2
 Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
 in 63 aa overlap (3-64:134-194)

```

                                10      20      30
AAD-12                        RQHSPAEWDDMMKVIVGNMAWHADSTY-MPVM
                                :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-119 SKKYLQAPKDVSQQIKMANKMKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
                                110      120      130      140      150      160

                                40      50      60      70      80
AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVY
                                :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-119 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFVWLEHGGIATDDDDY
                                170      180      190      200      210      220

gi+AHw-119 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTETEQAFLSAILEQPISVSIDAKDFH
                                230      240      250      260      270      280
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:52 2010 done: Fri Feb 5 12:55:52 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 89 - 168 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 4 library sequences
24	0	0:	
26	0	0:	
28	2	0:+AD0-	
30	2	2:+ACo-	
32	9	8:+AD0AKgA9-	
34	4	21:+AD0- +ACo-	


```

114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.96080.00297+ADs- mu+AD0- 0.3733
0.155
mean+AF8-var+AD0-37.4504 9.925, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.209578
Kolmogorov-Smirnov statistic: 0.1244 (N+AD0-29) at 46

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.0 1
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 57 22.6 1.8
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 55 22.0 2.6
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 22.5 2.9
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.5 3.3
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.1 4
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
( 158) 55 21.9 4.9
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379) 60 23.0 5.1
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.5 5.9
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.5 6.2
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 51 20.8 6.2
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.3 6.7
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.2 7.6
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.0 8.8
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.3
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 20.9 9.3
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.3
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.3
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.3

```

gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
 52 20.9 9.3
 gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
 52 20.9 9.3
 gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
 52 20.9 9.3
 gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 20.9 9.3
 gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
 52 20.9 9.3
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 20.9 9.4
 gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34
 (379) 57 22.1 9.6
 gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
 57 22.1 9.6
 gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
 53 21.2 9.8

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 init1: 55 opt: 62 Z-score: 102.3 bits: 24.0 E(): 1
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (24-72:5-52)

```

                10      20      30      40      50      60
AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDAL
                ..  ...  ...  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..  ..
gi+AHw-189                MASKSSITPLLLLA AVLASFVFAAAAATGQYCYAGMGLPSNPL
                        10      20      30      40
    
```

```

                70      80
AAD-12 DEATRALVHQRSARHSLVYS
                ..  :  :  :  ..
gi+AHw-189 -EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRVRYFIGRRSHPD
                50      60      70      80      90      100
    
```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 49 init1: 49 opt: 57 Z-score: 98.0 bits: 22.6 E(): 1.8
 Smith-Waterman score: 57+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (1-24:36-56)

```

                                10      20      30
AAD-12                                QHSPA EWDDMMKVIVGNMAWHADSTYMPVM
                                ...  ...  :  :  ...  ...  :
gi+AHw-126 TVEKGS DAKTLVLN I KYTRPGDTLAEVELRQH GSEEWEPMTKK--GNL-WEVKS AKPLTG
                10      20      30      40      50      60
    
```

```

                40      50      60      70      80
AAD-12 AQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS

gi+AHw-126 PMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                70      80      90
    
```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 45 initl: 45 opt: 55 Z-score: 94.8 bits: 22.0 E(): 2.6
Smith-Waterman score: 55+ADs- 36.000+ACU- identity (64.000+ACU- similar)
in 25 aa overlap (1-25:36-57)

```

                                10      20      30
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVM
                                ::.  ::.  . :  ::.  ::.  ::.
gi+AHw-144  KVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEEW EPLTKK--GNL-WEVKSSKPLTG
              10      20      30      40      50      60

```

```

              40      50      60      70      80
AAD-12  A QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYS

```

```

gi+AHw-144  PFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTP EE
              70      80      90

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
tetrameric (145 aa)
initn: 50 initl: 50 opt: 57 Z-score: 94.1 bits: 22.5 E(): 2.9
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (24-72:5-52)

```

              10      20      30      40      50      60
AAD-12  QHSPA EWDDMMKVIVGNMAWHADSTYMPVMA QGAVFSAEVVPAVGGRTCFADMRAAYDAL
                                ..  ...  ..  ..  ..  ..  ::.  :  . :
gi+AHw-439  MASKSSITPLLLLA AVLASF AAATATGQYCYAGMGLPSNPL
              10      20      30      40

```

```

              70      80
AAD-12  DEATR ALVHQRSARHSLVYS
              ..  :  :  ::.
gi+AHw-439  -EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHP
              50      60      70      80      90      100

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 initl: 55 opt: 57 Z-score: 93.1 bits: 22.5 E(): 3.3
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (18-46:23-50)

```

              10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMA QGAVFSAEVVPAVGGRTCFADMRA
                                ..  ::.  :  . :  . :  ::.  . :
gi+AHw-444  MG VFTYADESTSVIPPR LFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTIKKISF
              10      20      30      40      50

```

```

              60      70      80
AAD-12  AYDALDEATR ALVHQRSARHSLVYS

```

```

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
              60      70      80      90      100      110

```


gi+AHw-309 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
 230 240 250 260 270 280

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
 Lolium per (301 aa)

initn: 49 init1: 49 opt: 58 Z-score: 88.6 bits: 22.5 E(): 5.9
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (19-68:23-71)

10 20 30 40 50
 AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
 .. :: : : : . : ::::: : : .
 gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
 10 20 30 40 50

60 70 80
 AAD-12 YDALDEATRALVHQRSARHSLVYS
 : :
 gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
 60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 52 init1: 52 opt: 54 Z-score: 88.2 bits: 21.5 E(): 6.2
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (18-46:23-50)

10 20 30 40 50
 AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. :: : : : . : ::::: . : :
 gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIIAPQSVKTAIEIVEGDDGGVGTIKKISF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYS
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)

initn: 32 init1: 32 opt: 51 Z-score: 88.2 bits: 20.8 E(): 6.2
 Smith-Waterman score: 51+ADs- 28.571+ACU- identity (50.000+ACU- similar)
 in 56 aa overlap (1-56:37-86)

10 20 30
 AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVM
 ... :: . : : . . . : : .
 gi+AHw-126 TVEKGSDEKNLALSIIKYNKEGDSMAEVELKEHGSNEWLALKK--NGDGVWEIKSDK-PL-
 10 20 30 40 50 60

40 50 60 70 80
 AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS

```

      .:  .:  .:  .:  .:  .:  .:
gi+AHw-126 -KGP-FNFRFVSEKGMARNVFDVVPADFKVGTTYKPE
              70              80              90

```

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
  initn: 46 initl: 46 opt: 53 Z-score: 87.5 bits: 21.3 E(): 6.7
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (24-72:5-52)

```

```

              10              20              30              40              50              60
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL
              .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-217              MASKSSISPLLLATVLSVFAAATATGPYCYAGMLPINPL
              10              20              30              40

```

```

              70              80
AAD-12 DEATRALVHQRSARHSLVYS
      .:  .:  .:  .:
gi+AHw-217 -EGCREYVAQQTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDP
              50              60              70              80              90              100

```

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
  initn: 47 initl: 47 opt: 53 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (27-78:31-87)

```

```

              10              20              30              40              50
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCF
              .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-132 MGVFNYETETTSVIPPARLFKRFVLDSNDLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
              10              20              30              40              50

```

```

              60              70              80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYS
      :  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-132 DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
              60              70              80              90              100              110

```

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
  initn: 52 initl: 52 opt: 52 Z-score: 85.4 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (57-80:29-52)

```

```

              30              40              50              60              70              80
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
              :  :  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEEAARISAKNALESYAYSLRNTLS
              10              20              30              40              50

```

```

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
              60              70              80              90              100              110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVF TYESEFTS IIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGV DKNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-279  MGVF TYESEFTS V IIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-279  GEGSTYSYVKHRIDGV DKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVF TYESEFTS V IIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGV DKNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-131  MGVF NYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
 1.03A (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::..  .  ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLADNL-IPK IAPQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

gi+AHw-602  GEGSTYSYVKHRIDGV DKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 50 init1: 50 opt: 52 Z-score: 84.9 bits: 20.9 E(): 9.4
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (18-46:23-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  ::  :  :  :  .:  :::..  .  ::
gi+AHw-444  MGVF TYADESTSVITPPRLFKALVLEAD-TLIPK IAPQSVKGAEIVEG DGGVGTIKKISF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
 Full+AD0-P34 prob (379 aa)
 initn: 48 init1: 48 opt: 57 Z-score: 84.7 bits: 22.1 E(): 9.6
 Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
 in 63 aa overlap (2-63:134-194)

```

                                10      20      30
AAD-12                                QHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
                                :  ::  ::  :  .  .  .  .  .
gi+AHw-129  SKKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKG VITQVKYQGGCGRGWAFS
                110      120      130      140      150      160

                40      50      60      70      80
AAD-12  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
                :  ::.  .:..  .:  .  .:..  .  :  .:..
gi+AHw-129  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSF EWVLEHGGIATDDDDY
                170      180      190      200      210      220
    
```

gi+AHw-129 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
230 240 250 260 270 280

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
vacuola (379 aa)
initn: 48 init1: 48 opt: 57 Z-score: 84.7 bits: 22.1 E(): 9.6
Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
in 63 aa overlap (2-63:134-194)

AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
: : : : :
gi+AHw-119 SKKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
110 120 130 140 150 160

AAD-12 A QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYS
: : : : : : : :
gi+AHw-119 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSF EWVLEHGGIATDDDDY
170 180 190 200 210 220

gi+AHw-119 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
230 240 250 260 270 280

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
(196 aa)
initn: 34 init1: 34 opt: 53 Z-score: 84.6 bits: 21.2 E(): 9.8
Smith-Waterman score: 53+ADs- 28.571+ACU- identity (51.786+ACU- similar)
in 56 aa overlap (1-56:37-86)

AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVM
. . . : : : : :
gi+AHw-109 TVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWL LKK--NGDGVWEIKSDK-PL-
10 20 30 40 50 60

AAD-12 A QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYS
. : . . : : : :
gi+AHw-109 -KGP-FNFRFVSEKGM RNVFVDVVPADFKVGT TYKPEEAAAASARRRSSEVFQFLILSCQ
70 80 90 100 110 120

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:53 2010 done: Fri Feb 5 12:55:54 2010
Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1


```

66      56      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
68      48      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0-
70      13      16:+AD0APQA9AD0APQAq-
72      38      12:+AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0-
74      17      10:+AD0APQA9ACoAPQA9-
76      17      7:+AD0APQAqAD0APQA9-
78      22      6:+AD0AKgA9AD0APQA9AD0APQ-
80      7       4:+AD0AKgA9-
82      3       3:+ACo-
84      10      3:+ACoAPQA9AD0-
86      12      2:+ACoAPQA9AD0-
88      3       2:+ACo-          inset +AD0- represents 1 library sequences
90      3       1:+ACo-
92      1       1:+ACo-          :+ACo-
94      2       1:+ACo-          :+ACoAPQ-
96      0       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     1       0:+AD0-          +ACoAPQ-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.09580.00295+ADs- mu+AD0- -
0.5339 0.154
mean+AF8-var+AD0-36.5168 9.708, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.212240
Kolmogorov-Smirnov statistic: 0.1298 (N+AD0-29) at 46

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.2 0.88
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.7 2.6
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.6 2.9
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.3 3.6
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 54 21.8 4.4
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-G1
( 158) 55 22.0 4.4
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379) 60 23.2 4.7

```

gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 58 22.7 5.3
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 54 21.7 5.5
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.4 6
 gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po (97) 50 20.7 6.8
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.4 6.8
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.1 7.9
 gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po (97) 49 20.4 8.3
 gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.4
 gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.4
 gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159) 52 21.1 8.4
 gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.4
 gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.4
 gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.4
 gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.4
 gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159) 52 21.1 8.4
 gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.4
 gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.4
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160) 52 21.1 8.4
 gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34 (379) 57 22.3 8.9
 gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379) 57 22.3 8.9

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 103.4 bits: 24.2 E(): 0.88
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (23-71:5-52)

	10	20	30	40	50	60
AAD-12	HSPA	EWD	DDMMKVIVGNMAWHADSTYMPVMAQGA	VFSAEVVP	PAVGGRTCFADMRAAYDALD	
gi+AHw-189		
			MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-			
			10	20	30	40
	70	80				

AAD-12 EATRALVHQRSARHSLVYSQ

.. : : ..

gi+AHw-189 EGCREYVAQQTTCGVVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDW
 50 60 70 80 90 100

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)

initn: 50 init1: 50 opt: 57 Z-score: 95.0 bits: 22.7 E(): 2.6
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (23-71:5-52)

10 20 30 40 50 60
 AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD
 .. :.. :.. :. :. :. :. :. :.
 gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-
 10 20 30 40

70 80
 AAD-12 EATRALVHQRSARHSLVYSQ
 .. : : ..
 gi+AHw-439 EGCREYVAQQTTCGVVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPD
 50 60 70 80 90 100

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)

initn: 55 init1: 55 opt: 57 Z-score: 94.0 bits: 22.6 E(): 2.9
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (17-45:23-50)

10 20 30 40 50
 AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. :.. :. :. :. :. :. :.
 gi+AHw-444 MGVF TYADESTSVIPPR LFKALVLEAD-TLIPKIAPQSVKSAEIVEG DGGVGTIKKISF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQ
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)

initn: 55 init1: 55 opt: 56 Z-score: 92.4 bits: 22.3 E(): 3.6
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (21-45:27-50)

10 20 30 40 50
 AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 :.. :. :. :. :. :. :.
 gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIEGNGGPGTIKKITF
 10 20 30 40 50
 60 70 80

AAAD-12 AYDALDEATRALVHQRSARHSLVYSQ

gi+AHw-165 GEGSQFKYVVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
60 70 80 90 100 110

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 32 init1: 32 opt: 54 Z-score: 90.8 bits: 21.8 E(): 4.4
Smith-Waterman score: 54+ADs- 32.000+ACU- identity (64.000+ACU- similar)
in 50 aa overlap (33-80:9-54)

10 20 30 40 50 60
AAAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--D
: : : : . : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIE
10 20 30

70 80
AAAD-12 EATRALVHQRSARHSLVYSQ
: : : : : :
gi+AHw-111 QANHAI---EKGEHQLLYLQHQDELNENKSKELQEKIIRELDVVCAMIEGAQGalEREL
40 50 60 70 80 90

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
Full+AD0-Globin (158 aa)
initn: 39 init1: 39 opt: 55 Z-score: 90.8 bits: 22.0 E(): 4.4
Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
in 34 aa overlap (2-29:114-147)

10 20
AAAD-12 HSPAEWDDMMKVIV----GNMAWHA--DSTY
: : : : : : : :
gi+AHw-250 EVMDLLGNdANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGGATKWDSAVESSW
90 100 110 120 130 140

30 40 50 60 70 80
AAAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
: :
gi+AHw-250 APVLDFVVFSTLKNEL
150

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
max+AF0- (379 aa)
initn: 48 init1: 48 opt: 60 Z-score: 90.3 bits: 23.2 E(): 4.7
Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
in 63 aa overlap (1-62:134-194)

10 20
AAAD-12 HSPAEWDDMMKVIVGNMAWHAD-STYMPVM
: : : : : : : :
gi+AHw-309 SKKYLQAPKDVSQQIKMANKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGSGWAFS
110 120 130 140 150 160
30 40 50 60 70 80

AAAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQ

: :: : : : :

gi+AHw-309 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFVWLEHGGIATDDDDY
170 180 190 200 210 220

gi+AHw-309 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSDAKDFH
230 240 250 260 270 280

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)

initn: 49 initl: 49 opt: 58 Z-score: 89.3 bits: 22.7 E(): 5.3
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (18-67:23-71)

AAAD-12 10 20 30 40 50
HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGVFSAEVVPAVGGRTCFADMRAA

gi+AHw-663 MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
10 20 30 40 50

AAAD-12 60 70 80
YDALDEATRVLVHQRSARHSLVYSQ

gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSADAKAPGLILKLDTDYDVA
60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 89.0 bits: 21.7 E(): 5.5
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (17-45:23-50)

AAAD-12 10 20 30 40 50
HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGVFSAEVVPAVGGRTCFADMRA

gi+AHw-444 MGVTYSDESTSVIPPRLFKALVLEAD-TLIPKIAPQSVKTAEIVEGDDGGVGTIKKISF
10 20 30 40 50

AAAD-12 60 70 80
AYDALDEATRVLVHQRSARHSLVYSQ

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 88.4 bits: 21.4 E(): 6
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (23-71:5-52)

AAAD-12 10 20 30 40 50 60
HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGVFSAEVVPAVGGRTCFADMRAAYDALD

gi+AHw-217 MASKSSISPLLLATVLSVFAAATATGPYCYAGMGLPINPL-

```

                                10      20      30      40
AAD-12      70      80
EATRALVHQRSARHSLVYSQ
      .. : : ...
gi+AHw-217  EGREYVAQQTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRCEAVRYFIGRRSDPN
                                50      60      70      80      90      100

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 42 init1: 42 opt: 50 Z-score: 87.5 bits: 20.7 E(): 6.8
 Smith-Waterman score: 50+ADs- 39.130+ACU- identity (60.870+ACU- similar)
 in 23 aa overlap (1-23:37-56)

```

                                10      20      30
AAD-12      HSPAEWDDMMKVIVGNMAWHADSTYMPVMA
                                .. ::: : : ::: ... :
gi+AHw-126  VEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNL-WEVKSAPLTPG
                                10      20      30      40      50      60

```

```

                                40      50      60      70      80
AAD-12  QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
gi+AHw-126  MNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                                70      80      90

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 +AFs-Cor (160 aa)
 initn: 47 init1: 47 opt: 53 Z-score: 87.4 bits: 21.4 E(): 6.8
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (26-77:31-87)

```

                                10      20      30      40      50
AAD-12      HSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
                                .: .: .: : ... .: .: .:
gi+AHw-132  MGVFNJETETTSVIPPARLFKRFVLDSDNLIPKVAPKAIKSIEIIEGGPGTIKKICF-
                                10      20      30      40      50

```

```

                                60      70      80
AAD-12  DMRAAYDALDEATRALVHQR-SARHSLVYSQ
      : . . . . . . . . : ::...
gi+AHw-132  DEGSPFNLIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
 initn: 52 init1: 52 opt: 52 Z-score: 86.3 bits: 21.1 E(): 7.9
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (56-79:29-52)

```

                                30      40      50      60      70      80
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
                                : : :: : . .: .: .:
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEEAARISAKNALESYAYSLRNTLS

```

```

                10         20         30         40         50
gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
                60         70         80         90        100        110

```

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
  initn: 32 init1: 32 opt: 49 Z-score: 85.8 bits: 20.4 E(): 8.3
Smith-Waterman score: 49+ADs- 29.091+ACU- identity (49.091+ACU- similar)
in 55 aa overlap (1-55:38-86)

```

```

                                10         20         30
AAD-12                          HSPA EWDDMMKVIVGNMAWHADSTYMPVMA
                                ..  ::  . :  ::  ... :  ::
gi+AHw-126 VEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKK--NGDGVWEIKSDK-PL--
                10         20         30         40         50         60

```

```

                40         50         60         70         80
AAD-12 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
                ..  ..  . :  : ::  : ::  :
gi+AHw-126 KGP-FNFRFVSEKGM RNVFDDVVPADFKVGT TYKPE
                70         80         90

```

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)
  initn: 51 init1: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

```

```

                10         20         30         40         50
AAD-12          HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::  ..  . :  ::  ::  ::  ..  . ::
gi+AHw-602 MGVTYSEFTSIIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

```

```

gi+AHw-602 GEGSTYSYVKHRIDGV DKNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90        100        110

```

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
  initn: 51 init1: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

```

```

                10         20         30         40         50
AAD-12          HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::  ..  . :  ::  ::  ::  ..  . ::
gi+AHw-602 MGVTYSEFTSVIIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80

```

AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
           60           70           80           90          100          110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

```

           10           20           30           40           50
AAD-12      HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
           ::.  .: .:  ::  ::::. .  ::
gi+AHw-279  MGVF TYESEFTSVI PPARLFN AFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
           10           20           30           40           50

```

```

           60           70           80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

```

```

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
           60           70           80           90          100          110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

```

           10           20           30           40           50
AAD-12      HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
           ::.  .: .:  ::  ::::. .  ::
gi+AHw-602  MGVF TYESEFTSVI PPARLFN AFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
           10           20           30           40           50

```

```

           60           70           80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
           60           70           80           90          100          110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

```

           10           20           30           40           50
AAD-12      HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
           ::.  .: .:  ::  ::::. .  ::
gi+AHw-602  MGVF TYESEFTSVI PPARLFN AFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
           10           20           30           40           50

```

```

           60           70           80

```

AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
           60           70           80           90           100          110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (21-45:27-50)

```

           10           20           30           40           50
AAD-12      HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
           ..  .:  .:  .:  ::  ::::..  .  ::
gi+AHw-602 MGVF TYESEFTSVIPPARLFN AFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
           10           20           30           40           50

```

```

           60           70           80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
           60           70           80           90           100          110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (21-45:27-50)

```

           10           20           30           40           50
AAD-12      HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
           ..  .:  .:  .:  ::  ::::..  .  ::
gi+AHw-602 MGVF TYESEFTSVIPPARLFN AFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
           10           20           30           40           50

```

```

           60           70           80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
           60           70           80           90           100          110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (21-45:27-50)

```

           10           20           30           40           50
AAD-12      HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
           ..  .:  .:  .:  ::  ::::..  .  ::
gi+AHw-131 MGVF NYETEFTSVIPPARLFN AFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
           10           20           30           40           50

```

```

           60           70           80

```


AAAD-12 AYDALDEATRALLVHQRSARHSLVYSQ

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
Full+AD0-P34 prob (379 aa)
initn: 48 initl: 48 opt: 57 Z-score: 85.3 bits: 22.3 E(): 8.9
Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
in 63 aa overlap (1-62:134-194)

AAAD-12 HSPAEWDDMMKVIVGNMAWHADSTY-MPVM
: : : : :
gi+AHw-129 SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
110 120 130 140 150 160

30 40 50 60 70 80
AAAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQ
: : : : : :
gi+AHw-129 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFVLEHGGIATDDDDY
170 180 190 200 210 220

gi+AHw-129 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
230 240 250 260 270 280

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
vacuola (379 aa)
initn: 48 initl: 48 opt: 57 Z-score: 85.3 bits: 22.3 E(): 8.9
Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
in 63 aa overlap (1-62:134-194)

AAAD-12 HSPAEWDDMMKVIVGNMAWHADSTY-MPVM
: : : : :
gi+AHw-119 SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
110 120 130 140 150 160

30 40 50 60 70 80
AAAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQ
: : : : : :
gi+AHw-119 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFVLEHGGIATDDDDY
170 180 190 200 210 220

gi+AHw-119 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
230 240 250 260 270 280

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:54 2010 done: Fri Feb 5 12:55:54 2010
Total Scan time: 0.080 Total Display time: 0.010


```

58      69
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60      46      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
62      38      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      35      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
66      60      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
68      26      20:+AD0APQA9AD0APQA9ACoAPQA9-
70      35      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
72      28      12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
74      29      10:+AD0APQA9ACoAPQA9AD0APQA9AD0-
76      20      7:+AD0APQAqAD0APQA9AD0-
78      19      6:+AD0AKgA9AD0APQA9AD0-
80      7       4:+AD0AKgA9-
82      6       3:+ACoAPQ-
84      1       3:+ACo-
86      14      2:+ACoAPQA9AD0APQ-
88      3       2:+ACo-          inset +AD0- represents 1 library sequences
90      3       1:+ACo-
92      2       1:+ACo-          :+ACoAPQ-
94      1       1:+ACo-          :+ACo-
96      2       1:+ACo-          :+ACoAPQ-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     1       0:+AD0-          +ACoAPQ-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.05660.00294+ADs- mu+AD0- -
0.3656 0.153
mean+AF8-var+AD0-33.5864 9.201, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.221306
Kolmogorov-Smirnov statistic: 0.1224 (N+AD0-29) at 46

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 24.6 0.65

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145) 57 23.0 2

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 57 23.0 2.3

gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 56 22.7 2.8

gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-G1
 (158) 55 22.3 3.5

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 54 22.1 3.5

gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
 58 23.0 4.3

gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 22.0 4.4

gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145)
 53 21.7 4.8

gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160)
 53 21.7 5.5

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
 (152) 52 21.4 6.4

gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
 52 21.4 6.8

gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159)
 52 21.4 6.8

gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
 52 21.4 6.8

gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
 52 21.4 6.8

gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
 52 21.4 6.8

gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
 52 21.4 6.8

gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
 52 21.4 6.8

gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
 52 21.4 6.8

gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
 52 21.4 6.8

gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 21.4 6.8

gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.4 6.9

gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA (301)
 55 22.0 8.3

gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName: Full+AD0-P
 (133) 50 20.8 8.4

gi+AHw-320606+AHw-pir+AHwAfa-E37396 pollen allergen Agr a I - be (26)
 40 18.4 8.6

gi+AHw-320607+AHw-pir+AHwAfa-G37396 pollen allergen Ant o I - sw (26)
 40 18.4 8.6

gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 55 22.0 9.7

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 init1: 55 opt: 62 Z-score: 105.7 bits: 24.6 E(): 0.65
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (22-70:5-52)

10

20

30

40

50

60


```

                10         20         30         40         50
                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1.03A (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (20-44:27-50)

```

                10         20         30         40         50
AAD-12      SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  ::  ::::. .  ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (20-44:27-50)

```

                10         20         30         40         50
AAD-12      SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  ::  ::::. .  ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (20-44:27-50)

```

                10         20         30         40         50
AAD-12      SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  ::  ::::. .  ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF

```

```

                10          20          30          40          50
        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-602 GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (20-44:27-50)

                10          20          30          40          50
AAD-12      SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  ::  :::. .  ::
gi+AHw-279 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-279 GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (20-44:27-50)

                10          20          30          40          50
AAD-12      SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  ::  :::. .  ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-602 GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (20-44:27-50)

                10          20          30          40          50
AAD-12      SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  ::  :::. .  ::
gi+AHw-131 MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
```

```

                10          20          30          40          50
                60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

```

```

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (20-44:27-50)

```

                10          20          30          40          50
AAD-12          SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::. .: .: :: ::::. . ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (20-44:27-50)

```

                10          20          30          40          50
AAD-12          SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::. .: .: :: ::::. . ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen Pru a (160 aa)

initn: 50 init1: 50 opt: 52 Z-score: 87.3 bits: 21.4 E(): 6.9
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (16-44:23-50)

```

                10          20          30          40          50
AAD-12          SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                .. ::. : .: .: .: ::::. . ::
gi+AHw-444 MGVFYADESTSVITPPRLFKALVLEAD-TLIPKIAPQSVKGAEIVEGDDGGVGTIKKISF

```

```

                10         20         30         40         50
                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60         70         80         90         100         110

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA
pre (301 aa)
initn: 53 init1: 53 opt: 55 Z-score: 85.9 bits: 22.0 E(): 8.3
Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
in 47 aa overlap (11-56:16-62)

```

```

                10         20         30         40         50
AAD-12 SPAEWDDMMKVIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                ...: : . :: : : : . : . :.....
gi+AHw-441 MAVQKYTVALFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL
                10         20         30         40         50         60

                60         70         80
AAD-12 YDALDEATRALVHQRSARHSLVYSQS
:
gi+AHw-441 EDVNAGFKA AVAAAAANAPPADKFKIFEA AFSESSKGLLATSAAKAPGLIPKLD TAYDVAY
                70         80         90         100         110         120

```

```

+AD4APg-gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName:
Full+AD0-Proba (133 aa)
initn: 50 init1: 50 opt: 50 Z-score: 85.8 bits: 20.8 E(): 8.4
Smith-Waterman score: 50+ADs- 28.125+ACU- identity (59.375+ACU- similar)
in 32 aa overlap (11-42:11-42)

```

```

                10         20         30         40         50         60
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE
                :... :: ... : : : :...
gi+AHw-249 MRTVSMAALVVIAAALAWTSSAEPAPAPAGEEACGKVVQDIMPCLHFVKGEEKEPSKEC
                10         20         30         40         50         60

                70         80
AAD-12 ATRALVHQRSARHSLVYSQS

gi+AHw-249 CSGTKKLSEEVKTTEQKREACKCIVRATKGISGIKNELVAEVPKKCDIKTTLPPITADFD
                70         80         90         100         110         120

```

```

+AD4APg-gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - bent
g (26 aa)
initn: 40 init1: 40 opt: 40 Z-score: 85.6 bits: 18.4 E(): 8.6
Smith-Waterman score: 40+ADs- 57.143+ACU- identity (100.000+ACU- similar)
in 7 aa overlap (18-24:19-25)

```

```

                10         20         30         40         50
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD
                :.....
gi+AHw-320 YTTEGGTKAEAEVDVIPEGWKADTSYE

```

10 20

+AD4APg-gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I -
sweet (26 aa)

initn: 40 init1: 40 opt: 40 Z-score: 85.6 bits: 18.4 E(): 8.6
Smith-Waterman score: 40+ADs- 57.143+ACU- identity (100.000+ACU- similar)
in 7 aa overlap (18-24:19-25)

```

                10      20      30      40      50
AAD-12  SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD
                :.:.:.:
gi+AHw-320 YTTEGGKVKVEAEDVIPEGWKADTSYE
                10      20

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)

initn: 55 init1: 55 opt: 55 Z-score: 84.6 bits: 22.0 E(): 9.7
Smith-Waterman score: 55+ADs- 30.556+ACU- identity (58.333+ACU- similar)
in 36 aa overlap (3-38:155-190)

```

                                10      20      30
AAD-12                          SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
                                : . . . . . : : . . . :
gi+AHw-249 QLTSKLDAAALKLAYEAAQGATPEAKYDAYVATLLEALRVIAGTLEVHAVKPAEEVKVGA
                130      140      150      160      170      180

                40      50      60      70      80
AAD-12 VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS
                . . . . .
gi+AHw-249 IPAAEVQLIDKVDAAYRTAATAANAAPANDKFTVFENTFNNAIKVS LGAAAYDSYKFIPTL
                190      200      210      220      230      240

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:54 2010 done: Fri Feb 5 12:55:54 2010

Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 92 - 171 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

88      1      2:+ACo-      inset +AD0- represents 1 library sequences
90      3      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      2      1:+ACo-      :+ACoAPQ-
96      2      1:+ACo-      :+ACoAPQ-
98      0      0:      +ACo-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     1      0:+AD0-      +ACoAPQ-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.02820.00296+ADs- mu+AD0- -
0.2039 0.155
mean+AF8-var+AD0-33.9199 9.303, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.220215
Kolmogorov-Smirnov statistic: 0.1244 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.6 0.68
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 23.0 2.1
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.9 2.4
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 55 22.4 2.9
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.6 2.9
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.9 4.4
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 22.0 4.6
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.7 5
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.7 5.7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.4 6.6
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7

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gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
52 21.3 7

gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
52 21.3 7

gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
52 21.3 7

gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
52 21.3 7

gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
52 21.3 7

gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
52 21.3 7

gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
52 21.3 7

gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
52 21.3 7

gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
52 21.3 7.1

gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA (301)
55 22.0 8.5

gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName: Full+AD0-P
(133) 50 20.8 8.6

gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - be (26)
40 18.4 8.9

gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I - sw (26)
40 18.4 8.9

gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
(339) 55 21.9 9.9

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)

initn: 55 init1: 55 opt: 62 Z-score: 105.4 bits: 24.6 E(): 0.68
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (21-69:5-52)

	10	20	30	40	50	60
AAD-12	PAEWDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA					
gi+AHw-189		MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EG				
		10	20	30	40	

	70	80
AAD-12	TRALVHQRSARHSLVYSQSK	
gi+AHw-189	CREYVAQQTTCGVVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRV	
	50	60

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
tetrameric (145 aa)

initn: 50 init1: 50 opt: 57 Z-score: 96.7 bits: 23.0 E(): 2.1
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (21-69:5-52)

10	20	30	40	50	60
----	----	----	----	----	----


```

AAD-12          PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10          20          30          40          50

```

```

                60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs- Lolium per (301 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 90.9 bits: 22.9 E(): 4.4
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (16-65:23-71)

```

                10          20          30          40          50
AAD-12          PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                ..  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-663 MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                10          20          30          40          50

```

```

                60          70          80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSK
                . . . . .:  .:
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 52 initl: 52 opt: 54 Z-score: 90.5 bits: 22.0 E(): 4.6
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (15-43:23-50)

```

                10          20          30          40          50
AAD-12          PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-444 MGVFYTSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTAEIVEGDGGVGTIKKISF
                10          20          30          40          50

```

```

                60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs-Trit (145 aa)
 initn: 46 initl: 46 opt: 53 Z-score: 89.8 bits: 21.7 E(): 5
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (21-69:5-52)

```

                10          20          30          40          50          60

```

```

AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA
      :. :.. .. : :.. : :..
gi+AHw-217 MASKSSISPLLLATVVLVSVFAAATATGPYCYAGMGLPINPL-EG
      10      20      30      40

```

```

      70      80
AAD-12 TRALVHQRSARHSLVYSQSK
      : : :..
gi+AHw-217 CREYVAQQTTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRC EAVRYFIGRRSDPNSS
      50      60      70      80      90      100

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 +AFs-Cor (160 aa)
 initn: 47 initl: 47 opt: 53 Z-score: 88.8 bits: 21.7 E(): 5.7
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar) in 58 aa overlap (24-75:31-87)

```

      10      20      30      40
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
      :. :. :. :. :. :. :. :.
gi+AHw-132 MGVFN YETETTSVI PPARLFKRFVLDSDNLI PKVAPKAIKSIEIIEGNGGPGTIKKICF-
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSK
      : . . . . . : : : :
gi+AHw-132 DEGSPFN YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 87.6 bits: 21.4 E(): 6.6
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar) in 24 aa overlap (54-77:29-52)

```

      30      40      50      60      70      80
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK
      : : : : : . . : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAEARISAKNALESYAYSLRNTLS
      10      20      30      40      50

```

```

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar) in 25 aa overlap (19-43:27-50)

```

      10      20      30      40      50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      : : . : : : : : : :
gi+AHw-602 MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF

```

```

                10          20          30          40          50
                60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-602 GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

```

                10          20          30          40          50
AAD-12          PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  ::  ::::.  .  ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-602 GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

```

                10          20          30          40          50
AAD-12          PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  ::  ::::.  .  ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-602 GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

```

                10          20          30          40          50
AAD-12          PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  ::  ::::.  .  ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF

```

10 20 30 40 50
60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK
gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

10 20 30 40 50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :::: . :
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

10 20 30 40 50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :::: . :
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK
gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

10 20 30 40 50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :::: . :
gi+AHw-279 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF

10 20 30 40 50
60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK
gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

10 20 30 40 50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: ::::: . ::
gi+AHw-602 MGVFYSEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

10 20 30 40 50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: ::::: . ::
gi+AHw-131 MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK
gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

10 20 30 40 50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: ::::: . ::
gi+AHw-602 MGVFYSEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF

```

                10         20         30         40         50
                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                60         70         80         90         100        110

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)
  initn: 50 init1: 50 opt: 52 Z-score: 87.1 bits: 21.3 E(): 7.1
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (15-43:23-50)

                10         20         30         40         50
AAD-12      PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. .:: : .: .: .: .::: . :
gi+AHw-444 MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIA PQSVKGAEIVEGDGGVGTIKKISF
                10         20         30         40         50

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60         70         80         90         100        110

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA
pre (301 aa)
  initn: 53 init1: 53 opt: 55 Z-score: 85.7 bits: 22.0 E(): 8.5
Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
in 47 aa overlap (10-55:16-62)

                10         20         30         40         50
AAD-12      PAEWDDMMKVIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                ...: : . :: : :: : . : . : :::: . . .
gi+AHw-441 MAVQKYTVALFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL
                10         20         30         40         50         60

                60         70         80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSK
:
gi+AHw-441 EDVNAGFKA AVAAAANAPPADKFKIFEAFSESSKGLLATSAAKAPGLIPKLDTAYDVAY
                70         80         90         100        110        120

+AD4APg-gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName:
Full+AD0-Proba (133 aa)
  initn: 50 init1: 50 opt: 50 Z-score: 85.6 bits: 20.8 E(): 8.6
Smith-Waterman score: 50+ADs- 28.125+ACU- identity (59.375+ACU- similar)
in 32 aa overlap (10-41:11-42)

                10         20         30         40         50
AAD-12      PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE
                :... .:: ... .: : : .::: .
gi+AHw-249 MRTVSMAALVVIAAALAWTSSAEPAPAPAPGEEACGKVVQDIMPCLHFVKGEEKEPSKEC

```


gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 60 23.9 1
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145) 57 22.9 2.2
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 57 22.9 2.5
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 56 22.5 3.1
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 58 22.9 4.5
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 54 21.9 4.8
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.6 5.2
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.6 6
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.3 6.9
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.4
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.4
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.4
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.4
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.4
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.4
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159) 52 21.3 7.4
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.4
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159) 52 21.3 7.4
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.4
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160) 52 21.3 7.4
gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA (301) 55 22.0 8.7
gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName: Full+AD0-P (133) 50 20.7 9.1
gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - be (26) 40 18.2 9.9
gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I - sw (26) 40 18.2 9.9

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
initn: 55 init1: 55 opt: 62 Z-score: 104.9 bits: 24.5 E(): 0.72
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (20-68:5-52)

```

                10         20         30         40         50         60
AAD-12 AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
                :.  :..  ...  :.  .  .  .  :.  :.  :.  :.  :.  :.
gi+AHw-189                MASKSSITPLLLA AVLASVF AAAAATGQYCYAGMGLPSNPL-EGC
                        10         20         30         40
    
```

```

                70         80
AAD-12 RALVHQRSARHSLVYSQSKL
                :  :  :..
gi+AHw-189 REYVAQQTTCGVTTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRVRYFIGRRSHPDWRVL
                50         60         70         80         90         100
    
```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 34 init1: 34 opt: 60 Z-score: 102.2 bits: 23.9 E(): 1
Smith-Waterman score: 60+ADs- 32.075+ACU- identity (64.151+ACU- similar)
in 53 aa overlap (30-80:9-57)

```

                10         20         30         40         50
AAD-12 AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DE
                :  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-111                MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQ
                        10         20         30
    
```

```

                60         70         80
AAD-12 ATRALVHQRSARHSLVYSQSKL
                :...  .....  :  :
gi+AHw-111 ANHAI---EKGEHQLLYLQHQLDLLENKSKELQEKI IRELDVVCAMIEGAQGALERELK
                40         50         60         70         80         90
    
```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of
tetrameric (145 aa)
initn: 50 init1: 50 opt: 57 Z-score: 96.3 bits: 22.9 E(): 2.2
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (20-68:5-52)

```

                10         20         30         40         50         60
AAD-12 AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
                :.  :..  ...  :.  .  .  .  :.  :.  :.  :.  :.  :.
gi+AHw-439                MASKSSITPLLLA AVLASVF AAAATATGQYCYAGMGLPSNPL-EGC
                        10         20         30         40
    
```

```

                70         80
AAD-12 RALVHQRSARHSLVYSQSKL
                :  :  :..
gi+AHw-439 REYVAQQTTCGVTTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSV
                50         60         70         80         90         100
    
```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 init1: 55 opt: 57 Z-score: 95.3 bits: 22.9 E(): 2.5
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (14-42:23-50)

```

                10      20      30      40      50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  :::  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFITYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
                10      20      30      40      50

```

```

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 init1: 55 opt: 56 Z-score: 93.6 bits: 22.5 E(): 3.1
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

                10      20      30      40      50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  .:  :::.  .  ::
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10      20      30      40      50

```

```

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

gi+AHw-165  GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium per (301 aa)
 initn: 49 init1: 49 opt: 58 Z-score: 90.6 bits: 22.9 E(): 4.5
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (15-64:23-71)

```

                10      20      30      40      50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                ..  :::  :  :  :  .  :  :::::  :  .
gi+AHw-663  MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                10      20      30      40      50

```

```

                60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKL
                .  .  .  .  :  :
gi+AHw-663  LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 52 init1: 52 opt: 54 Z-score: 90.2 bits: 21.9 E(): 4.8
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (14-42:23-50)

```
          10      20      30      40      50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  .::  :  .:  .:  .:  .:::  .  .:
gi+AHw-444  MGVFYTSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
                10      20      30      40      50
```

```
          60      70      80
AAD-12      AYDALDEATRALVHQRSARHSLVYSQSKL
gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
                60      70      80      90      100      110
```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 89.4 bits: 21.6 E(): 5.2
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (20-68:5-52)

```
          10      20      30      40      50      60
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
                ..  .::  .  .:  .  .  .  .:  .:  .  .:  .:
gi+AHw-217      MASKSSISPLLLATVVLVSVFAAATATGPYCYAGMGLPINPL-EGC
                10      20      30      40
```

```
          70      80
AAD-12      RALVHQRSARHSLVYSQSKL
                :  :  :..
gi+AHw-217      REYVAQQTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRC EAVRYFIGRRSDPNSSV
                50      60      70      80      90      100
```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 88.5 bits: 21.6 E(): 6
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (23-74:31-87)

```
          10      20      30      40
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
                .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-132  MGVFNYETETTSVIPPARLFKRFVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
                10      20      30      40      50
```

```
          50      60      70      80
AAD-12      DMRAAYDALDEATRALVHQR-SARHSLVYSQSKL
                :  .  .  .  .  .  .  .  .:  .:  .:
gi+AHw-132  DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60      70      80      90      100      110
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 87.3 bits: 21.3 E(): 6.9
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (53-76:29-52)

```

          30          40          50          60          70          80
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
          : : : : : . . . : : : :
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
          10          20          30          40          50

```

```

gi+AHw-144  DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAG
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

          10          20          30          40          50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          : : . : : : : : : : : :
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL
gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

          10          20          30          40          50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          : : . : : : : : : : : :
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL
gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

          10          20          30          40          50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                ... .. : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1.03A (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

                10         20         30         40         50
AAD-12          AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                ... .. : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

                10         20         30         40         50
AAD-12          AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                ... .. : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

                10         20         30         40         50
AAD-12          AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                                ::. .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (18-42:27-50)

```

                                10         20         30         40         50
AAD-12          AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                                ::. .: .: :: :... . ::
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (18-42:27-50)

```

                                10         20         30         40         50
AAD-12          AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                                ::. .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (18-42:27-50)

```

                                10         20         30         40         50
AAD-12          AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                ::. .: .: :: :... . ::
gi+AHw-131 MGVFN YET EFTSV IPPARLFN A FVLDADNL-IPK IAPQAVKSAE ILEGDGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-131 GEGSTYSYVKHRIDGV DKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

                10         20         30         40         50
AAD-12          AEWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSAEVVPVAVGGRTCFADMRA
                ::. .: .: :: :... . ::
gi+AHw-602 MGVFTY ESEFTSV IPPARLFN A FVLDADNL-IPK IAPQAVKSAE ILEGDGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-602 GEGSTYSYVKHRIDGV DKNDFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen Pru a (160 aa)

initn: 50 init1: 50 opt: 52 Z-score: 86.7 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (14-42:23-50)

```

                10         20         30         40         50
AAD-12          AEWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSAEVVPVAVGGRTCFADMRA
                .. ::: : .: .: .: :...: . ::
gi+AHw-444 MGVFTY ADESTSVITPPRLFKALVLEAD-TLIPK IAPQSVKGAEI VEGDGGVGTIKKISF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA pre (301 aa)

initn: 53 init1: 53 opt: 55 Z-score: 85.5 bits: 22.0 E(): 8.7
 Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
 in 47 aa overlap (9-54:16-62)

```

                10         20         30         40         50
AAD-12          AEWDDMMKVIVGNMA-WHADSTYMPVMAQGA VFSAEVVPVAVGGRTCFADMRAA

```


gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 60 23.9 0.99
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145) 57 22.9 2.1
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 57 22.9 2.4
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 56 22.6 3
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 58 22.9 4.4
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 54 21.9 4.7
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.7 5.1
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.6 5.8
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.3 6.8
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.2
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.2
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.2
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.2
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.2
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.2
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159) 52 21.3 7.2
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.2
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159) 52 21.3 7.2
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159) 52 21.3 7.2
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160) 52 21.3 7.3
gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA (301) 55 22.0 8.6
gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName: Full+AD0-P (133) 50 20.8 8.9
gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - be (26) 40 18.3 9.5
gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I - sw (26) 40 18.3 9.5

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
initn: 55 init1: 55 opt: 62 Z-score: 105.1 bits: 24.5 E(): 0.7
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (19-67:5-52)


```

                10         20         30         40         50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  :::  :  ::  :  :  ::  :::::  .  ::
gi+AHw-444 MGVFYYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDDGGVGTIKKISF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 init1: 55 opt: 56 Z-score: 93.8 bits: 22.6 E(): 3
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

                10         20         30         40         50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  .:  ::::.  .  ::
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium per (301 aa)
 initn: 49 init1: 49 opt: 58 Z-score: 90.8 bits: 22.9 E(): 4.4
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (14-63:23-71)

```

                10         20         30         40         50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                ..  :::  :  ::  :  .  :  :::::  .  :  .
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                10         20         30         40         50

```

```

                60         70         80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLG
                .  .  .  .  ::  :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 52 init1: 52 opt: 54 Z-score: 90.3 bits: 21.9 E(): 4.7
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (13-41:23-50)

```

                10         20         30         40         50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  ...  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444 MGVFYTSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 89.6 bits: 21.7 E(): 5.1
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (19-67:5-52)

```

                10         20         30         40         50         60
AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
                :.  :..  .  :.  .  .  .  :  :..  :  .  :.  :
gi+AHw-217 MASKSSISPLLLATVILVSVFAAATATGPYCYAGMGLPINPL-EGCR
                10         20         30         40

```

```

                70         80
AAD-12 ALVHQRSARHSLVYSQSKLG
                :  :..
gi+AHw-217 EYVAQQTTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRC EAVRYFIGRRSDPNSSVL
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 88.6 bits: 21.6 E(): 5.8
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (22-73:31-87)

```

                10         20         30         40
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCF
                .:  :  :.  :  :..  .  :  .  :
gi+AHw-132 MGVFNYETETTSVIPPARLFKRFVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLG
                :  .  .  .  .  .  .  :  :..
gi+AHw-132 DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 87.4 bits: 21.3 E(): 6.8
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (52-75:29-52)

```

                30         40         50         60         70         80
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
                : : : : : : . . . : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
                10         20         30         40         50

```

```

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAG
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

                10         20         30         40         50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                : : . : : : : : : : : : . : :
gi+AHw-602 MGVTYSEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

                10         20         30         40         50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                : : . : : : : : : : : : . : :
gi+AHw-602 MGVTYSEFTSVIIPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

                10         20         30         40         50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                                ::. .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1.03A (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

                                10         20         30         40         50
AAD-12                EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                                ::. .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

                                10         20         30         40         50
AAD-12                EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                                ::. .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

                                10         20         30         40         50
AAD-12                EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                                ::. .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
              10          20          30          40          50

```

```

              60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (17-41:27-50)

```

              10          20          30          40          50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                                ::. .: .: :: :... . ::
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
              10          20          30          40          50

```

```

              60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (17-41:27-50)

```

              10          20          30          40          50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                                ::. .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
              10          20          30          40          50

```

```

              60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (17-41:27-50)

```

              10          20          30          40          50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                                ::. .: .: :: :... . ::
gi+AHw-131 MGVFN YET EFTSVI PPARLFN A FVLDADNL-IPK IAPQAVKSAE ILEGDGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

                                10         20         30         40         50
AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                                ::. .: .: :: :... . ::
gi+AHw-602 MGVFTY ESEFTSVI PPARLFN A FVLDADNL-IPK IAPQAVKSAE ILEGDGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen Pru a (160 aa)

initn: 50 init1: 50 opt: 52 Z-score: 86.9 bits: 21.3 E(): 7.3
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (13-41:23-50)

```

                                10         20         30         40         50
AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                                .. :: : .: .: .: :... . ::
gi+AHw-444 MGVFTYADESTSVITPPRLFKALVLEAD-TLIPK IAPQSVKGAEI VEGDGGVGTIKKISF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA pre (301 aa)

initn: 53 init1: 53 opt: 55 Z-score: 85.6 bits: 22.0 E(): 8.6
 Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
 in 47 aa overlap (8-53:16-62)

```

                                10         20         30         40         50
AAD-12 EWDDMMKVIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA

```

```

...: : . :: : : : . : . :.....
gi+AHw-441 MAVQKYTVLFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL
          10          20          30          40          50          60

```

```

          60          70          80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLG

```

```

:
gi+AHw-441 EDVNAGFKA AVAAAANAPPADKFKIFEAAFSESSKGLLATSAAKAPGLIPKLDTAYDVAY
          70          80          90          100          110          120

```

+AD4APg-gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName:
Full+AD0-Proba (133 aa)
initn: 50 initl: 50 opt: 50 Z-score: 85.4 bits: 20.8 E(): 8.9
Smith-Waterman score: 50+ADs- 28.125+ACU- identity (59.375+ACU- similar)
in 32 aa overlap (8-39:11-42)

```

          10          20          30          40          50
AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE
          :... ::... :. : : :... :
gi+AHw-249 MRTVSMAALVVIAAALAWTSSAEPAPAPGEEACGKVVQDIMPCLHFVKGEEKEPSKEC
          10          20          30          40          50          60

```

```

          60          70          80
AAD-12 ATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-249 CSGTKKLSEEVKTTEQKREACKCIVRATKGISGIKNELVAEVPKCKDIKTTLPPITADFD
          70          80          90          100          110          120

```

+AD4APg-gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - bent
g (26 aa)
initn: 40 initl: 40 opt: 40 Z-score: 84.8 bits: 18.3 E(): 9.5
Smith-Waterman score: 40+ADs- 57.143+ACU- identity (100.000+ACU- similar)
in 7 aa overlap (15-21:19-25)

```

          10          20          30          40          50
AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD
          :.....:
gi+AHw-320 YTTEGGTKAEAEVDVIPEGWKADTSYE
          10          20

```

+AD4APg-gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I -
sweet (26 aa)
initn: 40 initl: 40 opt: 40 Z-score: 84.8 bits: 18.3 E(): 9.5
Smith-Waterman score: 40+ADs- 57.143+ACU- identity (100.000+ACU- similar)
in 7 aa overlap (15-21:19-25)

```

          10          20          30          40          50
AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD
          :.....:
gi+AHw-320 YTTEGGKKVEAEVDVIPEGWKADTSYE
          10          20

```


54 80 91:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-
 +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
 56 72
 76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
 +ACo-
 58 61
 62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
 60 50 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
 62 44 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
 64 31 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
 66 55 25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
 68 35 20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
 70 33 16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
 72 30 12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
 74 20 10:+AD0APQA9ACoAPQA9AD0-
 76 16 7:+AD0APQAqAD0APQA9-
 78 20 6:+AD0AKgA9AD0APQA9AD0-
 80 7 4:+AD0AKgA9-
 82 5 3:+ACoAPQ-
 84 5 3:+ACoAPQ-
 86 13 2:+ACoAPQA9AD0APQ-
 88 1 2:+ACo- inset +AD0- represents 1 library sequences
 90 3 1:+ACo-
 92 0 1:+ACo- :+ACo-
 94 2 1:+ACo- :+ACoAPQ-
 96 1 1:+ACo- :+ACo-
 98 0 0: +ACo-
 100 0 0: +ACo-
 102 1 0:+AD0- +ACoAPQ-
 104 1 0:+AD0- +ACoAPQ-
 106 0 0: +ACo-
 108 0 0: +ACo-
 110 0 0: +ACo-
 112 0 0: +ACo-
 114 0 0: +ACo-
 116 0 0: +ACo-
 118 0 0: +ACo-
 +AD4-120 0 0: +ACo-
 331323 residues in 1471 sequences
 Expectation+AF8-n fit: rho(ln(x))+AD0- 5.88690.00284+ADs- mu+AD0- 0.6342
 0.149
 mean+AF8-var+AD0-33.9298 9.626, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
 Lambda+AD0- 0.220183
 Kolmogorov-Smirnov statistic: 0.1053 (N+AD0-29) at 46

 FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1
 join: 42, opt: 30, open/ext: -10/-2, width: 32
 Scan time: 0.080
 The best scores are: opt bits E(1471)
 gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 24.5 0.7
 gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 60 23.9 0.99

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145)
57 22.9 2.1
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
57 22.9 2.4
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
160) 56 22.6 3
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
301) 58 22.9 4.4
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
54 21.9 4.7
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145)
145) 53 21.7 5.1
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160)
53 21.6 5.8
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152)
(152) 52 21.3 6.8
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
52 21.3 7.2
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
52 21.3 7.2
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
52 21.3 7.3
gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA (301)
55 22.0 8.5
gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName: Full+AD0-P (133)
(133) 50 20.7 8.9
gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - be (26)
40 18.3 9.7
gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I - sw (26)
40 18.3 9.7

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
initn: 55 init1: 55 opt: 62 Z-score: 105.1 bits: 24.5 E(): 0.7
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (18-66:5-52)

10

20

30

40

50

60

AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. .:: : .: .: .: :::: . : :
 gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 init1: 55 opt: 56 Z-score: 93.8 bits: 22.6 E(): 3
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (16-40:27-50)

10 20 30 40
 AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: .: :::. . : :
 gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH
 gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium per (301 aa)
 initn: 49 init1: 49 opt: 58 Z-score: 90.8 bits: 22.9 E(): 4.4
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (13-62:23-71)

10 20 30 40 50
 AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
 .. .:: : .: .: .: :::: . : :
 gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
 10 20 30 40 50

60 70 80
 AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGH
 : :
 gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
 60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 52 init1: 52 opt: 54 Z-score: 90.3 bits: 21.9 E(): 4.7
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (12-40:23-50)

10 20 30 40

```

AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. .:: : .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-444 MGVTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
                10          20          30          40          50

```

```

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

```

```

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
                60          70          80          90          100          110

```

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
  initn: 46 initl: 46 opt: 53 Z-score: 89.6 bits: 21.7 E(): 5.1
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (18-66:5-52)

```

```

                10          20          30          40          50          60
AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                :. :.. .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-217          MASKSSISPLLLATVLVSVFAAATATGPYCYAGMLPINPL-EGCRE
                10          20          30          40

```

```

                70          80
AAD-12 LVHQRSARHSLVYSQSKLGH
                : :..
gi+AHw-217 YVAQQTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLK
                50          60          70          80          90          100

```

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
  initn: 47 initl: 47 opt: 53 Z-score: 88.6 bits: 21.6 E(): 5.8
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (21-72:31-87)

```

```

                10          20          30          40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
                .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-132 MGVFNYETETTSVIPPARLFKRFVLDSDNLIPKVPKAIKSIEIIEGGGPGTIKKICF-
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGH
                : . . . . . . . . . . : : : : .
gi+AHw-132 DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60          70          80          90          100          110

```

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
  initn: 52 initl: 52 opt: 52 Z-score: 87.4 bits: 21.3 E(): 6.8
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (51-74:29-52)

```

```

                30          40          50          60          70          80

```

AAAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
 : : ::: : . . . : : : :
 gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
 10 20 30 40 50

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (16-40:27-50)

AAAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: :::.. . ::
 gi+AHw-602 MGVFTYESEFTSIIPPAPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
 1.03D (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (16-40:27-50)

AAAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: :::.. . ::
 gi+AHw-602 MGVFTYESEFTSVIPPAPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (16-40:27-50)

AAAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: :::.. . ::
 gi+AHw-602 MGVFTYESEFTSVIPPAPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF

```

                10         20         30         40         50
50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

```

                10         20         30         40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  ::  :::. .  ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
          10          20          30          40          50

```

```

50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

```

                10         20         30         40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  ::  :::. .  ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
          10          20          30          40          50

```

```

50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

```

                10         20         30         40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  ::  :::. .  ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF

```

```

                10         20         30         40         50
50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

                10         20         30         40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  ::  ::::. .  ::
gi+AHw-279 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

                10         20         30         40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  ::  ::::. .  ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

                10         20         30         40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  ::  ::::. .  ::
gi+AHw-131 MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
```

```

                10         20         30         40         50
50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60         70         80         90         100        110

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)
  initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

                10         20         30         40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-602 MGVFTYESEFTSVIIPPARLFNAFVLDADNL-IPKIIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
        60         70         80         90         100        110

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)
  initn: 50 init1: 50 opt: 52 Z-score: 86.9 bits: 21.3 E(): 7.3
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (12-40:23-50)

                10         20         30         40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-444 MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIIAPQSVKGAEIVEGDDGGVGTIKKISF
                10         20         30         40         50

50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
        60         70         80         90         100        110

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA
pre (301 aa)
  initn: 53 init1: 53 opt: 55 Z-score: 85.7 bits: 22.0 E(): 8.5
Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
in 47 aa overlap (7-52:16-62)

                10         20         30         40         50
AAD-12          WDDMMKVIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                ...:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-441 MAVQKYTVALFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL

```

```

                10         20         30         40         50         60
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGH
      :
gi+AHw-441 EDVNAGFKA AVAAAANAPPADKFKIFEAAFSESSKGLLATSAAKAPGLIPKLDTAYDVAY
                70         80         90         100        110        120

```

+AD4APg-gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName: Full+AD0-Proba (133 aa)
 initn: 50 init1: 50 opt: 50 Z-score: 85.3 bits: 20.7 E(): 8.9
 Smith-Waterman score: 50+ADs- 28.125+ACU- identity (59.375+ACU- similar)
 in 32 aa overlap (7-38:11-42)

```

                10         20         30         40         50
AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDE
      :... .:: ... :: : : ...: .
gi+AHw-249 MRTVSMAALVVIAAALAWTSSAEPAPAPGEEACGKVVQDIMPCLHFVKGEEKEPSKEC
                10         20         30         40         50         60

```

```

                60         70         80
AAD-12 ATRALVHQRSARHSLVYSQSKLGH
gi+AHw-249 CSGTKKLSEEVKTTEQKREACKCIVRATKGISGIKNELVAEVPKCKDIKTTLPPITADFD
                70         80         90         100        110        120

```

+AD4APg-gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - bent g (26 aa)
 initn: 40 init1: 40 opt: 40 Z-score: 84.7 bits: 18.3 E(): 9.7
 Smith-Waterman score: 40+ADs- 57.143+ACU- identity (100.000+ACU- similar)
 in 7 aa overlap (14-20:19-25)

```

                10         20         30         40         50
AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALD
      :...:
gi+AHw-320 YTTEGGTKAEAEVDVIPEGWKADTSYE
                10         20

```

+AD4APg-gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I - sweet (26 aa)
 initn: 40 init1: 40 opt: 40 Z-score: 84.7 bits: 18.3 E(): 9.7
 Smith-Waterman score: 40+ADs- 57.143+ACU- identity (100.000+ACU- similar)
 in 7 aa overlap (14-20:19-25)

```

                10         20         30         40         50
AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALD
      :...:
gi+AHw-320 YTTEGGKKVEAEVDVIPEGWKADTSYE
                10         20

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences


```

56      79
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9-
58      54      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
60      53      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
62      39      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      29      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      57      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
68      49      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
70      22      16:+AD0APQA9AD0APQAqAD0APQ-
72      34      12:+AD0APQA9ACoAPQA9AD0APQA9--AD0APQA9-
74      14      10:+AD0APQA9ACoAPQ-
76      17      7:+AD0APQAqAD0APQA9-
78      23      6:+AD0AKgA9AD0APQA9AD0APQ-
80      7       4:+AD0AKgA9-
82      5       3:+ACoAPQ-
84      4       3:+ACoAPQ-
86      12      2:+ACoAPQA9AD0-
88      2       2:+ACo-          inset +AD0- represents 1 library sequences
90      2       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      2       1:+ACo-          :+ACoAPQ-
96      1       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     1       0:+AD0-          +ACoAPQ-
104     1       0:+AD0-          +ACoAPQ-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0 0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.89150.0031+ADs- mu+AD0- 0.5955
0.163
mean+AF8-var+AD0-34.7186 9.748, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.217667
Kolmogorov-Smirnov statistic: 0.1073 (N+AD0-29) at 46

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 24.4 0.76

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 60 23.8 1.1

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145) 57 22.8 2.3

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 22.8 2.6
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
 56 22.5 3.2
 gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
 58 22.9 4.7
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.9 5
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145)
 53 21.6 5.4
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160)
 53 21.5 6.2
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152)
 52 21.3 7.2
 gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
 52 21.2 7.6
 gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
 52 21.2 7.6
 gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.2 7.7
 gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA (301)
 55 21.9 9
 gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName: Full+AD0-P (133)
 50 20.7 9.3

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 104.5 bits: 24.4 E(): 0.76
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (17-65:5-52)

	10	20	30	40	50	60
AAD-12	DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRAL					
gi+AHw-189	
		MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREY				
		10	20	30	40	
	70	80				

AAD-12 V

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
 1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (15-39:27-50)

AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: ::::. . ::
 gi+AHw-602 MGVFTYESEFTSIIPPAPLRFNFAVFLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
 10 20 30 40 50

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV
 50 60 70 80

gi+AHw-602 GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
 1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (15-39:27-50)

AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: ::::. . ::
 gi+AHw-602 MGVFTYESEFTSVIPPAPLRFNFAVFLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
 10 20 30 40 50

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV
 50 60 70 80

gi+AHw-602 GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
 60 70 80 90 100 110

+AD4-+AD4-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
 1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (15-39:27-50)

AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: ::::. . ::
 gi+AHw-602 MGVFTYESEFTSVIPPAPLRFNFAVFLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
 10 20 30 40 50

50 60 70 80

AAAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

AAAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
10 20 30 40
::: .: .: :: ::::: . ::
gi+AHw-602 MGVFTYESEFTSVIPPAPLRFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

AAAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

AAAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
10 20 30 40
::: .: .: :: ::::: . ::
gi+AHw-602 MGVFTYESEFTSVIPPAPLRFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

AAAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

AAAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
10 20 30 40
::: .: .: :: ::::: . ::
gi+AHw-602 MGVFTYESEFTSVIPPAPLRFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

50 60 70 80

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

```
gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
           60           70           80           90          100          110
```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

```
           10           20           30           40
AAD-12          DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                   ::.  .: .:  ::  :::. . . ::
gi+AHw-279  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
           10           20           30           40           50
```

```
           50           60           70           80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV
```

```
gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
           60           70           80           90          100          110
```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

```
           10           20           30           40
AAD-12          DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                   ::.  .: .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
           10           20           30           40           50
```

```
           50           60           70           80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV
```

```
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
           60           70           80           90          100          110
```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

```
           10           20           30           40
AAD-12          DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                   ::.  .: .:  ::  :::. . . ::
gi+AHw-131  MGVFNJETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
           10           20           30           40           50
```

```
           50           60           70           80
```


AAAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHV

```

:
gi+AHw-441 EDVNAGFKA AVAAAANAPPADKFKIFEAAFSESSKGLLATSAAKAPGLIPKLDTAYDVAY
              70          80          90          100          110          120
    
```

```

+AD4APg-gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName:
Full+AD0-Proba (133 aa)
  initn: 50 initl: 50 opt: 50 Z-score: 84.9 bits: 20.7 E(): 9.3
Smith-Waterman score: 50+ADs- 28.125+ACU- identity (59.375+ACU- similar)
in 32 aa overlap (6-37:11-42)
    
```

```

              10          20          30          40          50
AAAD-12      DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVPAVGGRTCFADMRAAYDALDE
              :... ::: ...  :: : :  .... .
gi+AHw-249 MRTVSM AALVVIAAALAWTSSAEPAPAPGEEACGKVVQDIMPCLHFVKGEEKEPSKEC
              10          20          30          40          50          60
    
```

```

              60          70          80
AAAD-12 ATRALVHQRSARHSLVYSQSKLGHV
    
```

```

gi+AHw-249 CSGTKKLSEEVKTTEQKREACKCIVRATKGISGIKNELVAEVPPKCDIKTTLPPITADFD
              70          80          90          100          110          120
    
```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:54 2010 done: Fri Feb 5 12:55:55 2010
Total Scan time: 0.090 Total Display time: 0.010
    
```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448
    
```

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
    
```

```

1+AD4APgA+-AAD-12: 97 - 176 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
    
```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      1      0:+AD0-      one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      2      0:+AD0-
      30      3      2:+ACo-
      32      5      8:+AD0APQAq-
    
```



```

102    0    0:          +ACo-
104    1    0:+AD0-    +ACoAPQ-
106    0    0:          +ACo-
108    0    0:          +ACo-
110    0    0:          +ACo-
112    0    0:          +ACo-
114    0    0:          +ACo-
116    0    0:          +ACo-
118    0    0:          +ACo-
+AD4-120    0    0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.06190.00318+ADs- mu+AD0- -
0.2586 0.167
mean+AF8-var+AD0-35.9651 9.815, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.213862
Kolmogorov-Smirnov statistic: 0.1148 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.2 0.86
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 60 23.7 1.2
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 22.7 2.5
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.7 2.9
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.3 3.5
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.7 5.2
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.7 5.4
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.5 5.9
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.4 6.7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.1 7.8
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.3
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.3
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.3
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.3
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.3
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.3

```



```

                10         20         30         40         50         60
AAD-12 DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
                :. :.. ... :. . . . . : : : : : :
gi+AHw-439      MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYV
                10         20         30         40

```

```

                70         80
AAD-12 HQRSARHSLVYSQSKLGHVQ
                :..
gi+AHw-439 AQQTCGVTTIAGSPVSSEPGDTPKDRCCQELDEAPQHRCCEAVRYFIGRRSHPDWSVLKDL
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 init1: 55 opt: 57 Z-score: 94.2 bits: 22.7 E(): 2.9
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (10-38:23-50)

```

                10         20         30         40
AAD-12      DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. :. : : : : : : : : : :
gi+AHw-444 MGVFTYADESTSVIPPRLFKALVLEAD-TLIPKIAFQSVKSAEIVEGDGGVGTIKKISF
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 init1: 55 opt: 56 Z-score: 92.5 bits: 22.3 E(): 3.5
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (14-38:27-50)

```

                10         20         30         40
AAD-12      DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                :. :. : : : : : : : :
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs- Lolium per (301 aa)
 initn: 49 init1: 49 opt: 58 Z-score: 89.5 bits: 22.7 E(): 5.2
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (11-60:23-71)

```

                10         20         30         40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                .. ::: : : : . : .....: : .
gi+AHw-663 MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12          YDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                . . . . : :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLLILKLDTDYDVA
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 52 init1: 52 opt: 54 Z-score: 89.2 bits: 21.7 E(): 5.4
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (10-38:23-50)

```

                10         20         30         40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. ::: : : : . : .....: : .
gi+AHw-444 MGVFTYSDESTSVIPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12          AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs-Trit (145 aa)
 initn: 46 init1: 46 opt: 53 Z-score: 88.5 bits: 21.5 E(): 5.9
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (16-64:5-52)

```

                10         20         30         40         50         60
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
                :. :.. .. :. . . . : :. : . : : :
gi+AHw-217          MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYV
                10         20         30         40

```

```

                70         80
AAD-12          HQRSARHSLVYSQSKLGHVQ
                :..
gi+AHw-217 AQQTCGISISGSVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDL
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 +AFs-Cor (160 aa)
 initn: 47 init1: 47 opt: 53 Z-score: 87.5 bits: 21.4 E(): 6.7
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (19-70:31-87)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
                .: .: .: .: .: .: .: .: .:
gi+AHw-132  MGVFNJETETTSVIPPARLFKRFLDSDNLI PKVAPKAIKSIEIIEGNGGPGTIKKICF-
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  DMRAAYDALDEATR ALVHQR-SARHSLVYSQSKLGHVQ
                : . . . . . : : : :
gi+AHw-132  DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
 initn: 52 init1: 52 opt: 52 Z-score: 86.4 bits: 21.1 E(): 7.8
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (49-72:29-52)

```

                20      30      40      50      60      70
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGH
                : : : : : : . . . : : :
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
                10      20      30      40      50

```

```

                80
AAD-12  VQ
gi+AHw-144  DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .: .: .: .: .: .: .: .: .:
gi+AHw-602  MGVFTYESEFTSIIPPARLFNFAVFLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  AYDALDEATR ALVHQRSARHSLVYSQSKLGHVQ
gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1.03A (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-279 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-131 MGVFNYETETFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 50 init1: 50 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (10-38:23-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  :::  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFTYADESTSVITPPRLFALVLEAD-TLIPKIA PQSVKGAEIVEGDGGVGTIKKISF
                10      20      30      40      50

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA pre (301 aa)
 initn: 53 init1: 53 opt: 55 Z-score: 84.5 bits: 21.8 E(): 9.9
 Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
 in 47 aa overlap (5-50:16-62)

```

                10      20      30      40
AAD-12          DMMKVIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                ...:  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-441  MAVQKYTVALFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL
                10      20      30      40      50      60

                50      60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                :
gi+AHw-441  EDVNAGFKA AVAAAAANAPPADKFKIFEA AFSESSKGLLATSAAKAPGLIPKLD TAYDVAY
                70      80      90      100     110     120

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:55 2010 done: Fri Feb 5 12:55:55 2010
 Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 98 - 177 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

 98      0      0:      +ACo-
100      0      0:      +ACo-
102      1      0:+AD0-      +ACoAPQ-
104      1      0:+AD0-      +ACoAPQ-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.98190.00321+ADs- mu+AD0- 0.4037
0.169
mean+AF8-var+AD0-36.010810.064, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.213726
Kolmogorov-Smirnov statistic: 0.1053 (N+AD0-28) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 62 24.2 0.83
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.2 0.91
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 22.6 2.7
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.6 3
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.3 3.8
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.6 5.5
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.6 5.8
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.4 6.3
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.3 7.1
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.0 8.3
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 51 20.8 8.7
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
51 20.8 8.7
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 8.8
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 8.8
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 8.8

```

gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.8
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
52 21.0 8.8
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.8
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.8
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
52 21.0 8.8
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.8
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.8
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
52 21.0 8.8
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
50 20.5 9.3

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 36 init1: 36 opt: 62 Z-score: 103.8 bits: 24.2 E(): 0.83
Smith-Waterman score: 62+ADs- 29.310+ACU- identity (65.517+ACU- similar)
in 58 aa overlap (25-80:9-62)

```

                10         20         30         40         50
AAD-12 MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRAL
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111                MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI
                10         20         30         40

                60         70         80
AAD-12 VHQRSARHSLVYSQSKLGHVQQ
                .....: : : : :
gi+AHw-111 ---EKGEHQLLYLQHQLDLLENENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLN
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 init1: 55 opt: 62 Z-score: 103.1 bits: 24.2 E(): 0.91
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (15-63:5-52)

```

                10         20         30         40         50         60
AAD-12 MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
                : . : . . . : . . . : . : : : : : : : : : : : : : : :
gi+AHw-189                MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVA
                10         20         30         40

                70         80
AAD-12 QRSARHSLVYSQSKLGHVQQ
                : : .
gi+AHw-189 QQTGCVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRVRYFIGRRSHPDWRVLDLPG
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)
 initn: 50 init1: 50 opt: 57 Z-score: 94.7 bits: 22.6 E(): 2.7
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (15-63:5-52)

```

                10         20         30         40         50         60
AAD-12 MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVH
                :.  :..  ...  :.  .  .  .  :.  :.  :  :  :  :  :
gi+AHw-439      MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVA
                10         20         30         40

```

```

                70         80
AAD-12 QRSARHSLVYSQSKLGHVQQ
                :..
gi+AHw-439 QQTGCVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLF
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 init1: 55 opt: 57 Z-score: 93.7 bits: 22.6 E(): 3
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (9-37:23-50)

```

                10         20         30         40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  :.  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444 MGVTYADESTSVIPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEG DGGVGTIKKISF
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12 AYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQ
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVSADGGSIKSTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 init1: 55 opt: 56 Z-score: 92.1 bits: 22.3 E(): 3.8
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (13-37:27-50)

```

                10         20         30         40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                :..  :.  :  :  :  :  :  :  :
gi+AHw-165 MGVFTHENEITS AIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIEGNGGPGTIKKITF
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12 AYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQ
gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)

initn: 49 init1: 49 opt: 58 Z-score: 89.1 bits: 22.6 E(): 5.5
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (10-59:23-71)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                                .. ::: : : : . : .....: : .
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12      YDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
                                . . . . : :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 init1: 52 opt: 54 Z-score: 88.7 bits: 21.6 E(): 5.8
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (9-37:23-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                .. ::: : : : . : .....: : .
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12      AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)

initn: 46 init1: 46 opt: 53 Z-score: 88.0 bits: 21.4 E(): 6.3
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (15-63:5-52)

```

                                10      20      30      40      50      60
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
                                :. :.. .. : . . . : :. : : . : : :
gi+AHw-217      MASKSSISPLLLATVLSVFAAATATGPYCYAGMGLPINPL-EGCREYVA
                                10      20      30      40

```

```

                                70      80
AAD-12      QRSARHSLVYSQSKLGHVQQ
                                :..
gi+AHw-217 QQTCGISISGSAVSTEPGNTPRDRCCCKELYDASQHCRC EAVRYFIGRRSDPNSSVLKDLF
                                50      60      70      80      90      100

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)
 initn: 47 initl: 47 opt: 53 Z-score: 87.1 bits: 21.3 E(): 7.1
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (18-69:31-87)

```

      10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
              .: .: .: .: .: .: .: .: .:
gi+AHw-132  MGVFNJETETTSVIPPARLFKRFVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
              10      20      30      40      50

      50      60      70      80
AAD-12  DMRAAYDALDEATRALLVHQR-SARHSLVYSQSKLGHVQQ
          : . . . . . . . . : : : :
gi+AHw-132  DEGSPFNFIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
          60      70      80      90      100      110
  
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 85.9 bits: 21.0 E(): 8.3
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (48-71:29-52)

```

      20      30      40      50      60      70
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGH
              : : : : : . . . : : : :
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
              10      20      30      40      50

      80
AAD-12  VQQ

gi+AHw-144  DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
          60      70      80      90      100      110
  
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 36 initl: 36 opt: 51 Z-score: 85.5 bits: 20.8 E(): 8.7
 Smith-Waterman score: 51+ADs- 27.586+ACU- identity (63.793+ACU- similar)
 in 58 aa overlap (25-80:9-62)

```

      10      20      30      40      50
AAD-12  MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALL
              : : : : . : . : : : : : : : : :
gi+AHw-111  MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI
              10      20      30      40

      60      70      80
AAD-12  VHQRSARHSLVYSQSKLGHVQQ
          . . . . . : : . . . .
gi+AHw-111  ---EKGEHQLLYLQHLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLN
          50      60      70      80      90      100
  
```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein B1 (134 aa)
 initn: 36 init1: 36 opt: 51 Z-score: 85.5 bits: 20.8 E(): 8.7
 Smith-Waterman score: 51+ADs- 27.586+ACU- identity (63.793+ACU- similar)
 in 58 aa overlap (25-80:9-62)

```

                10         20         30         40         50
AAD-12 MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRAL
                : : : : . : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-420                MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI
                        10         20         30         40

```

```

                60         70         80
AAD-12 VHQRSARHSLVYSQSKLGHVQQ
                .....: : : : :
gi+AHw-420 ---EKGEHQLLYLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLN
                        50         60         70         80         90         100

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (13-37:27-50)

```

                10         20         30         40
AAD-12                MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                        10         20         30         40         50

```

```

                50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1.03A (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (13-37:27-50)

```

                10         20         30         40
AAD-12                MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-602 MGVFYTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                        10         20         30         40         50

```

```

                50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . .  ::
gi+AHw-602  MGVFTYESEFTSIIPPAPLRFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110
```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . .  ::
gi+AHw-602  MGVFTYESEFTSVIIPPAPLRFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110
```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . .  ::
gi+AHw-279  MGVFTYESEFTSVIIPPAPLRFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110
```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-131  MGVFNJETEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

```

```

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 50 init1: 50 opt: 52 Z-score: 85.4 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (9-37:23-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ..  ::  :  .:  .:  .:  :::. . . ::
gi+AHw-444  MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIA PQSVKGAEIVEG DGGVGTIKKISF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

```

```

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 36 initl: 36 opt: 50 Z-score: 85.0 bits: 20.5 E(): 9.3
 Smith-Waterman score: 50+ADs- 27.500+ACU- identity (72.500+ACU- similar)
 in 40 aa overlap (43-80:11-47)

```

                20      30      40      50      60      70
AAD-12 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                :.: : : .....: .....:
gi+AHw-160                GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQQLLY
                        10      20      30

                80
AAD-12 SQSKLGHVQQ
                :.: ....
gi+AHw-160 LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
                40      50      60      70      80      90
  
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:55 2010 done: Fri Feb 5 12:55:55 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 99 - 178 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 4 library sequences
24	0	0:	
26	0	0:	
28	1	0:+AD0-	
30	3	2:+ACo-	
32	5	8:+AD0AKg-	
34	13	21:+AD0APQA9AD0- +ACo-	
36	31	44:+AD0APQA9AD0APQA9AD0APQ- +ACo-	
38	48	72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-	

+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.01450.00323+ADs- mu+AD0- 0.2313
0.170
mean+AF8-var+AD0-36.389910.135, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.212610
Kolmogorov-Smirnov statistic: 0.1039 (N+AD0-28) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 62 24.1 0.86
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 24.1 0.94
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145) 57 22.6 2.7
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 57 22.5 3.1
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 56 22.2 3.9
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 58 22.6 5.7
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 54 21.6 5.9
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.3 6.4
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.3 7.3
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.0 8.5
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 51 20.8 8.9
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 51 20.8 8.9
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159) 52 21.0 9
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159) 52 21.0 9
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159) 52 21.0 9
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159) 52 21.0 9
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159) 52 21.0 9
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159) 52 21.0 9
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159) 52 21.0 9
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159) 52 21.0 9

gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9
 gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.0 9
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 50 20.5 9.5
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 50 20.5 9.7

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 36 initl: 36 opt: 62 Z-score: 103.6 bits: 24.1 E(): 0.86
 Smith-Waterman score: 62+ADs- 29.310+ACU- identity (65.517+ACU- similar)
 in 58 aa overlap (24-79:9-62)

	10	20	30	40	50
AAD-12	MKVIVGNMAWHADSTYMPVMAQGA	VFSAEVVPVAVGGRTCFADMRAAYDAL--DE	ATRALV		
		:	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI-				
	10	20	30	40	

	60	70	80
AAD-12	HQRSARHSLVYSQSKLGHVQQA		
	:	:
gi+AHw-111	--EKGEHQLLYLQHQLDDELNENKSKELQEKIIRELDVVCAMIEGAQ GALERELKRTDLNI		
	50	60	70

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 102.8 bits: 24.1 E(): 0.94
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (14-62:5-52)

	10	20	30	40	50	60
AAD-12	MKVIVGNMAWHADSTYMPVMAQGA	VFSAEVVPVAVGGRTCFADMRAAYDALDE	ATRALVHQ			
	:	:	:	:	:	:
gi+AHw-189	MASKSSITPLLLA AVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQ					
	10	20	30	40	50	

	70	80
AAD-12	RSARHSLVYSQSKLGHVQQA	
	..	
gi+AHw-189	QTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRV LKDLPGC	
	60	70

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
 tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 94.5 bits: 22.6 E(): 2.7
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (14-62:5-52)

	10	20	30	40	50	60
--	----	----	----	----	----	----


```

AAD-12          MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (12-36:27-50)

```

                10          20          30          40
AAD-12          MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (12-36:27-50)

```

                10          20          30          40
AAD-12          MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  :: :...  .  ::
gi+AHw-279  MGVFTYESEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (12-36:27-50)

```

                10          20          30          40

```

```

AAD-12          MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (12-36:27-50)

```

                10          20          30          40
AAD-12          MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (12-36:27-50)

```

                10          20          30          40
AAD-12          MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .: .:  :: :...  .  ::
gi+AHw-131  MGVFNYYETEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (12-36:27-50)

```

                10          20          30          40

```



```

AAD-12 ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                                :::  .:  :  .....  .....:
gi+AHw-160                      GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
                                10      20      30

```

```

      70      80
AAD-12 SQSKLGHVQQA
      :  .:  ....
gi+AHw-160 LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQT
      40      50      60      70      80      90

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 50 initl: 50 opt: 50 Z-score: 84.7 bits: 20.5 E(): 9.7
Smith-Waterman score: 50+ADs- 26.829+ACU- identity (58.537+ACU- similar)
in 41 aa overlap (40-80:26-66)

```

      10      20      30      40      50      60
AAD-12 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                                :::      .:  .  :  ....  :..
gi+AHw-527      MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
                                10      20      30      40      50

```

```

      70      80
AAD-12 SQSKLGHVQQA
      ..  .:  ....
gi+AHw-527 AKVNVVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQ
      60      70      80      90      100      110

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:55 2010 done: Fri Feb 5 12:55:55 2010
Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 100 - 179 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-

```



```

92      1      1:+ACo-      :+ACo-
94      2      1:+ACo-      :+ACoAPQ-
96      0      1:+ACo-      :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     2      0:+AD0-      +ACoAPQA9-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120  0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.96160.0032+ADs- mu+AD0- 0.4624
0.168
mean+AF8-var+AD0-35.842310.035, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.214228
Kolmogorov-Smirnov statistic: 0.1060 (N+AD0-28) at 46

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 62 24.2 0.81
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.2 0.89
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.6 2.6
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.6 3
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.3 3.7
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.7 5.4
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.7 5.6
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.4 6.2
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.4 7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.1 8.1
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 51 20.8 8.5
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
51 20.8 8.5
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.6

```

gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
52 21.1 8.6
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
52 21.1 8.6
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
52 21.1 8.6
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
52 21.1 8.6
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
52 21.1 8.6
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
52 21.1 8.6
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
52 21.1 8.6
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
52 21.1 8.6
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
52 21.1 8.6
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
52 21.1 8.6
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
50 20.6 9.1
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 50 20.5 9.3
gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumi (107)
49 20.3 9.8

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 36 initl: 36 opt: 62 Z-score: 104.0 bits: 24.2 E(): 0.81
Smith-Waterman score: 62+ADs- 29.310+ACU- identity (65.517+ACU- similar)
in 58 aa overlap (23-78:9-62)

	10	20	30	40	50
AAD-12	KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRVLVH				
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI--				
	10	20	30	40	
	60	70	80		
AAD-12	QRSARHSLVYSQSKLGHVQQAG				
gi+AHw-111	-EKGEHQLLYLQHQLDLNLNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNIL				
	50	60	70	80	90 100

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 initl: 55 opt: 62 Z-score: 103.3 bits: 24.2 E(): 0.89
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (13-61:5-52)

	10	20	30	40	50	60
AAD-12	KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQR					

gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQ
 10 20 30 40 50

70 80
 AAD-12 SARHSLVYSQSKLGHVQQAG

gi+AHw-189 TCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGCP
 60 70 80 90 100 110

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 94.9 bits: 22.6 E(): 2.6
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (13-61:5-52)

10 20 30 40 50 60
 AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQR

 gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQ
 10 20 30 40 50

70 80
 AAD-12 SARHSLVYSQSKLGHVQQAG

gi+AHw-439 TCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGC
 60 70 80 90 100 110

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 93.9 bits: 22.6 E(): 3
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (7-35:23-50)

10 20 30 40
 AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

 gi+AHw-444 MGVFTYADESTSVIPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 92.2 bits: 22.3 E(): 3.7
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (11-35:27-50)

10 20 30 40
 AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIEGNGGPGTIKKITF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
60 70 80 90 100 110

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)
initn: 49 initl: 49 opt: 58 Z-score: 89.3 bits: 22.7 E(): 5.4
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (8-57:23-71)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
.. :: : : : . : ::::: : :
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
10 20 30 40 50

50 60 70 80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
. . . . : :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 52 initl: 52 opt: 54 Z-score: 88.9 bits: 21.7 E(): 5.6
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (7-35:23-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
.. :: : : : . : ::::: . : :
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 88.2 bits: 21.4 E(): 6.2
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (13-61:5-52)

10 20 30 40 50 60
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQR
. . : : . . . : : : : : : : . .

gi+AHw-217 MASKSSISPLLLLATVLSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQ
10 20 30 40 50

70 80
AAD-12 SARHSLVYSQSKLGHVQQAG

gi+AHw-217 TCGISISGSAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGC
60 70 80 90 100 110

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 87.2 bits: 21.4 E(): 7
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (16-67:31-87)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
: : : : : : : :
gi+AHw-132 MGVFNJETETTSVIIPPARLFKRFVLDSDNLIKVPKAIKSIEIIEGNGGPGTIKKICF-
10 20 30 40 50

50 60 70 80
AAD-12 DMRAAYDALDEATRALLVHQR-SARHSLVYSQSKLGHVQQAG
: : : : : : : :
gi+AHw-132 DEGSPFNLIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
60 70 80 90 100 110

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (46-69:29-52)

20 30 40 50 60 70
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGH
: : : : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
10 20 30 40 50

80
AAD-12 VQQAG
gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
60 70 80 90 100 110

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 36 initl: 36 opt: 51 Z-score: 85.6 bits: 20.8 E(): 8.5
Smith-Waterman score: 51+ADs- 27.586+ACU- identity (63.793+ACU- similar)
in 58 aa overlap (23-78:9-62)

10 20 30 40 50
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALLVH
: : : : : : : :

```

gi+AHw-111          MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI--
                    10          20          30          40

```

```

        60          70          80
AAD-12 QRSARHSLVYSQSKLGHVQQAG
        .....: : :

```

```

gi+AHw-111 -EKGEHQLLYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNIL
                    50          60          70          80          90          100

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)
 initn: 36 initl: 36 opt: 51 Z-score: 85.6 bits: 20.8 E(): 8.5
 Smith-Waterman score: 51+ADs- 27.586+ACU- identity (63.793+ACU- similar)
 in 58 aa overlap (23-78:9-62)

```

                    10          20          30          40          50
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRVLVH
                    : : : : : . : : : : : : : : : : : : : : : : :
gi+AHw-420          MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI--
                    10          20          30          40

```

```

        60          70          80
AAD-12 QRSARHSLVYSQSKLGHVQQAG
        .....: : :

```

```

gi+AHw-420 -EKGEHQLLYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNIL
                    50          60          70          80          90          100

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (11-35:27-50)

```

                    10          20          30          40
AAD-12          KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                    : : . : : : : : : : : : : : : : : : : :
gi+AHw-602 MGVFYSEFTSVIPPARLFNFAVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                    10          20          30          40          50

```

```

        50          60          70          80
AAD-12 AYDALDEATRVLVHQRSARHSLVYSQSKLGHVQQAG

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
        60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1.03A (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (11-35:27-50)

```

                    10          20          30          40
AAD-12          KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                    : : . : : : : : : : : : : : : : : : : :

```

gi+AHw-602 MGVF¹⁰TYESEFTSVI²⁰PPARLFN³⁰AFVLDADNL-IPK⁴⁰IAPQAVKSAE⁵⁰IILEGDDGGVGTIKKINF

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
:: .: .: :: :::: . :
gi+AHw-602 MGVF¹⁰TYESEFTSII²⁰PPARLFN³⁰AFVLDADNL-IPK⁴⁰IAPQAVKSAE⁵⁰IILEGDDGGVGTIKKINF

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
:: .: .: :: :::: . :
gi+AHw-602 MGVF¹⁰TYESEFTSVI²⁰PPARLFN³⁰AFVLDADNL-IPK⁴⁰IAPQAVKSAE⁵⁰IILEGDDGGVGTIKKINF

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
:: .: .: :: :::: . :
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH

gi+AHw-279 MGVF¹⁰TYESEFTSVI²⁰PPARLFN³⁰AFVLDADNL-IPK⁴⁰IAPQAVKSAE⁵⁰IILEGDDGGVGTIKKINF

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
:: .: .: :: :::: . :
gi+AHw-602 MGVF¹⁰TYESEFTSVI²⁰PPARLFN³⁰AFVLDADNL-IPK⁴⁰IAPQAVKSAE⁵⁰IILEGDDGGVGTIKKINF

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
:: .: .: :: :::: . :
gi+AHw-602 MGVF¹⁰TYESEFTSVI²⁰PPARLFN³⁰AFVLDADNL-IPK⁴⁰IAPQAVKSAE⁵⁰IILEGDDGGVGTIKKINF

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
:: .: .: :: :::: . :
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH

gi+AHw-131 MGVFN¹⁰YETEFTSVI²⁰PPARLFN³⁰AFVLDADNL-IPK⁴⁰IAPQAVKSAE⁵⁰IILEGDDGGVGTIKKINF

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-131 GEGSTYSYV⁶⁰KHRIDGVDK⁷⁰ENFVYKYSVIEGDAI⁸⁰SETIEKISYET⁹⁰KLVASGSGSVIK¹⁰⁰STSH¹¹⁰

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGA¹⁰VFSAEVVP²⁰AVGGRTCFADM³⁰RA⁴⁰
:: .: .: :: :::: . : ::
gi+AHw-602 MGVFTY¹⁰ESEFTSVI²⁰PPARLFN³⁰AFVLDADNL-IPK⁴⁰IAPQAVKSAE⁵⁰IILEGDDGGVGTIKKINF

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYV⁶⁰KHRIDGVDK⁷⁰DNFVYKYSVIEGDAI⁸⁰SETIEKISYET⁹⁰KLVA¹⁰⁰SSNGSVIK¹¹⁰STSH

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGA¹⁰VFSAEVVP²⁰AVGGRTCFADM³⁰RA⁴⁰
:: .: .: :: :::: . : ::
gi+AHw-602 MGVFTY¹⁰ESEFTSVI²⁰PPARLFN³⁰AFVLDADNL-IPK⁴⁰IAPQAVKSAE⁵⁰IILEGDDGGVGTIKKINF

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYV⁶⁰KHRIDGVDK⁷⁰ENFVYKYSVIEGDAI⁸⁰SETIEKISYET⁹⁰KLVASGSGSVIK¹⁰⁰STSH¹¹⁰

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen Pru a (160 aa)
initn: 50 init1: 50 opt: 52 Z-score: 85.5 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (7-35:23-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGA¹⁰VFSAEVVP²⁰AVGGRTCFADM³⁰RA⁴⁰
.. :: : .: .: .: :::: . : ::

46 122 138:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9- +ACo-
48 174
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA
9AD0APQA9AD0-
50 121
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
52 100
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0- +ACo-
54 57 91:+AD0APQA9AD0APQA9AD0APQA9AD0-+AD0APQA9AD0APQA9AD0APQA9-
+ACo-
56 82
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0-
58 51 62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
60 55 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62 47 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
64 48 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
66 50 25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
68 46 20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0-
70 14 16:+AD0APQA9AD0APQAq-
72 34 12:+AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
74 14 10:+AD0APQA9ACoAPQ-
76 23 7:+AD0APQAqAD0APQA9AD0APQ-
78 10 6:+AD0AKgA9AD0-
80 7 4:+AD0AKgA9-
82 8 3:+ACoAPQA9-
84 12 3:+ACoAPQA9AD0-
86 5 2:+ACoAPQ-
88 6 2:+ACoAPQ- inset +AD0- represents 1 library

sequences

90 0 1:+ACo-
92 1 1:+ACo- :+ACo-
94 2 1:+ACo- :+ACoAPQ-
96 0 1:+ACo- :+ACo-
98 0 0: +ACo-
100 0 0: +ACo-
102 0 0: +ACo-
104 1 0:+AD0- +ACoAPQ-
106 1 0:+AD0- +ACoAPQ-
108 0 0: +ACo-
110 0 0: +ACo-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 5.80580.00317+ADs- mu+AD0- 1.2308
0.167

mean+AF8-var+AD0-35.883610.156, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.214105
Kolmogorov-Smirnov statistic: 0.1003 (N+AD0-29) at 58

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 64 24.8 0.53
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 24.2 0.89
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145) 57 22.6 2.6
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 57 22.6 3
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 56 22.3 3.7
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 58 22.7 5.2
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.4 5.6
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.4 5.6
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 54 21.7 5.6
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 21.2 6
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.4 6.2
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.4 7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.1 8.1
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159) 52 21.1 8.6
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159) 52 21.1 8.6
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6

gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.6
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.1 8.6
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 50 20.5 9.4
 gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumi (107)
 49 20.3 9.9
 gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA (301)
 55 21.8 10

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 107.3 bits: 24.8 E(): 0.53
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (22-80:9-65)

	10	20	30	40	50
AAD-12	VIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQ				
		:	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---				
	10	20	30	40	

	60	70	80
AAD-12	RSARHSLVYSQSKLGHVQQAGS		
: : : : : :		
gi+AHw-111	EKGEHQLLYLQHQLDLDELNENKSKELQEKI IRELDVVCAMIEGAQGalERELKRTDLNILE		
	50	60	70

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 103.3 bits: 24.2 E(): 0.89
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (12-60:5-52)

	10	20	30	40	50	60
AAD-12	VIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRS					
	:	:	:	:	:	:
gi+AHw-189	MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQT					
	10	20	30	40	50	

	70	80
AAD-12	ARHSLVYSQSKLGHVQQAGS	
gi+AHw-189	CGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRVRYFIGRRSHPDWRVLDLPGCPK	
	60	70

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
 tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 94.9 bits: 22.6 E(): 2.6
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (12-60:5-52)

	10	20	30	40	50	60
--	----	----	----	----	----	----

AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
 . : . : . : . : . : . :
 gi+AHw-132 MGVFN YETETTSVIPPARLFKRFLDSDNLI PKVAPKAIKSIEIIEGNGGPGTIKKICF-
 10 20 30 40 50

40 50 60 70 80
 AAD-12 DMRAAYDALDEATR ALVHQR-SARHSLVYSQSKLGHVQQAGS
 : : : : : :
 gi+AHw-132 DEGSPFN YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSI S
 60 70 80 90 100 110

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 init1: 52 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (45-68:29-52)

20 30 40 50 60 70
 AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGH
 : : : : : : . . . : : : : :
 gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
 10 20 30 40 50

80
 AAD-12 VQQAGS
 gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
 1.03D (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (10-34:27-50)

10 20 30 40
 AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 : : . : : : : : : : : : : :
 gi+AHw-602 MGVFTYSEFTSVIPPARLFN A FVLADNL-IPK IAPQAVKSAEILEG DGGVGTIKKINF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGS
 gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
 1.03A (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (10-34:27-50)

10 20 30 40

```

AAD-12          VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::...  .  ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEIELEGDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (10-34:27-50)

```

                10      20      30      40
AAD-12          VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::...  .  ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEIELEGDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (10-34:27-50)

```

                10      20      30      40
AAD-12          VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::...  .  ::
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEIELEGDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (10-34:27-50)

```

                10      20      30      40

```

```

AAD-12          VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::. .: .: :: :... . ::
gi+AHw-602 MGVF10TYESEFTSVI20PPARLFNA30FVLDADNL-IP40KIAPQAVKSAE50IILEGDDGGVGTIKKINF

```

```

                50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (10-34:27-50)

```

                10          20          30          40
AAD-12          VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::. .: .: :: :... . ::
gi+AHw-602 MGVF10TYESEFTSVI20PPARLFNA30FVLDADNL-IP40KIAPQAVKSAE50IILEGDDGGVGTIKKINF

```

```

                50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (10-34:27-50)

```

                10          20          30          40
AAD-12          VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::. .: .: :: :... . ::
gi+AHw-131 MGVF10NYETEFTSVI20PPARLFNA30FVLDADNL-IP40KIAPQAVKSAE50IILEGDDGGVGTIKKINF

```

```

                50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (10-34:27-50)

```

                10          20          30          40

```

```

AAD-12          VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::...  .  ::
gi+AHw-602  MGVFTYESEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (10-34:27-50)

```

                10          20          30          40
AAD-12          VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::...  .  ::
gi+AHw-602  MGVFTYESEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (10-34:27-50)

```

                10          20          30          40
AAD-12          VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::...  .  ::
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 50 init1: 50 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (6-34:23-50)

```

                10          20          30          40

```


331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.81550.00313+ADs- mu+AD0- 1.1633
0.165
mean+AF8-var+AD0-35.0524 9.934, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.216628
Kolmogorov-Smirnov statistic: 0.1044 (N+AD0-29) at 58

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 64 25.0 0.48
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 24.3 0.82
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145) 57 22.7 2.4
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 57 22.7 2.8
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 56 22.4 3.4
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 58 22.8 4.9
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.5 5.2
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.5 5.2
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 54 21.8 5.3
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 21.3 5.6
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.5 5.8
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.5 6.6
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.2 7.6
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.1
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.1
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.1
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159) 52 21.1 8.1
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.1
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.1
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159) 52 21.1 8.1
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.1

gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.1
 gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.1
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.1 8.1
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 50 20.6 8.8
 gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumi (107)
 49 20.4 9.4

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 108.0 bits: 25.0 E(): 0.48
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (21-79:9-65)

	10	20	30	40	50
AAD-12	IVGNMAWHADSTYMPVMAQGA	VFSAEVVP	AVGGRTCFADMRAAYDAL--	DEATR	LVHQ
		:	::	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---				
	10	20	30	40	

	60	70	80
AAD-12	SARHSLVYSQSKLGHVQQAGSA		
:::	: :
gi+AHw-111	KGEHQLLYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILER		
	50	60	70

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 103.9 bits: 24.3 E(): 0.82
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (11-59:5-52)

	10	20	30	40	50	60
AAD-12	IVGNMAWHADSTYMPVMAQGA	VFSAEVVP	AVGGRTCFADMRAAYDALDEATR	LVHQ	RS	
	:	:
gi+AHw-189	MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTC					
	10	20	30	40	50	

	70	80
AAD-12	RHSLVYSQSKLGHVQQAGSA	
gi+AHw-189	GVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRVRYFIGRRSHPDWRVLKDLPGCPKE	
	60	70

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
 tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 95.4 bits: 22.7 E(): 2.4
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (11-59:5-52)

	10	20	30	40	50	60
--	----	----	----	----	----	----

AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR¹ALVH²Q³RS⁴A

 gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTC
 10 20 30 40 50

AAD-12 RHSLVYSQSKLGHVQQAGSA
 70 80
 gi+AHw-439 GVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPK
 60 70 80 90 100 110

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 94.5 bits: 22.7 E(): 2.8
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (5-33:23-50)

AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

 gi+AHw-444 MGVFTYADESTSVI¹PP²RL³FK⁴AL⁵VLEAD-TLIPKIA⁶PQ⁷SV⁸KS⁹AEI¹⁰VEGDGGVGTIKKISF
 10 20 30 40 50

AAD-12 AYDALDEATR¹ALVH²Q³RSARHSLVYSQSKLGHVQQAGSA
 50 60 70 80
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKL¹VASADGG²SIIK³STS
 60 70 80 90 100 110

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
 sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 92.8 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

 gi+AHw-165 MGVFTHENEITSAI¹PP²GR³LF⁴KA⁵FVLDADNL-IPKLAPHA⁶IK⁷SAE⁸II⁹EGNGGPGT¹⁰IKK¹¹IT¹²F
 10 20 30 40 50

AAD-12 AYDALDEATR¹ALVH²Q³RSARHSLVYSQSKLGHVQQAGSA
 50 60 70 80
 gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGG¹SIL²K³N⁴TS
 60 70 80 90 100 110

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
 Lolium per (301 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 89.9 bits: 22.8 E(): 4.9
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (6-55:23-71)

10 20 30 40


```

AAD-12          IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
                .: .: .: .: .: .: .: .: .:
gi+AHw-132 MGVFNYETETTSVIPPARLFKRFLDSDNLI PKVAPKAIKSIEIIEGNGGPGTIKKICF-
                10      20      30      40      50

```

```

                40      50      60      70      80
AAD-12 DMRAAYDALDEATR LVHQR-SARHSLVYSQSKLGHVQQAGSA
                : . . . . . : : : :
gi+AHw-132 DEGSPFN YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 init1: 52 opt: 52 Z-score: 86.5 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (44-67:29-52)

```

                20      30      40      50      60      70
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR LVHQRSARHSLVYSQSKLGH
                : : : : : : . . . : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
                10      20      30      40      50

```

```

                80
AAD-12 VQQAGSA
gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (9-33:27-50)

```

                10      20      30      40
AAD-12          IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .: .: .: .: .: .: .: .:
gi+AHw-602 MGVF TYESEFTSVIPPARLFN AFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 AYDALDEATR LVHQRSARHSLVYSQSKLGHVQQAGSA
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (9-33:27-50)

```

                10      20      30      40

```

```

AAD-12                IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: :...  .  ::
gi+AHw-602  MGVTYSEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                    50          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

```

                    10          20          30          40
AAD-12                IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: :...  .  ::
gi+AHw-602  MGVTYSEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                    50          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

```

                    10          20          30          40
AAD-12                IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: :...  .  ::
gi+AHw-279  MGVTYSEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

                    50          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA

```

```

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

```

                    10          20          30          40

```

```

AAD-12                IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ...  .: .:  :: :...  .  ::
gi+AHw-602  MGVF10TYESEFTSVI20PPARLFN30AFVLDADNL-IP40KIAPQ50AVKSAEILEG60DGGVGTIKKINF

```

```

AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
           60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

```

AAD-12                IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ...  .: .:  :: :...  .  ::
gi+AHw-602  MGVF10TYESEFTSVI20PPARLFN30AFVLDADNL-IP40KIAPQ50AVKSAEILEG60DGGVGTIKKINF

```

```

AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
           60      70      80      90      100     110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

```

AAD-12                IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ...  .: .:  :: :...  .  ::
gi+AHw-131  MGVF10NYETEFTSVI20PPARLFN30AFVLDADNL-IP40KIAPQ50AVKSAEILEG60DGGVGTIKKINF

```

```

AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
           60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

10 20 30 40

```

AAD-12                IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ...  .: .:  :: :...  .  ::
gi+AHw-602  MGVFYSEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                        10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
            60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

```

                    10      20      30      40
AAD-12                IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ...  .: .:  :: :...  .  ::
gi+AHw-602  MGVFYSEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                        10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
            60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

```

                    10      20      30      40
AAD-12                IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ...  .: .:  :: :...  .  ::
gi+AHw-602  MGVFYSEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                        10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
            60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 50 init1: 50 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (5-33:23-50)

```

                    10      20      30      40

```

```

AAD-12          IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. ::: : : : : : : : : : : : : : : : : : :
gi+AHw-444 MGVFYADESTSVITPPRLFALVLEAD-TLIPKIA PQSVKGAEIVEGDGGVGTIKKISF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVSADGGSIKSTS
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 50 initl: 50 opt: 50 Z-score: 85.4 bits: 20.6 E(): 8.8
Smith-Waterman score: 50+ADs- 26.829+ACU- identity (58.537+ACU- similar)
in 41 aa overlap (37-77:26-66)

```

                10          20          30          40          50          60
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                :::: :. . . : : : : : : : :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
                10          20          30          40          50

```

```

                70          80
AAD-12 SQSKLGHVQQAGSA
                .. .. : : : :
gi+AHw-527 AKVNVVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AAEKLGGLAQ
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle
parvalbumin +AFs-T (107 aa)
initn: 42 initl: 42 opt: 49 Z-score: 84.9 bits: 20.4 E(): 9.4
Smith-Waterman score: 49+ADs- 22.414+ACU- identity (56.897+ACU- similar)
in 58 aa overlap (19-76:4-59)

```

                10          20          30          40          50          60
AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA
                .... : : : : : : : : : : : : : : : : : :
gi+AHw-777 MAFKGV LNDADVTAALDGCKSAFDHKAFFKACGLAAKSADDIKKA
                10          20          30          40

```

```

                70          80
AAD-12 RHSLVYSQSKLGHVQQAGSA
                . . . . : : . .
gi+AHw-777 FA--IIDQDKSGFIEEDELKLF LQNF CAGARALSDAETKAF LKAGDSGDGKIGVDEF AA
                50          60          70          80          90          100

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:56 2010 done: Fri Feb 5 12:55:57 2010
Total Scan time: 0.090 Total Display time: 0.000

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
57 22.7 2.7
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
56 22.4 3.4
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
58 22.8 4.8
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
53 21.5 5.2
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
53 21.5 5.2
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
54 21.8 5.2
gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116)
52 21.3 5.4
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
52 21.3 5.6
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145)
53 21.5 5.8
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160)
53 21.5 6.5
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152)
52 21.2 7.6
gi+AHw-60280849+AHw-gb+AHw-AAx18317.1+AHw- major allergen Mal d 1. (159)
52 21.2 8
gi+AHw-60280841+AHw-gb+AHw-AAx18313.1+AHw- major allergen Mal d 1. (159)
52 21.2 8
gi+AHw-60280859+AHw-gb+AHw-AAx18322.1+AHw- major allergen Mal d 1. (159)
52 21.2 8
gi+AHw-60280853+AHw-gb+AHw-AAx18319.1+AHw- major allergen Mal d 1. (159)
52 21.2 8
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
52 21.2 8
gi+AHw-60280861+AHw-gb+AHw-AAx18323.1+AHw- major allergen Mal d 1. (159)
52 21.2 8
gi+AHw-60280843+AHw-gb+AHw-AAx18314.1+AHw- major allergen Mal d 1. (159)
52 21.2 8
gi+AHw-60280851+AHw-gb+AHw-AAx18318.1+AHw- major allergen Mal d 1. (159)
52 21.2 8
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
52 21.2 8
gi+AHw-60280855+AHw-gb+AHw-AAx18320.1+AHw- major allergen Mal d 1. (159)
52 21.2 8
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
52 21.2 8.1
gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumi (107)
49 20.4 9.4

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
initn: 38 init1: 38 opt: 64 Z-score: 108.0 bits: 25.0 E(): 0.48
Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (20-78:9-65)

10

20

30

40

50

```

AAD-12 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111      MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EK
      10          20          30          40
  
```

```

      60          70          80
AAD-12 ARHSLVYSQSKLGHVQQAGSAY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 GEHQLLYLQHQLDLLENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERF
      50          60          70          80          90          100
  
```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 104.0 bits: 24.3 E(): 0.82
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (10-58:5-52)

```

      10          20          30          40          50          60
AAD-12 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-189      MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCG
      10          20          30          40          50
  
```

```

      70          80
AAD-12 HSLVYSQSKLGHVQQAGSAY
gi+AHw-189 VTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGCPKEP
      60          70          80          90          100          110
  
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 57 initl: 57 opt: 57 Z-score: 97.2 bits: 22.8 E(): 1.9
 Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (36-80:26-70)

```

      10          20          30          40          50          60
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527      MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
      10          20          30          40          50
  
```

```

      70          80
AAD-12 SQSKLGHVQQAGSAY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527 AKVNVVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQ
      60          70          80          90          100          110
  
```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
 tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 95.5 bits: 22.7 E(): 2.4
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (10-58:5-52)

```

      10          20          30          40          50          60
  
```



```

AAD-12          VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                .. ::: : : : . : .....: : .
gi+AHw-663 MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY
                . . . . .: :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLLILKLDTDYDVA
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 89.5 bits: 21.5 E(): 5.2
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (20-78:9-65)

```

                10      20      30      40      50
AAD-12 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRS
                : ::: : : . ::: : : .....: ..
gi+AHw-420          MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EK
                10      20      30      40

```

```

                60      70      80
AAD-12 ARHSLVYSQSKLGHVQQAGSAY
                .....: : : ..... :
gi+AHw-420 GEHQLLYLQHQLDDELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERF
                50      60      70      80      90      100

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 89.5 bits: 21.5 E(): 5.2
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (20-78:9-65)

```

                10      20      30      40      50
AAD-12 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRS
                : ::: : : . ::: : : .....: ..
gi+AHw-111          MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EK
                10      20      30      40

```

```

                60      70      80
AAD-12 ARHSLVYSQSKLGHVQQAGSAY
                .....: : : ..... :
gi+AHw-111 GEHQLLYLQHQLDDELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERF
                50      60      70      80      90      100

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 52 initl: 52 opt: 54 Z-score: 89.4 bits: 21.8 E(): 5.2
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (4-32:23-50)


```

AAD-12                VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                        10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
            60      70      80      90      100     110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (8-32:27-50)

```

                        10      20      30      40
AAD-12                VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: :...  .  ::
gi+AHw-131  MGVFN YETEFTSVIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                        10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

```

```

gi+AHw-131  GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
            60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (8-32:27-50)

```

                        10      20      30      40
AAD-12                VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                        10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
            60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (8-32:27-50)

```

                        10      20      30      40

```



```

AAD-12          VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFYSEFTSIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 50 initl: 50 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8.1
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (4-32:23-50)

```

                10      20      30      40
AAD-12          VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  ::  :  .:  .:  .:  ::::.  .  ::
gi+AHw-444  MGVFYADESTSVITPPRLFALVLEAD-TLIPKIA PQSVKGAEIVEGDDGGVGTIKKISF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumin +AFs-T (107 aa)
 initn: 42 initl: 42 opt: 49 Z-score: 84.9 bits: 20.4 E(): 9.4
 Smith-Waterman score: 49+ADs- 22.414+ACU- identity (56.897+ACU- similar)
 in 58 aa overlap (18-75:4-59)

```

                10      20      30      40      50      60
AAD-12  VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                ....  ::::.  .:  :  :  .:  .:  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-777  MAFKGV LNDADVTAALD GCKSAFDHKAFFKACGLA AKSADDIKKAF
                10      20      30      40

```

```

                70      80
AAD-12  HSLVYSQSKLGHVQQAGSAY
                .  ::::.  :  ...
gi+AHw-777  A--IIDQDKSGFIEEDELKLF LQNF CAGARALS DAETKAF LKAGDS DGDGKIGVDEFAAM
                50      60      70      80      90      100

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:57 2010 done: Fri Feb 5 12:55:57 2010
 Total Scan time: 0.090 Total Display time: 0.010

56 83
 76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
 A9AD0-
 58 50 62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
 60 61
 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
 62 42 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
 64 40 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
 66 62 25:+AD0APQA9AD0APQA9AD0-
 +AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
 68 43 20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
 70 11 16:+AD0APQA9AD0- +ACo-
 72 30 12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
 74 17 10:+AD0APQA9ACoAPQA9-
 76 15 7:+AD0APQAqAD0APQ-
 78 18 6:+AD0AKgA9AD0APQA9-
 80 8 4:+AD0AKgA9-
 82 8 3:+ACoAPQA9-
 84 4 3:+ACoAPQ-
 86 12 2:+ACoAPQA9AD0-
 88 5 2:+ACoAPQ- inset +AD0- represents 1 library

sequences

90 2 1:+ACo-
 92 1 1:+ACo- :+ACo-
 94 2 1:+ACo- :+ACoAPQ-
 96 1 1:+ACo- :+ACo-
 98 0 0: +ACo-
 100 0 0: +ACo-
 102 0 0: +ACo-
 104 1 0:+AD0- +ACoAPQ-
 106 0 0: +ACo-
 108 1 0:+AD0- +ACoAPQ-
 110 0 0: +ACo-
 112 0 0: +ACo-
 114 0 0: +ACo-
 116 0 0: +ACo-
 118 0 0: +ACo-

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 5.80120.00311+ADs- mu+AD0- 1.1680
 0.164

mean+AF8-var+AD0-35.492010.042, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42

Lambda+AD0- 0.215283

Kolmogorov-Smirnov statistic: 0.1067 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 64 24.9 0.5

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 24.3 0.84

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 57 22.8 2

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145)
 57 22.7 2.5

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 22.7 2.8

gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
 56 22.4 3.5

gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
 58 22.8 5

gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
 53 21.5 5.3

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 53 21.5 5.3

gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.7 5.4

gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116)
 52 21.2 5.5

gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 21.2 5.7

gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145)
 53 21.5 5.9

gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160)
 53 21.4 6.7

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
 (152) 52 21.1 7.7

gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.2

gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.2

gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.2

gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.2

gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
 52 21.1 8.2

gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.2

gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.2

gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.2

gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
 52 21.1 8.2

gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.2

gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.1 8.3

gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumi (107)
 49 20.3 9.5

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)

initn: 38 init1: 38 opt: 64 Z-score: 107.8 bits: 24.9 E(): 0.5

Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (19-77:9-65)

```

                10         20         30         40         50
AAD-12  GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATR
ALVHQRSA
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111      MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKG
                10         20         30         40

```

```

                60         70         80
AAD-12  RHSLVYSQSKLGHVQQAGSAYI
                . : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111  EHQLLYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQ
GALERELKRTDLNILERFN
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 init1: 55 opt: 62 Z-score: 103.7 bits: 24.3 E(): 0.84
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (9-57:5-52)

```

                10         20         30         40         50         60
AAD-12  GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
ALVHQRSARH
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-189      MASKSSITPLLLAASVLFVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQ
QTCGV
                10         20         30         40         50

```

```

                70         80
AAD-12  SLVYSQSKLGHVQQAGSAYI
gi+AHw-189  TIAGSPVSSEPGDTPKDRCCQELDEAPQHRCRVRVYFIGRRSH
PDRVRLKDLPGCPKEPQ
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 57 init1: 57 opt: 57 Z-score: 97.0 bits: 22.8 E(): 2
Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (35-79:26-70)

```

                10         20         30         40         50         60
AAD-12  WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
ALVHQRSARHSLVY
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527      MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQ
LSTKHSVPDVLAF
                10         20         30         40         50

```

```

                70         80
AAD-12  SQSKLGHVQQAGSAYI
                . . . : : : : : : : : : : : : : : : : :
gi+AHw-527  AKVNVVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGAD
PRTLGA-AAEKLGGLAQ
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
tetrameric (145 aa)
initn: 50 init1: 50 opt: 57 Z-score: 95.3 bits: 22.7 E(): 2.5

Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (4-53:23-71)

```

                10         20         30         40
AAD-12          GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                .. ::: : :. : . : .....: :. .
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                10         20         30         40         50

                50         60         70         80
AAD-12 YDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYI
                . . . . : :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)
initn: 38 init1: 38 opt: 53 Z-score: 89.3 bits: 21.5 E(): 5.3
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (19-77:9-65)

```

                10         20         30         40         50
AAD-12 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALLVHQRSA
                : ::: :. : . : : : : .....: ...
gi+AHw-420          MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKG
                10         20         30         40

                60         70         80
AAD-12 RHSLVYSQSKLGHVQQAGSAYI
                .....: : : ..... :
gi+AHw-420 EHQLLYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFN
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
initn: 38 init1: 38 opt: 53 Z-score: 89.3 bits: 21.5 E(): 5.3
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (19-77:9-65)

```

                10         20         30         40         50
AAD-12 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALLVHQRSA
                : ::: :. : . : : : : .....: ...
gi+AHw-111          MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKG
                10         20         30         40

                60         70         80
AAD-12 RHSLVYSQSKLGHVQQAGSAYI
                .....: : : ..... :
gi+AHw-111 EHQLLYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFN
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)
initn: 52 init1: 52 opt: 54 Z-score: 89.3 bits: 21.7 E(): 5.4

Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (3-31:23-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  :::  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
                10      20      30      40      50

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVSADGGSIKSTS
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytoctystatin +AFs-
Actinidia de (116 aa)
initn: 34 init1: 34 opt: 52 Z-score: 89.0 bits: 21.2 E(): 5.5
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (11-79:11-80)

```

                10      20      30      40      50
AAD-12  GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                ..  .  .  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-408  MVPKPLSLLLFLLLLALSAAVVGGRKLV AAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
                10      20      30      40      50

                60      70      80
AAD-12  HSLVYSQSKLGHVQQ-AGSAYI
                :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-408  DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMWHFRNLTSFRKV
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 init1: 38 opt: 52 Z-score: 88.8 bits: 21.2 E(): 5.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (37-77:11-50)

```

                10      20      30      40      50      60
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-160      GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
                10      20      30

                70      80
AAD-12  SQSKLGHVQQAGSAYI
                :  :  :  :  :
gi+AHw-160  LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQ GALERELKRTDLNILERFN YEEAQT
                40      50      60      70      80      90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 init1: 46 opt: 53 Z-score: 88.5 bits: 21.5 E(): 5.9

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12                        GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12                        GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-131  MGVFNYTEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12                        GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12                        GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12                        GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12                        GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-279  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 50 initl: 50 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (3-31:23-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ..  ::  :  .:  .:  .:  :::. . . ::
gi+AHw-444  MGVFTYADESTSVITPPRLF KALVLEAD-TLIPKIA PQSVKGA EIVEG DGGVGTIKKISF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

```

```

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle
parvalbumin +AFs-T (107 aa)

initn: 42 initl: 42 opt: 49 Z-score: 84.8 bits: 20.3 E(): 9.5
Smith-Waterman score: 49+ADs- 22.414+ACU- identity (56.897+ACU- similar)
in 58 aa overlap (17-74:4-59)

```

                                10      20      30      40      50      60
AAD-12  GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH
                                ....  :::. .:  :  :  .:  .:  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-777  MAFKGV LNDADVTAALDGCKSAFDHKAFFKACGLA AKSADDIKKAFA
                                10      20      30      40

                                70      80
AAD-12  SLVYSQSKLGHVQQAGSAYI

```

```

.  :::. .:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-777  --IIDQDKSGFIEEDELKLF LQNF CAGARALSDAETKAF LKAGDSGDGDKIGVDEFAAMV
                                50      60      70      80      90      100

```

80 residues in 1 query sequences


```

56      78
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58      52      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
60      61
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
62      47      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
64      50      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
66      53      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-
68      41      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
70      13      16:+AD0APQA9AD0APQAq-
72      30      12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
74      16      10:+AD0APQA9ACoAPQA9-
76      21      7:+AD0APQAqAD0APQA9AD0-
78      10      6:+AD0AKgA9AD0-
80      9       4:+AD0AKgA9-
82      9       3:+ACoAPQA9-
84      9       3:+ACoAPQA9-
86      5       2:+ACoAPQ-
88      7       2:+ACoAPQA9-          inset +AD0- represents 1 library

```

sequences

```

90      0       1:+ACo-
92      1       1:+ACo-          :+ACo-
94      2       1:+ACo-          :+ACoAPQ-
96      1       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     1       0:+AD0-          +ACo-+AD0-
104     0       0:          +ACo-
106     1       0:+AD0-          +ACoAPQ-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-

```

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 5.79830.00318+ADs- mu+AD0- 1.1997
0.167

mean+AF8-var+AD0-36.168910.134, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42

Lambda+AD0- 0.213259

Kolmogorov-Smirnov statistic: 0.1046 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 64 24.8 0.54

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 24.2 0.9

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 57 22.7 2.1

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145)
 57 22.6 2.6

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 22.6 3

gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
 56 22.3 3.7

gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
 58 22.7 5.3

gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
 53 21.4 5.6

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 53 21.4 5.6

gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.7 5.7

gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116)
 52 21.2 5.8

gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 21.2 6

gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145)
 53 21.4 6.2

gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160)
 53 21.4 7

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
 (152) 52 21.1 8.1

gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.6

gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.6

gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.6

gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.6

gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
 52 21.1 8.6

gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.6

gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.6

gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.6

gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
 52 21.1 8.6

gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.6

gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.1 8.7

gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumi (107)
 49 20.3 10

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)

initn: 38 init1: 38 opt: 64 Z-score: 107.2 bits: 24.8 E(): 0.54

Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (18-76:9-65)

```

                10         20         30         40         50
AAD-12 NMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSAR
                : : : : : : . : : : : : : : : : : : : : : :
gi+AHw-111      MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGE
                10         20         30         40

```

```

                60         70         80
AAD-12 HSLVYSQSKLGHVQQAGSAYIG
                : : : : : : : : : : : : : : : :
gi+AHw-111 HQLLYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNY
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 init1: 55 opt: 62 Z-score: 103.2 bits: 24.2 E(): 0.9
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (8-56:5-52)

```

                10         20         30         40         50         60
AAD-12 NMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-189      MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVT
                10         20         30         40         50

```

```

                70         80
AAD-12 LVYSQSKLGHVQQAGSAYIG
gi+AHw-189 IAGSPVSSEPGDTPKDRCCQELDEAPQHRCRCRVRYFIGRRSHPDWRVLKDLPGCPKEPQR
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 57 init1: 57 opt: 57 Z-score: 96.5 bits: 22.7 E(): 2.1
Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (34-78:26-70)

```

                10         20         30         40         50         60
AAD-12 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527      MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
                10         20         30         40         50

```

```

                70         80
AAD-12 SQSKLGHVQQAGSAYIG
                : : : : : : : : : : : : : : : :
gi+AHw-527 AKVNVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQ
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
tetrameric (145 aa)
initn: 50 init1: 50 opt: 57 Z-score: 94.8 bits: 22.6 E(): 2.6

Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (3-52:23-71)

```

                                10      20      30      40
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
              .. ::: : :. : . : .....: :. .
gi+AHw-663  MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
              10      20      30      40      50

              50      60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG
              . . . . : :
gi+AHw-663  LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)
initn: 38 init1: 38 opt: 53 Z-score: 88.9 bits: 21.4 E(): 5.6
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (18-76:9-65)

```

              10      20      30      40      50
AAD-12  NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSAR
              : ::: : : . : : : : .....: ....
gi+AHw-420  MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGE
              10      20      30      40

              60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIG
              : : : : : : : : : :
gi+AHw-420  HQLLYLQHQLDDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNY
              50      60      70      80      90      100

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
initn: 38 init1: 38 opt: 53 Z-score: 88.9 bits: 21.4 E(): 5.6
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (18-76:9-65)

```

              10      20      30      40      50
AAD-12  NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSAR
              : ::: : : . : : : : .....: ....
gi+AHw-111  MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGE
              10      20      30      40

              60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIG
              : : : : : : : : : :
gi+AHw-111  HQLLYLQHQLDDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNY
              50      60      70      80      90      100

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)
initn: 52 init1: 52 opt: 54 Z-score: 88.9 bits: 21.7 E(): 5.7

Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (2-30:23-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ..  :::  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
              10      20      30      40      50

              40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
              60      70      80      90      100     110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)
initn: 34 initl: 34 opt: 52 Z-score: 88.6 bits: 21.2 E(): 5.8
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (10-78:11-80)

```

                                10      20      30      40      50
AAD-12  NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
              ..  .  .  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-408  MVPKPLSLLLFLLLLALSAAVVGGRKLV AAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
              10      20      30      40      50

              60      70      80
AAD-12  HSLVYSQSKLGHVQQ-AGSAYIG
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-408  DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMWHFRNLTSFRKV
              60      70      80      90      100     110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 88.4 bits: 21.2 E(): 6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (36-76:11-50)

```

                                10      20      30      40      50      60
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-160      GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
              10      20      30

              70      80
AAD-12  SQSKLGHVQQAGSAYIG
              :  :  :  :  :
gi+AHw-160  LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQ GALERELKRTDLNILERFN YEEAQT
              40      50      60      70      80      90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 88.2 bits: 21.4 E(): 6.2

Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (8-56:5-52)

```

                10         20         30         40         50         60
AAD-12 NMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHS
                :.  :..  ..  :.  . . . . :  ::  :  .  :  :  :  :  :..
gi+AHw-217  MASKSSISPLLLLATVLSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTCGIS
                10         20         30         40         50

```

```

                70         80
AAD-12 LVYSQSKLGHVQQAGSAYIG

gi+AHw-217 ISGSAVSTEPGNTPRDRCKELYDASQHCRC EAVRYFIGRRSDPNSSVLKDLPGCPREPQ
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 init1: 47 opt: 53 Z-score: 87.2 bits: 21.4 E(): 7
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (11-62:31-87)

```

                10         20         30
AAD-12 NMAWHADSTYMPVMAQGAVFSAEVPVAVGG-----RTCFA
                .:  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-132 MGVFN YETETTSVIPPARLFKRFVLDSDNLI PKVAPKAIKSIEIIEGNGGPGTIKKICF-
                10         20         30         40         50

```

```

                40         50         60         70         80
AAD-12 DMRAAYDALDEATRALLVHQR-SARHSLVYSQSKLGHVQQAGSAYIG
                :  .  .  .  .  .  .  .  :  :  :  :  :
gi+AHw-132 DEGSPFN YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 init1: 52 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.1
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (41-64:29-52)

```

                20         30         40         50         60         70
AAD-12 MPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVYSQSKLGH
                :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
                10         20         30         40         50

```

```

                80
AAD-12 VQQAGSAYIG

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12                          NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12                          NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12                          NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12                        NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 AYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12                        NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-131 MGVFNYTEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 AYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12                        NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 AYDALDEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12                          NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12                          NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12                          NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. .  ::
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 50 initl: 50 opt: 52 Z-score: 85.5 bits: 21.1 E(): 8.7
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (2-30:23-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ..  ::  :  .:  .:  .:  :::. .  ::
gi+AHw-444  MGVFTYADESTSVITPPRLFALVLEAD-TLIPKIA PQSVKGA EIVEGDDGGVGTIKKISF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle
parvalbumin +AFs-T (107 aa)

initn: 42 initl: 42 opt: 49 Z-score: 84.4 bits: 20.3 E(): 10
Smith-Waterman score: 49+ADs- 22.414+ACU- identity (56.897+ACU- similar)
in 58 aa overlap (16-73:4-59)

```

    10      20      30      40      50      60
AAD-12  NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
                                ....  :::. .:  :  :  .:  .:  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-777  MAFKGV LNDADVTAALDGCKSAFDHKAFFKACGLA AKSADDIKKAFA-
                                10      20      30      40

```

```

    70      80
AAD-12  LVYSQSKLGHVQQAGSAYIG
.  :::. .:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-777  -IIDQDKSGFIEEDELKLF LQNF CAGARALS DAETKAF LKAGDS DGDGKIGVDEFAAMVK
    50      60      70      80      90      100

```

80 residues in 1 query sequences

54 73
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56 82
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0-
58 53 62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
60 55 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62 47 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
64 69
32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
66 36 25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
68 43 20:+AD0APQA9AD0APQA9ACoAPQA9AD0-+AD0APQA9AD0APQ-
70 16 16:+AD0APQA9AD0APQAq-
72 30 12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
74 19 10:+AD0APQA9ACoAPQA9AD0-
76 23 7:+AD0APQAqAD0APQA9AD0APQ-
78 6 6:+AD0AKg-
80 11 4:+AD0AKgA9AD0-
82 6 3:+ACoAPQ-
84 13 3:+ACoAPQA9AD0APQ-
86 1 2:+ACo-
88 7 2:+ACoAPQA9- inset +AD0- represents 1 library
sequences
90 0 1:+ACo-
92 2 1:+ACo- :+ACoAPQ-
94 1 1:+ACo- :+ACo-
96 1 1:+ACo- :+ACo-
98 0 0: +ACo-
100 0 0: +ACo-
102 1 0:+AD0- +ACoAPQ-
104 0 0: +ACo-
106 1 0:+AD0- +ACoAPQ-
108 0 0: +ACo-
110 0 0: +ACo-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.81910.00326+ADs- mu+AD0- 1.1377
0.172
mean+AF8-var+AD0-37.029210.120, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.210767
Kolmogorov-Smirnov statistic: 0.1121 (N+AD0-29) at 46
FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are: opt bits E(1471)
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 64 24.7 0.59

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 24.0 0.98
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T (121) 57 22.6 2.3
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145) 57 22.5 2.8
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 57 22.5 3.2
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 56 22.2 4
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 58 22.6 5.6
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.3 6
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.3 6
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 54 21.6 6
gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 21.1 6.2
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 21.1 6.4
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.3 6.6
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.3 7.5
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.0 8.7
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159) 52 21.0 9.1
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159) 52 21.0 9.1
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159) 52 21.0 9.1
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159) 52 21.0 9.1
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159) 52 21.0 9.1
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159) 52 21.0 9.1
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159) 52 21.0 9.1
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159) 52 21.0 9.1
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159) 52 21.0 9.1
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159) 52 21.0 9.1
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160) 52 21.0 9.2

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)

initn: 38 init1: 38 opt: 64 Z-score: 106.5 bits: 24.7 E(): 0.59

Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (17-75:9-65)

```

                10         20         30         40         50
AAD-12 MAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARH
                : : : : . : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111      MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEH
                10         20         30         40

```

```

                60         70         80
AAD-12 SLVYSQSKLGHVQQAGSAYIGY
                . : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 QLLYLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYE
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 init1: 55 opt: 62 Z-score: 102.5 bits: 24.0 E(): 0.98
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (7-55:5-52)

```

                10         20         30         40         50         60
AAD-12 MAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-189      MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTI
                10         20         30         40         50

```

```

                70         80
AAD-12 VYSQSKLGHVQQAGSAYIGY
gi+AHw-189      AGSPVSSEPGDTPKDRCCQELDEAPQHCRVRYFIGRRSHPDWRVLKDLPGCPKEPQRD
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 57 init1: 57 opt: 57 Z-score: 95.9 bits: 22.6 E(): 2.3
Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (33-77:26-70)

```

                10         20         30         40         50         60
AAD-12 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527      MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQVSTKHSVPDVLAF
                10         20         30         40         50

```

```

                70         80
AAD-12 SQSKLGHVQQAGSAYIGY
                . . . : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527      AKVNVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQ
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
tetrameric (145 aa)
initn: 50 init1: 50 opt: 57 Z-score: 94.2 bits: 22.5 E(): 2.8

Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (2-51:23-71)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
              .. ::: : :. : . : .....: :. .
gi+AHw-663  MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
              10      20      30      40      50

              40      50      60      70      80
AAD-12      YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
              . . . . : :
gi+AHw-663  LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLLILKLDTDYDVA
              60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 88.4 bits: 21.3 E(): 6
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (17-75:9-65)

```

                                10      20      30      40      50
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARH
              : ::: : : . : : : : .....: .....:
gi+AHw-420      MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEH
              10      20      30      40

              60      70      80
AAD-12      SLVYSQSKLGHVQQAGSAYIGY
              . . . : : : . . . :
gi+AHw-420  QLLYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYE
              50      60      70      80      90      100
    
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 88.4 bits: 21.3 E(): 6
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (17-75:9-65)

```

                                10      20      30      40      50
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARH
              : ::: : : . : : : : .....: .....:
gi+AHw-111      MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEH
              10      20      30      40

              60      70      80
AAD-12      SLVYSQSKLGHVQQAGSAYIGY
              . . . : : : . . . :
gi+AHw-111  QLLYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYE
              50      60      70      80      90      100
    
```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)
initn: 52 initl: 52 opt: 54 Z-score: 88.3 bits: 21.6 E(): 6

Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (1-29:23-50)

```

                10      20      30
AAD-12          MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. ::: : : : : : : : : : : : :
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
                10      20      30      40      50

```

```

        40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
        60      70      80      90      100     110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)
initn: 34 initl: 34 opt: 52 Z-score: 88.1 bits: 21.1 E(): 6.2
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (9-77:11-80)

```

                10      20      30      40      50
AAD-12          MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                .. . .::: . . . :::: . . . : . . : : : : : : : : : :
gi+AHw-408 MVPKPLSLLLFLLLLALSAAVVGGRKLV AAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
                10      20      30      40      50

```

```

        60      70      80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGY
        : :. .::: :. :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMWHFRNLTSFRKV
        60      70      80      90      100     110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.9 bits: 21.1 E(): 6.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (35-75:11-50)

```

                10      20      30      40      50      60
AAD-12 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                :. : : : : : : : : : : : : : : : : :
gi+AHw-160          GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
                10      20      30

```

```

        70      80
AAD-12 SQSKLGHVQQAGSAYIGY
        : :. :. :
gi+AHw-160 LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQ GALERELKRTDLNILERFN YEEAQT
        40      50      60      70      80      90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 87.6 bits: 21.3 E(): 6.6

Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar) in 49 aa overlap (7-55:5-52)

10 20 30 40 50 60
AAD-12 MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR...
gi+AHw-217 MASKSSISPLLLATVLSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTCGISI

70 80
AAD-12 VYSQSKLGHVQQAGSAYIGY
gi+AHw-217 SGSAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPREPQR

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 +AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 86.7 bits: 21.3 E(): 7.5
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar) in 58 aa overlap (10-61:31-87)

10 20 30
AAD-12 MAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
gi+AHw-132 MGVFN...ETETTSVIPPARL...FKRFVLDSDNLI...PKVAPKAIKSIEII...EGNGGPGTIKKICF-

40 50 60 70 80
AAD-12 DMRAAYDALDEATR...SARHSLVYSQSKLGHVQQAGSAYIGY
gi+AHw-132 DEGSPFN...YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar) in 24 aa overlap (40-63:29-52)

10 20 30 40 50 60
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR...SARHSLVYSQSKLGH
gi+AHw-144 KTNKIVITNDKGR...LSKEEIERMLAEAEKYKAEDAEAEARISAKNALESYAYSLRNTLS

70 80
AAD-12 VQQAGSAYIGY
gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12                          MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12                          MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12                          MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12                          MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12                          MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-131  MGVFNYTEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

```

```

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12                          MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12                          MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12                          MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12                          MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

```

```

    40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

```

```

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
    60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 50 initl: 50 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (1-29:23-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ..  ::  :  .:  .:  .:  ::  :::. . . ::
gi+AHw-444  MGVFTYADESTSVITPPRLF KALVLEAD-TLIPKIA PQSVKGA EIVEG DGGVGTIKKISF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
                                60      70      80      90      100     110

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:00 2010 done: Fri Feb 5 12:56:00 2010
Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 107 - 186 80 aa - 80 aa


```

82      4      3:+ACoAPQ-
84     12     3:+ACoAPQA9AD0-
86      3     2:+ACo-
88      7     2:+ACoAPQA9-      inset +AD0- represents 1 library
sequences
90      1     1:+ACo-
92      2     1:+ACo-      :+ACoAPQ-
94      1     1:+ACo-      :+ACo-
96      0     1:+ACo-      :+ACo-
98      0     0:      +ACo-
100     0     0:      +ACo-
102     1     0:+AD0-      +ACoAPQ-
104     0     0:      +ACo-
106     1     0:+AD0-      +ACoAPQ-
108     0     0:      +ACo-
110     0     0:      +ACo-
112     0     0:      +ACo-
114     0     0:      +ACo-
116     0     0:      +ACo-
118     0     0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.00980.00333+ADs- mu+AD0- -
0.1006 0.176
mean+AF8-var+AD0-39.083210.559, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.205154
Kolmogorov-Smirnov statistic: 0.1216 (N+AD0-29) at 46

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 64 24.5 0.67
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 23.9 1.1
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 57 22.4 2.5
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 22.4 3.1
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.1 4.3
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
56 22.1 4.3
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
56 22.0 5.7
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204) 56 22.0 5.8
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.4 6.3
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.2 6.4

```

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.2 6.4
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 21.0 6.6
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 21.0 6.8
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.2 7.1
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 53 21.2 8
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.2 8
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 20.9 9.2
 gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159) 52 20.9 9.8
 gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159) 52 20.9 9.8
 gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159) 52 20.9 9.8
 gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159) 52 20.9 9.8
 gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159) 52 20.9 9.8
 gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159) 52 20.9 9.8
 gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159) 52 20.9 9.8
 gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159) 52 20.9 9.8
 gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159) 52 20.9 9.8
 gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159) 52 20.9 9.8

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 105.5 bits: 24.5 E(): 0.67
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (16-74:9-65)

```

                10          20          30          40          50
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHS
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111      MKFAIVLIACFAASVL-AQGHPKPKDDFRNEFDHLLIEQANHAI---EKGEHQ
                10          20          30          40

                60          70          80
AAD-12 LVYSQSKLGHVQQAGSAYIGY
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 LLYLQHQLDLLENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYE
                50          60          70          80          90          100
    
```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 initl: 55 opt: 62 Z-score: 101.6 bits: 23.9 E(): 1.1
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (6-54:5-52)

```

                10         20         30         40         50         60
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
      .. ... .. . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIA
                10         20         30         40         50

```

```

                70         80
AAD-12 YSQSKLGHVQQAGSAYIGYG

```

```

gi+AHw-189 GSPVSSEPGDTPKDRCCQELDEAPQHCRCRVRYFIGRRSHPDWRVLKDLPGCPKEPQRDF
        60         70         80         90         100         110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 57 initl: 57 opt: 57 Z-score: 95.2 bits: 22.4 E(): 2.5
Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (32-76:26-70)

```

                10         20         30         40         50         60
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
      ::: .. . . : .... :..
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
                10         20         30         40         50

```

```

                70         80
AAD-12 SQSKLGHVQQAGSAYIGYG

```

```

      .. .. ::::: . .
gi+AHw-527 AKVNVVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQ
        60         70         80         90         100         110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
tetrameric (145 aa)
initn: 50 initl: 50 opt: 57 Z-score: 93.5 bits: 22.4 E(): 3.1
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (6-54:5-52)

```

                10         20         30         40         50         60
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
      .. ... .. . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIA
                10         20         30         40         50

```

```

                70         80
AAD-12 YSQSKLGHVQQAGSAYIGYG

```

```

gi+AHw-439 GSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQRD
        60         70         80         90         100         110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)

initn: 55 init1: 55 opt: 56 Z-score: 90.9 bits: 22.1 E(): 4.3
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  .:  ::::.  .  ::
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG

```

```

gi+AHw-165  GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)

initn: 55 init1: 55 opt: 56 Z-score: 90.9 bits: 22.1 E(): 4.3
Smith-Waterman score: 56+ADs- 48.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::  :  .:  .:  .:  ::::.  .  ::
gi+AHw-444  MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG

```

```

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)

initn: 40 init1: 40 opt: 56 Z-score: 88.8 bits: 22.0 E(): 5.7
Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
in 53 aa overlap (33-80:93-144)

```

                                10      20      30      40      50
AAD-12  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                .....  :::  ::  .  ..  ..
gi+AHw-144  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                                70      80      90      100     110     120

```

```

                                60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYG
.. :  .:  .:  .:  .:  .:  .:  .:

```

```

gi+AHw-144  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 88.6 bits: 22.0 E(): 5.8
 Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
 in 53 aa overlap (33-80:97-148)

```

      10      20      30      40      50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
      . . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
      70      80      90      100     110     120
  
```

```

      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGY
      . . : . . . : . . . . . :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
      130     140     150     160     170     180
  
```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
 Lolium per (301 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 88.1 bits: 22.4 E(): 6.3
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (1-50:23-71)

```

      10      20      30
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
      . . . . .
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
      10      20      30      40      50
  
```

```

      40      50      60      70      80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
      . . . . . :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
      60      70      80      90      100     110
  
```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein B1 (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 87.9 bits: 21.2 E(): 6.4
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (16-74:9-65)

```

      10      20      30      40      50
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHS
      : : : : : . : : : . . . . .
gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQ
      10      20      30      40
  
```

```

      60      70      80
AAD-12 LVYSQSKLGHVQQAGSAYIGY
      : : : . . . :
gi+AHw-420 LLYLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEE
      50      60      70      80      90      100
  
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 87.9 bits: 21.2 E(): 6.4
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (16-74:9-65)

```

                10         20         30         40         50
AAD-12 AWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHS
                : : : : : . : : : : : : : : : : : : : : : :
gi+AHw-111      MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQ
                10         20         30         40

```

```

                60         70         80
AAD-12 LVYSQSKLGHVQQAGSAYIGYG
                : : : : : :
gi+AHw-111 LLYLQHQLDLLENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEE
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)
initn: 34 initl: 34 opt: 52 Z-score: 87.6 bits: 21.0 E(): 6.6
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (8-76:11-80)

```

                10         20         30         40         50
AAD-12 AWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                . . . . : : : : . : : : . . . : : : : : : : : : : : :
gi+AHw-408 MVPKPLSLLLFLLLLALSAAVVGGRKLVAAAGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
                10         20         30         40         50

```

```

                60         70         80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYG
                : : . : : : : : : :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMWHFRNLTSFRKV
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.4 bits: 21.0 E(): 6.8
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (34-74:11-50)

```

                10         20         30         40         50         60
AAD-12 ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-160      GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
                10         20         30

```

```

                70         80
AAD-12 SQSKLGHVQQAGSAYIGYG
                : : : : : :
gi+AHw-160 LQHQLDLLENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQT
                40         50         60         70         80         90

```


+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 init1: 52 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.2
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (39-62:29-52)

```

      10      20      30      40      50      60
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
      : : : : : . . . : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
      10      20      30      40      50

```

```

      70      80
AAD-12 VQQAGSAYIGYG

```

```

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

      10      20      30
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      : : : : : : : : : : : :
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
      10      20      30      40      50

```

```

      40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

      10      20      30
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      : : : : : : : : : : : :
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
      10      20      30      40      50

```

```

      40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSG SVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKL VASSNGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKL VASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
 +AFs-Mal (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-131  MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
 1.03B (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
 +AFs-Mal (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. . . ::
gi+AHw-279  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
 1.03D (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. .  ::
gi+AHw-602  MGVFTYSEFTSVIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
 1.03E (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::. .  ::
gi+AHw-602  MGVFTYSEFTSVIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:00 2010 done: Fri Feb 5 12:56:00 2010
 Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

78      8      6:+AD0AKgA9-
80      8      4:+AD0AKgA9-
82      6      3:+ACoAPQ-
84     12     3:+ACoAPQA9AD0-
86      5      2:+ACoAPQ-
88      3      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      1      1:+ACo-          :+ACo-
94      1      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:              +ACo-
104     1      0:+AD0-          +ACoAPQ-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-

```

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 6.04060.00337+ADs- mu+AD0- -
0.2234 0.177

mean+AF8-var+AD0-40.063710.748, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42

Lambda+AD0- 0.202628

Kolmogorov-Smirnov statistic: 0.1271 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 64 24.3 0.74

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 23.7 1.2

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T (121) 57 22.3 2.7

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145) 57 22.3 3.4

gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 56 22.0 4.6

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 56 22.0 4.6

gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200) 56 21.9 6.1

gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-G1 (204) 56 21.9 6.3

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.1 6.9

gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.1 6.9

gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.9 7
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.9 7.3
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.1 7.6
 gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 57 22.0 8.2
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 53 21.1 8.5
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.1 8.5
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 20.8 9.8

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)

initn: 38 init1: 38 opt: 64 Z-score: 104.7 bits: 24.3 E(): 0.74
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (15-73:9-65)

	10	20	30	40	50
AAD-12	WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSL				
		:	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQQL				
	10	20	30	40	50

	60	70	80
AAD-12	VYSQSKLGHVQQAGSAYIGYGM		
	:	:	:
gi+AHw-111	LYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEA		
	60	70	80

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)

initn: 55 init1: 55 opt: 62 Z-score: 100.9 bits: 23.7 E(): 1.2
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (5-53:5-52)

	10	20	30	40	50	60
AAD-12	WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY					
	:	:	:	:	:	:
gi+AHw-189	MASKSSITPLLLAASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIAG					
	10	20	30	40	50	

	70	80
AAD-12	SQSKLGHVQQAGSAYIGYGM	
gi+AHw-189	SPVSSEPGDTPKDRCCQELDEAPQHCRVRYFIGRRSHPDWRVLKDLPGCPKEPQRDFA	
	60	70

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)

initn: 57 init1: 57 opt: 57 Z-score: 94.6 bits: 22.3 E(): 2.7

Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (31-75:26-70)

```

                10         20         30         40         50         60
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRLVHQSSARHSLVY
                :::         :. . . : . . . : . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
                10         20         30         40         50

```

```

                70         80
AAD-12 SQSKLGHVQQAGSAYIGYGM
                .. .. : . . . . . :
gi+AHw-527 AKVNVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAAEKLGGLAQ
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)
initn: 50 init1: 50 opt: 57 Z-score: 92.9 bits: 22.3 E(): 3.4
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (5-53:5-52)

```

                10         20         30         40         50         60
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRLVHQSSARHSLVY
                :. :. . . . :. . . . : : : : : : : :
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIAG
                10         20         30         40         50

```

```

                70         80
AAD-12 SQSKLGHVQQAGSAYIGYGM
gi+AHw-439 SPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQRDF
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
initn: 55 init1: 55 opt: 56 Z-score: 90.4 bits: 22.0 E(): 4.6
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (3-27:27-50)

```

                10         20         30
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                :. . : : : : : :
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIEGNGGGPGTIKKITF
                10         20         30         40         50

```

```

                40         50         60         70         80
AAD-12 AYDALDEATRLVHQSSARHSLVYSQSKLGHVQQAGSAYIGYGM
gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
initn: 55 init1: 55 opt: 56 Z-score: 90.4 bits: 22.0 E(): 4.6

Smith-Waterman score: 56+ADs- 48.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (3-27:27-50)

```

                                10      20      30
AAD-12      WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              :: : .: .: .: ::::: . ::
gi+AHw-444  MGVFTYADESTSVIPPPRLFALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
              10      20      30      40      50
    
```

```

              40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVSADGGSIKSTS
              60      70      80      90      100     110
    
```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 40 init1: 40 opt: 56 Z-score: 88.3 bits: 21.9 E(): 6.1
Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
in 53 aa overlap (32-79:93-144)

```

              10      20      30      40      50
AAD-12  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
              .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-144  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
              70      80      90      100     110     120
    
```

```

              60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGM
              .. : .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-144  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130     140     150     160     170     180
    
```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 40 init1: 40 opt: 56 Z-score: 88.1 bits: 21.9 E(): 6.3
Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
in 53 aa overlap (32-79:97-148)

```

              10      20      30      40      50
AAD-12  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
              .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-622  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
              70      80      90      100     110     120
    
```

```

              60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGM
              .. : .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-622  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130     140     150     160     170     180
    
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 init1: 38 opt: 53 Z-score: 87.3 bits: 21.1 E(): 6.9

Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (15-73:9-65)

```

                10         20         30         40         50
AAD-12 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSL
                : : : : : . : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111      MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQL
                10         20         30         40         50

```

```

                60         70         80
AAD-12 VYSQSKLGHVQQAGSAYIGYGM
                . : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi+AHw-111 LYLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNVEEA
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 init1: 38 opt: 53 Z-score: 87.3 bits: 21.1 E(): 6.9
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (15-73:9-65)

```

                10         20         30         40         50
AAD-12 WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSL
                : : : : : . : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-420      MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQL
                10         20         30         40         50

```

```

                60         70         80
AAD-12 VYSQSKLGHVQQAGSAYIGYGM
                . : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi+AHw-420 LYLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNVEEA
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)

initn: 34 init1: 34 opt: 52 Z-score: 87.1 bits: 20.9 E(): 7
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (7-75:11-80)

```

                10         20         30         40         50
AAD-12      WHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                . . . . : : : : . . . . : : : : . . . . : : : : . . . . :
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
                10         20         30         40         50

```

```

                60         70         80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGM
                : : . : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNVEAVVWVKPMMHFRNLTSFRKV
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 init1: 38 opt: 52 Z-score: 86.9 bits: 20.9 E(): 7.3

Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (33-73:11-50)

```

                10         20         30         40         50         60
AAD-12 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                :.: .: : .....: .....:
gi+AHw-160                GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
                        10         20         30

```

```

                70         80
AAD-12 SQSKLGHVQQAGSAYIGYGM
                :.: .....:
gi+AHw-160 LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
                40         50         60         70         80         90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 86.6 bits: 21.1 E(): 7.6
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (5-53:5-52)

```

                10         20         30         40         50         60
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                :. :.. .. :. . . . : :.: : . :.: : : :..
gi+AHw-217 MASKSSISPLLLATVLSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTCGISISG
                10         20         30         40         50

```

```

                70         80
AAD-12 SQSKLGHVQQAGSAYIGYGM
gi+AHw-217 SAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPREPQRDF
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)
initn: 48 initl: 48 opt: 57 Z-score: 85.9 bits: 22.0 E(): 8.2
Smith-Waterman score: 57+ADs- 27.660+ACU- identity (55.319+ACU- similar)
in 47 aa overlap (3-49:26-71)

```

                        10         20         30
AAD-12                WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                        :.: :.: : . : .....: :. .
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                        10         20         30         40         50

```

```

                40         50         60         70         80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
                . . . . :.:
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 52 initl: 52 opt: 53 Z-score: 85.7 bits: 21.1 E(): 8.5

Smith-Waterman score: 53+ADs- 44.000+ACU- identity (68.000+ACU- similar) in 25 aa overlap (3-27:27-50)

AAAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
:: : .: .: .: .: .: .: .: .:
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEG DGGVGTIKKISF
10 20 30 40 50

AAAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
40 50 60 70 80
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVNYTLVEGDALSDKIEKITYEIKLVSADGGSIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 85.7 bits: 21.1 E(): 8.5
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (8-59:31-87)

AAAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
.: .: .: .: .: .: .: .:
gi+AHw-132 MGVFN YETETTSVIPPARL FKRFVLDSDN LIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
10 20 30 40 50

AAAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGSAYIGYGM
: : : : :
gi+AHw-132 DEGSPFN YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
60 70 80 90 100 110

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 84.6 bits: 20.8 E(): 9.8
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (38-61:29-52)

AAAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
: : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
10 20 30 40 50

AAAD-12 VQQAGSAYIGYGM
70 80
gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
60 70 80 90 100 110

80 residues in 1 query sequences

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 23.8 1.2
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T (121) 57 22.3 2.7
 gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145) 57 22.3 3.3
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po (396) 62 23.5 3.8
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 56 22.0 4.6
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 56 22.0 4.6
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200) 56 21.9 5.9
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl (204) 56 21.9 6
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.1 6.8
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.1 6.8
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.9 7.1
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.9 7.3
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.1 7.5
 gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 57 22.1 7.7
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 53 21.1 8.4
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.1 8.4
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 20.8 9.6

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
 initn: 38 init1: 38 opt: 64 Z-score: 104.7 bits: 24.3 E(): 0.74
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (14-72:9-65)

```

                10          20          30          40          50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLV
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQGHPKPKDDFRNEFDHLLIEQANHAI---EKGEHQLL
                10          20          30          40          50

                60          70          80
AAD-12 YSQSKLGHVQQAGSAYIGYGM
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 YLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQ
                60          70          80          90          100          110
    
```


+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 45 init1: 45 opt: 62 Z-score: 91.9 bits: 23.5 E(): 3.8
Smith-Waterman score: 62+ADs- 23.214+ACU- identity (53.571+ACU- similar)
in 56 aa overlap (25-80:309-358)

```

                10         20         30         40         50
AAD-12      HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                : : : : : : : : : : : :
gi+AHw-113  HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
            280       290       300       310       320       330

```

```

                60         70         80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGM
            : : . . : . : . : : : :
gi+AHw-113  ESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEPEGESALSLTSSAGVLSCQP
            340       350       360       370       380       390

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 init1: 55 opt: 56 Z-score: 90.5 bits: 22.0 E(): 4.6
Smith-Waterman score: 56+ADs- 48.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (2-26:27-50)

```

                10         20         30
AAD-12      HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                : : : : : : : : : : : :
gi+AHw-444  MGVFITYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDDGGVGTIKKISF
            10         20         30         40         50

```

```

                40         50         60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
            60         70         80         90         100        110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 init1: 55 opt: 56 Z-score: 90.5 bits: 22.0 E(): 4.6
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (2-26:27-50)

```

                10         20         30
AAD-12      HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                : : . . : : : : : : : :
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
            10         20         30         40         50

```

```

                40         50         60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
gi+AHw-165  GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
            60         70         80         90         100        110

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
 allergen +AFs- (200 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 88.6 bits: 21.9 E(): 5.9
 Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
 in 53 aa overlap (31-78:93-144)

```

                10         20         30         40         50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRAlVHQRSARH
                .....:   ::: :: .. .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100        110        120

                60         70         80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGM
                .. :   .. :   .....:
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
                130        140        150        160        170        180
  
```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 88.4 bits: 21.9 E(): 6
 Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
 in 53 aa overlap (31-78:97-148)

```

                10         20         30         40         50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRAlVHQRSARH
                .....:   ::: :: .. .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100        110        120

                60         70         80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGM
                .. :   .. :   .....:
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
                130        140        150        160        170        180
  
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 87.4 bits: 21.1 E(): 6.8
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (14-72:9-65)

```

                10         20         30         40         50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRAlVHQRSARHSLV
                : ::: : . :   ::: : : .....: .....:
gi+AHw-111 MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLL
                10         20         30         40         50

                60         70         80
AAD-12 YSQSKLGHVQQAGSAYIGYGM
                : :   .. :   .....:
gi+AHw-111 YLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQ
                60         70         80         90         100        110
  
```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein B1 (134 aa)

initn: 38 init1: 38 opt: 53 Z-score: 87.4 bits: 21.1 E(): 6.8
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (14-72:9-65)

```

                10         20         30         40         50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLV
                : : : : . : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-420      MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLL
                10         20         30         40         50

```

```

                60         70         80
AAD-12 YSQSKLGHVQQAGSAYIGYGM
                : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-420      YLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQ
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs- Actinidia de (116 aa)

initn: 34 init1: 34 opt: 52 Z-score: 87.1 bits: 20.9 E(): 7.1
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (6-74:11-80)

```

                10         20         30         40         50
AAD-12      HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                . . . . : : : : . : : : . . . . : : : : : : : : : : : :
gi+AHw-408      MVPKPLSLLLFLLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
                10         20         30         40         50

```

```

                60         70         80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGM
                : : . : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-408      DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMWHFRNLTSFRKV
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Structur (119 aa)

initn: 38 init1: 38 opt: 52 Z-score: 86.9 bits: 20.9 E(): 7.3
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (32-72:11-50)

```

                10         20         30         40         50
AAD-12 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-160      GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
                10         20         30

```

```

                60         70         80
AAD-12 SQSKLGHVQQAGSAYIGYGM
                : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-160      LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
                40         50         60         70         80         90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
 +AFs-Trit (145 aa)
 initn: 46 initl: 46 opt: 53 Z-score: 86.7 bits: 21.1 E(): 7.5
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (4-52:5-52)

```

                10      20      30      40      50
AAD-12  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
          ::  ::  ..  ::  ..  ..  :  :::  :  .  :  ::  :  :  ::
gi+AHw-217 MASKSSISPLLLATVLSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTTCGISISG
                10      20      30      40      50

```

```

        60      70      80
AAD-12  SQSKLGHVQQAGSAYIGYGM

```

```

gi+AHw-217 SAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPREPQRDF
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
 Lolium per (301 aa)
 initn: 48 initl: 48 opt: 57 Z-score: 86.5 bits: 22.1 E(): 7.7
 Smith-Waterman score: 57+ADs- 27.660+ACU- identity (55.319+ACU- similar)
 in 47 aa overlap (2-48:26-71)

```

                                10      20      30
AAD-12                                HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                                ::  :  ::  :  .  :  :::  :::  .  :  .
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                                10      20      30      40      50

```

```

        40      50      60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
          .  .  .  .  :  :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAASFESCKGLLATSADAKAPGLILKLDTDYDVA
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 52 initl: 52 opt: 53 Z-score: 85.8 bits: 21.1 E(): 8.4
 Smith-Waterman score: 53+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (2-26:27-50)

```

                                10      20      30
AAD-12                                HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::  :  ::  :  .  :  :::  .  :  :
gi+AHw-444 MGVTYSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTAEIVEGDDGGVGTIKKISF
                                10      20      30      40      50

```

```

        40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM

```

```

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (7-58:31-87)

10 20 30
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
.: .: .: .: .: .: .: .:
gi+AHw-132 MGVFN YETETTSVIPPARLFKRFVLDSDNLIPKVAPKAIKSIEIIIEGNGGPGTIKKICF-
10 20 30 40 50
40 50 60 70 80
AAD-12 DMRAAYDALDEATR ALVHQR-SARHSLVYSQSKLGHVQQAGSAYIGYGM
: : : : : :
gi+AHw-132 DEGSPFN YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
60 70 80 90 100 110

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 84.7 bits: 20.8 E(): 9.6
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (37-60:29-52)

10 20 30 40 50 60
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKLGH
: : : : : : . . . : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEEAARISAKNALESYAYSLRNTLS
10 20 30 40 50
70 80
AAD-12 VQQAGSAYIGYGM
gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
60 70 80 90 100 110

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:01 2010 done: Fri Feb 5 12:56:01 2010
Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

76      27      7:+AD0APQAqAD0APQA9AD0APQA9-
78      8      6:+AD0AKgA9-
80      8      4:+AD0AKgA9-
82      5      3:+ACoAPQ-
84     12      3:+ACoAPQA9AD0-
86      6      2:+ACoAPQ-
88      2      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      1      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      0      0:          +ACo-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:          +ACo-
104     1      0:+AD0-          +ACoAPQ-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120  0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.56990.00353+ADs- mu+AD0- 2.0442
0.185
mean+AF8-var+AD0-40.979410.974, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.200351
Kolmogorov-Smirnov statistic: 0.1232 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:          opt bits E(1471)
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  64 24.2  0.79
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)  62 23.7  1.3
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 22.5  2.4
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.2  3.5
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  62 23.5  4
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
56 21.9  4.8
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)  56 21.9  4.8
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
56 21.9  6.2
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-G1
( 204)  56 21.9  6.3

```

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.1 7.2
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.1 7.2
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.8 7.5
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.8 7.7
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.1 7.9
 gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 57 22.1 8
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 53 21.0 8.8
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.0 8.8

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 104.2 bits: 24.2 E(): 0.79
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (13-71:9-65)

```

                10         20         30         40         50
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                :  ::  .  :  .  .  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-111  MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
                10         20         30         40         50

                60         70         80
AAD-12  SQSKLGHVQQAGSAYIGYGMT
                :  ::  ....  :
gi+AHw-111  LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
                60         70         80         90         100         110
    
```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 100.4 bits: 23.7 E(): 1.3
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (3-51:5-52)

```

                10         20         30         40         50
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                ::  ...  ...  :  .  .  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-189  MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTGCVTIAG
                10         20         30         40         50

                60         70         80
AAD-12  SQSKLGHVQQAGSAYIGYGMT

gi+AHw-189  SPVSSEPGDTPKDRCCQELDEAPQHCRVRYFIGRRSHPDWRVLKDLPGCPKEPQRDFA
                60         70         80         90         100         110
    
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 58 init1: 58 opt: 58 Z-score: 95.7 bits: 22.5 E(): 2.4
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (29-80:26-77)

```

                10         20         30         40         50         60
AAD-12 ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
                :::         :. . . : ..... :....
gi+AHw-527  MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQQLSTKHSVDPDLAFAK
                10         20         30         40         50
  
```

```

                70         80
AAD-12 SKLGHVQQAGSAYIGYGMT
                .. :::::.. : .: :
gi+AHw-527 VNVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQKR
                60         70         80         90         100         110
  
```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
 tetrameric (145 aa)
 initn: 50 init1: 50 opt: 57 Z-score: 92.5 bits: 22.2 E(): 3.5
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (3-51:5-52)

```

                10         20         30         40         50
AAD-12 ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                :. :.. ... :. . . . : ::: : . : : : : : :
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIAG
                10         20         30         40         50
  
```

```

                60         70         80
AAD-12 SQSKLGHVQQAGSAYIGYGMT
gi+AHw-439 SPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQRDF
                60         70         80         90         100         110
  
```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 45 init1: 45 opt: 62 Z-score: 91.6 bits: 23.5 E(): 4
 Smith-Waterman score: 62+ADs- 23.214+ACU- identity (53.571+ACU- similar)
 in 56 aa overlap (24-79:309-358)

```

                10         20         30         40         50
AAD-12 ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                ::: : : :. ... : : :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA
                280         290         300         310         320         330
  
```

```

                60         70         80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMT
                :. . . : . : . . . : :
gi+AHw-113 ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAE PGESALS LTSSAGVLSCQP
                340         350         360         370         380         390
  
```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
 Smith-Waterman score: 56+ADs- 48.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (1-25:27-50)

```

                                10      20      30
AAD-12      ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              :: : .: .: .: ::::: . ::
gi+AHw-444  MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEG DGGVGTIKKISF
              10      20      30      40      50

              40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
              60      70      80      90      100     110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (1-25:27-50)

```

                                10      20      30
AAD-12      ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              :: .: .: .: ::::: . ::
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
              10      20      30      40      50

              40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
gi+AHw-165  GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
              60      70      80      90      100     110

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 88.2 bits: 21.9 E(): 6.2
 Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
 in 53 aa overlap (30-77:93-144)

```

              10      20      30      40      50
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
              .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-144  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
              70      80      90      100     110     120

              60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMT
              .. : .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-144  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130     140     150     160     170     180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 88.0 bits: 21.9 E(): 6.3
 Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
 in 53 aa overlap (30-77:97-148)

```

                10      20      30      40      50
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRLVHQSSARH
                . . . . .   . . . . .   . . . . .   . . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70      80      90      100     110     120

                60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMT
                . . : . . . : . . . . . :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130     140     150     160     170     180
    
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 init1: 38 opt: 53 Z-score: 87.0 bits: 21.1 E(): 7.2
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (13-71:9-65)

```

                10      20      30      40      50
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRLVHQSSARHSLVY
                : : : : : . : : : : . . . . . :
gi+AHw-111  MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLLY
                10      20      30      40      50

                60      70      80
AAD-12  SQSKLGHVQQAGSAYIGYGMT
                : . : . . . :
gi+AHw-111 LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQT
                60      70      80      90      100     110
    
```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein Bl (134 aa)
 initn: 38 init1: 38 opt: 53 Z-score: 87.0 bits: 21.1 E(): 7.2
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (13-71:9-65)

```

                10      20      30      40      50
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRLVHQSSARHSLVY
                : : : : : . : : : : . . . . . :
gi+AHw-420  MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLLY
                10      20      30      40      50

                60      70      80
AAD-12  SQSKLGHVQQAGSAYIGYGMT
                : . : . . . :
gi+AHw-420 LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQT
                60      70      80      90      100     110
    
```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)
initn: 34 initl: 34 opt: 52 Z-score: 86.7 bits: 20.8 E(): 7.5
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (5-73:11-80)

```

                10         20         30         40         50
AAD-12      ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                .. .  ...:  ... .  ...:  . . .:  . . :  :  .:  ....:
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
                10         20         30         40         50

```

```

                60         70         80
AAD-12      HSLVYSQSKLGHVQQ-AGSAYIGYGMT
                :  ...  ...:  ... :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 86.5 bits: 20.8 E(): 7.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (31-71:11-50)

```

                10         20         30         40         50
AAD-12      ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                ::  :  :  .....  .....:
gi+AHw-160      GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
                10         20         30

```

```

                60         70         80
AAD-12      SQSKLGHVQQAGSAYIGYGMT
                :  ::  ....  :
gi+AHw-160 LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
                40         50         60         70         80         90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 86.3 bits: 21.1 E(): 7.9
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (3-51:5-52)

```

                10         20         30         40         50
AAD-12      ADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                :.  ...  ..  .  .  .  :  ::  :  .  :  :  :  :  :
gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTTCGISISG
                10         20         30         40         50

```

```

                60         70         80
AAD-12      SQSKLGHVQQAGSAYIGYGMT
gi+AHw-217 SAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPREPQRDF
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
 Lolium per (301 aa)
 initn: 48 init1: 48 opt: 57 Z-score: 86.2 bits: 22.1 E(): 8
 Smith-Waterman score: 57+ADs- 27.660+ACU- identity (55.319+ACU- similar)
 in 47 aa overlap (1-47:26-71)

```

                                10      20      30
AAD-12                        ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                                :: : : : . : ..... : .
gi+AHw-663 MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
        . . . . : :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
        60      70      80      90      100     110
    
```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 52 init1: 52 opt: 53 Z-score: 85.4 bits: 21.0 E(): 8.8
 Smith-Waterman score: 53+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (1-25:27-50)

```

                                10      20      30
AAD-12                        ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                :: : : : . : ..... : :
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
        60      70      80      90      100     110
    
```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)
 initn: 47 init1: 47 opt: 53 Z-score: 85.4 bits: 21.0 E(): 8.8
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (6-57:31-87)

```

                                10      20      30
AAD-12                        ADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
                                . : . : . : . : . : . : . :
gi+AHw-132 MGVFN YETETTSVIPPARLFKRFVLDSDNLIPKVPKAIKSIEIIEGNGGPGTIKKICF-
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGSAYIGYGMT
        : . . . . : : : :
gi+AHw-132 DEGSPFN YIKQKV EIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
        60      70      80      90      100     110
    
```


The best scores are:

opt bits E(1471)

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 64 24.3 0.76
 gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 23.7 1.2
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T (121) 58 22.6 2.3
 gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145) 57 22.3 3.4
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po (396) 62 23.5 3.8
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 55 21.7 5.7
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 55 21.7 5.7
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200) 56 21.9 6
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl (204) 56 21.9 6.1
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.1 7
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.1 7
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.8 7.3
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.8 7.5
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.1 7.6
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.1 8.5
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 20.8 9.8

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
 initn: 38 init1: 38 opt: 64 Z-score: 104.5 bits: 24.3 E(): 0.76
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (12-70:9-65)

```

                10          20          30          40          50
AAD-12 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYS
                : : : : . : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQGHPKPKDDFRNEFDHLLIEQANHAI---EKGEHQLLYL
                10          20          30          40          50

                60          70          80
AAD-12 QSKLGHVQQAGSAYIGYGMDDT
                : : . . . :
gi+AHw-111 QHQDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEAAQTL
                60          70          80          90          100          110
    
```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)

initn: 45 init1: 45 opt: 62 Z-score: 92.0 bits: 23.5 E(): 3.8
 Smith-Waterman score: 62+ADs- 23.214+ACU- identity (53.571+ACU- similar)
 in 56 aa overlap (23-78:309-358)

```

                10      20      30      40      50
AAD-12          DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                : : : : :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA
                280      290      300      310      320      330

```

```

                60      70      80
AAD-12          HSLVYSQSKLGHVQQAGSAYIGYGMDDT
                : : : : :
gi+AHw-113 ESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
                340      350      360      370      380      390

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 55 init1: 55 opt: 55 Z-score: 88.8 bits: 21.7 E(): 5.7
 Smith-Waterman score: 55+ADs- 45.455+ACU- identity (68.182+ACU- similar)
 in 22 aa overlap (3-24:29-50)

```

                10      20      30
AAD-12          DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                : : : : :
gi+AHw-444 MGVFTYADESTSVIIPPRLFKALVLEADTLIPKIA PQSVKSAEIVEGDDGGVGTIKKISFG
                10      20      30      40      50      60

```

```

                40      50      60      70      80
AAD-12          YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDT
                : : : : :
gi+AHw-444 EGSYYSYVVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTSN
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
 sativa+AF0- (160 aa)

initn: 55 init1: 55 opt: 55 Z-score: 88.8 bits: 21.7 E(): 5.7
 Smith-Waterman score: 55+ADs- 40.000+ACU- identity (70.000+ACU- similar)
 in 20 aa overlap (5-24:31-50)

```

                10      20      30
AAD-12          DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                : : : : :
gi+AHw-165 MGVFTHENEITSAIIPGRLFKAFVLDADNLIPKLAPHAIKSAEIIIEGNGGPGTIKKITFG
                10      20      30      40      50      60

```

```

                40      50      60      70      80
AAD-12          YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDT
                : : : : :
gi+AHw-165 EGSQFKYVVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTSK
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
 allergen +AFs- (200 aa)

initn: 40 initl: 40 opt: 56 Z-score: 88.4 bits: 21.9 E(): 6
 Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
 in 53 aa overlap (29-76:93-144)

```

                10         20         30         40         50
AAD-12  DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRLVHQSARH
                . . . . . : : : : : . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100        110        120

                60         70         80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDTT
                . . : . . . : . . . . . :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130        140        150        160        170        180
    
```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 88.3 bits: 21.9 E(): 6.1
 Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
 in 53 aa overlap (29-76:97-148)

```

                10         20         30         40         50
AAD-12  DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRLVHQSARH
                . . . . . : : : : : . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100        110        120

                60         70         80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDTT
                . . : . . . : . . . . . :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130        140        150        160        170        180
    
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 87.2 bits: 21.1 E(): 7
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (12-70:9-65)

```

                10         20         30         40         50
AAD-12  DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRLVHQSARHSLVYS
                : : : : : : : : : : . . . . . :
gi+AHw-111  MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYL
                10         20         30         40         50

                60         70         80
AAD-12  QSKLGHVQQAGSAYIGYGMDTT
                : : . . . :
gi+AHw-111 QHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL
                60         70         80         90         100        110
    
```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein B1 (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 87.2 bits: 21.1 E(): 7
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (12-70:9-65)

```

                10         20         30         40         50
AAD-12  DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYS
                : : : : . : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-420  MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYL
                10         20         30         40         50

                60         70         80
AAD-12  QSKLGHVQQAGSAYIGYGMDDT
                : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-420  QHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
 Actinidia de (116 aa)

initn: 34 initl: 34 opt: 52 Z-score: 86.9 bits: 20.8 E(): 7.3
 Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
 in 71 aa overlap (4-72:11-80)

```

                10         20         30         40         50
AAD-12  DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                . . . . : : : : . : : : . . . . : : : : : : : : : : : :
gi+AHw-408  MVPKPLSLLLFLLLLALSAAVVGGRKLVAAAGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
                10         20         30         40         50

                60         70         80
AAD-12  HSLVYSQSKLGHVQQ-AGSAYIGYGMDDT
                : : . : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-408  DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMWHFRNLTSFRKV
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 86.7 bits: 20.8 E(): 7.5
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (30-70:11-50)

```

                10         20         30         40         50
AAD-12  DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYS
                : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-160  GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYL
                10         20         30

                60         70         80
AAD-12  QSKLGHVQQAGSAYIGYGMDDT
                : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-160  QHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
                40         50         60         70         80         90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
 +AFs-Trit (145 aa)

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 23.7 1.2
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T (121) 58 22.6 2.3
 gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145) 57 22.3 3.4
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po (396) 62 23.5 3.8
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200) 57 22.2 4.9
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl (204) 57 22.2 5
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 55 21.7 5.7
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 55 21.7 5.7
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.1 6.9
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.1 6.9
 gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281) 57 22.1 7.1
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.9 7.2
 gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P (284) 57 22.1 7.2
 gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 (287) 57 22.1 7.3
 gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290) 57 22.1 7.4
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.8 7.4
 gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295) 57 22.1 7.5
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.1 7.6
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.1 8.5
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 20.8 9.8

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 104.5 bits: 24.3 E(): 0.76
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (11-69:9-65)

	10	20	30	40	50
AAD-12	STYMPVMAQGAVFSAEVPVAVGGRTCFADMR	AAAYDAL--DEATRALVHQRSARHSLVYSQ			
	:	::	::	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI--EKGEHQLLYLQ				
	10	20	30	40	50
	60	70	80		


```

                10         20         30         40         50
                60         70         80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGMDTTA
      : ..  :...  :...  :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
      60         70         80         90         100        110

```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
 Full+AD0-Polle (284 aa)
 initn: 34 init1: 34 opt: 57 Z-score: 86.9 bits: 22.1 E(): 7.2
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (11-80:186-267)

```

                10         20         30
AAD-12          STYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
      :...  .  :...  :.  :...:
gi+AHw-285 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
      160        170        180        190        200        210

```

```

                40         50         60         70         80
AAD-12 LDEATRVLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTA
      :: : . :  ..: . . . . . :...  :...  :.  :...
gi+AHw-285 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
      220        230        240        250        260        270

```

gi+AHw-285 TVAAGGYKV
 280

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
 5.020 (287 aa)
 initn: 34 init1: 34 opt: 57 Z-score: 86.9 bits: 22.1 E(): 7.3
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (11-80:189-270)

```

                10         20         30
AAD-12          STYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
      :...  .  :...  :.  :...:
gi+AHw-330 GELQIIDKIDAAFKVAATAAATAPADTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
      160        170        180        190        200        210

```

```

                40         50         60         70         80
AAD-12 LDEATRVLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTA
      :: : . :  ..: . . . . . :...  :...  :.  :...
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
      220        230        240        250        260        270

```

gi+AHw-330 TVAAGGYKV
 280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
 5.020 (290 aa)
 initn: 34 init1: 34 opt: 57 Z-score: 86.8 bits: 22.1 E(): 7.4

Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (11-80:192-273)

```

                                10      20      30
AAD-12      STYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...: .. ...:
gi+AHw-330  QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPLSLEAAVKQ
                                170      180      190      200      210      220

                                40      50      60      70      80
AAD-12  LDEATRNLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTA
                                :: : . : ..: . . .... :...: .. : :::
gi+AHw-330  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                                230      240      250      260      270      280

gi+AHw-330  TVAAGGYKV
                                290

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 init1: 38 opt: 52 Z-score: 86.7 bits: 20.8 E(): 7.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (29-69:11-50)

```

                                10      20      30      40      50
AAD-12  STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRNLVHQRSARHSLVYSQ
                                :: : : ..... : .....: :
gi+AHw-160  GSQEHKPKKDDFRNEFDHLLIEQANHAI--EKGEHQLLYLQ
                                10      20      30

                                60      70      80
AAD-12  SKLGHVQQAGSAYIGYGMDDTTA
                                :: .... :
gi+AHw-160  HQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLS
                                40      50      60      70      80      90

```

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)
initn: 34 init1: 34 opt: 57 Z-score: 86.6 bits: 22.1 E(): 7.5
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (11-80:197-278)

```

                                10      20      30
AAD-12      STYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...: .. ...:
gi+AHw-330  QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPLSLEAAVKQ
                                170      180      190      200      210      220

                                40      50      60      70      80
AAD-12  LDEATRNLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTA
                                :: : . : ..: . . .... :...: .. : :::
gi+AHw-330  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                                230      240      250      260      270      280

```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 86.6 bits: 21.1 E(): 7.6
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (1-49:5-52)

```

                10         20         30         40         50
AAD-12      STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
             ::  ::  ..  ::  ..  ..  :  ::  :  .  :  ::  :  :  ::
gi+AHw-217 MASKSSISPLLLATVLSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTTCGISISG
                10         20         30         40         50

```

```

                60         70         80
AAD-12      SQSKLGHVQQAGSAYIGYGMDDTTA

```

```

gi+AHw-217 SAVSTEPGNTPRDRCCCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPREPQRDF
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 85.7 bits: 21.1 E(): 8.5
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (4-55:31-87)

```

                                10         20
AAD-12                                STYMPVMAQGAVFSAEVVPAVGG-----RTCFA
                                ::  ::  ::  :  ::  .  ::  .  ::
gi+AHw-132 MGVFNJETETTSVIPPARLFKRFVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
                                10         20         30         40         50

```

```

                30         40         50         60         70         80
AAD-12      DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTA
             :  .  .  .  .  .  .  .  :  ::  ::
gi+AHw-132 DEGSPFNFIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 84.6 bits: 20.8 E(): 9.8
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (34-57:29-52)

```

                10         20         30         40         50         60
AAD-12      MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
             :  :  ::  :  .  .  ::  :  ::
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
                10         20         30         40         50

```

```

                70         80
AAD-12      VQQAGSAYIGYGMDDTTA

```

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
 60 70 80 90 100 110

80 residues in 1 query sequences
 331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:03 2010 done: Fri Feb 5 12:56:03 2010

Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 113 - 192 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	0	0:	
30	2	2:+ACo-	
32	4	8:+AD0APQAq-	
34	7	21:+AD0APQA9- +ACo-	
36	33	44:+AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-	
38	35	72:+AD0APQA9AD0APQA9AD0APQA9-+AD0APQA9- +ACo-	
40	65		

101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-

+ACo-

42 92

123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP

QA9AD0APQA9AD0- +ACo-

44 107

136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP

QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-

46 123

138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP

QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-

48 129

132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP

QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-

Scan time: 0.090

The best scores are: opt bits E(1471)
 gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 64 24.4 0.73
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T (121) 58 22.6 2.2
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po (396) 64 24.2 2.5
 gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281) 62 23.7 2.5
 gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290) 62 23.6 2.6
 gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 57 22.3 3.3
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200) 57 22.3 4.7
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl (204) 57 22.3 4.8
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 55 21.7 5.5
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 55 21.7 5.5
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.2 6.7
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.2 6.7
 gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P (284) 57 22.2 7
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.9 7
 gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 (287) 57 22.2 7.1
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.9 7.2
 gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295) 57 22.2 7.3
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.1 8.2
 gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145) 52 20.9 9
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 20.8 9.5

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
 initn: 38 init1: 38 opt: 64 Z-score: 104.8 bits: 24.4 E(): 0.73
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (10-68:9-65)

	10	20	30	40	50
AAD-12	TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQS				
	:	:	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQH				
	10	20	30	40	50

```

        60          70          80
AAD-12 KLGHVQQAGSAYIGYGMDDTAT
        .: . . . . :
gi+AHw-111 QLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISK
        60          70          80          90          100          110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 initl: 58 opt: 58 Z-score: 96.3 bits: 22.6 E(): 2.2
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (26-77:26-77)

```

        10          20          30          40          50          60
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
        .: . . . . : . . . . : . . . . : . . . . :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQNSTKHSVPDVLAFKRVNV
        10          20          30          40          50          60

```

```

        70          80
AAD-12 GHVQQAGSAYIGYGMDDTAT
        .: . . . . : . . . . :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQKRVAG
        70          80          90          100          110          120

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 47 initl: 47 opt: 64 Z-score: 95.4 bits: 24.2 E(): 2.5
Smith-Waterman score: 64+ADs- 23.333+ACU- identity (53.333+ACU- similar)
in 60 aa overlap (21-80:309-362)

```

        10          20          30          40          50
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
        .: . . . . : . . . . : . . . . : . . . . :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
        280          290          300          310          320          330

```

```

        60          70          80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDTAT
        .: . . . . : . . . . : . . . . : . . . . :
gi+AHw-113 ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPEGESALSLSAGVLSQCP
        340          350          360          370          380          390

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
+AFs-Phl (281 aa)
initn: 39 initl: 39 opt: 62 Z-score: 95.2 bits: 23.7 E(): 2.5
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (10-80:183-265)

```

        10          20          30
AAD-12 TYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
        .: . . . . : . . . . : . . . . :
gi+AHw-168 QIIDKIDAAFKAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPLSLEAAVKQ
        160          170          180          190          200          210

```



```

                10         20         30         40         50
AAD-12      TYPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                . . . . .      . . . . .      . . . . .
gi+AHw-144  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100        110        120

```

```

                60         70         80
AAD-12      SLVYSQSKLGHVQQAGSAYIGYGMTTAT
                .. :   .. :   . . . . . :   :   :
gi+AHw-144  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
                130        140        150        160        170        180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 init1: 41 opt: 57 Z-score: 90.1 bits: 22.3 E(): 4.8
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (27-79:97-153)

```

                10         20         30         40         50
AAD-12      TYPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                . . . . .      . . . . .      . . . . .
gi+AHw-622  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100        110        120

```

```

                60         70         80
AAD-12      SLVYSQSKLGHVQQAGSAYIGYGMTTAT
                .. :   .. :   . . . . . :   :   :
gi+AHw-622  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
                130        140        150        160        170        180

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 init1: 55 opt: 55 Z-score: 89.1 bits: 21.7 E(): 5.5
Smith-Waterman score: 55+ADs- 45.455+ACU- identity (68.182+ACU- similar)
in 22 aa overlap (1-22:29-50)

```

                                10         20         30
AAD-12      TYPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                                : . : . : . : . : . : . :
gi+AHw-444  MGVFYADESTSVIPPPRLFKALVLEADTLIPKIA PQSVKSAEIVEGDGGVGTIKKISFG
                                10         20         30         40         50         60

```

```

                40         50         60         70         80
AAD-12      YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTAT
gi+AHw-444  EGSYYSVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTSN
                70         80         90         100        110        120

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 init1: 55 opt: 55 Z-score: 89.1 bits: 21.7 E(): 5.5
Smith-Waterman score: 55+ADs- 40.000+ACU- identity (70.000+ACU- similar)
in 20 aa overlap (3-22:31-50)

```

                                10      20      30
AAD-12      TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                                .: .: .: :... . :
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLDADNLI PKLAPHAIKSAEIIIEGNGGPGTIKKITFG
                                10      20      30      40      50      60

```

```

                                40      50      60      70      80
AAD-12      YDALDEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT
gi+AHw-165  EGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTSK
                                70      80      90      100     110     120

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 87.5 bits: 21.2 E(): 6.7
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (10-68:9-65)

```

                                10      20      30      40      50
AAD-12      TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATR ALVHQRSARHSLVYSQS
                                : : : : . . : : : : : : : : : : : : : : : :
gi+AHw-111  MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQH
                                10      20      30      40      50

```

```

                                60      70      80
AAD-12      KLGHVQQAGSAYIGYGMDDTTAT
                                .: .: .: :
gi+AHw-111  QLDELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFN YEEAQTL SK
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 87.5 bits: 21.2 E(): 6.7
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (10-68:9-65)

```

                                10      20      30      40      50
AAD-12      TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATR ALVHQRSARHSLVYSQS
                                : : : : . . : : : : : : : : : : : : : : : :
gi+AHw-420  MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQH
                                10      20      30      40      50

```

```

                                60      70      80
AAD-12      KLGHVQQAGSAYIGYGMDDTTAT
                                .: .: .: :
gi+AHw-420  QLDELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFN YEEAQTL SK
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
Full+AD0-Polle (284 aa)
initn: 34 initl: 34 opt: 57 Z-score: 87.2 bits: 22.2 E(): 7
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (10-79:186-267)

```

                                10      20      30
AAD-12      TYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... .  ...:  .. ...:
gi+AHw-285  QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
            160      170      180      190      200      210

```

```

            40      50      60      70      80
AAD-12  LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTAT
            :: : . :      ..: . . . . . . : : : : : : : : :
gi+AHw-285  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
            220      230      240      250      260      270

```

gi+AHw-285 TVAAGGYKV
280

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)
initn: 34 initl: 34 opt: 52 Z-score: 87.2 bits: 20.9 E(): 7
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (2-70:11-80)

```

                                10      20      30      40      50
AAD-12      TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVL-HQRSAR
                                .. .  ...:  ... .  : : : : : : : : :
gi+AHw-408  MVPKPLSLLLFLLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
            10      20      30      40      50

```

```

            60      70      80
AAD-12  HSLVYSQSKLGHVQQ-AGSAYIGYGMDTTAT
            : ...  ...:  ... :
gi+AHw-408  DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMHFRNLTSFRKV
            60      70      80      90      100      110

```

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
5.020 (287 aa)
initn: 34 initl: 34 opt: 57 Z-score: 87.1 bits: 22.2 E(): 7.1
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (10-79:189-270)

```

                                10      20      30
AAD-12      TYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... .  ...:  .. ...:
gi+AHw-330  GELQIIDKIDAAFKVAATAAATAPADTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
            160      170      180      190      200      210

```

```

            40      50      60      70      80
AAD-12  LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTAT
            :: : . :      ..: . . . . . . : : : : : : : : :
gi+AHw-330  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
            220      230      240      250      260      270

```

gi+AHw-330 TVAAGGYKV
280

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 init1: 38 opt: 52 Z-score: 86.9 bits: 20.9 E(): 7.2
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (28-68:11-50)

```

                10         20         30         40         50
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQS
                :::  :::  :  .....  .....:::  :
gi+AHw-160                GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQH
                        10         20         30         40

```

```

                60         70         80
AAD-12 KLGHVQQAGSAYIGYGMDDTTAT
                ::  ....  :
gi+AHw-160 QLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSK
                        50         60         70         80         90         100

```

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)

initn: 34 init1: 34 opt: 57 Z-score: 86.9 bits: 22.2 E(): 7.3
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (10-79:197-278)

```

                        10         20         30
AAD-12                TYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                        :...  .  ...:  ..  ....:
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                170         180         190         200         210         220

```

```

                40         50         60         70         80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTAT
                ::  :  .  :  ..:  .  .....  ...:  ...:  .  :  :::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                230         240         250         260         270         280

```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)

initn: 47 init1: 47 opt: 53 Z-score: 85.9 bits: 21.1 E(): 8.2
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (3-54:31-87)

```

                        10         20
AAD-12                TYMPVMAQGAVFSAEVVPAVGG----RTCF
                        ::  ::  :  :  ...  .  :  .  ::
gi+AHw-132 MGVFNJETETTSVIPPARLFKRFVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
                10         20         30         40         50

```

```

                30         40         50         60         70         80
AAD-12 DMRAAYDALDEATRALVHQ-RSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT

```

```

      : . . . . . : : : :
gi+AHw-132 DEGSPFNLIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKXIS
      60          70          80          90          100          110

```

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
tetrameric (145 aa)
  initn: 37 initl: 37 opt: 52 Z-score: 85.2 bits: 20.9 E(): 9
Smith-Waterman score: 52+ADs- 24.444+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (4-48:9-52)

```

```

      10          20          30          40          50
AAD-12      TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY
      :..  ...  :.  ..  ..  :.  : : :  .  : : :  : : :
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTTCGVTIAG
      10          20          30          40          50

```

```

      60          70          80
AAD-12 SQSKLGHVQQAGSAYIGYGMDDTTAT

```

```

gi+AHw-439 SPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQRDF
      60          70          80          90          100          110

```

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
  initn: 52 initl: 52 opt: 52 Z-score: 84.8 bits: 20.8 E(): 9.5
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (33-56:29-52)

```

```

      10          20          30          40          50          60
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGH
      : : : : : .  .. : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
      10          20          30          40          50

```

```

      70          80
AAD-12 VQQAGSAYIGYGMDDTTAT

```

```

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
      60          70          80          90          100          110

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:03 2010 done: Fri Feb 5 12:56:04 2010
Total Scan time: 0.090 Total Display time: 0.010

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

```


64 63
 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
 66 55 25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
 68 35 20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
 70 20 16:+AD0APQA9AD0APQAqAD0-
 72 13 12:+AD0APQA9ACoAPQ-
 74 18 10:+AD0APQA9ACoAPQA9-
 76 8 7:+AD0APQAq-
 78 5 6:+AD0AKg-
 80 18 4:+AD0AKgA9AD0APQA9-
 82 2 3:+ACo-
 84 1 3:+ACo-
 86 7 2:+ACoAPQA9-
 88 5 2:+ACoAPQ- inset +AD0- represents 1 library

sequences

90 1 1:+ACo-
 92 1 1:+ACo- :+ACo-
 94 3 1:+ACo- :+ACoAPQA9-
 96 0 1:+ACo- :+ACo-
 98 0 0: +ACo-
 100 0 0: +ACo-
 102 1 0:+AD0- +ACoAPQ-
 104 0 0: +ACo-
 106 0 0: +ACo-
 108 0 0: +ACo-
 110 1 0:+AD0- +ACoAPQ-
 112 0 0: +ACo-
 114 0 0: +ACo-
 116 0 0: +ACo-
 118 0 0: +ACo-

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 5.10670.00357+ADs- mu+AD0- 5.1625
 0.186

mean+AF8-var+AD0-40.349010.483, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42

Lambda+AD0- 0.201910

Kolmogorov-Smirnov statistic: 0.1147 (N+AD0-29) at 54

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 74 26.9 0.36

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
 134) 64 24.1 0.89

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 58 22.3 2.7

gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281)
 62 23.5 2.9

gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290)
 62 23.5 3

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 57 22.0 4
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 57 22.0 4.4
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200) 57 22.0 5.5
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-G1 (204) 57 22.0 5.7
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 55 21.4 6.6
 gi+AHw-60280809+AHw-gb+AHw-AAX18297.1+AHw- major allergen Mal d 1. (160) 55 21.4 6.6
 gi+AHw-60280807+AHw-gb+AHw-AAX18296.1+AHw- major allergen Mal d 1. (160) 55 21.4 6.6
 gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P (284) 57 22.0 8
 gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 (287) 57 22.0 8
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 20.9 8.2
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 20.9 8.2
 gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295) 57 22.0 8.3
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.6 8.7
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.6 8.9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 57 init1: 57 opt: 74 Z-score: 110.3 bits: 26.9 E(): 0.36
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar) in 61 aa overlap (20-80:309-363)

		10	20	30	40	
AAD-12		YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR				
			:: :	: ::	... :	: ...
gi+AHw-113	HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA					
	280 290 300 310 320 330					
	50	60	70	80		
AAD-12	HSLVYSQSKLGHVQQAGSAYIGYGMDDTATP					
	: ::	. ::		
gi+AHw-113	ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPEGESALSLTSSAGVLSCQP					
	340 350 360 370 380 390					

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
 initn: 38 init1: 38 opt: 64 Z-score: 103.3 bits: 24.1 E(): 0.89

Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar) in 61 aa overlap (9-67:9-65)

10 20 30 40 50
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
: : : : : . : : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQGHPKPKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
10 20 30 40 50

60 70 80
AAD-12 LGHVQQAGSAYIGYGMDDTTATP
: :
gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
60 70 80 90 100 110

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
initn: 58 init1: 58 opt: 58 Z-score: 94.6 bits: 22.3 E(): 2.7
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar) in 52 aa overlap (25-76:26-77)

10 20 30 40 50
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
: : : : : : : : : : : : : : : : :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAIPVYEQLSTKHSVPDVLAFQKRVNV
10 20 30 40 50 60

60 70 80
AAD-12 GHVQQAGSAYIGYGMDDTTATP
: : : : : : : : : : : : : : : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGLAQKRVAG
70 80 90 100 110 120

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 +AFs-Phl (281 aa)
initn: 39 init1: 39 opt: 62 Z-score: 94.1 bits: 23.5 E(): 2.9
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar) in 83 aa overlap (9-79:183-265)

10 20 30
AAD-12 YMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
: : : . : : : : : : : : : : : : : : : :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDITYKCIPSLEAAVKQ
160 170 180 190 200 210

40 50 60 70 80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATP
: : : . : : : : : : : : : : : : : : :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
220 230 240 250 260 270

gi+AHw-168 TVAAGGYKV
280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
 5.020 (290 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 93.9 bits: 23.5 E(): 3
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (9-79:192-274)

```

                                10      20      30
AAD-12      YMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :.:. . .: : :. .: :
gi+AHw-330  QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPLSLEAAVKQ
                170      180      190      200      210      220

                40      50      60      70      80
AAD-12  LDEATRALLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATP
                :: : . : . : . . . . . : : : . : : : :
gi+AHw-330  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                230      240      250      260      270      280

gi+AHw-330  TVAAGGYKV
                290
  
```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 91.7 bits: 22.0 E(): 4
 Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (3-47:9-52)

```

                                10      20      30      40      50
AAD-12      YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARHSLVY
                                :. . . . : . : : : . : : : : : :
gi+AHw-189  MASKSSITPLLLA AVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIAG
                10      20      30      40      50

                60      70      80
AAD-12  SQSKLGHVQQAGSAYIGYGMDDTTATP

gi+AHw-189  SPVSSEPGDTPKDRCCQELDEAPQHCRVRYFIGRRSHDPWRVLDLPGCPKEPQRDFA
                60      70      80      90      100      110
  
```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)
 initn: 47 initl: 47 opt: 57 Z-score: 90.8 bits: 22.0 E(): 4.4
 Smith-Waterman score: 57+ADs- 20.000+ACU- identity (55.294+ACU- similar)
 in 85 aa overlap (2-80:31-109)

```

                                10      20
AAD-12      YMPVMAQGAVFSAEVVPAVGG----RTCF
                                :. : : . : . : : . :
gi+AHw-132  MGVFN YETETTSVIPPARLFKRFVLDSDNLI PKVAPKAIKSIEIIEGNGGPGTIKKICF-
                10      20      30      40      50

                30      40      50      60      70      80
AAD-12  DMRAAYDALDEATRALLVHQ--SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP
                : . . . . . : : : . . . . . : : : . . . :
  
```

gi+AHw-132 DEGSPFN...INYEIKIVASPHGGSI
60 70 80 90 100 110

gi+AHw-132 LKSISKYHTIGDHELIKDEQIKAGKEKASGLFKAVEGYLLAHS DAYN
120 130 140 150 160

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 89.0 bits: 22.0 E(): 5.5
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (26-78:93-149)

AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATR...
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
70 80 90 100 110 120

AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMTTATP
.. : ... : : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
130 140 150 160 170 180

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 88.9 bits: 22.0 E(): 5.7
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (26-78:97-153)

AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATR...
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
70 80 90 100 110 120

AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMTTATP
.. : ... : : : :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
130 140 150 160 170 180

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 initl: 55 opt: 55 Z-score: 87.7 bits: 21.4 E(): 6.6
Smith-Waterman score: 55+ADs- 40.000+ACU- identity (70.000+ACU- similar)
in 20 aa overlap (2-21:31-50)

AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
.. : ... : : : :
gi+AHw-165 MGVFTHENEITS AIPPGR LFKAFVLDADN LIPK LAPHAIKSAEII EGNGGPGTIKKITFG
10 20 30 40 50 60

40 50 60 70 80
 AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATP

gi+AHw-165 EGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTSK
 70 80 90 100 110 120

+AD4APg-gi+AHw-60280809+AHw-gb+AHw-AAX18297.1+AHw- major allergen Mal d
 1.0502 (160 aa)
 initn: 49 initl: 49 opt: 55 Z-score: 87.7 bits: 21.4 E(): 6.6
 Smith-Waterman score: 55+ADs- 23.750+ACU- identity (51.250+ACU- similar)
 in 80 aa overlap (2-80:31-109)

10 20 30
 AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRRA
 .: .: .: .: .: .: .: .: .: .: .:
 gi+AHw-602 MGVFTYETEFSSAIPAPGLFKAFILDGDNLIPKIAPOAIKSTEIVEGDGGVGTIKKITFG
 10 20 30 40 50 60

40 50 60 70 80
 AAD-12 YDALDEATRALVHQRSARHSLVYSQSKL-GHVQQAGSAYIGYGMTTATP
 . . : . .: .: .: .: .: .: .: .: .: .:
 gi+AHw-602 EGSQYGYVKHKVDGID-KHNFTYSYSMIEGDALSDKIEKIAIYETKLTASPDGGSIIKTTS
 70 80 90 100 110

gi+AHw-602 HCHTKGGVEIKEEHVKAGKEKASSLFKLLLETYL VANPNAYN
 120 130 140 150 160

+AD4APg-gi+AHw-60280807+AHw-gb+AHw-AAX18296.1+AHw- major allergen Mal d
 1.0501 (160 aa)
 initn: 49 initl: 49 opt: 55 Z-score: 87.7 bits: 21.4 E(): 6.6
 Smith-Waterman score: 55+ADs- 23.750+ACU- identity (51.250+ACU- similar)
 in 80 aa overlap (2-80:31-109)

10 20 30
 AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRRA
 .: .: .: .: .: .: .: .: .: .: .:
 gi+AHw-602 MGVFTYETEFSSAIPAPRLFKAFILDGDNLIPKIAPOAIKSTEIVEGDGGVGTIKKITFG
 10 20 30 40 50 60

40 50 60 70 80
 AAD-12 YDALDEATRALVHQRSARHSLVYSQSKL-GHVQQAGSAYIGYGMTTATP
 . . : . .: .: .: .: .: .: .: .: .: .:
 gi+AHw-602 EGSQYGYVKHKVDGID-KHNFTYSYSMIEGDALSDKIEKIAIYETKLTASPDGGSIIKTTS
 70 80 90 100 110

gi+AHw-602 HCHTKGGVEIKEEHVKAGKEKASGLFKLLLETYL VANPNAYN
 120 130 140 150 160

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
 Full+AD0-Polle (284 aa)
 initn: 34 initl: 34 opt: 57 Z-score: 86.2 bits: 22.0 E(): 8
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (9-78:186-267)

```

                                10      20      30
AAD-12      YMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... .   ...:   .. ...:
gi+AHw-285  QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPSLEAAVKQ
                                160      170      180      190      200      210

```

```

                                40      50      60      70      80
AAD-12  LDEATR LVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATP
                                :: : . :   ..: . . . . . . : : : : : : : : :
gi+AHw-285  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                                220      230      240      250      260      270

```

gi+AHw-285 TVAAGGYKV
280

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5.020 (287 aa)
 initn: 34 initl: 34 opt: 57 Z-score: 86.1 bits: 22.0 E(): 8
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (9-78:189-270)

```

                                10      20      30
AAD-12      YMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... .   ...:   .. ...:
gi+AHw-330  GELQIIDKIDAAFKVAATAAATAPADTVFEEAFNKAIKESTGGAYDXYKCIPSLEAAVKQ
                                160      170      180      190      200      210

```

```

                                40      50      60      70      80
AAD-12  LDEATR LVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATP
                                :: : . :   ..: . . . . . . : : : : : : : : :
gi+AHw-330  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                                220      230      240      250      260      270

```

gi+AHw-330 TVAAGGYKV
280

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 85.9 bits: 20.9 E(): 8.2
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (9-67:9-65)

```

                                10      20      30      40      50
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATR LVHQRSARHSLVYSQSK
                                : : : : .   : : :   : : : : : : : : : : :
gi+AHw-111  MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                                10      20      30      40      50

```

```

                                60      70      80
AAD-12  LGHVQQAGSAYIGYGMDDTTATP
                                : . . . . :
gi+AHw-111  LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein B1 (134 aa)
 initn: 38 init1: 38 opt: 53 Z-score: 85.9 bits: 20.9 E(): 8.2
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (9-67:9-65)

```

                10         20         30         40         50
AAD-12  YMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                : : : : . : : : : : : : : : : : : : : : : :
gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                10         20         30         40         50
  
```

```

                60         70         80
AAD-12  LGHVQQAGSAYIGYGMDDTTATP
                : : : : :
gi+AHw-420 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
                60         70         80         90         100        110
  
```

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5.020 (295 aa)
 initn: 34 init1: 34 opt: 57 Z-score: 85.9 bits: 22.0 E(): 8.3
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (9-78:197-278)

```

                                10         20         30
AAD-12                                YMPVMAQGAVFSAEVPVAVGG----RTCFADMRAAYDA
                                : : . : : : : : : : : : : : : : : :
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDITYKCIPLSLEAAVKQ
                170         180         190         200         210         220
  
```

```

                40         50         60         70         80
AAD-12  LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATP
                : : : . : : : : : : : : : : : : : : : : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                230         240         250         260         270         280
  
```

gi+AHw-330 TVAAGGYKV
 290

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs- Actinidia de (116 aa)
 initn: 34 init1: 34 opt: 52 Z-score: 85.5 bits: 20.6 E(): 8.7
 Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
 in 71 aa overlap (1-69:11-80)

```

                                10         20         30         40
AAD-12                                YMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                                . . . : : : : . : : : . . : : : : : : : : : :
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
                10         20         30         40         50
  
```

```

                50         60         70         80
AAD-12  HSLVYSQSKLGHVQQ-AGSAYIGYGMDDTTATP
                : : . : : : : : : :
  
```

gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMMHFRNLTSFRKV
60 70 80 90 100 110

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 85.3 bits: 20.6 E(): 8.9
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (27-67:11-50)

10 20 30 40 50
AAD-12 YMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
: : : : :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
10 20 30 40

60 70 80
AAD-12 LGHVQQAGSAYIGYGMDDTTATP
: : :
gi+AHw-160 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
50 60 70 80 90 100

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:05 2010 done: Fri Feb 5 12:56:05 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 115 - 194 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

opt E()
+ADw- 20 2 0:+AD0-
22 0 0: one +AD0- represents 3 library sequences
24 0 0:
26 0 0:
28 2 0:+AD0-
30 2 2:+ACo-
32 4 8:+AD0APQAq-
34 19 21:+AD0APQA9AD0APQA9ACo-
36 36 44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-

```

38      45      72 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
40      61
101 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42      103
123 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
44      117
136 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
46      123
138 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
48      121
132 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
50      128
121 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
52      95
106 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ-      +ACo-
54      75
91 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56      97
76 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
58      65
62 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
60      58      50 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
62      62
40 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
64      67
32 :+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
66      52      25 :+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-
68      35      20 :+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
70      18      16 :+AD0APQA9AD0APQAq-
72      15      12 :+AD0APQA9ACoAPQ-
74      16      10 :+AD0APQA9ACoAPQA9-
76      8       7 :+AD0APQAq-
78      5       6 :+AD0AKg-
80      19      4 :+AD0AKgA9AD0APQA9AD0-
82      1       3 :+ACo-
84      2       3 :+ACo-
86      6       2 :+ACoAPQ-
88      5       2 :+ACoAPQ-      inset +AD0- represents 1 library
sequences
90      1       1 :+ACo-
92      1       1 :+ACo-      :+ACo-
94      3       1 :+ACo-      :+ACoAPQA9-
96      0       1 :+ACo-      :+ACo-
98      0       0 :      +ACo-
100     0       0 :      +ACo-

```

```

102      1      0:+AD0-          +ACoAPQ-
104      0      0:              +ACo-
106      0      0:              +ACo-
108      0      0:              +ACo-
110      1      0:+AD0-          +ACoAPQ-
112      0      0:              +ACo-
114      0      0:              +ACo-
116      0      0:              +ACo-
118      0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.08810.00359+ADs- mu+AD0- 5.3253
0.187
mean+AF8-var+AD0-40.169610.344, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.202360
Kolmogorov-Smirnov statistic: 0.1113 (N+AD0-29) at 54

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  74 26.9    0.36
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  64 24.1    0.89
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 22.3    2.7
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 ( 281)
62 23.5    2.9
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 ( 290)
62 23.5    3
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)  57 22.0    4
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
57 22.0    4.4
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.0    5.6
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.0    5.7
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)  55 21.4    6.6
gi+AHw-60280809+AHw-gb+AHw-AAX18297.1+AHw- major allergen Mal d 1. ( 160)
55 21.4    6.6
gi+AHw-60280807+AHw-gb+AHw-AAX18296.1+AHw- major allergen Mal d 1. ( 160)
55 21.4    6.6
gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
( 284)  57 22.0    8
gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 ( 287)
57 22.0    8.1
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  53 20.9    8.3
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 20.9    8.3

```

gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295)
 57 22.0 8.3
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 20.6 9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 57 initl: 57 opt: 74 Z-score: 110.3 bits: 26.9 E(): 0.36
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (19-79:309-363)

```

                10         20         30         40
AAD-12      MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                : : : : : : : : : : : : : : : : : :
gi+AHw-113  HGFFQVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
            280       290       300       310       320       330

            50         60         70         80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL
            : : : : : : : : : : : : : : : : : :
gi+AHw-113  ESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
            340       350       360       370       380       390

```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 103.3 bits: 24.1 E(): 0.89
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (8-66:9-65)

```

                10         20         30         40         50
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                : : : : : : : : : : : : : : : : : :
gi+AHw-111  MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
            10         20         30         40         50

            60         70         80
AAD-12  LGHVQQAGSAYIGYGMDDTTATPL
            : : : : : :
gi+AHw-111  LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
            60         70         80         90         100        110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 94.6 bits: 22.3 E(): 2.7
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (24-75:26-77)

```

                10         20         30         40         50
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                : : : : : : : : : : : : : : : : : :
gi+AHw-527  MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQVSTKHSVPDVLAFKVN

```

```

                10         20         30         40         50         60
AAD-12  60      70      80
        GHVQQAGSAYIGYGMDDTTATPL
        ::::: . : . :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQKRVAG
                70         80         90         100        110        120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 +AFs-Phl (281 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 94.2 bits: 23.5 E(): 2.9
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (8-78:183-265)

```

                                10         20         30
AAD-12  MPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                ::. . .:: . . .::
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDITYKCIPSLEAAVKQ
                160        170        180        190        200        210

```

```

                40         50         60         70         80
AAD-12  LDEATRVLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPL
                :: : . : . : . . . . . : : : . : : :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                220        230        240        250        260        270

```

gi+AHw-168 TVAAGGYKV
 280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5.020 (290 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 93.9 bits: 23.5 E(): 3
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (8-78:192-274)

```

                                10         20         30
AAD-12  MPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                ::. . .:: . . .::
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDITYKCIPSLEAAVKQ
                170        180        190        200        210        220

```

```

                40         50         60         70         80
AAD-12  LDEATRVLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPL
                :: : . : . : . . . . . : : : . : : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                230        240        250        260        270        280

```

gi+AHw-330 TVAAGGYKV
 290

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 91.6 bits: 22.0 E(): 4

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 88.8 bits: 22.0 E(): 5.7
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (25-77:97-153)

```

                10      20      30      40
AAD-12      MPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                . . . . .      : : : : :      . . . . .
gi+AHw-622  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70      80      90      100      110      120

```

```

                50      60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL
                . . : . . . : . . . . . : : :
gi+AHw-622  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130      140      150      160      170      180

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
 sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 55 Z-score: 87.6 bits: 21.4 E(): 6.6
 Smith-Waterman score: 55+ADs- 40.000+ACU- identity (70.000+ACU- similar)
 in 20 aa overlap (1-20:31-50)

```

                10      20      30
AAD-12      MPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                . : . : . : : : . . : :
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLDADNLI PKLAPHAIKSAEIIIEGNGGPGTIKKITFG
                10      20      30      40      50      60

```

```

                40      50      60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL
gi+AHw-165  EGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTSK
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-60280809+AHw-gb+AHw-AAX18297.1+AHw- major allergen Mal d
 1.0502 (160 aa)
 initn: 49 initl: 49 opt: 55 Z-score: 87.6 bits: 21.4 E(): 6.6
 Smith-Waterman score: 55+ADs- 23.750+ACU- identity (51.250+ACU- similar)
 in 80 aa overlap (1-79:31-109)

```

                10      20      30
AAD-12      MPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                . : . : . : : : . . : . .
gi+AHw-602  MGVFYETEFSSAIPAPGLFKAFILDGDNLI PKIAPQAIKSTEIVEGDGGVGTIKKITFG
                10      20      30      40      50      60

```

```

                40      50      60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKL-GHVQQAGSAYIGYGMDDTTATPL
                . . : . . . . . : . : . . : : :
gi+AHw-602  EGSQYGYVKKHKVDGID-KHNFTYSYSMIEGDALSDKIEKIAYETKLTASPDGGSIIKTTS
                70      80      90      100      110

```

gi+AHw-602 HCHTKGGVEIKEEHVKAGKEKASSLFLKLETYLVANPNAYN
 120 130 140 150 160

+AD4APg-gi+AHw-60280807+AHw-gb+AHw-AAX18296.1+AHw- major allergen Mal d
 1.0501 (160 aa)

initn: 49 init1: 49 opt: 55 Z-score: 87.6 bits: 21.4 E(): 6.6
 Smith-Waterman score: 55+ADs- 23.750+ACU- identity (51.250+ACU- similar)
 in 80 aa overlap (1-79:31-109)

AAD-12 10 20 30
 MPVMAQGAVFSAEVVPAVGGRTCFADMRAA
 .: .: .: .: .: .: .: .: .: .: .:
 gi+AHw-602 MGVTYETEFSSAIPAPRLFKAFILDGDNLIPKIAPOAIKSTEIVEGDGGVGTIKKITFG
 10 20 30 40 50 60

AAD-12 40 50 60 70 80
 YDALDEATRALVHQRSARHSLVYSQSKL-GHVQQAGSAYIGYMDTTATPL
 . . .: .: .: .: .: .: .: .: .: .: .:
 gi+AHw-602 EGSQYGYVKHKVDGID-KHNFTYSYSMIEGDALSDKIEKIAYETKLTASPDGGSIIKTTS
 70 80 90 100 110

gi+AHw-602 HCHTKGGVEIKEEHVKAGKEKASGLFLKLETYLVANPNAYN
 120 130 140 150 160

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
 Full+AD0-Polle (284 aa)

initn: 34 init1: 34 opt: 57 Z-score: 86.2 bits: 22.0 E(): 8
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (8-77:186-267)

AAD-12 10 20 30
 MPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
 :.:. .: .: .: .: .: .: .: .: .: .:
 gi+AHw-285 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPLSLEAAVKQ
 160 170 180 190 200 210

AAD-12 40 50 60 70 80
 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYMDTTATPL
 :: .: .: .: .: .: .: .: .: .: .: .:
 gi+AHw-285 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
 220 230 240 250 260 270

gi+AHw-285 TVAAGGYKV
 280

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
 5.020 (287 aa)

initn: 34 init1: 34 opt: 57 Z-score: 86.1 bits: 22.0 E(): 8.1
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (8-77:189-270)

AAD-12 10 20 30
 MPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
 :.:. .: .: .: .: .: .: .: .: .: .:


```

                                10      20      30
AAD-12      MPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...:  :. ....:
gi+AHw-330  QIIDKIDA AFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYD TYKCIPSLEAAVKQ
                                170      180      190      200      210      220

```

```

                                40      50      60      70      80
AAD-12  LDEATR ALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPL
                                :: : . :  ..: . . ....: ...: .. :  :::
gi+AHw-330  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                                230      240      250      260      270      280

```

```

gi+AHw-330  TVAAGGYKV
                                290

```

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
  initn: 38 initl: 38 opt: 52 Z-score: 85.3 bits: 20.6 E(): 9
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (26-66:11-50)

```

```

                                10      20      30      40      50
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATR ALVHQRSARHSLVYSQSKL
                                :: : :  .....: .....: : :
gi+AHw-160  GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                                10      20      30      40

```

```

                                60      70      80
AAD-12  GHVQQAGSAYIGYGMDTTATPL
                                .... :
gi+AHw-160  DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFN YEEAQTL SKIL
                                50      60      70      80      90      100

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:05 2010 done: Fri Feb 5 12:56:05 2010
Total Scan time: 0.080 Total Display time: 0.010

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

1+AD4APgA+-AAD-12: 116 - 195 80 aa - 80 aa


```

76      9      7:+AD0APQAq-
78     15     6:+AD0AKgA9AD0APQ-
80      3     4:+AD0AKg-
82      4     3:+ACoAPQ-
84      5     3:+ACoAPQ-
86      8     2:+ACoAPQA9-
88      1     2:+ACo-          inset +AD0- represents 1 library sequences
90      2     1:+ACo-
92      1     1:+ACo-          :+ACo-
94      3     1:+ACo-          :+ACoAPQA9-
96      0     1:+ACo-          :+ACo-
98      0     0:              +ACo-
100     0     0:              +ACo-
102     0     0:              +ACo-
104     1     0:+AD0-          +ACoAPQ-
106     0     0:              +ACo-
108     0     0:              +ACo-
110     1     0:+AD0-          +ACoAPQ-
112     0     0:              +ACo-
114     0     0:              +ACo-
116     0     0:              +ACo-
118     0     0:              +ACo-

```

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 5.02070.00354+ADs- mu+AD0- 5.6837
0.185

mean+AF8-var+AD0-38.799010.102, 0's: 2 Z-trim: 3 B-trim: 213 in 1/42

Lambda+AD0- 0.205904

Kolmogorov-Smirnov statistic: 0.1092 (N+AD0-29) at 54

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 74 27.2 0.31

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134)
64 24.2 0.8

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 58 22.5 2.5

gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281)
62 23.6 2.6

gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290)
62 23.6 2.7

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144)
57 22.2 3.6

gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)
57 22.1 5.1

gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-G1
(204) 57 22.1 5.2

gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160)
55 21.6 6.1

gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
 (284) 57 22.1 7.3
 gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 (287)
 57 22.1 7.4
 gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295)
 57 22.1 7.6
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 53 21.0 7.7
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
 53 21.0 7.7
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 22.7 8.1
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 20.7 8.3
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
 53 21.0 9.2
 gi+AHw-60280809+AHw-gb+AHw-AAX18297.1+AHw- major allergen Mal d 1. (160)
 53 21.0 9.2
 gi+AHw-60280807+AHw-gb+AHw-AAX18296.1+AHw- major allergen Mal d 1. (160)
 53 21.0 9.2
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116)
 51 20.4 10

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 57 init1: 57 opt: 74 Z-score: 111.5 bits: 27.2 E(): 0.31
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (18-78:309-363)

```

                                10      20      30      40
AAD-12      PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                :: : : . . . . : . . .
gi+AHw-113  HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEGAAA
            280      290      300      310      320      330

            50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
            . . . . : . . . . . . . . . .
gi+AHw-113  ESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
            340      350      360      370      380      390

```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 init1: 38 opt: 64 Z-score: 104.1 bits: 24.2 E(): 0.8
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (7-65:9-65)

```

                                10      20      30      40      50
AAD-12      PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                                : . . . . : : . . . . . . . . . . . . . . . . . .
gi+AHw-111  MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ

```

```

                10          20          30          40          50
    60          70          80
AAD-12 LGHVQQAGSAYIGYGMDDTTATPLR
      : . . . . :
gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
    60          70          80          90          100          110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 58 init1: 58 opt: 58 Z-score: 95.3 bits: 22.5 E(): 2.5
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (23-74:26-77)

```

                10          20          30          40          50
AAD-12  PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKL
      ::: . . . : . . . : . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQNSTKHSVPDVLAFKVN
    10          20          30          40          50          60

```

```

    60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLR
      :: . . . : . : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAAEKLGGLAQKRVAG
    70          80          90          100          110          120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
 +AFs-Phl (281 aa)
 initn: 39 init1: 39 opt: 62 Z-score: 95.0 bits: 23.6 E(): 2.6
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (7-77:183-265)

```

                10          20          30
AAD-12  PVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
      :: . . . : . . . :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPSLEAAVKQ
    160          170          180          190          200          210

```

```

    40          50          60          70          80
AAD-12 LDEATRNLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLR
      :: : . : . . : . . . . . : . . : . . : : :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
    220          230          240          250          260          270

```

```

gi+AHw-168 TVAAGGYKV
    280

```

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
 5.020 (290 aa)
 initn: 39 init1: 39 opt: 62 Z-score: 94.7 bits: 23.6 E(): 2.7
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (7-77:192-274)

Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar) in 58 aa overlap (24-76:97-153)

Sequence alignment for AAD-12 and gi+AHw-622. AAD-12: PVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATR... gi+AHw-622: AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE... Alignment markers at 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180.

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 +AFs-Cor (160 aa) initn: 45 initl: 45 opt: 55 Z-score: 88.3 bits: 21.6 E(): 6.1 Smith-Waterman score: 55+ADs- 20.238+ACU- identity (54.762+ACU- similar) in 84 aa overlap (1-78:32-109)

Sequence alignment for AAD-12 and gi+AHw-132. AAD-12: PVMAQGAVFSAEVVPAVGG-----RTCFAD... gi+AHw-132: GVFNYETETTSVIPPARLFKRFVLDSDNLIPKVAPKAIKSIEIEGNGGPGTIKKICF-D... Alignment markers at 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160.

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-Polle (284 aa) initn: 34 initl: 34 opt: 57 Z-score: 86.9 bits: 22.1 E(): 7.3 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar) in 82 aa overlap (7-76:186-267)

Sequence alignment for AAD-12 and gi+AHw-285. AAD-12: PVMAQGAVFSAEVVPAVGG-----RTCFADMRAAYDA... gi+AHw-285: QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPLSLEAAVKQ... Alignment markers at 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270.

gi+AHw-285 TVAAGGYKV
280

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
5.020 (287 aa)

initn: 34 init1: 34 opt: 57 Z-score: 86.8 bits: 22.1 E(): 7.4
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (7-76:189-270)

```

                                10          20          30
AAD-12          PVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...:   .. ...:
gi+AHw-330 GELQIIDKIDAAFKVAATAAATAPADTVFEAAFNKAIKESTGGAYDITYKCIPSLEAAVKQ
          160      170      180      190      200      210

```

```

          40          50          60          70          80
AAD-12 LDEATRNLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLR
          :: : . :      ..: . . . . . . : : . : : : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          220      230      240      250      260      270

```

gi+AHw-330 TVAAGGYKV
280

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)

initn: 34 init1: 34 opt: 57 Z-score: 86.5 bits: 22.1 E(): 7.6
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (7-76:197-278)

```

                                10          20          30
AAD-12          PVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...:   .. ...:
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDITYKCIPSLEAAVKQ
          170      180      190      200      210      220

```

```

          40          50          60          70          80
AAD-12 LDEATRNLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLR
          :: : . :      ..: . . . . . . : : . : : : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          230      240      250      260      270      280

```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 init1: 38 opt: 53 Z-score: 86.5 bits: 21.0 E(): 7.7
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (7-65:9-65)

```

          10          20          30          40          50
AAD-12  PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRNLVHQRSARHSLVYSQSK
          : ... : . :      ..: . : : . . . . . . . . . . . . . . . . . .

```



```

82      2      3:+ACo-
84      2      3:+ACo-
86      7      2:+ACoAPQA9-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      3      1:+ACo-          :+ACoAPQA9-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     1      0:+AD0-          +ACoAPQ-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     1      0:+AD0-          +ACoAPQ-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.03520.0034+ADs- mu+AD0- 6.7115
0.176
mean+AF8-var+AD0-34.7883 8.923, 0's: 2 Z-trim: 4 B-trim: 30 in 1/42
Lambda+AD0- 0.217449
Kolmogorov-Smirnov statistic: 0.0250 (N+AD0-28) at 32

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 74 27.4 0.26

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 64 24.5 0.69

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 58 22.6 2.3

gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281)
62 23.7 2.4

gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290)
62 23.7 2.5

gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)
57 22.2 4.9

gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-G1
(204) 57 22.2 5

gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
(284) 57 22.2 7.1

gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 (287)
57 22.2 7.2

gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295)
57 22.2 7.4

gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
53 21.0 7.5

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.0 7.5
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465) 59 22.7 7.9
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.7 8.2
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 51 20.4 9.9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 57 init1: 57 opt: 74 Z-score: 113.0 bits: 27.4 E(): 0.26
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar) in 61 aa overlap (17-77:309-363)

```

                                10      20      30      40
AAD-12      VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                : : : : : : : : : :
gi+AHw-113  HGFFQVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA
            280      290      300      310      320      330

            50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP
            : : : : : : : : : :
gi+AHw-113  ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
            340      350      360      370      380      390
    
```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
 initn: 38 init1: 38 opt: 64 Z-score: 105.3 bits: 24.5 E(): 0.69
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar) in 61 aa overlap (6-64:9-65)

```

                                10      20      30      40      50
AAD-12      VMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                                : : : : : : : : : : : :
gi+AHw-111  MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
            10      20      30      40      50

            60      70      80
AAD-12  LGHVQQAGSAYIGYGMDDTTATPLRP
            : : : : :
gi+AHw-111  LDELNENKSKELQEKI IRELDVVCAMIEGAQ GALERELKRTDLNILERFN YEEAQTL SKI
            60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 init1: 58 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar) in 52 aa overlap (22-73:26-77)

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
 allergen +AFs- (200 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 90.0 bits: 22.2 E(): 4.9
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (23-75:93-149)

```

                10         20         30         40
AAD-12          VMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRLVHQSSARH
                .....:   ::: :: .. .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100        110        120

                50         60         70         80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP
                .. :   .. :   .....:   :   :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130        140        150        160        170        180
  
```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 89.9 bits: 22.2 E(): 5
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (23-75:97-153)

```

                10         20         30         40
AAD-12          VMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRLVHQSSARH
                .....:   ::: :: .. .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100        110        120

                50         60         70         80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP
                .. :   .. :   .....:   :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130        140        150        160        170        180
  
```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
 Full+AD0-Polle (284 aa)
 initn: 34 initl: 34 opt: 57 Z-score: 87.0 bits: 22.2 E(): 7.1
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (6-75:186-267)

```

                10         20         30
AAD-12          VMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                .... .   ....:   .. .....:
gi+AHw-285 QIIDKIDAAFKVAATAAATAPADDKFTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                160        170        180        190        200        210

                40         50         60         70         80
AAD-12 LDEATRLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRP
                :: : . :   ..: . . .....:   ::: .. :   :::
gi+AHw-285 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                220        230        240        250        260        270
  
```

gi+AHw-285 TVAAGGYKV
280

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
5.020 (287 aa)

initn: 34 init1: 34 opt: 57 Z-score: 86.9 bits: 22.2 E(): 7.2
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (6-75:189-270)

```

                                10          20          30
AAD-12          VMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...:   .. ...:
gi+AHw-330 GELQIIDKIDAAFKVAATAAATAPADTVFEAAFNKAIKESTGGAYDITYKCIPSLEAAVKQ
          160          170          180          190          200          210
    
```

```

          40          50          60          70          80
AAD-12 LDEATRNLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRP
          :: : . :   ..: . . . . . . : :   . : : . :   : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          220          230          240          250          260          270
    
```

gi+AHw-330 TVAAGGYKV
280

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)

initn: 34 init1: 34 opt: 57 Z-score: 86.7 bits: 22.2 E(): 7.4
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (6-75:197-278)

```

                                10          20          30
AAD-12          VMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...:   .. ...:
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAKESTGGAYDITYKCIPSLEAAVKQ
          170          180          190          200          210          220
    
```

```

          40          50          60          70          80
AAD-12 LDEATRNLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRP
          :: : . :   ..: . . . . . . : :   . : : . :   : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          230          240          250          260          270          280
    
```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 init1: 38 opt: 53 Z-score: 86.7 bits: 21.0 E(): 7.5
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (6-64:9-65)

```

          10          20          30          40          50
AAD-12          VMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRNLVHQRSARHSLVYSQSK
          : : : : . :   : : :   : : :   : : :   : :
    
```

gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
10 20 30 40 50

60 70 80
AAD-12 LGHVQQAGSAYIGYGMDDTTATPLRP
: :

gi+AHw-420 LDELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
60 70 80 90 100 110

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 86.7 bits: 21.0 E(): 7.5
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (6-64:9-65)

10 20 30 40 50
AAD-12 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
: : : : : . : : : : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
10 20 30 40 50

60 70 80
AAD-12 LGHVQQAGSAYIGYGMDDTTATPLRP
: :

gi+AHw-111 LDELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
60 70 80 90 100 110

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)

initn: 47 initl: 47 opt: 59 Z-score: 86.2 bits: 22.7 E(): 7.9
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (42-79:198-242)

20 30 40 50 60
AAD-12 VVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
: : : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHF FLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
170 180 190 200 210 220

70 80
AAD-12 YIGYGMDT-TATPLRP
. : : . :

gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
230 240 250 260 270 280

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 86.0 bits: 20.7 E(): 8.2
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (24-64:11-50)

10 20 30 40 50
AAD-12 VMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGH
: : : : : : : : .

```

gi+AHw-160          GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQLDE
                   10          20          30          40

                   60          70          80
AAD-12 VQQAGSAYIGYGMDDTTATPLRP
      ... :
gi+AHw-160 L N E N K S K E L Q E K I I R E L D V V C A M I E G A Q G A L E R E L K R T D L N I L E R F N Y E E A Q T L S K I L L K
                   50          60          70          80          90          100
    
```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
 Actinidia de (116 aa)
 initn: 34 initl: 34 opt: 51 Z-score: 84.5 bits: 20.4 E(): 9.9
 Smith-Waterman score: 51+ADs- 28.571+ACU- identity (60.317+ACU- similar)
 in 63 aa overlap (6-66:19-80)

```

                   10          20          30          40
AAD-12          VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                   :: ... . :::: . . .: . . : : . : :...:
gi+AHw-408 M V P K P L S L L L F L L L A L S A A V V G G R K L V A A G G W R P I E S L N S A - E V Q D V A Q F A V S E H N K Q A N
                   10          20          30          40          50

                   50          60          70          80
AAD-12 H S L V Y S Q S K L G H V Q Q - A G S A Y I G Y G M D T T A T P L R P
      : ... :...: :... :
gi+AHw-408 D E L Q Y Q S V V R G Y T Q V V A G T N Y R L V I A A K D G A V V G N Y E A V V W D K P W M H F R N L T S F R K V
                   60          70          80          90          100          110
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:06 2010 done: Fri Feb 5 12:56:06 2010
 Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 118 - 197 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
    
```



```

 94      1      1:+ACo-      :+ACo-
 96      2      1:+ACo-      :+ACoAPQ-
 98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     1      0:+AD0-      +ACoAPQ-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     1      0:+AD0-      +ACoAPQ-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120  0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.14520.00342+ADs- mu+AD0- 6.0269
0.177
mean+AF8-var+AD0-35.2009 9.134, 0's: 2 Z-trim: 4 B-trim: 30 in 1/42
Lambda+AD0- 0.216171
Kolmogorov-Smirnov statistic: 0.0250 (N+AD0-28) at 32

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  74 27.4    0.27
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  64 24.4    0.69
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 22.6    2.3
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 ( 281)
62 23.7    2.4
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 ( 290)
62 23.7    2.5
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.2    4.9
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.2    5
gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
( 284)  57 22.1    7.2
gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 ( 287)
57 22.1    7.3
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.0    7.5
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  53 21.0    7.5
gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 ( 295)
57 22.1    7.6
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 20.7    8.1
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)  59 22.7    8.1

```

gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 51 20.4 9.8

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
initn: 57 initl: 57 opt: 74 Z-score: 112.7 bits: 27.4 E(): 0.27
Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
in 61 aa overlap (16-76:309-363)

MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
gi+AHw-113 HGFFQVNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
280 290 300 310 320 330

HSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPL
ESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
340 350 360 370 380 390

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
initn: 38 initl: 38 opt: 64 Z-score: 105.2 bits: 24.4 E(): 0.69
Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (5-63:9-65)

MAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
10 20 30 40 50

LGHVQQAGSAYIGYMDTTATPLRPL
LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
60 70 80 90 100 110

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
initn: 58 initl: 58 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (21-72:26-77)

MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQVSTKHSVPDVLAFKVVN
10 20 30 40 50 60


```

                10      20      30      40
AAD-12      MAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATR1ALVHQ2SARH
                . . . . .      . . . . .
gi+AHw-144 AISRYL1GKQ2FGLSGKDDWENLEIDMIVDTISDFRAA3IANYHYDA-DEN4SKQ5KKWDPLKKE
                70      80      90      100      110      120

```

```

                50      60      70      80
AAD-12 SLVYSQSKLGHVQ1QAGSAYIGYGM2TTATPLRPL
                . . : . . . : . . . . . : : :
gi+AHw-144 TIPYYTKKFDE1VVKANGGYLAAGKLTWADFYFVA2ILDYLNHMAKEDLVANQP3NLKALREK
                130      140      150      160      170      180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 init1: 41 opt: 57 Z-score: 89.8 bits: 22.2 E(): 5
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (22-74:97-153)

```

                10      20      30      40
AAD-12      MAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATR1ALVHQ2SARH
                . . . . .      . . . . .
gi+AHw-622 AISRYL1GKQ2FGLSGKDDWENLEIDMIVDTISDFRAA3IANYHYDA-DEN4SKQ5KKWDPLKKE
                70      80      90      100      110      120

```

```

                50      60      70      80
AAD-12 SLVYSQSKLGHVQ1QAGSAYIGYGM2TTATPLRPL
                . . : . . . : . . . . . : : :
gi+AHw-622 TIPYYTKKFDE1VVKANGGYLAAGKLTWADFYFVA2ILDYLNHMAKEDLVANQP3NLKALREK
                130      140      150      160      170      180

```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
 Full+AD0-Polle (284 aa)
 initn: 34 init1: 34 opt: 57 Z-score: 86.9 bits: 22.1 E(): 7.2
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (5-74:186-267)

```

                10      20      30
AAD-12      MAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                . . . . .      . . . . .
gi+AHw-285 QIIDKIDAAFKVAATAAATAPAD1DKFTVF2EAAFNKAIKESTGGAYD3TYKCIPSLEAAV4KQ
                160      170      180      190      200      210

```

```

                40      50      60      70      80
AAD-12 LDEATR1ALVHQ-----RSARHSLVYSQSKLGHVQ2Q--AGSAYIGYGM3TTATPLRPL
                . . : . . : . . . . . : . . : . . :
gi+AHw-285 AYAATVAAAPQ1VKYAVFEAALTKAITAMSEVQ2KVSPATGAATVAAGAATTAAGAASGAA
                220      230      240      250      260      270

```

gi+AHw-285 TVAAGGYKV
 280

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
 5.020 (287 aa)
 initn: 34 init1: 34 opt: 57 Z-score: 86.8 bits: 22.1 E(): 7.3

Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (5-74:189-270)

```

                                10          20          30
AAD-12          MAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                   :... . ...:      .. ...:
gi+AHw-330 GELQIIDKIDAAFKVAATAAATAPADTVFEAAFNKAIKESTGGAYDITYKCIPSLEAAVKQ
           160      170      180      190      200      210
    
```

```

                   40          50          60          70          80
AAD-12 LDEATRVLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPL
                   :: : . :      ..: . . .... :...: .. : :::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
           220      230      240      250      260      270
    
```

gi+AHw-330 TVAAGGYKV
280

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 86.7 bits: 21.0 E(): 7.5
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (5-63:9-65)

```

                                10          20          30          40          50
AAD-12          MAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRVLVHQRSARHSLVYSQSK
                   : ::: : . :      :: : : : .....: .....: : .
gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
           10          20          30          40          50
    
```

```

                   60          70          80
AAD-12 LGHVQQAGSAYIGYGMDDTTATPLRPL
                   : .... :
gi+AHw-420 LDELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
           60          70          80          90          100          110
    
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 86.7 bits: 21.0 E(): 7.5
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (5-63:9-65)

```

                                10          20          30          40          50
AAD-12          MAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRVLVHQRSARHSLVYSQSK
                   : ::: : . :      :: : : : .....: .....: : .
gi+AHw-111 MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
           10          20          30          40          50
    
```

```

                   60          70          80
AAD-12 LGHVQQAGSAYIGYGMDDTTATPLRPL
                   : .... :
gi+AHw-111 LDELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
           60          70          80          90          100          110
    
```

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)

initn: 34 initl: 34 opt: 57 Z-score: 86.6 bits: 22.1 E(): 7.6
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (5-74:197-278)

```

                                10          20          30
AAD-12          MAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                   :.:. . .: : : : : : : : : :
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
           170          180          190          200          210          220

```

```

                   40          50          60          70          80
AAD-12 LDEATRNLVHQ-----RSARHSLVYSQSKLGHVQ--AGSAYIGYGMDDTATPLRPL
                   :: : . : . : . : . : . : . : . : . : . : . : . : . :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
           230          240          250          260          270          280

```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 86.0 bits: 20.7 E(): 8.1
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (23-63:11-50)

```

                   10          20          30          40          50
AAD-12 MAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRNLVHQRSARHSLVYSQSKLGHV
                   :. : . : : : : : : : : : : : : : : :
gi+AHw-160          GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQLDEL
                   10          20          30          40

```

```

                   60          70          80
AAD-12 QQAGSAYIGYGMDDTATPLRPL
                   .. :
gi+AHw-160 NENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKD
           50          60          70          80          90          100

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)

initn: 47 initl: 47 opt: 59 Z-score: 86.0 bits: 22.7 E(): 8.1
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (41-78:198-242)

```

                   20          30          40          50          60
AAD-12 VVPAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKL-----GHVQQAGSA
                   :. : : : : : : : : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
           170          180          190          200          210          220

```

```

                   70          80
AAD-12 YIGYGMT-TATPLRPL
                   ..... : :

```

gi+AHw-303 VLGFGMDTETARKVVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
 230 240 250 260 270 280

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
 Actinidia de (116 aa)
 initn: 34 initl: 34 opt: 51 Z-score: 84.6 bits: 20.4 E(): 9.8
 Smith-Waterman score: 51+ADs- 28.571+ACU- identity (60.317+ACU- similar)
 in 63 aa overlap (5-65:19-80)

```

                                10      20      30      40
AAD-12      MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
              :: ... . :::: . . .: . . : : :. :...:
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAAGGWRPIESLSA-EVQDVAQFAVSEHNKQAN
              10      20      30      40      50

              50      60      70      80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGMDTTATPLRPL
              : ... :...: ::. :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
              60      70      80      90      100      110
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:06 2010 done: Fri Feb 5 12:56:07 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 119 - 198 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
	22	0	0: one +AD0- represents 3 library sequences
	24	0	0:
	26	4	0:+AD0APQ-
	28	5	0:+AD0APQ-
	30	16	2:+ACoAPQA9AD0APQA9-
	32	10	8:+AD0APQAqAD0-
	34	22	21:+AD0APQA9AD0APQA9ACoAPQ-
	36	33	44:+AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-


```

102      0      0:      +ACo-
104      0      0:      +ACo-
106      1      0:+AD0-      +ACoAPQ-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      1      0:+AD0-      +ACoAPQ-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.19370.00341+ADs- mu+AD0- 5.3399
0.177
mean+AF8-var+AD0-34.2961 8.821, 0's: 2 Z-trim: 4 B-trim: 30 in 1/42
Lambda+AD0- 0.219004
Kolmogorov-Smirnov statistic: 0.0333 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 74 27.7 0.22
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 64 24.7 0.57
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 58 22.8 1.9
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 ( 281)
62 23.9 2.1
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 ( 290)
62 23.9 2.1
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.4 4.2
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204) 57 22.4 4.3
gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
( 284) 57 22.4 6.2
gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 ( 287)
57 22.4 6.3
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.2 6.4
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 53 21.2 6.4
gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 ( 295)
57 22.3 6.5
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 20.9 6.9
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465) 59 22.9 7
gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (
116) 51 20.6 8.4
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 20.9 9.1

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 57 init1: 57 opt: 74 Z-score: 114.2 bits: 27.7 E(): 0.22
Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
in 61 aa overlap (15-75:309-363)

```

                                10      20      30      40
AAD-12      AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                :.: : :.: .: .: :.:
gi+AHw-113  HGFFQVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
              280      290      300      310      320      330

```

```

                    50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLV
          :.: .: .: .: .: .: .: .: .: .: .:
gi+AHw-113  ESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
              340      350      360      370      380      390

```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 init1: 38 opt: 64 Z-score: 106.7 bits: 24.7 E(): 0.57
Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (4-62:9-65)

```

                                10      20      30      40      50
AAD-12      AQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                                :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi+AHw-111  MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
              10      20      30      40      50

```

```

                    60      70      80
AAD-12  LGHVQQAGSAYIGYGMDDTATPLRPLV
          :.: .: .: .: .: .: .: .: .: .: .:
gi+AHw-111  LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 init1: 58 opt: 58 Z-score: 97.4 bits: 22.8 E(): 1.9
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (20-71:26-77)

```

                                10      20      30      40      50
AAD-12      AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                :.: :.: :.: :.: :.: :.: :.:
gi+AHw-527  MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQVSTKHSVPDVLAFKVN
              10      20      30      40      50      60

```

```

                    60      70      80
AAD-12  GHVQQAGSAYIGYGMDDTATPLRPLV

```

```

      ::::: :  : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAAEKLGGLAQKRVAG
              70          80          90          100          110          120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
+AFs-Phl (281 aa)
initn: 39 initl: 39 opt: 62 Z-score: 96.7 bits: 23.9 E(): 2.1
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (4-74:183-265)

```

                                10          20
AAD-12                        AQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                ::. . .:::  :. ....:
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPSLEAAVKQ
              160          170          180          190          200          210

```

```

      30          40          50          60          70          80
AAD-12 LDEATRVLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLV
      :: : . :      ..: . . . . . .::: .::: . . :  ::::
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
              220          230          240          250          260          270

```

gi+AHw-168 TVAAGGYKV
280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
5.020 (290 aa)
initn: 39 initl: 39 opt: 62 Z-score: 96.5 bits: 23.9 E(): 2.1
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (4-74:192-274)

```

                                10          20
AAD-12                        AQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                ::. . .:::  :. ....:
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPSLEAAVKQ
              170          180          190          200          210          220

```

```

      30          40          50          60          70          80
AAD-12 LDEATRVLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLV
      :: : . :      ..: . . . . . .::: .::: . . :  ::::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
              230          240          250          260          270          280

```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 91.2 bits: 22.4 E(): 4.2
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (21-73:93-149)

```

                                10          20          30          40
AAD-12                        AQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRVLVHQRSARH

```

```

          . . . . .      : : : : :
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
          70          80          90          100          110          120

```

```

          50          60          70          80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLV
          .. :   .. :   .. :   .. :   .. :   .. :

```

```

gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
          130          140          150          160          170          180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 init1: 41 opt: 57 Z-score: 91.0 bits: 22.4 E(): 4.3
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (21-73:97-153)

```

          10          20          30          40
AAD-12          AQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATR LVHQRSARH
          . . . . .      : : : : :
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
          70          80          90          100          110          120

```

```

          50          60          70          80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLV
          .. :   .. :   .. :   .. :   .. :   .. :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
          130          140          150          160          170          180

```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
Full+AD0-Polle (284 aa)
initn: 34 init1: 34 opt: 57 Z-score: 88.1 bits: 22.4 E(): 6.2
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (4-73:186-267)

```

          10          20
AAD-12          AQGAVFSAEVVPAVGG----RTCFADMRAAYDA
          . . . . .      : : : : :
gi+AHw-285 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYD TYKCIPSLEAAVKQ
          160          170          180          190          200          210

```

```

          30          40          50          60          70          80
AAD-12  LDEATR LVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPLV
          :: :   . :   .. :   . . . . .      : : : : :
gi+AHw-285 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          220          230          240          250          260          270

```

```

gi+AHw-285 TVAAGGYKV
          280

```

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
5.020 (287 aa)
initn: 34 init1: 34 opt: 57 Z-score: 88.0 bits: 22.4 E(): 6.3
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (4-73:189-270)

```

                                10          20
AAD-12          AQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                   :... . ...:   :. ....:
gi+AHw-330 GELQIIDKIDAAFKVAATAAATAPADTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          160      170      180      190      200      210
    
```

```

          30      40          50          60      70      80
AAD-12 LDEATRVLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTATPLRPLV
          :: : . :          ..: . . ....: ...: .. : :::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          220      230      240      250      260      270
    
```

gi+AHw-330 TVAAGGYKV
280

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)
initn: 38 init1: 38 opt: 53 Z-score: 87.9 bits: 21.2 E(): 6.4
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (4-62:9-65)

```

                                10      20      30      40      50
AAD-12          AQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRVLVHQRSARHSLVYSQSK
                   : :: : . : .      :: : : .....: .....: : .
gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
          10      20      30      40      50
    
```

```

          60      70      80
AAD-12 LGHVQQAGSAYIGYGMDDTATPLRPLV
          : .... :
gi+AHw-420 LDELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEAAQTLSKI
          60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
initn: 38 init1: 38 opt: 53 Z-score: 87.9 bits: 21.2 E(): 6.4
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (4-62:9-65)

```

                                10      20      30      40      50
AAD-12          AQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRVLVHQRSARHSLVYSQSK
                   : :: : . : .      :: : : .....: .....: : .
gi+AHw-111 MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
          10      20      30      40      50
    
```

```

          60      70      80
AAD-12 LGHVQQAGSAYIGYGMDDTATPLRPLV
          : .... :
gi+AHw-111 LDELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEAAQTLSKI
          60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5.020 (295 aa)

initn: 34 initl: 34 opt: 57 Z-score: 87.8 bits: 22.3 E(): 6.5
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (4-73:197-278)

```

                                10          20
AAD-12          AQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...: .. ...:
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDITYKCIPSLEAAVKQ
              170          180          190          200          210          220

              30          40          50          60          70          80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPLV
              :: : . :          ..: . . .... :...: .. : :::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
              230          240          250          260          270          280

gi+AHw-330 TVAAGGYKV
              290

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.3 bits: 20.9 E(): 6.9
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (22-62:11-50)

```

              10          20          30          40          50
AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQ
              :: : : .....: .....: : : ...
gi+AHw-160          GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDLDELN
              10          20          30          40

              60          70          80
AAD-12 QAGSAYIGYGMDDTTATPLRPLV
              . :
gi+AHw-160 ENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNIEEAQTLKILLKDL
              50          60          70          80          90          100

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)

initn: 47 initl: 47 opt: 59 Z-score: 87.2 bits: 22.9 E(): 7
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (40-77:198-242)

```

              10          20          30          40          50          60
AAD-12 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
              :... :... :... :          : ...
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
              170          180          190          200          210          220

              70          80
AAD-12 YIGYGMT-TATPLRPLV
              .....: : :
gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
              230          240          250          260          270          280

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
 Actinidia de (116 aa)
 initn: 34 initl: 34 opt: 51 Z-score: 85.8 bits: 20.6 E(): 8.4
 Smith-Waterman score: 51+ADs- 28.571+ACU- identity (60.317+ACU- similar)
 in 63 aa overlap (4-64:19-80)

```

                                10      20      30      40
AAD-12      A Q G A V F S A E V V P A V G G R T C F A D M R A A Y D A L D E A T R A L V - H Q R S A R
              :: ... . :::: . . .: . . : : : . : : : :
gi+AHw-408  M V P K P L S L L L F L L L A L S A A V V G G R K L V A A G G W R P I E S L N S A - E V Q D V A Q F A V S E H N K Q A N
              10      20      30      40      50
  
```

```

                    50      60      70      80
AAD-12  H S L V Y S Q S K L G H V Q Q - A G S A Y I G Y G M D T T A T P L R P L V
          : : . . : . : : : . : . :
gi+AHw-408  D E L Q Y Q S V V R G Y T Q V V A G T N Y R L V I A A K D G A V V G N Y E A V V W D K P W M H F R N L T S F R K V
          60      70      80      90      100      110
  
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 85.1 bits: 20.9 E(): 9.1
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (27-50:29-52)

```

                                10      20      30      40      50
AAD-12      A Q G A V F S A E V V P A V G G R T C F A D M R A A Y D A L D E A T R A L V H Q R S A R H S L V Y S Q S K L G H V Q
              : : :: : : . . .: . : : :
gi+AHw-144  K T N K I V I T N D K G R L S K E E I E R M L A E A E K Y K A E D E A E A A R I S A K N A L E S Y A Y S L R N T L S D S
              10      20      30      40      50      60
  
```

```

                    60      70      80
AAD-12  Q A G S A Y I G Y G M D T T A T P L R P L V
gi+AHw-144  K V D E K L D A G D K Q K L T A E I D K T V Q W L D D N Q T A T K D E Y E S Q Q K E L E G V A N P I M M K F Y G A G G E
              70      80      90      100      110      120
  
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:08 2010 done: Fri Feb 5 12:56:08 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

84      1      3:+ACo-
86      2      2:+ACo-
88      6      2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      1      1:+ACo-
92      1      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      3      1:+ACo-          :+ACoAPQA9-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     1      0:+AD0-          +ACoAPQ-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     1      0:+AD0-          +ACoAPQ-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120 0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.21610.00345+ADs- mu+AD0- 4.7967
0.179
mean+AF8-var+AD0-35.3882 8.775, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.215598
Kolmogorov-Smirnov statistic: 0.0556 (N+AD0-29) at 46

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  74 27.6    0.23
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   64 24.7    0.58
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 22.8    1.9
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 ( 281)
62 23.9    2.1
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 ( 290)
62 23.9    2.1
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.4    4.1
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-G1
( 204)  57 22.4    4.2
gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
( 284)  57 22.4    6.1
gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 ( 287)
57 22.4    6.2
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.3    6.2
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   53 21.3    6.2

```

gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295)
 57 22.4 6.4
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 21.0 6.8
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 22.9 6.9
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116)
 51 20.7 8.2
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152)
 52 20.9 8.9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 57 initl: 57 opt: 74 Z-score: 113.9 bits: 27.6 E(): 0.23
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (14-74:309-363)

```

                                10      20      30      40
AAD-12      QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                : : : : : : : : : :
gi+AHw-113  HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA
            280      290      300      310      320      330

                    50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVK
            : : : : : : : : : :
gi+AHw-113  ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
            340      350      360      370      380      390
    
```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 106.6 bits: 24.7 E(): 0.58
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (3-61:9-65)

```

                                10      20      30      40      50
AAD-12      QGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                                : : : : : : : : : :
gi+AHw-111  MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
            10      20      30      40      50

                    60      70      80
AAD-12  LGHVQQAGSAYIGYGMDDTTATPLRPLVK
            : : : : :
gi+AHw-111  LDELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
            60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 97.4 bits: 22.8 E(): 1.9

Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (19-70:26-77)

```

                10         20         30         40         50
AAD-12      QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                :::         :. . . :     . . . :     . . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVN
                10         20         30         40         50         60

                60         70         80
AAD-12      GHVQQAGSAYIGYGMDDTTATPLRPLVK
                ::::: . . :     . : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAAEKLGGLAQKRVAG
                70         80         90         100        110        120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
+AFs-Phl (281 aa)

initn: 39 init1: 39 opt: 62 Z-score: 96.7 bits: 23.9 E(): 2.1
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (3-73:183-265)

```

                                10         20
AAD-12      QGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :. . . . :     :. . . . :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                160        170        180        190        200        210

                30         40         50         60         70         80
AAD-12      LDEATRALVHQ-----RSARHSLVYSQSKLGHVQO--AGSAYIGYGMDDTTATPLRPLVK
                :: : . :     . : : . . . . . :     . : : . . :     : : :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                220        230        240        250        260        270

gi+AHw-168 TVAAGGYKV
                280

```

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
5.020 (290 aa)

initn: 39 init1: 39 opt: 62 Z-score: 96.4 bits: 23.9 E(): 2.1
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (3-73:192-274)

```

                                10         20
AAD-12      QGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :. . . . :     :. . . . :
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                170        180        190        200        210        220

                30         40         50         60         70         80
AAD-12      LDEATRALVHQ-----RSARHSLVYSQSKLGHVQO--AGSAYIGYGMDDTTATPLRPLVK
                :: : . :     . : : . . . . . :     . : : . . :     : : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                230        240        250        260        270        280

```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 init1: 41 opt: 57 Z-score: 91.3 bits: 22.4 E(): 4.1
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (20-72:93-149)

```

                                10      20      30      40
AAD-12      QGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRLVHQSARH
                                .....:   ::: :: .. . ..
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                                70      80      90      100     110     120

                                50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVK
.. :   .. :   .....:   :   :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180
```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 init1: 41 opt: 57 Z-score: 91.1 bits: 22.4 E(): 4.2
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (20-72:97-153)

```

                                10      20      30      40
AAD-12      QGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRLVHQSARH
                                .....:   ::: :: .. . ..
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                                70      80      90      100     110     120

                                50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVK
.. :   .. :   .....:   :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180
```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
Full+AD0-Polle (284 aa)
initn: 34 init1: 34 opt: 57 Z-score: 88.2 bits: 22.4 E(): 6.1
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (3-72:186-267)

```

                                10      20
AAD-12      QGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... .   :::   :. ....:
gi+AHw-285 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                                160     170     180     190     200     210

                                30      40      50      60      70      80
AAD-12 LDEATRLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPLVK
                                :: : . :   ... . . .... :... :... : . :   :::
```

gi+AHw-285 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
220 230 240 250 260 270

gi+AHw-285 TVAAGGYKV
280

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
5.020 (287 aa)

initn: 34 initl: 34 opt: 57 Z-score: 88.1 bits: 22.4 E(): 6.2
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (3-72:189-270)

AAD-12 10 20
QGAVFSAEVVPAVGG----RTCFADMRAAYDA
:.: . .: .: .:
gi+AHw-330 GELQIIDKIDAAFKVAATAAATAPADTVFEAAFNKAIKESTGGAYDITYKCIPLSLEAAVKQ
160 170 180 190 200 210

30 40 50 60 70 80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTATPLRPLVK
:: : . : .: . . .: .: .: .:
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
220 230 240 250 260 270

gi+AHw-330 TVAAGGYKV
280

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 88.1 bits: 21.3 E(): 6.2
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (3-61:9-65)

AAD-12 10 20 30 40 50
QGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
10 20 30 40 50

60 70 80
AAD-12 LGHVQQAGSAYIGYGMDDTATPLRPLVK
: .: .:
gi+AHw-420 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
60 70 80 90 100 110

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 88.1 bits: 21.3 E(): 6.2
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (3-61:9-65)

AAD-12 10 20 30 40 50
QGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
: .: .: .: .: .: .: .: .: .: .: .: .:


```

      10      20      30      40      50      60
AAD-12 VVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKL-----GHVQQAGSA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHF FLA GNIQRSQKQ RGER YGLRGGQQILADNVFKGFNMEALAD
      170      180      190      200      210      220

```

```

      70      80
AAD-12 YIGYGMDT-TATPLRPLVK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-303 VLGF GMDTETARKV RGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230      240      250      260      270      280

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)
initn: 34 initl: 34 opt: 51 Z-score: 86.0 bits: 20.7 E(): 8.2
Smith-Waterman score: 51+ADs- 28.571+ACU- identity (60.317+ACU- similar)
in 63 aa overlap (3-63:19-80)

```

      10      20      30      40
AAD-12 QGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRVLV-HQRSAR
      : : . . . : : : . . : : . : : : : : : : : : : : : : : :
gi+AHw-408 MVPKPLSLLLFLLLLALSAAVVGGRKLV AAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGMDTTATPLRPLVK
      : : . : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGN YEAVVWDKPMHFRNLTSFRKV
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 85.3 bits: 20.9 E(): 8.9
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (26-49:29-52)

```

      10      20      30      40      50
AAD-12 QGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKLGHVQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
      10      20      30      40      50      60

```

```

      60      70      80
AAD-12 QAGSAYIGYGMDTTATPLRPLVK
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTQVWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
      70      80      90      100      110      120

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:08 2010 done: Fri Feb 5 12:56:09 2010

56 82
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0-
58 60
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
60 67
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
62 62 40:+AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
64 23 32:+AD0APQA9AD0APQA9AD0APQ- +ACo-
66 26 25:+AD0APQA9AD0APQA9AD0APQAq-
68 18 20:+AD0APQA9AD0APQA9ACo-
70 16 16:+AD0APQA9AD0APQAq-
72 5 12:+AD0APQ- +ACo-
74 9 10:+AD0APQA9ACo-
76 8 7:+AD0APQAq-
78 2 6:+AD0AKg-
80 4 4:+AD0AKg-
82 6 3:+ACoAPQ-
84 1 3:+ACo-
86 3 2:+ACo-
88 5 2:+ACoAPQ- inset +AD0- represents 1 library
sequences
90 2 1:+ACo-
92 0 1:+ACo- :+ACo-
94 0 1:+ACo- :+ACo-
96 3 1:+ACo- :+ACoAPQA9-
98 0 0: +ACo-
100 0 0: +ACo-
102 0 0: +ACo-
104 0 0: +ACo-
106 1 0:+AD0- +ACoAPQ-
108 0 0: +ACo-
110 0 0: +ACo-
112 1 0:+AD0- +ACoAPQ-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.08520.00338+ADs- mu+AD0- 5.5129
0.175
mean+AF8-var+AD0-35.8947 9.001, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.214072
Kolmogorov-Smirnov statistic: 0.0474 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are: opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 74 27.5 0.24

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 64 24.6 0.62
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T (121) 58 22.8 2
 gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281) 62 23.9 2.1
 gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290) 62 23.9 2.2
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200) 57 22.4 4.3
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl (204) 57 22.4 4.4
 gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P (284) 57 22.3 6.3
 gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 (287) 57 22.3 6.4
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.2 6.6
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.2 6.6
 gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295) 57 22.3 6.6
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465) 59 22.9 7
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.9 7.2
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 51 20.6 8.6
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 20.9 9.3

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 57 initl: 57 opt: 74 Z-score: 113.5 bits: 27.5 E(): 0.24
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (13-73:309-363)

			10	20	30	40
AAD-12			GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR			
			:: :	: :	.. :	: .. :
gi+AHw-113	HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA					
	280 290 300 310 320 330					
		50	60	70	80	
AAD-12	HSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKV					
		.. .	: . :	... :	:: . :	
gi+AHw-113	ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAE PGESALS LTSSAGVLSQCP					
	340 350 360 370 380 390					

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)

initn: 38 initl: 38 opt: 64 Z-score: 106.0 bits: 24.6 E(): 0.62
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (2-60:9-65)

```

                10      20      30      40      50
AAD-12      GAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                : : : : . : : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                10      20      30      40      50

                60      70      80
AAD-12 LGHVQQAGSAYIGYGMDDTTATPLRPLVKV
                : : : : :
gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
                60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 96.9 bits: 22.8 E(): 2
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (18-69:26-77)

```

                10      20      30      40      50
AAD-12      GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                : : : : : : : : : : : : : : : : : :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAIPVYEQNSTKHSVPDVLAFQVNV
                10      20      30      40      50      60

                60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKV
                : : : : : : : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGLAQKRVAG
                70      80      90      100      110      120
    
```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
 +AFs-Phl (281 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 96.4 bits: 23.9 E(): 2.1
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (2-72:183-265)

```

                                10      20
AAD-12      GAVFSAEVVPAVGG----RTCFADMRAAYDA
                                : : : . : : : : : : : : :
gi+AHw-168 QIIDKIDAAFVVAATAAATAPADDKFTVFEAAFNKAIKESTGGAYDXYKCIPLSLEAAVKQ
                160      170      180      190      200      210

                30      40      50      60      70
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPLVK
                : : : . : : : . . . . . : : : : : : : : : :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                220      230      240      250      260      270
    
```

80
 AAD-12 V

gi+AHw-168 TVAAGGYKV
280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
5.020 (290 aa)

initn: 39 init1: 39 opt: 62 Z-score: 96.2 bits: 23.9 E(): 2.2
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (2-72:192-274)

```

                                10          20
AAD-12                        GAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...:   :. ....:
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                170          180          190          200          210          220

```

```

                30          40          50          60          70
AAD-12 LDEATRVLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLVK
                :: : . :   ..: . . .... :.: :.: . . :   :::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                230          240          250          260          270          280

```

80
AAD-12 V

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)

initn: 41 init1: 41 opt: 57 Z-score: 91.0 bits: 22.4 E(): 4.3
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (19-71:93-149)

```

                                10          20          30          40
AAD-12                        GAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRVLVHQRSARH
                                .....:   ::: :. . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKQKWDPLKKE
                70          80          90          100          110          120

```

```

                50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKV
                .. :   .. :   ..... :   : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130          140          150          160          170          180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)

initn: 41 init1: 41 opt: 57 Z-score: 90.8 bits: 22.4 E(): 4.4
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (19-71:97-153)

```

                                10          20          30          40
AAD-12                        GAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRVLVHQRSARH

```


gi+AHw-330 TVAAGGYKV
280

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 init1: 38 opt: 53 Z-score: 87.7 bits: 21.2 E(): 6.6
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (2-60:9-65)

	10	20	30	40	50
AAD-12	GAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATR ¹ ALVHQRSARHSLVYSQSK				
	:	:	:	:	:
gi+AHw-420	MKFAIVLIACFAASVL-AQE ¹ HKPKKDDFRNEFDHLLIEQANHAI---EKGEHQ ¹ LLYLQHQ				
	10	20	30	40	50

	60	70	80		
AAD-12	LGHVQQAGSAYIGYGM ¹ DTTATPLRPLVKV				
	:	:	:	:	:
gi+AHw-420	LDELNENKSKELQE ¹ KIIRELDVVCAMIEGAQ ¹ GALERELKRTDLNILERFN ¹ YEEAQ ¹ TLSKI				
	60	70	80	90	100

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 init1: 38 opt: 53 Z-score: 87.7 bits: 21.2 E(): 6.6
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (2-60:9-65)

	10	20	30	40	50
AAD-12	GAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATR ¹ ALVHQRSARHSLVYSQSK				
	:	:	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQE ¹ HKPEKDDFRNEFDHLLIEQANHAI---EKGEHQ ¹ LLYLQHQ				
	10	20	30	40	50

	60	70	80		
AAD-12	LGHVQQAGSAYIGYGM ¹ DTTATPLRPLVKV				
	:	:	:	:	:
gi+AHw-111	LDELNENKSKELQE ¹ KIIRELDVVCAMIEGAQ ¹ GALERELKRTDLNILERFN ¹ YEEAQ ¹ TLSKI				
	60	70	80	90	100

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)
initn: 34 init1: 34 opt: 57 Z-score: 87.7 bits: 22.3 E(): 6.6
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (2-71:197-278)

		10		20	
AAD-12		GAVFSAEVVPAVGG----		RTCFADMRAAYDA	
		:	:	:	:
gi+AHw-330	QI	IDKIDAA	FKVAATAA	ATAPAD	DKFTVF
	170	180	190	200	210

	30	40	50	60	70
AAD-12	LDEATR ¹ ALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGM ¹ DTTATPLRPLVK				


```

      :: . . . . : : : : . . . : . . : : : : : : : : : :
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
      10          20          30          40          50
      50          60          70          80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGMDTTATPLRPLVKV
      : : . . : : : : : : : : : :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMHFRNLTSFRKV
      60          70          80          90          100          110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 init1: 52 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (25-48:29-52)

```

      10          20          30          40          50
AAD-12 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGHVQ
      : : : : : : : . . . : : : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
      10          20          30          40          50          60
      60          70          80
AAD-12 QAGSAYIGYGMDTTATPLRPLVKV
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
      70          80          90          100          110          120

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:10 2010 done: Fri Feb 5 12:56:10 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 122 - 201 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 3 library sequences

```


88 5 2:+ACoAPQ- inset +AD0- represents 1 library
sequences
90 2 1:+ACo-
92 0 1:+ACo- :+ACo-
94 0 1:+ACo- :+ACo-
96 3 1:+ACo- :+ACoAPQA9-
98 0 0: +ACo-
100 0 0: +ACo-
102 0 0: +ACo-
104 0 0: +ACo-
106 1 0:+AD0- +ACoAPQ-
108 0 0: +ACo-
110 0 0: +ACo-
112 1 0:+AD0- +ACoAPQ-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.19250.0032+ADs- mu+AD0- 4.9319
0.166
mean+AF8-var+AD0-35.7991 8.999, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.214357
Kolmogorov-Smirnov statistic: 0.0474 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 74 27.5 0.24
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134)
64 24.6 0.61
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 58 22.8 2
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281)
62 23.9 2.1
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290)
62 23.9 2.2
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)
57 22.4 4.3
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
(204) 57 22.4 4.4
gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
(284) 57 22.3 6.3
gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 (287)
57 22.3 6.4
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
53 21.2 6.5
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
53 21.2 6.5
gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295)
57 22.3 6.6

gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 20.9 7
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 22.9 7.1
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116)
 51 20.6 8.4
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152)
 52 20.9 9.2

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 57 init1: 57 opt: 74 Z-score: 113.5 bits: 27.5 E(): 0.24
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (12-72:309-363)

```

                                10      20      30      40
AAD-12      AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                : : : : . . . . : : :
gi+AHw-113  HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA
            280      290      300      310      320      330
    
```

```

                    50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVH
            : . . : . : . . . : : . : :
gi+AHw-113  ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
            340      350      360      370      380      390
    
```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
 initn: 38 init1: 38 opt: 64 Z-score: 106.2 bits: 24.6 E(): 0.61
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (1-59:9-65)

```

                                10      20      30      40      50
AAD-12      AVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                                : : : : . : . : : : : : : : : : :
gi+AHw-111  MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
            10      20      30      40      50
    
```

```

                    60      70      80
AAD-12  LGHVQQAGSAYIGYGMDDTTATPLRPLVKVH
            : . . . :
gi+AHw-111  LDELNENKSKELQEKI IRELDVVCAMIEGAQ GALERELKRTDLNILERFN YEEAQTL SKI
            60      70      80      90      100      110
    
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 init1: 58 opt: 58 Z-score: 97.1 bits: 22.8 E(): 2
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (17-68:26-77)

```

                10      20      30      40      50
AAD-12      AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                :::      :. . . : . . . : . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVN
                10      20      30      40      50      60

```

```

                60      70      80
AAD-12      GHVQQAGSAYIGYGMDDTATPLRPLVKVH
                : . . . . : . : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AEKLGGLAQKRVAG
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 +AFs-Phl (281 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 96.4 bits: 23.9 E(): 2.1
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (1-71:183-265)

```

                                10      20
AAD-12      AVFSAEVVPAVGG----RTCFADMRAAYDA
                                : . . . : . . . :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYD TYKCIPSLEAAVKQ
                160      170      180      190      200      210

```

```

                30      40      50      60      70
AAD-12      LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTATPLRPLVK
                : : . . : . : . . . . . : : : . . : : :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                220      230      240      250      260      270

```

```

                80
AAD-12      VH
gi+AHw-168 TVAAGGYKV
                280

```

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5.020 (290 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 96.2 bits: 23.9 E(): 2.2
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (1-71:192-274)

```

                                10      20
AAD-12      AVFSAEVVPAVGG----RTCFADMRAAYDA
                                : . . . : . . . :
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYD TYKCIPSLEAAVKQ
                170      180      190      200      210      220

```

```

                30      40      50      60      70
AAD-12      LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTATPLRPLVK
                : : . . : . : . . . . . : : : . . : : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                230      240      250      260      270      280

```

80
AAD-12 VH

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 init1: 41 opt: 57 Z-score: 91.0 bits: 22.4 E(): 4.3
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (18-70:93-149)

	10	20	30	40
AAD-12	AVFSAEVVPAVGGRTCFADMRAA-----YDALDEATR ^L VHQ ^S SARH			
		::: ::
gi+AHw-144	AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIA ^N YHYDA-DENSKQ ^K KWDPLKKE			
	70	80	90	100
	110	120		
	50	60	70	80
AAD-12	SLVYSQSKLGHVQ ^Q AGSAYIGYGMTTATPLRPLVKVH			
	.. :	... : :	: :
gi+AHw-144	TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAI ^L DYLNHMAKEDLVANQP ^N LKALREK			
	130	140	150	160
	170	180		

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 init1: 41 opt: 57 Z-score: 90.9 bits: 22.4 E(): 4.4
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (18-70:97-153)

	10	20	30	40
AAD-12	AVFSAEVVPAVGGRTCFADMRAA-----YDALDEATR ^L VHQ ^S SARH			
		::: ::
gi+AHw-622	AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIA ^N YHYDA-DENSKQ ^K KWDPLKKE			
	70	80	90	100
	110	120		
	50	60	70	80
AAD-12	SLVYSQSKLGHVQ ^Q AGSAYIGYGMTTATPLRPLVKVH			
	.. :	... : :	: :
gi+AHw-622	TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAI ^L DYLNHMAKEDLVANQP ^N LKALREK			
	130	140	150	160
	170	180		

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
Full+AD0-Polle (284 aa)
initn: 34 init1: 34 opt: 57 Z-score: 88.0 bits: 22.3 E(): 6.3
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (1-70:186-267)

	10	20
AAD-12	AVFSAEVVPAVGG----RTCFADMRAAYDA	

gi+AHw-285	QIIDKIDAAFKVAATAAATAPADDKFTVF ^E AAFNKAIKESTGGAYD ^T YKCI ^P SLEAAVKQ	
	160	170
	180	190
	200	210

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 init1: 38 opt: 53 Z-score: 87.8 bits: 21.2 E(): 6.5
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (1-59:9-65)

```

                10         20         30         40         50
AAD-12          AVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                : : : : . : : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQECHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                10         20         30         40         50

                60         70         80
AAD-12 LGHVQQAGSAYIGYGMDDTATPLRPLVKVH
                : : : : :
gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)
initn: 34 init1: 34 opt: 57 Z-score: 87.7 bits: 22.3 E(): 6.6
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (1-70:197-278)

```

                                10         20
AAD-12                          AVFSAEVVPAVGG----RTCFADMRAAYDA
                                : : . : : : : : : : : : : :
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDITYKIPSLEAAVKQ
                170         180         190         200         210         220

                30         40         50         60         70
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTATPLRPLVK
                : : : . : : : : : : : : : : : : : : : : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                230         240         250         260         270         280

                80
AAD-12 VH

gi+AHw-330 TVAAGGYKV
                290

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.2 bits: 20.9 E(): 7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (19-59:11-50)

```

                10         20         30         40         50
AAD-12 AVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAG
                : : : : : : : : : : : : : : : : : :
gi+AHw-160          GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDDELNENK
                10         20         30         40

```

```

      60      70      80
AAD-12 SAYIGYGMDDTTATPLRPLVKVH
      :
gi+AHw-160 SKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKILLKDLKET
      50      60      70      80      90      100

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 87.1 bits: 22.9 E(): 7.1
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (37-74:198-242)

```

      10      20      30      40      50      60
AAD-12 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
      : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNPRHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
      170      180      190      200      210      220

```

```

      70      80
AAD-12 YIGYGMDDTTATPLRPLVKVH
      : : : : : :
gi+AHw-303 VLGFGMDTETARKVVRGEGDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230      240      250      260      270      280

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
 Actinidia de (116 aa)
 initn: 34 initl: 34 opt: 51 Z-score: 85.7 bits: 20.6 E(): 8.4
 Smith-Waterman score: 51+ADs- 28.571+ACU- identity (60.317+ACU- similar)
 in 63 aa overlap (1-61:19-80)

```

      10      20      30      40
AAD-12 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
      : : . . . : : : . . . : : : : : : : : :
gi+AHw-408 MVPKPLSLLLFLLLLALSAAVVGGRKLVAAAGWRPIESLSNSA-EVQDVAQFAVSEHNKQAN
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGMDDTTATPLRPLVKVH
      : : . : : : : :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMWFRNLTSFRKV
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 85.1 bits: 20.9 E(): 9.2
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (24-47:29-52)

```

      10      20      30      40      50
AAD-12 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
      : : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
      10      20      30      40      50      60

```


FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 74 27.5 0.25

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134)
60 23.4 1.4

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 58 22.9 1.9

gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)
57 22.5 4

gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
(204) 57 22.5 4.1

gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281)
57 22.4 5.9

gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290)
57 22.4 6.1

gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
52 21.0 6.5

gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
59 22.9 6.8

gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
52 21.0 7.4

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
52 21.0 7.4

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
(152) 52 21.0 8.5

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 57 init1: 57 opt: 74 Z-score: 113.3 bits: 27.5 E(): 0.25
Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
in 61 aa overlap (11-71:309-363)

```

                                10      20      30      40
AAD-12      VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                :: : : : : : : : :
gi+AHw-113  HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA
                280      290      300      310      320      330
    
```

```

                                50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP
                .. . : . : . . . : : . : :
gi+AHw-113  ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSQCP
                340      350      360      370      380      390
    
```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 init1: 38 opt: 60 Z-score: 99.8 bits: 23.4 E(): 1.4
 Smith-Waterman score: 60+ADs- 28.814+ACU- identity (64.407+ACU- similar)
 in 59 aa overlap (2-58:11-65)

```

                10      20      30      40
AAD-12      VFSAEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                ::: . . . . . ::: . . . . . : . . . . . : . . . . . : . . . . .
gi+AHw-111 MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                10      20      30      40      50

                50      60      70      80
AAD-12 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHP
                : . . . . :
gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)

initn: 58 init1: 58 opt: 58 Z-score: 97.5 bits: 22.9 E(): 1.9
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (16-67:26-77)

```

                10      20      30      40      50
AAD-12      VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                ::: . . . . . : . . . . . : . . . . . : . . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAIPVYEQQLSTKHSVPDVLAFAKVVN
                10      20      30      40      50      60

                60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHP
                ::: . . . . : . . . . :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQKRVAG
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
 allergen +AFs- (200 aa)

initn: 41 init1: 41 opt: 57 Z-score: 91.5 bits: 22.5 E(): 4
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (17-69:93-149)

```

                10      20      30      40
AAD-12      VFSAEVVPVAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                . . . . . : . . . . . : . . . . . : . . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70      80      90      100      110      120

                50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHP
                .. : . . . . : . . . . . : . . . . . : . . . . .
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130      140      150      160      170      180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)

initn: 41 initl: 41 opt: 57 Z-score: 91.3 bits: 22.5 E(): 4.1
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (17-69:97-153)

```

                                10      20      30      40
AAD-12      VFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                .....:   ::: :: .. . ..
gi+AHw-622  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
              70      80      90      100     110     120

```

```

                    50      60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP
          .. :   .. : . : ..... : : :
gi+AHw-622  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
            130     140     150     160     170     180

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
 +AFs-Phl (281 aa)

initn: 39 initl: 39 opt: 57 Z-score: 88.5 bits: 22.4 E(): 5.9
 Smith-Waterman score: 57+ADs- 25.926+ACU- identity (54.321+ACU- similar)
 in 81 aa overlap (2-70:185-265)

```

                                10      20
AAD-12      VFSAEVVPAVGG----RTCFADMRAAYDALD
                                .. . ....:   .. .....:
gi+AHw-168  IDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYD TYKCIPSLEAAVKQAY
            160     170     180     190     200     210

```

```

                30      40      50      60      70
AAD-12  EATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPLVKVH
          :: : . :   ..: . . ..... : ::: . : : : :::
gi+AHw-168  AATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAATV
            220     230     240     250     260     270

```

80
 AAD-12 P

gi+AHw-168 AAGGYKV
 280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
 5.020 (290 aa)

initn: 39 initl: 39 opt: 57 Z-score: 88.2 bits: 22.4 E(): 6.1
 Smith-Waterman score: 57+ADs- 25.926+ACU- identity (54.321+ACU- similar)
 in 81 aa overlap (2-70:194-274)

```

                                10      20
AAD-12      VFSAEVVPAVGG----RTCFADMRAAYDALD
                                .. . ....:   .. .....:
gi+AHw-330  IDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYD TYKCIPSLEAAVKQAY
            170     180     190     200     210     220

```

```

                30      40      50      60      70
AAD-12  EATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPLVKVH

```



```

      ::  :  :  .....  .....  :  :
gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
      10      20      30      40      50

```

```

      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHP
      ....  :

```

```

gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNIEEAQTLISKIL
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 86.8 bits: 21.0 E(): 7.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (18-58:26-65)

```

      10      20      30      40      50
AAD-12      VFSAEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      ::  :  :  .....  .....  :  :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
      10      20      30      40      50

```

```

      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHP
      ....  :

```

```

gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNIEEAQTLISKIL
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)

initn: 52 initl: 52 opt: 52 Z-score: 85.7 bits: 21.0 E(): 8.5
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (23-46:29-52)

```

      10      20      30      40      50
AAD-12      VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
      :  :  ::  :  .  ..  :  :  :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
      10      20      30      40      50      60

```

```

      60      70      80
AAD-12 QAGSAYIGYGMDDTATPLRPLVKVHP

```

```

gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAGGE
      70      80      90      100      110      120

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:10 2010 done: Fri Feb 5 12:56:11 2010
Total Scan time: 0.080 Total Display time: 0.010


```

60      68
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
62      60      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
64      48      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
66      22      25:+AD0APQA9AD0APQA9AD0APQAq-
68      20      20:+AD0APQA9AD0APQA9ACo-
70      24      16:+AD0APQA9AD0APQAqAD0APQ-
72      11      12:+AD0APQA9ACo-
74      5       10:+AD0APQ- +ACo-
76      11      7:+AD0APQAqAD0-
78      6       6:+AD0AKg-
80      7       4:+AD0AKgA9-
82      4       3:+ACoAPQ-
84      2       3:+ACo-
86      1       2:+ACo-
88      5       2:+ACoAPQ-          inset +AD0- represents 1 library

```

sequences

```

90      1       1:+ACo-
92      2       1:+ACo-          :+ACoAPQ-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     1       0:+AD0-          +ACoAPQ-
116     0       0:              +ACo-
118     0       0:              +ACo-

```

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 5.39720.00318+ADs- mu+AD0- 2.8909
0.165

mean+AF8-var+AD0-36.1929 9.478, 0's: 2 Z-trim: 3 B-trim: 30 in 1/42

Lambda+AD0- 0.213188

Kolmogorov-Smirnov statistic: 0.0612 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 74 27.7 0.21

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134)
60 23.7 1.2

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 58 23.1 1.6

gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)
57 22.6 3.6

gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
 (204) 57 22.6 3.7
 gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281)
 57 22.6 5.3
 gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290)
 57 22.6 5.5
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 21.2 5.7
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 23.1 6.2
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
 52 21.2 6.6
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 52 21.2 6.6
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
 (152) 52 21.2 7.6

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 57 initl: 57 opt: 74 Z-score: 114.5 bits: 27.7 E(): 0.21
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (10-70:309-363)

```

                                10      20      30
AAD-12      FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                :: : : : : : : : : : :
gi+AHw-113  HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA
            280      290      300      310      320      330

            40      50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE
            .. . . : . : . . . : : . : :
gi+AHw-113  ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
            340      350      360      370      380      390
    
```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 60 Z-score: 101.0 bits: 23.7 E(): 1.2
 Smith-Waterman score: 60+ADs- 28.814+ACU- identity (64.407+ACU- similar)
 in 59 aa overlap (1-57:11-65)

```

                                10      20      30      40
AAD-12      FSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                                :: : : : : : : : : : : : : : : : :
gi+AHw-111  MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
            10      20      30      40      50

            50      60      70      80
AAD-12  LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE
            : . . . :
gi+AHw-111  LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
    
```


130 140 150 160 170 180

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
+AFs-Phl (281 aa)

initn: 39 init1: 39 opt: 57 Z-score: 89.4 bits: 22.6 E(): 5.3
Smith-Waterman score: 57+ADs- 25.926+ACU- identity (54.321+ACU- similar)
in 81 aa overlap (1-69:185-265)

```

                                10          20
AAD-12                        FSAEVVPAVGG----RTCFADMRAAYDALD
                                .. . .:::   .. .:::
gi+AHw-168 IDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPLSLEAAVKQAY
                160          170          180          190          200          210

```

```

                30          40          50          60          70
AAD-12 EATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLVKVH
                :: : . :      ..: . . . . . .::: .::: . . :  ::::
gi+AHw-168 AATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAATV
                220          230          240          250          260          270

```

80
AAD-12 PE

gi+AHw-168 AAGGYKV
280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
5.020 (290 aa)

initn: 39 init1: 39 opt: 57 Z-score: 89.1 bits: 22.6 E(): 5.5
Smith-Waterman score: 57+ADs- 25.926+ACU- identity (54.321+ACU- similar)
in 81 aa overlap (1-69:194-274)

```

                                10          20
AAD-12                        FSAEVVPAVGG----RTCFADMRAAYDALD
                                .. . .:::   .. .:::
gi+AHw-330 IDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPLSLEAAVKQAY
                170          180          190          200          210          220

```

```

                30          40          50          60          70
AAD-12 EATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLVKVH
                :: : . :      ..: . . . . . .::: .::: . . :  ::::
gi+AHw-330 AATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAATV
                230          240          250          260          270          280

```

80
AAD-12 PE

gi+AHw-330 AAGGYKV
290

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 init1: 38 opt: 52 Z-score: 88.8 bits: 21.2 E(): 5.7

Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (17-57:11-50)

```

                10         20         30         40         50
AAD-12  FSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
                :::  :::  :  .....  .....:::  :  ::  ....  :
gi+AHw-160  GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDLDELNENKSK
                10         20         30         40         50
    
```

```

                60         70         80
AAD-12  YIGYGMDTTATPLRPLVKVHPE

gi+AHw-160  ELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKILLKDLKETEQ
                60         70         80         90         100         110
    
```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 init1: 47 opt: 59 Z-score: 88.2 bits: 23.1 E(): 6.2
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (35-72:198-242)

```

                10         20         30         40         50
AAD-12  VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                :::  :::  :::  :  :  :::  .
gi+AHw-303  LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                170        180        190        200        210        220
    
```

```

                60         70         80
AAD-12  YIGYGMDT-TATPLRPLVKVHPE
                .....:  ::  .:
gi+AHw-303  VLGFGMDTETARKVVRGEDDQRGHIVRVEQGLKVI RPPRIREELEQQEGGGYNGLEETICS
                230        240        250        260        270        280
    
```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.7 bits: 21.2 E(): 6.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (17-57:26-65)

```

                10         20         30         40
AAD-12  FSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                :::  :::  :  .....  .....:::  :  ::
gi+AHw-420  MKFAIVLIACFAASVLAQEHPKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10         20         30         40         50
    
```

```

                50         60         70         80
AAD-12  GHVQQAGSAYIGYGMDTTATPLRPLVKVHPE
                ....  :
gi+AHw-420  DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKIL
                60         70         80         90         100         110
    
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.7 bits: 21.2 E(): 6.6

Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (17-57:26-65)

```

                10         20         30         40
AAD-12          FSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                ::  :  :  .....  .....  :  :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                10         20         30         40         50

                50         60         70         80
AAD-12          GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE
                ....  :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 init1: 52 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (22-45:29-52)

```

                10         20         30         40         50
AAD-12          FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                :  :  ::  :  .  ...  :  :  :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEAEARISAKNALESYAYSLRNTLSDS
                10         20         30         40         50         60

                60         70         80
AAD-12          QAGSAYIGYGMDDTTATPLRPLVKVHPE

gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
                70         80         90         100         110         120

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:11 2010 done: Fri Feb 5 12:56:11 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 125 - 204 80 aa - 80 aa


```

82      5      3:+ACoAPQ-
84      3      3:+ACo-
86      1      2:+ACo-
88      4      2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      0      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      1      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     1      0:+AD0-          +ACoAPQ-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120 0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.25560.00328+ADs- mu+AD0- 3.5122
0.170
mean+AF8-var+AD0-36.6945 9.509, 0's: 2 Z-trim: 3 B-trim: 30 in 1/42
Lambda+AD0- 0.211726
Kolmogorov-Smirnov statistic: 0.0604 (N+AD0-29) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  74 27.7    0.21
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 23.0    1.7
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  56 22.4    2.9
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.6    3.6
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.6    3.7
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.2    5.9
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)  59 23.1    6.1
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  52 21.2    6.7
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.2    6.7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)  52 21.1    7.7

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 57 initl: 57 opt: 74 Z-score: 114.5 bits: 27.7 E(): 0.21
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (9-69:309-363)

```

                                10      20      30
AAD-12          SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSSAR
                                ::: : : : . . . : : :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
                280      290      300      310      320      330

                40      50      60      70      80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET
                .:. . . : . : . . . : . : . :
gi+AHw-113 ESMKWNWRTNKDVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
                340      350      360      370      380      390

gi+AHw-113 GAPC

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 98.3 bits: 23.0 E(): 1.7
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (14-65:26-77)

```

                                10      20      30      40
AAD-12          SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSSARHSLVYSQSKL
                                :::      :. . . : . . . : . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAFAKVNV
                10      20      30      40      50      60

                50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPET
                : . . . . : . : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAAEKLGGLAQKRVAG
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 56 Z-score: 94.2 bits: 22.4 E(): 2.9
 Smith-Waterman score: 56+ADs- 28.070+ACU- identity (61.404+ACU- similar)
 in 57 aa overlap (2-56:12-65)

```

                                10      20      30      40
AAD-12          SAEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSSARHSLVYSQSKL
                                : : : : . : . : : . . . . . : . . . . . : :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQL
                10      20      30      40      50

                50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPET
                . . . . :

```

gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 92.3 bits: 22.6 E(): 3.6
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (15-67:93-149)

10 20 30
AAD-12 SAEVVPVAVGGRTCFADMRAA-----YDALDEATRALLVHQRSARH
.:.:.: :.:.:
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
70 80 90 100 110 120

40 50 60 70 80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPET
.:.:.: :.:.: :.:.: :.:.: :.:.:
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
130 140 150 160 170 180

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 92.2 bits: 22.6 E(): 3.7
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (15-67:97-153)

10 20 30
AAD-12 SAEVVPVAVGGRTCFADMRAA-----YDALDEATRALLVHQRSARH
.:.:.: :.:.:
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
70 80 90 100 110 120

40 50 60 70 80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPET
.:.:.: :.:.: :.:.: :.:.: :.:.:
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
130 140 150 160 170 180

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 88.6 bits: 21.2 E(): 5.9
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (16-56:11-50)

10 20 30 40 50
AAD-12 SAEVVPVAVGGRTCFADMRAAYDAL--DEATRALLVHQRSARHSLVYSQSKLGHVQQAGSAY
.:.:.: :.:.: :.:.: :.:.: :.:.:
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDLENENKSKE
10 20 30 40 50

60 70 80
AAD-12 IGYGMTTATPLRPLVKVHPET

gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNIEEAQTLISKIL
 60 70 80 90 100 110

+AD4--+AD4-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 86.5 bits: 21.1 E(): 7.7
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (21-44:29-52)

10 20 30 40 50
 AAD-12 SAEVVPVAVGGRTCFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGHVQ
 : : : : : . . . : : : :
 gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
 10 20 30 40 50 60

60 70 80
 AAD-12 QAGSAYIGYGMDDTTATPLRPLVKVHPET

gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
 70 80 90 100 110 120

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:12 2010 done: Fri Feb 5 12:56:12 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 126 - 205 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	1	0:+AD0-	
30	3	2:+ACo-	
32	8	8:+AD0APQAq-	
34	28	21:+AD0APQA9AD0APQA9ACoAPQA9AD0-	
36	24	44:+AD0APQA9AD0APQA9AD0APQ-	+ACo-


```

106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      1      0:+AD0-      +ACoAPQ-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.30480.00328+ADs- mu+AD0- 3.0729
0.170
mean+AF8-var+AD0-37.1335 9.635, 0's: 2 Z-trim: 3 B-trim: 30 in 1/42
Lambda+AD0- 0.210471
Kolmogorov-Smirnov statistic: 0.0694 (N+AD0-29) at 48

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  77 28.6  0.11
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 23.0  1.7
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  56 22.4  2.8
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.6  3.6
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.6  3.7
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.2  5.8
gi+AHw-30313867+AHw-gb+AHw-AA038859.1+AHw- 11S globulin +AFs-Bertholle (
465)  59 23.1  6.1
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  52 21.2  6.6
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.2  6.6
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)  52 21.2  7.6

```

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 60 initl: 60 opt: 77 Z-score: 119.2 bits: 28.6 E(): 0.11
Smith-Waterman score: 77+ADs- 23.288+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (8-80:309-375)

```

```

                                10      20      30
AAD-12      AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                : : : : : : : : : :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA
      280      290      300      310      320      330

      40      50      60      70      80

```

```

AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETG
      . . . . . : . . . . . : : . : : . : : . : :
gi+AHw-113 ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALS LTSSAGVLSCQP
           340           350           360           370           380           390
    
```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 98.4 bits: 23.0 E(): 1.7
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (13-64:26-77)

```

AAD-12           10           20           30           40
      AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
      . . . . . : . . . . . : : . : : . : : . : :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAIPVYEQLSTKHSVPDVLAFKVN
           10           20           30           40           50           60
    
```

```

AAD-12           50           60           70           80
      GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETG
      . . . . . : . : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAAEKLGGLAQKRVAG
           70           80           90           100           110           120
    
```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
 initn: 38 initl: 38 opt: 56 Z-score: 94.2 bits: 22.4 E(): 2.8
 Smith-Waterman score: 56+ADs- 28.070+ACU- identity (61.404+ACU- similar)
 in 57 aa overlap (1-55:12-65)

```

AAD-12           10           20           30           40
      AEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      : : : : . : : : . : : : . : : : . : : : . : :
gi+AHw-111 MKFAIVLIACFAASVLAQGHPKPKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
           10           20           30           40           50
    
```

```

AAD-12           50           60           70           80
      GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETG
      . . . . . :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
           60           70           80           90           100           110
    
```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 92.4 bits: 22.6 E(): 3.6
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (14-66:93-149)

```

AAD-12           10           20           30
      AEVVPVAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
      . . . . . : : : : : . . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
    
```

```

              70          80          90          100          110          120
AAD-12  40      50      60      70      80
SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETG
.. :   .. :   ..... :   :   :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
              130          140          150          160          170          180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 92.2 bits: 22.6 E(): 3.7
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (14-66:97-153)

```

              10          20          30
AAD-12  AEVVPVAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
              ..... :   :   :   .   .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
              70          80          90          100          110          120

```

```

              40      50      60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETG
.. :   .. :   ..... :   :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
              130          140          150          160          170          180

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 88.7 bits: 21.2 E(): 5.8
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (15-55:11-50)

```

              10          20          30          40          50
AAD-12  AEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
              :   :   :   ..... :   :   :   :   :
gi+AHw-160  GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDDELNENKSKEL
              10          20          30          40          50

```

```

              60      70      80
AAD-12  GYGMDDTATPLRPLVKVHPETG
gi+AHw-160 QEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQKV
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 88.3 bits: 23.1 E(): 6.1
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (33-70:198-242)

```

              10          20          30          40          50
AAD-12  VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
              :   :   :   :   :   :   :   :
gi+AHw-303  LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD

```

```

170      180      190      200      210      220
      60      70      80
AAD-12 YIGYGMTD-TATPLRPLVKVHPETG
      ..... :: .:
gi+AHw-303 VLFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230      240      250      260      270      280

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.7 bits: 21.2 E(): 6.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (15-55:26-65)

```

      10      20      30      40
AAD-12      AEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      :: : : ..... : : :
gi+AHw-111 MKFAIVLIACFAASVLAQEHEKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETG
      .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.7 bits: 21.2 E(): 6.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (15-55:26-65)

```

      10      20      30      40
AAD-12      AEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      :: : : ..... : : :
gi+AHw-420 MKFAIVLIACFAASVLAQEHEKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETG
      .... :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 init1: 52 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (20-43:29-52)

```

      10      20      30      40      50
AAD-12      AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
      : : :: : . .: : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEEAARISAKNALESYAYSLRNTLSDS

```


FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 77 28.4 0.13

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 58 22.9 1.8

gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)
57 22.6 3.8

gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
(204) 57 22.6 3.9

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134)
54 21.7 4.6

gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
52 21.1 6.1

gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
59 23.0 6.4

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
52 21.1 6.9

gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
52 21.1 6.9

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
(152) 52 21.1 7.9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 60 initl: 60 opt: 77 Z-score: 118.4 bits: 28.4 E(): 0.13
Smith-Waterman score: 77+ADs- 23.288+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (7-79:309-375)

```

                                10      20      30
AAD-12      EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                :: : : : . . . . : . . .
gi+AHw-113  HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA
            280      290      300      310      320      330
    
```

```

                40      50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGR
                . . . . : . . . . . . . . . . . . . . . . . . . . .
gi+AHw-113  ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPEGESALSLSAGVLSLSCQP
            340      350      360      370      380      390
    
```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)

initn: 58 initl: 58 opt: 58 Z-score: 97.9 bits: 22.9 E(): 1.8
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (12-63:26-77)

```

                10         20         30         40
AAD-12          EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                :::         :. . . : . . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVN
                10         20         30         40         50         60

```

```

                50         60         70         80
AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGR
                ::::: . : . :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AEKLGGLAQKRVAG
                70         80         90         100        110        120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 91.9 bits: 22.6 E(): 3.8
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (13-65:93-149)

```

                10         20         30
AAD-12          EVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                . . . . . : : : : . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100        110        120

```

```

                40         50         60         70         80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGR
                .. : . . . : . . . . . : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130        140        150        160        170        180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 91.8 bits: 22.6 E(): 3.9
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (13-65:97-153)

```

                10         20         30
AAD-12          EVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                . . . . . : : : : . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100        110        120

```

```

                40         50         60         70         80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGR
                .. : . . . : . . . . . : : :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130        140        150        160        170        180

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
 initn: 38 initl: 38 opt: 54 Z-score: 90.5 bits: 21.7 E(): 4.6
 Smith-Waterman score: 54+ADs- 27.778+ACU- identity (62.963+ACU- similar)
 in 54 aa overlap (3-54:15-65)

```

                10         20         30         40
AAD-12      EVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
              : : : .   . : : .   . : : .   . : : .   . : : .
gi+AHw-111  MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
              10         20         30         40         50

```

```

                50         60         70         80
AAD-12      GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGR
              . . . . :
gi+AHw-111  DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
              60         70         80         90         100        110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 88.3 bits: 21.1 E(): 6.1
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (14-54:11-50)

```

                10         20         30         40         50
AAD-12      EVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG
              : : : .   . : : .   . : : .   . : : .   . : : .
gi+AHw-160  GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQDELNENKSKELQ
              10         20         30         40         50

```

```

                60         70         80
AAD-12      YGMDDTATPLRPLVKVHPETGR
              . . . . :
gi+AHw-160  EKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKILLKDLKETEQKVK
              60         70         80         90         100        110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 87.9 bits: 23.0 E(): 6.4
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (32-69:198-242)

```

                10         20         30         40         50
AAD-12      VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
              : : : .   . : : .   . : : .   . : : .   . : : .
gi+AHw-303  LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
              170        180        190        200        210        220

```

```

                60         70         80
AAD-12      YIGYGMDDT-TATPLRPLVKVHPETGR
              . . : : : : : : : : : : : :
gi+AHw-303  VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
              230        240        250        260        270        280

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.3 bits: 21.1 E(): 6.9
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (14-54:26-65)

```

                10         20         30         40
AAD-12          EVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                :::  :: :  :::::  :::::  :::  ::
gi+AHw-111 MKFAIVLIACFAASVLAQEHEKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGR
                .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein B1 (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.3 bits: 21.1 E(): 6.9
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (14-54:26-65)

```

                10         20         30         40
AAD-12          EVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                :::  :: :  :::::  :::::  :::  ::
gi+AHw-420 MKFAIVLIACFAASVLAQEHEKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGR
                .... :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 86.2 bits: 21.1 E(): 7.9
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (19-42:29-52)

```

                10         20         30         40         50
AAD-12          EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                : : ::: : .  :::  :::  :::
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
                10         20         30         40         50         60

```

```

                60         70         80
AAD-12 QAGSAYIGYGMDDTTATPLRPLVKVHPETGR
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
                70         80         90         100         110         120

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:12 2010 done: Fri Feb 5 12:56:13 2010

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 54 21.6 4.8
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 21.1 6.3
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465) 59 22.9 7
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 52 21.1 7.2
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 52 21.1 7.2
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.0 8.3

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 60 initl: 60 opt: 77 Z-score: 117.2 bits: 28.2 E(): 0.15
 Smith-Waterman score: 77+ADs- 23.288+ACU- identity (50.685+ACU- similar)
 in 73 aa overlap (6-78:309-375)

```

                                10      20      30
AAD-12      VVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                :::  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-113  HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA
            280      290      300      310      320      330

            40      50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRP
            ..  .  :  .  :  .  .  :  :  .  :  :  .  :  :
gi+AHw-113  ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALS LTSSAGVLSCQP
            340      350      360      370      380      390
    
```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 97.4 bits: 22.8 E(): 1.9
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (11-62:26-77)

```

                                10      20      30      40
AAD-12      VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                :::  :  .  .  :  :  :  :  :  :  :  :
gi+AHw-527  MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQ LSTKHSVPDVLAFKVN
            10      20      30      40      50      60

            50      60      70      80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRP
            :  :  :  :  :  :  :  :  :  :  :
gi+AHw-527  DHVQDAAQQYGITAMP TFMFFKEGKQVAVNGQAVIKGADPRTLGA AAEKLGGLAQKR
            70      80      90      100      110      120
    
```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)

initn: 41 initl: 41 opt: 57 Z-score: 91.4 bits: 22.5 E(): 4.1
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (12-64:93-149)

```

                                10          20          30
AAD-12          VVPAVGGRTCFADMRAA-----YDALDEATR LVHQRSARH
                                . . . . .   . . . . .   . . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                   70          80          90          100          110          120

                   40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRP
                   . . :   . . . :   . . . . . :   :   :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
                   130          140          150          160          170          180
    
```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 91.2 bits: 22.5 E(): 4.2
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (12-64:97-153)

```

                                10          20          30
AAD-12          VVPAVGGRTCFADMRAA-----YDALDEATR LVHQRSARH
                                . . . . .   . . . . .   . . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                   70          80          90          100          110          120

                   40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRP
                   . . :   . . . :   . . . . . :   :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
                   130          140          150          160          170          180
    
```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 54 Z-score: 90.1 bits: 21.6 E(): 4.8
 Smith-Waterman score: 54+ADs- 27.778+ACU- identity (62.963+ACU- similar)
 in 54 aa overlap (2-53:15-65)

```

                                10          20          30          40
AAD-12          VVPAVGGRTCFADMRAAYDAL--DEATR LVHQRSARHSLVYSQSKL
                                : : : .   . . :   . : :   . . . . .   . . . . . : :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                   10          20          30          40          50

                   50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRP
                   . . . . :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFN YEEAQTL SKIL
                   60          70          80          90          100          110
    
```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 88.0 bits: 21.1 E(): 6.3
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (13-53:11-50)

```

                10         20         30         40         50
AAD-12 VVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
                ::  :: :  .....  .....: :  ::  ....  :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDLLENKSKELQE
                10         20         30         40         50
    
```

```

                60         70         80
AAD-12 GMDTTATPLRPLVKVHPETGRP

gi+AHw-160 KIIRELDVVCAMIEGAQGALERELKRTDLNILERFNIEEAQTLKILLKDLKETEQKVKD
                60         70         80         90         100         110
    
```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 87.2 bits: 22.9 E(): 7
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (31-68:198-242)

```

                10         20         30         40         50
AAD-12 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                ::  :::  :: :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-303 LVQHTASDLNQLDQNP RHF FLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                170        180        190        200        210        220
    
```

```

                60         70         80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRP
                .....: :  ::  :
gi+AHw-303 VLGFGMDTETARKVVRGEDDQRGHIVRVEQGLKIVRPPRIREELEQQEGGGYNGLEETICS
                230        240        250        260        270        280
    
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.0 bits: 21.1 E(): 7.2
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (13-53:26-65)

```

                10         20         30         40
AAD-12 VVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                ::  :: :  .....  .....: :  ::  ....  :
gi+AHw-111 MKFAIVLIACFAASVLAQEHEKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10         20         30         40         50
    
```

```

                50         60         70         80
AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRP
                ....  :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNIEEAQTLKILL
                60         70         80         90         100         110
    
```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein B1 (134 aa)

initn: 38 init1: 38 opt: 52 Z-score: 87.0 bits: 21.1 E(): 7.2
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (13-53:26-65)

```

                                10      20      30      40
AAD-12      VVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                ::  :: :  .....  .....:  ::
gi+AHw-420  MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                                10      20      30      40      50

                                50      60      70      80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRP
        .... :
gi+AHw-420  DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)

initn: 52 init1: 52 opt: 52 Z-score: 85.9 bits: 21.0 E(): 8.3
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (18-41:29-52)

```

                                10      20      30      40
AAD-12      VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                                : : ::: : .  .: .: .:
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
                                10      20      30      40      50      60

                                50      60      70      80
AAD-12  QAGSAYIGYGMDDTTATPLRPLVKVHPETGRP

gi+AHw-144  KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
                                70      80      90      100      110      120

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:13 2010 done: Fri Feb 5 12:56:13 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

76      13      7:+AD0APQAcAD0APQ-
78      4      6:+AD0AKg-
80      4      4:+AD0AKg-
82      5      3:+ACoAPQ-
84      1      3:+ACo-
86      3      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      3      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     1      0:+AD0-          +ACoAPQ-
116     0      0:          +ACo-
118     0      0:          +ACo-

```

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: $\rho(\ln(x))+AD0-$ 5.72930.00338+ADs- $\mu+AD0-$ 0.5494
0.175

mean+AF8-var+AD0-41.562910.663, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43

Lambda+AD0- 0.198940

Kolmogorov-Smirnov statistic: 0.0856 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  77 27.9  0.19
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 22.7  2.1
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.3  4.6
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.3  4.7
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  54 21.5  5.3
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.0  6.9
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  52 20.9  7.9
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 20.9  7.9
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)  59 22.7  8.1

```

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
(152) 52 20.9 9.1

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 60 init1: 60 opt: 77 Z-score: 115.4 bits: 27.9 E(): 0.19
Smith-Waterman score: 77+ADs- 23.288+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (5-77:309-375)

```

                                10      20      30
AAD-12                        VPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                :::  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-113 HGFFQVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
                280      290      300      310      320      330

                40      50      60      70      80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPS
                .:. . .  :  .  :  .  .  .  :  :  .  :  :  .  .  :  :
gi+AHw-113 ESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
                340      350      360      370      380      390
    
```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 init1: 58 opt: 58 Z-score: 96.5 bits: 22.7 E(): 2.1
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (10-61:26-77)

```

                                10      20      30      40
AAD-12                        VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                :::  :  .  .  :  :  :  :  :  :  :  :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQVSTKHSVPDVLAFAKVVN
                10      20      30      40      50      60

                50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPS
                :::. . .  :  .  :  :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQKRVAG
                70      80      90      100      110      120
    
```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 init1: 41 opt: 57 Z-score: 90.5 bits: 22.3 E(): 4.6
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (11-63:93-149)

```

                                10      20      30
AAD-12                        VPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                .:  :  :  :  :  :  :  :  :  :  :
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70      80      90      100      110      120
    
```

```

      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPS
      .. :   .. :   ..... :   :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
      130      140      150      160      170      180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 90.3 bits: 22.3 E(): 4.7
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (11-63:97-153)

```

      10      20      30
AAD-12          VPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
      ..... :   :   :   .   .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
      70      80      90      100      110      120

```

```

      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPS
      .. :   .. :   ..... :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
      130      140      150      160      170      180

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
 initn: 38 initl: 38 opt: 54 Z-score: 89.4 bits: 21.5 E(): 5.3
 Smith-Waterman score: 54+ADs- 27.778+ACU- identity (62.963+ACU- similar)
 in 54 aa overlap (1-52:15-65)

```

      10      20      30      40
AAD-12          VPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      : : : .   : :   :   ..... :   ..... :   :
gi+AHw-111 MKFAIVLIACFAASVLAQGHPKPKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPS
      .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.3 bits: 21.0 E(): 6.9
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (12-52:11-50)

```

      10      20      30      40      50
AAD-12 VPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
      : : : :   ..... :   ..... :   :   :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQLDELNENKSKELQEK
      10      20      30      40      50

```



```

        60          70          80
AAD-12  YIGYGMTD-TATPLRPLVKVHPETGRPS
        .:.:.:.: :. :.
gi+AHw-303 VLGFGMTETARKVVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
        230          240          250          260          270          280
    
```

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
  initn: 52 initl: 52 opt: 52 Z-score: 85.2 bits: 20.9 E(): 9.1
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (17-40:29-52)
    
```

```

                10          20          30          40
AAD-12          VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                : : :.: : . .: : :.:
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
                10          20          30          40          50          60
    
```

```

        50          60          70          80
AAD-12  QAGSAYIGYGMTTATPLRPLVKVHPETGRPS
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
                70          80          90          100          110          120
    
```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:13 2010 done: Fri Feb 5 12:56:14 2010
Total Scan time: 0.080 Total Display time: 0.000
    
```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448
    
```

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
    
```

```

1+AD4APgA+-AAD-12: 130 - 209 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
    
```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      1      2:+ACo-
    
```



```

gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
          280          290          300          310          320          330

```

```

AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL
          40          50          60          70          80

```

```

gi+AHw-113 ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
          340          350          360          370          380          390

```

gi+AHw-113 GAPC

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 init1: 58 opt: 58 Z-score: 96.7 bits: 22.7 E(): 2.1
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (9-60:26-77)

```

```

AAD-12 PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
          10          20          30          40
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAIPVYEQLSTKHSVPDVLAFAKVVN
          10          20          30          40          50          60

```

```

AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL
          50          60          70          80
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAAEKLGGLAQKRVAG
          70          80          90          100          110          120

```

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 init1: 41 opt: 57 Z-score: 90.7 bits: 22.3 E(): 4.5
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (10-62:93-149)

```

```

AAD-12 PAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
          10          20          30
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
          70          80          90          100          110          120

```

```

AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL
          40          50          60          70          80
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
          130          140          150          160          170          180

```

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 init1: 41 opt: 57 Z-score: 90.5 bits: 22.3 E(): 4.6
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (10-62:97-153)

```

```

                                10          20          30
AAD-12          PAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                .....:   ::  ::  ..  .  ..
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
              70          80          90          100          110          120

```

```

              40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL
              .. :   ... :. : ..... :   :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130          140          150          160          170          180

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 init1: 38 opt: 53 Z-score: 88.1 bits: 21.3 E(): 6.3
Smith-Waterman score: 53+ADs- 26.923+ACU- identity (63.462+ACU- similar)
in 52 aa overlap (2-51:17-65)

```

                                10          20          30          40
AAD-12          PAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                : : .   ::  : :  .....  .....: : :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
              10          20          30          40          50

```

```

              50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL
              .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.6 bits: 21.0 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (11-51:11-50)

```

              10          20          30          40          50
AAD-12 PAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
              ::  : :  .....  .....: :  .... :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQLDELNENKSKELQEKI
              10          20          30          40          50

```

```

              60          70          80
AAD-12 DTTATPLRPLVKVHPETGRPSL

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQVKVDIQ
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 init1: 38 opt: 52 Z-score: 86.5 bits: 21.0 E(): 7.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (11-51:26-65)

```

                10          20          30          40
AAD-12          PAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                :::  :::  :  :::::  :::::  :  ::
gi+AHw-111 MKFAIVLIACFAASVLAQEHEKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL
                ....  :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 86.5 bits: 21.0 E(): 7.6
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (11-51:26-65)

```

                10          20          30          40
AAD-12          PAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                :::  :::  :  :::::  :::::  :  ::
gi+AHw-420 MKFAIVLIACFAASVLAQEHEKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL
                ....  :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 86.2 bits: 22.7 E(): 8
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (29-66:198-242)

```

                10          20          30          40          50
AAD-12          PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                :::  :::  :  :::  :  :  :  :  :  :  :  :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                170          180          190          200          210          220

```

```

                60          70          80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSL
                :::::  ::  :
gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                230          240          250          260          270          280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 85.4 bits: 20.9 E(): 8.8
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (16-39:29-52)


```
+AD4-120      1      0:+AD0-      +ACoAPQ-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.84200.00329+ADs- mu+AD0- -
0.4717 0.171
mean+AF8-var+AD0-41.992010.518, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.197921
Kolmogorov-Smirnov statistic: 0.1001 (N+AD0-28) at 50
```

```
FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
```

```
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
```

```
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  82 29.4  0.068
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 22.8   2
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.4   4.3
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.4   4.4
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  53 21.3   6
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.1   6.4
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  52 21.0   7.3
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.0   7.3
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)  59 22.8   7.7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)  52 21.0   8.5
```

```
+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 82 Z-score: 123.3 bits: 29.4 E(): 0.068
Smith-Waterman score: 82+ADs- 23.377+ACU- identity (51.948+ACU- similar)
in 77 aa overlap (3-79:309-379)
```

```

                                10      20      30
AAD-12                          AVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                :: : : : . . . . : . . .
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA
                                280      290      300      310      320      330
```

```

                                40      50      60      70      80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLL
                                . . . . : . . . . . . . . . . . . . . . .
gi+AHw-113 ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
                                340      350      360      370      380      390
```

```
gi+AHw-113 GAPC
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 initl: 58 opt: 58 Z-score: 97.0 bits: 22.8 E(): 2
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (8-59:26-77)

```

                                10      20      30      40
AAD-12          AVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKL
                                :::      . . . : . . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQQLSTKHSVPDVLAFAKVVN
                                10      20      30      40      50      60

```

```

                                50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                                ::::: . : . :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQKRVAG
                                70      80      90      100     110     120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 90.9 bits: 22.4 E(): 4.3
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (9-61:93-149)

```

                                10      20      30
AAD-12          AVGGRTCFADMRAA-----YDALDEATRVLVHQRSARH
                                . . . . . : : : . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDP LKKE
                                70      80      90      100     110     120

```

```

                                40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                                .. : . . . : . . . . . : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 90.7 bits: 22.4 E(): 4.4
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (9-61:97-153)

```

                                10      20      30
AAD-12          AVGGRTCFADMRAA-----YDALDEATRVLVHQRSARH
                                . . . . . : : : . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDP LKKE
                                70      80      90      100     110     120

```

```

                                40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                                .. : . . . : . . . . . : : :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 88.4 bits: 21.3 E(): 6
Smith-Waterman score: 53+ADs- 26.923+ACU- identity (63.462+ACU- similar)
in 52 aa overlap (1-50:17-65)

```

                                10         20         30         40
AAD-12          AVGGRTCFAADMRAAYDAL--DEATRAlVHQRSARHSLVYSQSKL
                   : : .   ::  : :  .....  .....: : :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                   10         20         30         40         50

                                50         60         70         80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                   .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNyEEAQTLskIL
                   60         70         80         90         100         110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.9 bits: 21.1 E(): 6.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (10-50:11-50)

```

                                10         20         30         40         50
AAD-12          AVGGRTCFAADMRAAYDAL--DEATRAlVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
                   ::  : :  .....  .....: : :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQDELNENKSKELQEKI
                   10         20         30         40         50

                                60         70         80
AAD-12 DTTATPLRPLVKVHPETGRPSLL

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNyEEAQTLskILLKDLKETEQKVkDIQ
                   60         70         80         90         100         110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 86.8 bits: 21.0 E(): 7.3
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (10-50:26-65)

```

                                10         20         30         40
AAD-12          AVGGRTCFAADMRAAYDAL--DEATRAlVHQRSARHSLVYSQSKL
                   ::  : :  .....  .....: : :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                   10         20         30         40         50

                                50         60         70         80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                   .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNyEEAQTLskIL
                   60         70         80         90         100         110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein B1 (134 aa)
 initn: 38 init1: 38 opt: 52 Z-score: 86.8 bits: 21.0 E(): 7.3
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (10-50:26-65)

```

                                10          20          30          40
AAD-12          AVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                :::  :::  :  .....:  .....:  :  ::
gi+AHw-420 MKFAIVLIACFAASVLAQEHPKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                10          20          30          40          50

```

```

                    50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                    .... :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs- Bertholletia (465 aa)
 initn: 47 init1: 47 opt: 59 Z-score: 86.4 bits: 22.8 E(): 7.7
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (28-65:198-242)

```

                                10          20          30          40          50
AAD-12          AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                :::  :::  :  :  :  :  :  :  :  :  :  :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                170          180          190          200          210          220

```

```

                    60          70          80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLL
                    .....:  ::  .:
gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                230          240          250          260          270          280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
 initn: 52 init1: 52 opt: 52 Z-score: 85.7 bits: 21.0 E(): 8.5
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (15-38:29-52)

```

                                10          20          30          40
AAD-12          AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                                :  :  :::  :  .  ...:  :  ...:
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
                10          20          30          40          50          60

```

```

                    50          60          70          80
AAD-12 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                    .....:  ::  .:
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
                70          80          90          100          110          120

```


The best scores are:

opt bits E(1471)
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 82 29.5 0.062
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 58 22.9 1.9
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)
 57 22.4 4.1
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
 (204) 57 22.4 4.2
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 21.1 6.1
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 52 21.1 7
 gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 52 21.1 7
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
 52 21.1 7
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 22.8 7.4
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
 (152) 52 21.1 8.1
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
 (38) 43 18.8 9.7

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 65 init1: 65 opt: 82 Z-score: 124.1 bits: 29.5 E(): 0.062
 Smith-Waterman score: 82+ADs- 23.377+ACU- identity (51.948+ACU- similar)
 in 77 aa overlap (2-78:309-379)

				10	20	30
AAD-12				VGGRTCFADMRAAYDALDEATRALVHQRSAR		
				::: : :		: . . :
gi+AHw-113	HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAA					
	280	290	300	310	320	330

				40	50	60	70	80
AAD-12	HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLI							
	.:. . .	:	::: : : : : : . . .
gi+AHw-113	ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLSAGVLSLSCQP							
	340	350	360	370	380	390		

gi+AHw-113 GAPC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 58 init1: 58 opt: 58 Z-score: 97.5 bits: 22.9 E(): 1.9
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (7-58:26-77)

				10	20	30	40
AAD-12				VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL			
				:::	:	:

gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDLLENENKSKELQEKI
10 20 30 40 50

60 70 80
AAD-12 DTTATPLRPLVKVHPETGRPSLLI

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLKILLKDLKETEQKVKDIQ
60 70 80 90 100 110

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.2 bits: 21.1 E(): 7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (9-49:26-65)

10 20 30 40
AAD-12 VGGRTCFADMRAAYDAL--DEATRAlVHQRSARHSLVYSQSKL
:: : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
10 20 30 40 50

50 60 70 80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI
.... :
gi+AHw-111 DELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.2 bits: 21.1 E(): 7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (9-49:26-65)

10 20 30 40
AAD-12 VGGRTCFADMRAAYDAL--DEATRAlVHQRSARHSLVYSQSKL
:: : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
10 20 30 40 50

50 60 70 80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI
.... :
gi+AHw-111 DELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.2 bits: 21.1 E(): 7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (9-49:26-65)

10 20 30 40
AAD-12 VGGRTCFADMRAAYDAL--DEATRAlVHQRSARHSLVYSQSKL
:: : : : : : : : : : : :

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 initl: 58 opt: 58 Z-score: 97.8 bits: 22.9 E(): 1.8
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (6-57:26-77)

```

                                10      20      30      40
AAD-12                        GGRTCFADMRAAYDALDEATRVLVHQRSARHSLVYSQSKL
                                :::      . . . : . . . : . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQVSTKHSVPDVLAFAKVVN
                                10      20      30      40      50      60

                                50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG
                                ::::: . : . :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQKRVAG
                                70      80      90      100     110     120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 91.5 bits: 22.5 E(): 4
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (7-59:93-149)

```

                                10      20      30
AAD-12                        GGRTCFADMRAA-----YDALDEATRVLVHQRSARH
                                . . . . : . : . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPKKE
                                70      80      90      100     110     120

                                40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG
                                .. : . . : . . . . . : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 91.3 bits: 22.5 E(): 4.1
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (7-59:97-153)

```

                                10      20      30
AAD-12                        GGRTCFADMRAA-----YDALDEATRVLVHQRSARH
                                . . . . : . : . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPKKE
                                70      80      90      100     110     120

                                40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG
                                .. : . . : . . . . . : : :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 88.6 bits: 21.2 E(): 5.9
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (8-48:11-50)

```

                10         20         30         40         50
AAD-12      GGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
                ::  :: :  .....  .....:: :  ::  ....  :
gi+AHw-160  GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDENENKSKELQEKI
                10         20         30         40         50

```

```

                60         70         80
AAD-12  DTTATPLRPLVKVHPETGRPSLLIG

```

```

gi+AHw-160  IRELDVVCAMIEGAQGALERELKRTDLNILERFNIEEAQTLKILLKDLKETEQKVKDIQ
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.4 bits: 21.1 E(): 6.8
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (8-48:26-65)

```

                10         20         30         40
AAD-12      GGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                ::  :: :  .....  .....:: :  ::
gi+AHw-111  MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG

```

```

                ....  :
gi+AHw-111  DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNIEEAQTLKIL
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.4 bits: 21.1 E(): 6.8
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (8-48:26-65)

```

                10         20         30         40
AAD-12      GGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                ::  :: :  .....  .....:: :  ::
gi+AHw-111  MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG

```

```

                ....  :
gi+AHw-111  DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNIEEAQTLKIL
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein B1 (134 aa)
 initn: 38 init1: 38 opt: 52 Z-score: 87.4 bits: 21.1 E(): 6.8
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (8-48:26-65)

```

                                10         20         30         40
AAD-12                GGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                :::  :::  :::  :::  :::  :::  :::  :::
gi+AHw-420 MKFAIVLIACFAASVLAQEHEKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                10         20         30         40         50

                50         60         70         80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG
                .... :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs- Bertholletia (465 aa)
 initn: 47 init1: 47 opt: 59 Z-score: 86.6 bits: 22.8 E(): 7.5
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (26-63:198-242)

```

                                10         20         30         40
AAD-12                GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                :::  :::  :::  :::  :  :::  .
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                170         180         190         200         210         220

                50         60         70         80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIG
                ..... ::  .:
gi+AHw-303 VLGFGMDTETARKVVRGEDDQRGHIVRVEQGLKVI RPPRIREELEQQEGGGYNGLEETICS
                230         240         250         260         270         280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
 initn: 52 init1: 52 opt: 52 Z-score: 86.2 bits: 21.1 E(): 7.9
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (13-36:29-52)

```

                                10         20         30         40
AAD-12                GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                                :  :  :::  :  .  ...  ::  ...
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
                10         20         30         40         50         60

                50         60         70         80
AAD-12 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG

gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
                70         80         90         100         110         120

```



```

112      1      0:+AD0-          +ACoAPQ-
114      0      0:              +ACo-
116      0      0:              +ACo-
118      0      0:              +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.01930.00319+ADs- mu+AD0- -
1.5633 0.165
mean+AF8-var+AD0-41.013810.136, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.200267
Kolmogorov-Smirnov statistic: 0.0985 (N+AD0-28) at 50

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 74 27.2 0.3
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 58 22.9 1.8
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.5 4
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204) 57 22.5 4.1
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.2 5.8
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 52 21.2 6.6
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 52 21.2 6.6
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.2 6.6
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465) 59 22.8 7.3
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.1 7.7
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38) 43 19.0 8.8

```

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 initl: 65 opt: 74 Z-score: 111.8 bits: 27.2 E(): 0.3
Smith-Waterman score: 74+ADs- 22.667+ACU- identity (50.667+ACU- similar)
in 75 aa overlap (2-76:311-379)

```

```

                                10      20      30
AAD-12                        GRTCFAADMRAAYDALDEATRALVHQRSARHS
                                : : : : . . . . : . . . :
gi+AHw-113 FFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAAES
                                290      300      310      320      330

                                40      50      60      70      80
AAD-12 LVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR

```

```

. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi+AHw-113 MKWNRWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLSLTSSAGVLSCQPGA
          340          350          360          370          380          390

```

gi+AHw-113 PC

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
  initn: 58 init1: 58 opt: 58 Z-score: 97.9 bits: 22.9 E(): 1.8
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (5-56:26-77)

```

```

          10          20          30
AAD-12          GRTCFADMRAAYDALDEATR ALVHQRSARHSLVYSQSKL
          :::          . . . : . . . : . . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQ LSTKHSVPDVLAFAKVN V
          10          20          30          40          50          60

```

```

          40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR
          ::: . . . : . . . :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTL GAAAEKLGGLAQKR VAG
          70          80          90          100          110          120

```

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
  initn: 41 init1: 41 opt: 57 Z-score: 91.6 bits: 22.5 E(): 4
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (6-58:93-149)

```

```

          10          20          30
AAD-12          GRTCFADMRAA-----YDALDEATR ALVHQRSARH
          . . . . . : . . . : . . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
          70          80          90          100          110          120

```

```

          40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR
          .. : . . . : . . . . . : . . . :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
          130          140          150          160          170          180

```

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
  initn: 41 init1: 41 opt: 57 Z-score: 91.5 bits: 22.5 E(): 4.1
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (6-58:97-153)

```

```

          10          20          30
AAD-12          GRTCFADMRAA-----YDALDEATR ALVHQRSARH
          . . . . . : . . . : . . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
          70          80          90          100          110          120

```

```

                40          50          60          70          80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR
      .. :  .. :  .. :  ..... :  :  :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
          130          140          150          160          170          180
    
```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 88.7 bits: 21.2 E(): 5.8
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (7-47:11-50)

```

                10          20          30          40          50
AAD-12  GRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
      :: :  :  :  ..... :  ..... :  :  :  :  :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDLLENKSKELQEKI
          10          20          30          40          50
    
```

```

                60          70          80
AAD-12  DTTATPLRPLVKVHPETGRPSLLIGR
gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQVKVDIQ
          60          70          80          90          100          110
    
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.6
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (7-47:26-65)

```

                10          20          30
AAD-12  GRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      :: :  :  :  ..... :  ..... :  :  :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
          10          20          30          40          50
    
```

```

                40          50          60          70          80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR
      .... :
gi+AHw-111 DELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
          60          70          80          90          100          110
    
```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.6
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (7-47:26-65)

```

                10          20          30
AAD-12  GRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      :: :  :  :  ..... :  ..... :  :  :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
          10          20          30          40          50
    
```

```

      40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR
      .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
      60          70          80          90          100          110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.6
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (7-47:26-65)

```

                                10          20          30
AAD-12                          GRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                :: : : ..... : ..... : : :
gi+AHw-420 MKFAIVLIACFAASVLAQEHEKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                                10          20          30          40          50

```

```

      40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR
      .... :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
      60          70          80          90          100          110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs- Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 86.8 bits: 22.8 E(): 7.3
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (25-62:198-242)

```

                                10          20          30          40
AAD-12                          GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                :: : : : : : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
      170          180          190          200          210          220

```

```

      50          60          70          80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIGR
      ..... : : :
gi+AHw-303 VLGFGMDTETARKVVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230          240          250          260          270          280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 86.4 bits: 21.1 E(): 7.7
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (12-35:29-52)

```

                                10          20          30          40
AAD-12                          GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                                : : : : : : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
      10          20          30          40          50          60

```

50 60 70 80
 AAD-12 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR

gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
 70 80 90 100 110 120

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 85.4 bits: 19.0 E(): 8.8
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (40-60:5-25)

10 20 30 40 50 60
 AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP
: . .:: . :::
 gi+AHw-462 AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
 10 20 30

70 80
 AAD-12 ETGRPSLLIGR

gi+AHw-462 LNSA

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:14 2010 done: Fri Feb 5 12:56:15 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 135 - 214 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	0	0:	


```
  98      1      0:+AD0-          +ACoAPQ-
 100      0      0:              +ACo-
 102      0      0:              +ACo-
 104      0      0:              +ACo-
 106      0      0:              +ACo-
 108      0      0:              +ACo-
 110      0      0:              +ACo-
 112      1      0:+AD0-          +ACoAPQ-
 114      0      0:              +ACo-
 116      0      0:              +ACo-
 118      0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.95530.00322+ADs- mu+AD0- -
1.2225 0.167
mean+AF8-var+AD0-40.818610.074, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.200745
Kolmogorov-Smirnov statistic: 0.0937 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   74 27.3   0.29
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   58 23.0   1.8
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.5   3.9
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)   57 22.5   4
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.2   5.7
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   52 21.2   6.6
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   52 21.2   6.6
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.2   6.6
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 22.9   7.2
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)   52 21.2   7.7
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38)   43 18.9   8.9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 74 Z-score: 112.0 bits: 27.3 E(): 0.29
Smith-Waterman score: 74+ADs- 22.667+ACU- identity (50.667+ACU- similar)
in 75 aa overlap (1-75:311-379)
```

```

AAD-12                      RTCFADMRAAYDALDEATR10ALVHQ20SARHS
                             : : : : . . . : : : : :
gi+AHw-113 FFQVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAAES
                             290      300      310      320      330

```

```

AAD-12 LVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH
         . . . : . : . . . : . : . . . : . : . . . : . : . . . :
gi+AHw-113 MKWNRWRTNKDVL40ENGAI50FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGA
         340      350      360      370      380      390

```

gi+AHw-113 PC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 init1: 58 opt: 58 Z-score: 98.0 bits: 23.0 E(): 1.8
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (4-55:26-77)

```

AAD-12                      RTCFADMRAAYDALDEATR10ALVHQ20SARHS30LVYSQSKL
                             :::      :. . . : . . . : . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAIPVYEQLSTKHSVPDVLAFAKVVN
                             10      20      30      40      50      60

```

```

AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH
         :::. . . : . : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA40AAEKLGG50LAQ60KRVAG
         70      80      90      100      110      120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)
 initn: 41 init1: 41 opt: 57 Z-score: 91.7 bits: 22.5 E(): 3.9
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (5-57:93-149)

```

AAD-12                      RTCFADMRAA-----YDALDEATR10ALVHQ20SARH
                             . . . . : : : : . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIA70NYHYDA-DENSKQ80KKWD90PLKKE
                             70      80      90      100      110      120

```

```

AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH
         .. : . . . : . . . . . : : :
gi+AHw-144 TIPYYTKKFDE30VVKANG40G50YLAAGKLTWAD60FYFVAILDYL70NHMAKEDLVANQ80PNLKALREK
         130      140      150      160      170      180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Glutat (204 aa)
 initn: 41 init1: 41 opt: 57 Z-score: 91.6 bits: 22.5 E(): 4

Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (5-57:97-153)

```

                                10          20
AAD-12          RTCFADMRAA-----YDALDEATRLVHQRSARH
                .....:   :: :. . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70          80          90          100          110          120

                30          40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH
                .. :   ... :. : .....: : : :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130          140          150          160          170          180

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 init1: 38 opt: 52 Z-score: 88.8 bits: 21.2 E(): 5.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (6-46:11-50)

```

                                10          20          30          40          50
AAD-12          RTCFADMRAAYDAL--DEATRLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
                :: :. : : .....: .....: : : : : :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLLYLQHQLDELNENKSKELQEKI
                10          20          30          40          50

                60          70          80
AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRH

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKILLKDLKETEQKVKDIQ
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 init1: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (6-46:26-65)

```

                                10          20          30
AAD-12          RTCFADMRAAYDAL--DEATRLVHQRSARHSLVYSQSKL
                :: :. : : .....: .....: : : :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLLYLQHQL
                10          20          30          40          50

                40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH
                .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKIL
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 init1: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.6

Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (6-46:26-65)

```

                                10          20          30
AAD-12          RTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                ::  :  :  .....  .....  :  :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                                10          20          30          40          50

                                40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH
                                ....  :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLISKIL
                                60          70          80          90          100          110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein B1 (134 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (6-46:26-65)

```

                                10          20          30
AAD-12          RTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                ::  :  :  .....  .....  :  :
gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                                10          20          30          40          50

                                40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH
                                ....  :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLISKIL
                                60          70          80          90          100          110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs- Bertholletia (465 aa)
initn: 47 init1: 47 opt: 59 Z-score: 87.0 bits: 22.9 E(): 7.2
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (24-61:198-242)

```

                                10          20          30          40
AAD-12          RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                ::  ::  :  :  :  :  :  :  :  :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                                170          180          190          200          210          220

                                50          60          70          80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRH
                                .....  :  :
gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                                230          240          250          260          270          280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
initn: 52 init1: 52 opt: 52 Z-score: 86.5 bits: 21.2 E(): 7.7

Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (11-34:29-52)

```

                10      20      30      40
AAD-12          RTCFADMRAAYDALDEATR10LVHQRSARHSLVYSQSKLGHVQ
                : : : : : . . . : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
                10      20      30      40      50      60

                50      60      70      80
AAD-12 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
                70      80      90      100     110     120

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
Full+AD0-Non-sp (38 aa)
initn: 43 init1: 43 opt: 43 Z-score: 85.3 bits: 18.9 E(): 8.9
Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
in 21 aa overlap (39-59:5-25)

```

                10      20      30      40      50      60
AAD-12 AAYDALDEATR10LVHQRSARHSLVYSQSKLGHVQVQAGSAYIGYGMDDTTATPLRPLVKVHP
                : : : : : . . . : : :
gi+AHw-462          AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
                10      20      30

                70      80
AAD-12 ETGRPSLLIGRH
gi+AHw-462 LNSA

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:15 2010 done: Fri Feb 5 12:56:15 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 136 - 215 80 aa - 80 aa


```

82      7      3:+ACoAPQA9-
84      1      3:+ACo-
86      2      2:+ACo-
88      4      2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      0      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     1      0:+AD0-          +ACoAPQ-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120  0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.82030.00319+ADs- mu+AD0- -
0.4515 0.165
mean+AF8-var+AD0-40.128610.001, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.202464
Kolmogorov-Smirnov statistic: 0.1026 (N+AD0-28) at 50

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  69 25.9    0.74
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 23.0    1.7
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.6    3.8
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.6    3.9
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.2    5.6
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  52 21.2    6.5
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  52 21.2    6.5
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.2    6.5
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)  59 22.9    6.8
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)  52 21.2    7.5

```

gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No (38) 43 18.9 9.1

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 69 Z-score: 104.7 bits: 25.9 E(): 0.74
Smith-Waterman score: 69+ADs- 21.918+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (2-74:313-379)

AAAD-12 TCFADMRAAYDALDEATRALVHQRSARHSLV
: : : . . . : : : . .
gi+AHw-113 QVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAAESMK
290 300 310 320 330

AAAD-12 YSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHA
. . : . : . . . : : . . : : . .
gi+AHw-113 WNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEFGESALSLTSSAGVLSCQPGAPC
340 350 360 370 380 390

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
initn: 58 init1: 58 opt: 58 Z-score: 98.2 bits: 23.0 E(): 1.7
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (3-54:26-77)

AAAD-12 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
::: : . . : : . . : : . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFAKVN
10 20 30 40 50 60

AAAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHA
::: . . : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGLAQKRVAG
70 80 90 100 110 120

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)
initn: 41 init1: 41 opt: 57 Z-score: 92.0 bits: 22.6 E(): 3.8
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (4-56:93-149)

AAAD-12 TCFADMRAA-----YDALDEATRALVHQRSARH
. . . . : : : :
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKQKWDPLKKE
70 80 90 100 110 120

AAAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHA
. . : : : :

gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
 60 70 80 90 100 110

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)

initn: 38 init1: 38 opt: 52 Z-score: 87.8 bits: 21.2 E(): 6.5
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (5-45:26-65)

10 20 30
 AAD-12 TCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
 :: : ::::: ::::: : :
 gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
 10 20 30 40 50

40 50 60 70 80
 AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA
 :

gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
 60 70 80 90 100 110

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein B1 (134 aa)

initn: 38 init1: 38 opt: 52 Z-score: 87.8 bits: 21.2 E(): 6.5
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (5-45:26-65)

10 20 30
 AAD-12 TCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
 :: : ::::: ::::: : :
 gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
 10 20 30 40 50

40 50 60 70 80
 AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA
 :

gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
 60 70 80 90 100 110

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)

initn: 47 init1: 47 opt: 59 Z-score: 87.4 bits: 22.9 E(): 6.8
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (23-60:198-242)

10 20 30 40
 AAD-12 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
 ::::: ::::: ::::: : :::::
 gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
 170 180 190 200 210 220

50 60 70 80
 AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHA
 ::::: :::::

gi+AHw-303 VLGFGMDETETARKVVRGEDDQRGHIVRVEQGLKVI RPPRIREELEQQEGGGYNGLEETICS
 230 240 250 260 270 280

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.5
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (10-33:29-52)

10 20 30 40
 AAD-12 TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
 : : : : : . . . : : : :
 gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
 10 20 30 40 50 60

50 60 70 80
 AAD-12 QAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHA

gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
 70 80 90 100 110 120

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 85.2 bits: 18.9 E(): 9.1
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (38-58:5-25)

10 20 30 40 50 60
 AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQAGSAYIGYMDTTATPLRPLVKVHP
 : : : : : . . . : : : :
 gi+AHw-462 AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
 10 20 30

70 80
 AAD-12 ETGRPSLLIGRHA

gi+AHw-462 LNSA

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:15 2010 done: Fri Feb 5 12:56:15 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

72      28      12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
74      11      10:+AD0APQA9ACo-
76      9       7:+AD0APQAq-
78      10      6:+AD0AKgA9AD0-
80      2       4:+AD0AKg-
82      6       3:+ACoAPQ-
84      1       3:+ACo-
86      2       2:+ACo-
88      4       2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      0       1:+ACo-
92      2       1:+ACo-          :+ACoAPQ-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     1       0:+AD0-          +ACoAPQ-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0 0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.98500.00322+ADs- mu+AD0- -
1.2648 0.167
mean+AF8-var+AD0-40.0529 9.937, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.202655
Kolmogorov-Smirnov statistic: 0.1067 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  69 25.9    0.76
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 23.0    1.7
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.6    3.8
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.6    3.9
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.3    5.6
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  52 21.2    6.4
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  52 21.2    6.4
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.2    6.4

```

gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465) 59 22.9 7.1
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.2 7.5
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No (38) 43 19.0 8.7

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 65 init1: 65 opt: 69 Z-score: 104.5 bits: 25.9 E(): 0.76
 Smith-Waterman score: 69+ADs- 21.918+ACU- identity (50.685+ACU- similar)
 in 73 aa overlap (1-73:313-379)

```

                                10      20      30
AAD-12                        CFADMRAAYDALDEATRALVHQRSARHSLV
                                :  :  :  .  .  :  .  :  :  :  .
gi+AHw-113 QVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEEAAESMK
                290      300      310      320      330
    
```

```

                40      50      60      70      80
AAD-12 YSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAH
                ..  :  .  :  .  .  :  :  .  :  .  :  :  .  :  :  .
gi+AHw-113 WNWRTNKDVLENGAI FV ASGVDPVLTPEQSAGMIPAE PGESALSLTSSAGVLS CQPGAPC
                340      350      360      370      380      390
    
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 init1: 58 opt: 58 Z-score: 98.3 bits: 23.0 E(): 1.7
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (2-53:26-77)

```

                                10      20      30
AAD-12                        CFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                ::  :  .  .  :  .  :  :  :  .  .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQ LSTKHSVPDVLAFAKVN
                10      20      30      40      50      60
    
```

```

                40      50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAH
                ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AAEKLGGLAQKRVAG
                70      80      90      100      110      120
    
```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)
 initn: 41 init1: 41 opt: 57 Z-score: 92.0 bits: 22.6 E(): 3.8
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (3-55:93-149)

```

                                10      20
AAD-12                        CFADMRAA-----YDALDEATRALVHQRSARH
                                .  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKQKWDPLKKE
                70      80      90      100      110      120
    
```

```

      30      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAH
      .. :   .. :   .. :   .. :   .. :   .. :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
      130      140      150      160      170      180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 91.8 bits: 22.6 E(): 3.9
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (3-55:97-153)

```

                                10      20
AAD-12                          CFADMRAA-----YDALDEATR ALVHQRSARH
                                .. :   .. :   .. :   .. :   .. :
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
      70      80      90      100      110      120

```

```

      30      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAH
      .. :   .. :   .. :   .. :   .. :   .. :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
      130      140      150      160      170      180

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 89.0 bits: 21.3 E(): 5.6
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (4-44:11-50)

```

                                10      20      30      40      50
AAD-12          CFADMRAAYDAL--DEATR ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
                                .. :   .. :   .. :   .. :   .. :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQ LLYLQHQ LDELNENKSKELQEKI
      10      20      30      40      50

```

```

                                60      70      80
AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRHAH
gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFN YEEAQ T LSKILLKDLKETEQKV KDIQ
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.8 bits: 21.2 E(): 6.4
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (4-44:26-65)

```

                                10      20      30
AAD-12          CFADMRAAYDAL--DEATR ALVHQRSARHSLVYSQSKL
                                .. :   .. :   .. :   .. :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQ LLYLQHQ L
      10      20      30      40      50

```



```
          50          60          70          80
AAD-12  YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAH
          ..... :: ..
gi+AHw-303 VLGFGMTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
          230          240          250          260          270          280
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 init1: 52 opt: 52 Z-score: 86.7 bits: 21.2 E(): 7.5
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (9-32:29-52)

```
          10          20          30          40
AAD-12          CFADMRAAYDALDEATRNLVHQRSARHSLVYSQSKLGHVQ
          : : : : : . . . : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
          10          20          30          40          50          60
```

```
          50          60          70          80
AAD-12  QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAH
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
          70          80          90          100          110          120
```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
Full+AD0-Non-sp (38 aa)
initn: 43 init1: 43 opt: 43 Z-score: 85.5 bits: 19.0 E(): 8.7
Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
in 21 aa overlap (37-57:5-25)

```
          10          20          30          40          50          60
AAD-12  AAYDALDEATRNLVHQRSARHSLVYSQSKLGHVQAGSAYIGYGMTTATPLRPLVKVHP
          ..... : . : : . : :
gi+AHw-462          AITCGQVSSALSSCLGYLKNNGGAVPPGSSCGIKN
          10          20          30
```

```
          70          80
AAD-12  ETGRPSLLIGRHAH
```

gi+AHw-462 LNSA

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:15 2010 done: Fri Feb 5 12:56:15 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1


```

62 48 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
64 42 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66 34 25:+AD0APQA9AD0-+AD0APQA9AD0AKgA9AD0APQ-
68 17 20:+AD0APQA9AD0APQA9ACo-
70 18 16:+AD0APQA9AD0APQAq-
72 28 12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
74 10 10:+AD0APQA9ACo-
76 10 7:+AD0APQAqAD0-
78 9 6:+AD0AKgA9-
80 2 4:+AD0AKg-
82 5 3:+ACoAPQ-
84 1 3:+ACo-
86 2 2:+ACo-
88 4 2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90 0 1:+ACo-
92 2 1:+ACo-          :+ACoAPQ-
94 0 1:+ACo-          :+ACo-
96 0 1:+ACo-          :+ACo-
98 1 0:+AD0-          +ACoAPQ-
100 1 0:+AD0-          +ACoAPQ-
102 0 0:          +ACo-
104 0 0:          +ACo-
106 0 0:          +ACo-
108 0 0:          +ACo-
110 0 0:          +ACo-
112 0 0:          +ACo-
114 0 0:          +ACo-
116 0 0:          +ACo-
118 0 0:          +ACo-
+AD4-120 0 0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.96790.00323+ADs- mu+AD0- -
1.1491 0.167
mean+AF8-var+AD0-39.9025 9.854, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.203036
Kolmogorov-Smirnov statistic: 0.0971 (N+AD0-29) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:          opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 67 25.3 1.1
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 58 23.0 1.7
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.6 3.8
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-G1
( 204) 57 22.6 3.9
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.3 5.6

```

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 52 21.2 6.4
 gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 52 21.2 6.4
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 52 21.2 6.4
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465) 59 22.9 7
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.2 7.5
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No (38) 43 19.0 8.7

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 65 init1: 65 opt: 67 Z-score: 101.4 bits: 25.3 E(): 1.1
 Smith-Waterman score: 67+ADs- 24.242+ACU- identity (53.030+ACU- similar)
 in 66 aa overlap (10-72:314-379)

```

                                10          20          30
AAD-12          FADMRAAYDALDEATRALV---HQRSARHSLVYSQSKLG
                                : : : . . : : : . . . .
gi+AHw-113 VVNNNYDKWGSYAIGGSASPTILSQGNRFPCAPDERSKKNVLGRHGEEAAESMKWNWRTNK
                290          300          310          320          330          340

                40          50          60          70          80
AAD-12 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHA
                : . : . . . : : . : : . . : : . :
gi+AHw-113 DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSILTSSAGVLSCQPGAPC
                350          360          370          380          390
    
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 init1: 58 opt: 58 Z-score: 98.3 bits: 23.0 E(): 1.7
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (1-52:26-77)

```

                                10          20          30
AAD-12          FADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                : : : . . : : : . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQQLSTKHSVPDVLAFKVVNV
                10          20          30          40          50          60

                40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHA
                : : : . . : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQKRVAG
                70          80          90          100          110          120
    
```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)
 initn: 41 init1: 41 opt: 57 Z-score: 92.0 bits: 22.6 E(): 3.8
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (2-54:93-149)

```

                                10      20
AAD-12                          FADMRAA-----YDALDEATRALVHQRSARH
                                .....:   ::: :: .. . ..
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                   70      80      90      100      110      120

```

```

                   30      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA
                   .. :   ... :: .....:   :: :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
                   130     140     150     160     170     180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 init1: 41 opt: 57 Z-score: 91.8 bits: 22.6 E(): 3.9
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (2-54:97-153)

```

                                10      20
AAD-12                          FADMRAA-----YDALDEATRALVHQRSARH
                                .....:   ::: :: .. . ..
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                   70      80      90      100      110      120

```

```

                   30      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA
                   .. :   ... :: .....:   :: :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREK
                   130     140     150     160     170     180

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 init1: 38 opt: 52 Z-score: 89.0 bits: 21.3 E(): 5.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (3-43:11-50)

```

                   10      20      30      40      50
AAD-12          FADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
                   ::: :: : .....:   .....:   :: ..... :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDLNLNENKSKELQEKI
                   10      20      30      40      50

```

```

                   60      70      80
AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRHAHA

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQKVVDIQ
                   60      70      80      90      100      110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.9 bits: 21.2 E(): 6.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (3-43:26-65)

```

                                10          20          30
AAD-12          FADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                   ::  :  :  .....  .....  :  :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                   10          20          30          40          50

                   40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA
                   ....  :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                   60          70          80          90          100          110

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.9 bits: 21.2 E(): 6.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (3-43:26-65)

```

                                10          20          30
AAD-12          FADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                   ::  :  :  .....  .....  :  :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                   10          20          30          40          50

                   40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA
                   ....  :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                   60          70          80          90          100          110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.9 bits: 21.2 E(): 6.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (3-43:26-65)

```

                                10          20          30
AAD-12          FADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                   ::  :  :  .....  .....  :  :
gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                   10          20          30          40          50

                   40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA
                   ....  :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                   60          70          80          90          100          110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 init1: 47 opt: 59 Z-score: 87.2 bits: 22.9 E(): 7
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (21-58:198-242)

```

                10         20         30         40
AAD-12          FADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                : : : : : : : : : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHF FLAGNIQRSQKQ RGERYGLRGGQQILADNVFKGFNMEALAD
                170         180         190         200         210         220

```

```

                50         60         70         80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAHA
                . : : : : : : : : : : :
gi+AHw-303 VLGFGMTETARKV RGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                230         240         250         260         270         280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 86.7 bits: 21.2 E(): 7.5
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (8-31:29-52)

```

                10         20         30
AAD-12          FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                : : : : : : : : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEEAARISAKNALESYAYSLRNTLSDS
                10         20         30         40         50         60

```

```

                40         50         60         70         80
AAD-12 QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
                70         80         90         100        110        120

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 85.5 bits: 19.0 E(): 8.7
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (36-56:5-25)

```

                10         20         30         40         50         60
AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP
                : : : : : : : : : : : :
gi+AHw-462          AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
                10         20         30

```

```

                70         80
AAD-12 ETGRPSLLIGRHAHA

```

gi+AHw-462 LNSA

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-


```

56      78
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58      81
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9-
60      68
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
62      52      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
64      44      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
66      29      25:+AD0APQA9AD0APQA9AD0APQAqAD0-
68      21      20:+AD0APQA9AD0APQA9ACo-
70      22      16:+AD0APQA9AD0APQAqAD0APQ-
72      28      12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
74      8       10:+AD0APQA9ACo-
76      10      7:+AD0APQAqAD0-
78      9       6:+AD0AKgA9-
80      2       4:+AD0AKg-
82      3       3:+ACo-
84      1       3:+ACo-
86      2       2:+ACo-
88      4       2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      0       1:+ACo-
92      2       1:+ACo-          :+ACoAPQ-
94      1       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.08370.00326+ADs- mu+AD0- -
1.7127 0.169
mean+AF8-var+AD0-40.599010.047, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.201287
Kolmogorov-Smirnov statistic: 0.0890 (N+AD0-29) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:          opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 67 25.2 1.2

```

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 56 22.4 2.6
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)
 57 22.5 4
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
 (204) 57 22.5 4.1
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 21.2 5.8
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 52 21.2 6.7
 gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 52 21.2 6.7
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
 52 21.2 6.7
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 22.8 7.5
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
 (152) 52 21.1 7.8
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
 (38) 43 19.0 8.8

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 65 init1: 65 opt: 67 Z-score: 100.7 bits: 25.2 E(): 1.2
 Smith-Waterman score: 67+ADs- 24.242+ACU- identity (53.030+ACU- similar)
 in 66 aa overlap (9-71:314-379)

```

                                10          20          30
AAD-12                        ADMRAAYDALDEATRALV---HQRSARHSLVYSQSKLG
                                : : . . : : . . . .
gi+AHw-113 VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNK
                290          300          310          320          330          340

                40          50          60          70          80
AAD-12 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI
                : . : . . . : : . : : . . : : . :
gi+AHw-113 DVLENGAIFVASGVDFVLTPEQSAGMIPAEPGESALSILTSSAGVLSCQPGAPC
                350          360          370          380          390
    
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 50 init1: 50 opt: 56 Z-score: 94.8 bits: 22.4 E(): 2.6
 Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
 in 44 aa overlap (12-51:34-77)

```

                                10          20          30
AAD-12                        ADMRAAYDALDEATRALVHQRSARHS----LVYSQSKLGHV
                                . : . : : : : : : : : : : :
gi+AHw-527 HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQVSTKHSVPDVLAFKVNVDHV
                10          20          30          40          50          60

                40          50          60          70          80
AAD-12 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI
                : : : : : : : :
    
```

gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA... 70 80 90 100 110 120

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa) initn: 41 initl: 41 opt: 57 Z-score: 91.6 bits: 22.5 E(): 4 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar) in 58 aa overlap (1-53:93-149)

AAAD-12 ADMRAA-----YDALDEATR... gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE 70 80 90 100 110 120

AAAD-12 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAI .. : ... : : : : gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP... 130 140 150 160 170 180

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Glutat (204 aa) initn: 41 initl: 41 opt: 57 Z-score: 91.4 bits: 22.5 E(): 4.1 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar) in 58 aa overlap (1-53:97-153)

AAAD-12 ADMRAA-----YDALDEATR... gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE 70 80 90 100 110 120

AAAD-12 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAI .. : ... : : : : gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP... 130 140 150 160 170 180

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Structur (119 aa) initn: 38 initl: 38 opt: 52 Z-score: 88.7 bits: 21.2 E(): 5.8 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar) in 43 aa overlap (2-42:11-50)

AAAD-12 ADMRAAYDAL--DEATR... gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ... 10 20 30 40 50

AAAD-12 DTTATPLRPLVKVHPETGRPSLLIGRHAHAI 50 60 70 80

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLKILLKDLKETEQKVKDIQ
60 70 80 90 100 110

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.5 bits: 21.2 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (2-42:26-65)

AAD-12 ADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
:: : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVLAQEHEKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
10 20 30 40 50

AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI
.... :

gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.5 bits: 21.2 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (2-42:26-65)

AAD-12 ADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
:: : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
10 20 30 40 50

AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI
.... :

gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.5 bits: 21.2 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (2-42:26-65)

AAD-12 ADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
:: : : : : : : : : : : :
gi+AHw-420 MKFAIVLIACFAASVLAQEHEKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
10 20 30 40 50

AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI
.... :

gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 initl: 47 opt: 59 Z-score: 86.6 bits: 22.8 E(): 7.5
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (20-57:198-242)

10 20 30 40
AAD-12 ADMRAAYDALDEATR...LHVHQR...SARHSLVYSQSKL-----GHVQQAGSA
::: ::: .:: : : ::
gi+AHw-303 LVQHTASDLNQLDQNP...RHHFFLAGNIQRSQKQ...RGERYGLRGGQQILADNVFKGFNMEALAD
170 180 190 200 210 220

50 60 70 80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAI
.::.: : : .:
gi+AHw-303 VLGF...GMDTETARKV...RGEDDQRGHIVRVEQGLK...VIRPPRIREELEQQEGGGYNGLEETICS
230 240 250 260 270 280

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 86.3 bits: 21.1 E(): 7.8
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (7-30:29-52)

10 20 30
AAD-12 ADMRAAYDALDEATR...LHVHQR...SARHSLVYSQSKLGHVQ
: : :: : . .: : :
gi+AHw-144 KTNKIVITNDKGR...LSKEEIERMLAEAEKYKA...EAEAAARISAKNALESYAYSLRNTLSDS
10 20 30 40 50 60

40 50 60 70 80
AAD-12 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAI
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
70 80 90 100 110 120

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
Full+AD0-Non-sp (38 aa)
initn: 43 initl: 43 opt: 43 Z-score: 85.4 bits: 19.0 E(): 8.8
Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
in 21 aa overlap (35-55:5-25)

10 20 30 40 50 60
AAD-12 AAYDALDEATR...LHVHQR...SARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP
: : : : : : . : : . : :
gi+AHw-462 AITCGQVSSALSSCLGYLKN...GGAVPPGSSCGIKN
10 20 30

70 80
AAD-12 ETGRPSLLIGRHAHAI

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR	RecName: Full+AD0-Po
(396)	67 25.2 1.2
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU	RecName: Full+AD0-T
(121)	56 22.4 2.6
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg	(200)
56 22.2	4.9
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE	RecName: Full+AD0-Gl
(204)	56 22.2 5
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru	(119)
52 21.2	5.8
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom	(134)
52 21.2	6.7
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom	(134)
52 21.2	6.7
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei	(134)
52 21.2	6.7
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle	(465)
59 22.8	7.4
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL	RecName: Full+AD0-
(152)	52 21.1 7.8
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX	RecName: Full+AD0-No
(38)	43 19.0 8.8

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 65 init1: 65 opt: 67 Z-score: 100.8 bits: 25.2 E(): 1.2
Smith-Waterman score: 67+ADs- 24.242+ACU- identity (53.030+ACU- similar)
in 66 aa overlap (8-70:314-379)

		10	20	30	
AAD-12		DMRAAYDALDEATRALV	---HQRSARHSLVYSQSKLG		
		:	::	..	: : : : . . .
gi+AHw-113	VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNK				
	290	300	310	320	330
	40	50	60	70	80
AAD-12	HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIP				
	:	::	. : : .
gi+AHw-113	DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSILTSSAGVLSCQPGAPC				
	350	360	370	380	390

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)

initn: 45 init1: 45 opt: 56 Z-score: 94.8 bits: 22.4 E(): 2.6
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (11-50:34-77)


```

AAD-12          DMRAAYDAL--DEATRALVHQRSARHSLVYSQSCLGHVQQAGSAYIGYGM
                :::  :: :  .....  .....:::  ::  ....  :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDENENKSKELQEKI
                10          20          30          40          50

```

```

AAD-12          50          60          70          80
AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRHAHAIP

```

```

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLKILLKDLKETEQKVKDIQ
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (1-41:26-65)

```

AAD-12          10          20          30
                DMRAAYDAL--DEATRALVHQRSARHSLVYSQSCL
                :::  :: :  .....  .....:::  ::  ....  :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLD
                10          20          30          40          50

```

```

AAD-12          40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP

```

```

gi+AHw-111 DELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLKIL
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (1-41:26-65)

```

AAD-12          10          20          30
                DMRAAYDAL--DEATRALVHQRSARHSLVYSQSCL
                :::  :: :  .....  .....:::  ::  ....  :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLD
                10          20          30          40          50

```

```

AAD-12          40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP

```

```

gi+AHw-111 DELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLKIL
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (1-41:26-65)

```

AAD-12                      DMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                               :::  :: :  .....  .....  :  ::
gi+AHw-420 MKFAIVLIACFAASVLAQEHPKPKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
              10          20          30          40          50

```

```

AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIP
        ....  :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 86.7 bits: 22.8 E(): 7.4
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (19-56:198-242)

```

AAD-12                      10          20          30          40
                               DMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                               :::  :::  :::  :  :  :::  .
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
              170          180          190          200          210          220

```

```

AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAHAIP
        .....  ::  .:
gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
              230          240          250          260          270          280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 86.4 bits: 21.1 E(): 7.8
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (6-29:29-52)

```

AAD-12                      10          20          30
                               DMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                               :  :  :::  :  .  ..:  :  :::
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
              10          20          30          40          50          60

```

```

AAD-12 QAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIP
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAGGE
              70          80          90          100          110          120

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 85.4 bits: 19.0 E(): 8.8
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (34-54:5-25)

```

10          20          30          40          50          60

```

```

AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHP
      ..... :. .:: . .::
gi+AHw-462 AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
              10          20          30

```

```

      70          80
AAD-12 ETGRPSLLIGRHAHAIP
gi+AHw-462 LNSA

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:15 2010 done: Fri Feb 5 12:56:15 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 141 - 220 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      1      8:+AD0- +ACo-
      34      3      21:+AD0- +ACo-
      36      25     44:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38      59     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      40     104
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQ-
      42      91
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-

```


+AD4-120 0 0: +ACo-
 331323 residues in 1471 sequences
 Expectation+AF8-n fit: rho(ln(x))+AD0- 6.00400.00326+ADs- mu+AD0- -
 1.3123 0.169
 mean+AF8-var+AD0-38.7001 9.412, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
 Lambda+AD0- 0.206167
 Kolmogorov-Smirnov statistic: 0.0808 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
 Scan time: 0.080

The best scores are: opt bits E(1471)
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 69 26.0 0.69
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 56 22.6 2.3
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465) 59 23.0 6.6
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
 (152) 52 21.3 7
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
 (38) 43 19.1 8

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 65 init1: 65 opt: 69 Z-score: 105.3 bits: 26.0 E(): 0.69
 Smith-Waterman score: 69+ADs- 23.750+ACU- identity (51.250+ACU- similar)
 in 80 aa overlap (7-80:314-393)

		10	20	30	
AAD-12		MRAAYDALDEATRALV---HQRSARHSLVYSQSKLG			
		:	:	:	:
gi+AHw-113	VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNK				
	290 300 310 320 330 340				
	40 50 60 70 80				
AAD-12	HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PG				
	:	:	:	:	:
gi+AHw-113	DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSILTSSAGVLSCQPGAPC				
	350 360 370 380 390				

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 45 init1: 45 opt: 56 Z-score: 95.8 bits: 22.6 E(): 2.3
 Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
 in 44 aa overlap (10-49:34-77)

		10	20	30	
AAD-12		MRAAYDALDEATRALVHQRSARHS----LVYSQSKLGHV			
		:	:	:	:
gi+AHw-527	HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVNVDHV				
	10 20 30 40 50 60				

```

      40      50      60      70      80
AAD-12 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPG
      :. . . . : . : :
gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AAAEKLGLA QKR VAGA
      70      80      90      100     110     120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 87.7 bits: 23.0 E(): 6.6
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (18-55:198-242)

```

      10      20      30      40
AAD-12      MRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
      :. . : . . : . : : . : . :
gi+AHw-303 LVQHTASDLNQLDQNPRHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
      170     180     190     200     210     220

```

```

      50      60      70      80
AAD-12 YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPG
      :. . : . : : . :
gi+AHw-303 VLGFGMDTETARKVVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230     240     250     260     270     280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (5-28:29-52)

```

      10      20      30
AAD-12      MRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
      : : : : : . . : . : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEEAARISAKNALESYAYSLRNTLSDS
      10      20      30      40      50      60

```

```

      40      50      60      70      80
AAD-12 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPG
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
      70      80      90      100     110     120

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 86.1 bits: 19.1 E(): 8
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (33-53:5-25)

```

      10      20      30      40      50      60
AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP
      :. . : . : : . : :
gi+AHw-462      AITCGQVSSALSSCLGYLKNNGGAVPPGSSCGIKN
      10      20      30

```


Kolmogorov-Smirnov statistic: 0.0815 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po (396) 69 26.1 0.65

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T (121) 56 22.6 2.2

gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465) 59 23.1 6.2

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.3 6.8

gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No (38) 43 19.1 8.1

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)

initn: 65 init1: 65 opt: 69 Z-score: 105.8 bits: 26.1 E(): 0.65
Smith-Waterman score: 69+ADs- 23.750+ACU- identity (51.250+ACU- similar)
in 80 aa overlap (6-79:314-393)

```

                                10          20          30
AAD-12          RAAVDALDEATRALV---HQRSARHSLVYSQSKLG
                                : : . . : : . . . .
gi+AHw-113 VVNNNYDKWGSYAIGGSASPTILSQGNRFPCAPDERSKKNVLGRHGEEAAESMKWNWRTNK
          290          300          310          320          330          340

          40          50          60          70          80
AAD-12 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGM
          : . : . . . : : . : : . . : : . : . : . . : :
gi+AHw-113 DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSILTSSAGVLSCQPGAPC
          350          360          370          380          390
    
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)

initn: 45 init1: 45 opt: 56 Z-score: 96.0 bits: 22.6 E(): 2.2
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (9-48:34-77)

```

                                10          20          30
AAD-12          RAAVDALDEATRALVHQRSARHS----LVYSQSKLGHV
                                . : . : : : : : : : . . . . : :
gi+AHw-527 HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQVSTKHSVPDVLAFQKVNVDHV
          10          20          30          40          50          60

          40          50          60          70          80
AAD-12 QQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAI PGM
          : : : . : : :
gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQKRVAGA
          70          80          90          100          110          120
    
```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 88.1 bits: 23.1 E(): 6.2
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (17-54:198-242)

```

                10      20      30      40
AAD-12          RAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHF FLAGNIQRSQKQ RGER YGLRGGQQILADNVFKGFNMEALAD
                170      180      190      200      210      220
    
```

```

                50      60      70      80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGM
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-303 VLGFGMTETARKVRGEDDQRGHIVRVEQGLKVI RPPRIREELEQQEGGGYNGLEETICS
                230      240      250      260      270      280
    
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 87.4 bits: 21.3 E(): 6.8
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (4-27:29-52)

```

                10      20      30
AAD-12          RAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKA EDEAEAAARISAKNALESYAYSLRNTLSDS
                10      20      30      40      50      60
    
```

```

                40      50      60      70      80
AAD-12 QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
                70      80      90      100      110      120
    
```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 86.0 bits: 19.1 E(): 8.1
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (32-52:5-25)

```

                10      20      30      40      50      60
AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-462          AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
                10      20      30
    
```

```

                70      80
AAD-12 ETGRPSLLIGRHAHAIPGM
    
```

gi+AHw-462 LNSA

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 56 22.7 2.2
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 23.2 5.8
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
 (152) 52 21.4 6.6
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
 (38) 43 19.0 8.4

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 65 initl: 65 opt: 69 Z-score: 106.8 bits: 26.3 E(): 0.57
 Smith-Waterman score: 69+ADs- 23.750+ACU- identity (51.250+ACU- similar)
 in 80 aa overlap (5-78:314-393)

```

                                10          20          30
AAD-12                AAYDALDEATRALV---HQRSARHSLVYSQSKLG
                        : : : . . : : : . . . . .
gi+AHw-113 VVNNNYDKWGSYAIGGSASPTILSQGNRFPCAPDERSKKNVLGRHGEEAAESMKWNWRTNK
                290          300          310          320          330          340

                        40          50          60          70          80
AAD-12 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMD
                : . : . . . : : . : : . . : : . : . : . : :
gi+AHw-113 DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
                350          360          370          380          390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 45 initl: 45 opt: 56 Z-score: 96.4 bits: 22.7 E(): 2.2
 Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
 in 44 aa overlap (8-47:34-77)

```

                                10          20          30
AAD-12                AAYDALDEATRALVHQRSARHS----LVYSQSKLGHV
                        . : . . : : : : : : : . . . . . : :
gi+AHw-527 HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQSLTKHSVPDVLAFQKVNVDHV
                10          20          30          40          50          60

                        40          50          60          70          80
AAD-12 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD
                : : : . : : :
gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQKRVAGA
                70          80          90          100          110          120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 88.7 bits: 23.2 E(): 5.8
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (16-53:198-242)

```

                                10          20          30
AAD-12                AAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                        : : : . . : : : . . . . . : : . . . .

```

gi+AHw-303 LVQHTASDLNQLDQNP RHF FLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
170 180 190 200 210 220

40 50 60 70 80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD
.:.:.:.: .: .:

gi+AHw-303 VLGFGMTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
230 240 250 260 270 280

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 87.6 bits: 21.4 E(): 6.6
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (3-26:29-52)

10 20 30
AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
: : : : : . . . : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
10 20 30 40 50 60

40 50 60 70 80
AAD-12 QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD

gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
70 80 90 100 110 120

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
Full+AD0-Non-sp (38 aa)
initn: 43 initl: 43 opt: 43 Z-score: 85.8 bits: 19.0 E(): 8.4
Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
in 21 aa overlap (31-51:5-25)

10 20 30 40 50 60
AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQAGSAYIGYGMTTATPLRPLVKVHP
: : : : : . . . : : : :
gi+AHw-462 AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
10 20 30

70 80
AAD-12 ETGRPSLLIGRHAHAIPGMD

gi+AHw-462 LNSA

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:18 2010 done: Fri Feb 5 12:56:18 2010
Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

```
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 144 - 223 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      0      8: +ACo-
      34      5      21:+AD0APQ- +ACo-
      36      45     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
      38      68
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
      40      74
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      42      100
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0- +ACo-
      44      144
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
      46      106
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      48      125
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      50      109
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      52      114
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
      54      124
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9-
      56      82
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0-
```

```

58      68
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60      57      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      61
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
64      40      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      26      25:+AD0APQA9AD0APQA9AD0APQAq-
68      27      20:+AD0APQA9AD0APQA9ACoAPQA9-
70      20      16:+AD0APQA9AD0APQAqAD0-
72      18      12:+AD0APQA9ACoAPQA9-
74      22      10:+AD0APQA9ACoAPQA9AD0APQ-
76      13      7:+AD0APQAqAD0APQ-
78      6       6:+AD0AKg-
80      7       4:+AD0AKgA9-
82      1       3:+ACo-
84      2       3:+ACo-
86      1       2:+ACo-
88      2       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     1       0:+AD0-          +ACoAPQ-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.70930.00309+ADs- mu+AD0- 0.5536
0.160
mean+AF8-var+AD0-36.0156 8.639, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.213712
Kolmogorov-Smirnov statistic: 0.0828 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.070
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  69 26.4    0.54
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  56 22.7    2.1
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.2    5.6
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)  52 21.4    6.4

```


gi+AHw-303 VLGFGMDETETARKVVRGEDDQRGHIVRVEQGLKVI RPPRIREELEQQEGGGYNGLEETICS
 230 240 250 260 270 280

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)

initn: 52 init1: 52 opt: 52 Z-score: 87.9 bits: 21.4 E(): 6.4
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (2-25:29-52)

AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
 : : : : : . . . : : : :
 gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
 10 20 30 40 50 60

QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA
 40 50 60 70 80

KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
 70 80 90 100 110 120

+AD4-+AD4-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)

initn: 43 init1: 43 opt: 43 Z-score: 86.1 bits: 19.1 E(): 8
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (30-50:5-25)

AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE
 : : : : : . . . : : : :
 gi+AHw-462 AITCGQVSSALSSCLGYLKNNGAVPPGSSCGIKNL
 10 20 30

TGRPSLLIGRHAHAIPGMDA
 70 80

gi+AHw-462 NSA

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:19 2010 done: Fri Feb 5 12:56:19 2010
 Total Scan time: 0.070 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

72    16    12:+AD0APQA9ACoAPQA9-
74    22    10:+AD0APQA9ACoAPQA9AD0APQ-
76    11    7:+AD0APQAqAD0-
78    13    6:+AD0AKgA9AD0APQ-
80     6    4:+AD0AKg-
82     7    3:+ACoAPQA9-
84     2    3:+ACo-
86     1    2:+ACo-
88     1    2:+ACo-          inset +AD0- represents 1 library sequences
90     1    1:+ACo-
92     0    1:+ACo-          :+ACo-
94     0    1:+ACo-          :+ACo-
96     0    1:+ACo-          :+ACo-
98     1    0:+AD0-          +ACoAPQ-
100    0    0:              +ACo-
102    0    0:              +ACo-
104    0    0:              +ACo-
106    0    0:              +ACo-
108    0    0:              +ACo-
110    1    0:+AD0-          +ACoAPQ-
112    0    0:              +ACo-
114    0    0:              +ACo-
116    0    0:              +ACo-
118    0    0:              +ACo-
+AD4-120    0    0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.06930.00331+ADs- mu+AD0- 3.6737
0.170
mean+AF8-var+AD0-34.1757 8.340, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.219389
Kolmogorov-Smirnov statistic: 0.0917 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   69 26.9   0.38
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   56 22.9   1.8
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.7   4.1
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)   52 21.6   5.5
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
(  38)   43 19.0   8.5
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
51 21.3   9.3
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)   51 21.3   9.5

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

```


initn: 52 init1: 52 opt: 52 Z-score: 89.1 bits: 21.6 E(): 5.5
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (1-24:29-52)

```

                                10      20      30
AAD-12      YDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                                : : : : : . . . : : : :
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAARISAKNALESYAYSLRNTLSDS
                                10      20      30      40      50      60
    
```

```

                                40      50      60      70      80
AAD-12  QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA
gi+AHw-144  KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
                                70      80      90      100     110     120
    
```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 init1: 43 opt: 43 Z-score: 85.7 bits: 19.0 E(): 8.5
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (29-49:5-25)

```

                                10      20      30      40      50      60
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET
                                : : : : : . . . : : : :
gi+AHw-462  AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLN
                                10      20      30
    
```

```

                                70      80
AAD-12  GRPSLLIGRHAHAIPGMDAA
    
```

gi+AHw-462 SA

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
 allergen +AFs- (200 aa)
 initn: 41 init1: 41 opt: 51 Z-score: 85.0 bits: 21.3 E(): 9.3
 Smith-Waterman score: 51+ADs- 27.660+ACU- identity (61.702+ACU- similar)
 in 47 aa overlap (1-47:104-149)

```

                                10      20      30
AAD-12      YDALDEATRALVHQRSARHSLVYSQSKLGH
                                : : : : : . . . : : : :
gi+AHw-144  LSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKETIPYYTKKFDE
                                80      90      100     110     120     130
    
```

```

                                40      50      60      70      80
AAD-12  VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA
                                : : : : : . . . : : : :
gi+AHw-144  VVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREKVLGLPAIKAWV
                                140     150     160     170     180     190
    
```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)

initn: 41 init1: 41 opt: 51 Z-score: 84.8 bits: 21.3 E(): 9.5
 Smith-Waterman score: 51+ADs- 27.660+ACU- identity (61.702+ACU- similar)
 in 47 aa overlap (1-47:108-153)

```

                                10      20      30
AAD-12      YDALDEATRALVHQRSARHSLVYSQSKLGH
                                ::: :: .. . .... : ...
gi+AHw-622 LSGKDDWENLEIDMIVDTISDFRAAIIANYHYDA-DENSKQKKWDPLKKETIPYYTKKFDE
            80      90      100      110      120      130

                                40      50      60      70      80
AAD-12      VQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA
            : ..... : :
gi+AHw-622 VVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALREKVLGLPAIKAWV
            140      150      160      170      180      190
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:20 2010 done: Fri Feb 5 12:56:20 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 146 - 225 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

    opt      E()
+ADw- 20    2    0:+AD0-
    22      0    0:      one +AD0- represents 3 library sequences
    24      0    0:
    26      0    0:
    28      0    0:
    30      0    2:+ACo-
    32      1    8:+AD0- +ACo-
    34      7    21:+AD0APQA9- +ACo-
    36     46    44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
    38     74
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
    40     55   101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
    
```



```

114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.10760.0033+ADs- mu+AD0- 3.4677
0.170
mean+AF8-var+AD0-33.6122 8.210, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.221221
Kolmogorov-Smirnov statistic: 0.0903 (N+AD0-27) at 50

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  69 26.9  0.36
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  56 23.0  1.7
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)  59 23.7  3.9
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38)  43 19.1  8

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 69 Z-score: 110.3 bits: 26.9 E(): 0.36
Smith-Waterman score: 69+ADs- 23.750+ACU- identity (51.250+ACU- similar) in 80 aa overlap (2-75:314-393)

```

                                10                20
AAD-12                        DALDEATRALV---HQRSARHSLVYSQSKLG
                                : : . . : : . . : . . .
gi+AHw-113 VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNK
                290          300          310          320          330          340

                30          40          50          60          70          80
AAD-12 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAE
                : . : . . . : : . : : . . : : . : . : . : . :
gi+AHw-113 DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSILTSSAGVLSCQPGAPC
                350          360          370          380          390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
initn: 45 init1: 45 opt: 56 Z-score: 98.4 bits: 23.0 E(): 1.7
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar) in 44 aa overlap (5-44:34-77)

```

                                10                20                30
AAD-12                        DALDEATRALVHQRSARHS----LVYSQSKLGHV
                                : : . . : : : : : : : : : :
gi+AHw-527 HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQVSTKHSVPDVLAFKVNVDHV
                10          20          30          40          50          60

```

```

                40          50          60          70          80
AAD-12 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAE
      :.:.:. : .: :
gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AAAEKLGLA QKR VAGA
                70          80          90          100         110         120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 init1: 47 opt: 59 Z-score: 91.7 bits: 23.7 E(): 3.9
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (13-50:198-242)

```

                10          20          30
AAD-12          DALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
      :.:. :.:. :.:. : : .:. .
gi+AHw-303 LVQHTASDLNQLDQNP RHF LAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                170         180         190         200         210         220

```

```

                40          50          60          70          80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAE
      :.:.:. :. :.
gi+AHw-303 VLGFGMDTETARKV RGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                230         240         250         260         270         280

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 init1: 43 opt: 43 Z-score: 86.1 bits: 19.1 E(): 8
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (28-48:5-25)

```

                10          20          30          40          50          60
AAD-12 DALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETG
      :.:.:. :. :. :. :.
gi+AHw-462          AITCGQVSSALSSCLGYLKNNGGAVPPGSSCGIKNLNS
                10          20          30

```

```

                70          80
AAD-12 RPSLLIGRHAHAIPGMDAAE

```

gi+AHw-462 A

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:21 2010 done: Fri Feb 5 12:56:21 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1


```

60      76
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ
-
62      44      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
64      43      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
66      36      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
68      23      20:+AD0APQA9AD0APQA9ACoAPQ-
70      31      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      14      12:+AD0APQA9ACoAPQ-
74      18      10:+AD0APQA9ACoAPQA9-
76      19      7:+AD0APQAqAD0APQA9AD0-
78      13      6:+AD0AKgA9AD0APQ-
80      5       4:+AD0AKg-
82      9       3:+ACoAPQA9-
84      0       3:+ACo-
86      1       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      1       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     1       0:+AD0-          +ACoAPQ-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.09990.0033+ADs- mu+AD0- 3.2779
0.170
mean+AF8-var+AD0-34.4388 8.386, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.218550
Kolmogorov-Smirnov statistic: 0.0896 (N+AD0-27) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  69 26.9    0.38
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  56 23.0    1.7
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.7    4
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38)   43 19.1    8.1

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 69 Z-score: 110.0 bits: 26.9 E(): 0.38
Smith-Waterman score: 69+ADs- 23.750+ACU- identity (51.250+ACU- similar)
in 80 aa overlap (1-74:314-393)

```

                                10          20
AAD-12                ALDEATRALV---HQRSARHSLVYSQSKLG
                        : : : . : : : . : : .
gi+AHw-113 VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNK
                290          300          310          320          330          340

                30          40          50          60          70          80
AAD-12 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAES
                : . : . . . : : . : : . : : . : : . : : :
gi+AHw-113 DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSQPGAPC
                350          360          370          380          390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 init1: 45 opt: 56 Z-score: 98.2 bits: 23.0 E(): 1.7
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (4-43:34-77)

```

                                10          20
AAD-12                ALDEATRALVHQRSARHS----LVYSQSKLGHV
                        . : . : : : : : : : : : : :
gi+AHw-527 HITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQQLSTKHSVPDVLAFKVNVDHV
                10          20          30          40          50          60

                30          40          50          60          70          80
AAD-12 QQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIIPGMDAAES
                : : : . : : :
gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQKRVAGA
                70          80          90          100          110          120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 init1: 47 opt: 59 Z-score: 91.6 bits: 23.7 E(): 4
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (12-49:198-242)

```

                                10          20          30
AAD-12                ALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                        : : : : : : : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                170          180          190          200          210          220

                40          50          60          70          80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAHAIIPGMDAAES
                . : : : : : : : :
gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                230          240          250          260          270          280

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 init1: 43 opt: 43 Z-score: 86.1 bits: 19.1 E(): 8.1
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (27-47:5-25)

```

                10         20         30         40         50         60
AAD-12 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGR
                .....: .: .: .: .:
gi+AHw-462                AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLNSA
                        10         20         30

                70         80
AAD-12 PSLLLIGRHAHAIPGMDDAAES
  
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:21 2010 done: Fri Feb 5 12:56:22 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 148 - 227 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      1      8:+AD0- +ACo-
      34      3     21:+AD0- +ACo-
      36     22     44:+AD0APQA9AD0APQA9AD0APQ- +ACo-
      38     76     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9ACoAPQA9-
      40     73
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
  
```



```

116      0      0:          +ACo-
118      0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.13440.00328+ADs- mu+AD0- 3.1328
0.170
mean+AF8-var+AD0-34.2358 8.315, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.219197
Kolmogorov-Smirnov statistic: 0.0849 (N+AD0-27) at 50

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 68 26.6 0.46
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 56 23.0 1.7
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465) 59 23.7 4
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38) 43 19.1 7.9

```

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 68 Z-score: 108.4 bits: 26.6 E(): 0.46
Smith-Waterman score: 68+ADs- 23.077+ACU- identity (51.282+ACU- similar)
in 78 aa overlap (2-73:316-393)

```

```

                                10      20
AAD-12                          LDEATRALV---HQRSARHSLVYSQSKLGHV
                                :: .. : : :: :: .. :
gi+AHw-113 NNNYDKWGSYAIGGSASPTILSQQGNRFCAPDERSKKNVLGRHGEGAAAESMKWNWRTNKDV
                290      300      310      320      330      340

```

```

                30      40      50      60      70      80
AAD-12 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESE
                . :. ... :: . :: . . : : . : . : .. ::
gi+AHw-113 LENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSILTSSAGVLSCQPGAPC
                350      360      370      380      390

```

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 init1: 45 opt: 56 Z-score: 98.3 bits: 23.0 E(): 1.7
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (3-42:34-77)

```

```

                                10      20
AAD-12                          LDEATRALVHQRSARHS----LVYSQSKLGHV
                                .: . : : :: : : : : : : : : : :
gi+AHw-527 HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVNVDHV
                10      20      30      40      50      60

```

```

      30          40          50          60          70          80
AAD-12 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAEASE
      :.:.:. : .: :
gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQKRVAGA
      70          80          90          100         110         120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 init1: 47 opt: 59 Z-score: 91.6 bits: 23.7 E(): 4
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (11-48:198-242)

```

                                10          20          30
AAD-12                                LDEATRVLVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                :.:. :.:. : .: : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHF LAGNIQRSQKQ RGER YGLRGGQQILADNVFKGFNMEALAD
      170          180          190          200          210          220

```

```

      40          50          60          70          80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAEASE
      :.:.:. :. :
gi+AHw-303 VLGFGMDTETARKVVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230          240          250          260          270          280

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 init1: 43 opt: 43 Z-score: 86.2 bits: 19.1 E(): 7.9
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (26-46:5-25)

```

      10          20          30          40          50          60
AAD-12 LDEATRVLVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRP
      :.:. :. :. : .: :
gi+AHw-462                                AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLNSA
      10          20          30

```

```

      70          80
AAD-12 SLLIGRHAHAIPGMDAEASE

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:22 2010 done: Fri Feb 5 12:56:22 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

66      28      25:+AD0APQA9AD0APQA9AD0APQAqAD0-
68      26      20:+AD0APQA9AD0APQA9ACoAPQA9-
70      20      16:+AD0APQA9AD0APQAqAD0-
72      18      12:+AD0APQA9ACoAPQA9-
74      26      10:+AD0APQA9ACoAPQA9AD0APQA9-
76      10      7:+AD0APQAqAD0-
78      11      6:+AD0AKgA9AD0-
80      7       4:+AD0AKgA9-
82      3       3:+ACo-
84      0       3:+ACo-
86      1       2:+ACo-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     1       0:+AD0-          +ACoAPQ-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.57350.00325+ADs- mu+AD0- 0.9983
0.168
mean+AF8-var+AD0-36.6232 8.752, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.211932
Kolmogorov-Smirnov statistic: 0.0774 (N+AD0-28) at 50

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 68 26.1 0.66

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 56 22.7 2.1

gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465) 59 23.3 5.4

gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
(38) 43 19.0 8.3

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 65 init1: 65 opt: 68 Z-score: 105.6 bits: 26.1 E(): 0.66

Smith-Waterman score: 68+ADs- 23.077+ACU- identity (51.282+ACU- similar)
in 78 aa overlap (1-72:316-393)

```

                                10      20
AAD-12      DEATRALV---HQRSARHSLVYSQSKLGHV
                                :: .. : : ... .. :
gi+AHw-113  NNNYDKWGSYAIGGSASPTILSQGNRFPCAPDERSKKNVLGRHGEEAAESMKWNWRTNKDV
                290      300      310      320      330      340

```

```

                30      40      50      60      70      80
AAD-12  QQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESER
                . :. ... ::. . ::. . : :. :. . : .. ::
gi+AHw-113  LENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLSAGVLSLSCQPGAPC
                350      360      370      380      390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 45 init1: 45 opt: 56 Z-score: 96.7 bits: 22.7 E(): 2.1
 Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
 in 44 aa overlap (2-41:34-77)

```

                                10      20
AAD-12      DEATRALVHQRSARHS----LVYSQSKLGHV
                                .: . : : : : : : . . . . . : :
gi+AHw-527  HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAIPVYEQSLSTKHSVPDVLAFQKVNVDHV
                10      20      30      40      50      60

```

```

                30      40      50      60      70      80
AAD-12  QQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
                : : : : . : : :
gi+AHw-527  QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQKRVAGA
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 init1: 47 opt: 59 Z-score: 89.3 bits: 23.3 E(): 5.4
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (10-47:198-242)

```

                                10      20      30
AAD-12      DEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                :: : : : : : : : : : : : :
gi+AHw-303  LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                170      180      190      200      210      220

```

```

                40      50      60      70      80
AAD-12  YIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
                . : : : : : : : : :
gi+AHw-303  VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVI RPPRIREELEQQEGGGYNGLEETICS
                230      240      250      260      270      280

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 init1: 43 opt: 43 Z-score: 85.9 bits: 19.0 E(): 8.3
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (25-45:5-25)

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 89.5 bits: 23.3 E(): 5.2
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (9-46:198-242)

```

                                10      20      30
AAD-12      EATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                ::. ::. :  .:  :  .:  .
gi+AHw-303  LVQHTASDLNQLDQNP RHF FLAGNIQRSQKQ RGER YGLRGGQQILADNVFKGFNMEALAD
              170      180      190      200      210      220

```

```

                40      50      60      70      80
AAD-12  YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF
                .....: :  .:
gi+AHw-303  VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVI RPPRIREELEQQEGGGYNGLEETICS
              230      240      250      260      270      280

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 85.9 bits: 19.0 E(): 8.3
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (24-44:5-25)

```

                10      20      30      40      50      60
AAD-12  EATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSL
                .....: :  .:  .:  .:
gi+AHw-462  AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLNSA
              10      20      30

                70      80
AAD-12  LIGRHAHAIPGMDAAESERF

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:22 2010 done: Fri Feb 5 12:56:22 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 151 - 230 80 aa - 80 aa


```

      40          50          60          70          80
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFL
      .: . :. . . : :. :. . . : . . :.
gi+AHw-113 VDPVLTPEQSAGMIPAEPGESALSLSAGVLSQPGAPC
      360          370          380          390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 initl: 45 opt: 55 Z-score: 95.2 bits: 22.4 E(): 2.5
Smith-Waterman score: 55+ADs- 30.233+ACU- identity (62.791+ACU- similar)
in 43 aa overlap (1-39:35-77)

```

                                10          20
AAD-12                          ATRALVHQRSARHS----LVYSQSKLGHVQ
                                : . .: :...: :.... . . :.
gi+AHw-527 ITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQSTKHSVPDVLAFKVNVDHVQ
      10          20          30          40          50          60

```

```

      30          40          50          60          70          80
AAD-12 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL
      .: . :. :. :
gi+AHw-527 DAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAAELGGLAQKRVAGA
      70          80          90          100          110          120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 initl: 47 opt: 59 Z-score: 89.8 bits: 23.4 E(): 5
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (8-45:198-242)

```

                                10          20          30
AAD-12                          ATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                :. .: :. : : : :. :. :
gi+AHw-303 LVQHTASDLNQLDQNP RHF LAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
      170          180          190          200          210          220

```

```

      40          50          60          70          80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL
      .: .: .: .: .: .: .:
gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230          240          250          260          270          280

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
Full+AD0-Non-sp (38 aa)
initn: 43 initl: 43 opt: 43 Z-score: 85.7 bits: 19.0 E(): 8.5
Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
in 21 aa overlap (23-43:5-25)

```

      10          20          30          40          50          60
AAD-12 ATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLL
      :. .: :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.
gi+AHw-462 AITCGQVSSALSSCLGYLKNNGGAVPPGSSCGIKNLNSA
      10          20          30

```


FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 67 26.4 0.54
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 54 22.4 2.6
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
59 23.8 3.7
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
(339) 56 22.9 5.1
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
(38) 43 19.0 8.6
gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (875)
58 23.5 8.9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 65 init1: 65 opt: 67 Z-score: 107.2 bits: 26.4 E(): 0.54
Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)
in 67 aa overlap (6-69:327-393)

```

                                10      20      30
AAD-12                      TRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
                                :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-113 IGGASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNKDVLENGAI FV ASG
          300      310      320      330      340      350

          40      50      60      70      80
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLE
          :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-113 VDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
          360      370      380      390
    
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)

initn: 45 init1: 45 opt: 54 Z-score: 94.8 bits: 22.4 E(): 2.6
Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)
in 36 aa overlap (7-38:42-77)

```

                                10      20      30
AAD-12                      TRALVHQRSARHS----LVYSQSKLGHVQQAGSAYI
                                :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-527 QKLLSSTTYVVVDFADWCPPCKAIAPVYEQ LSTKH SVPDVLAFAKVNVDHVQDAAQQYG
          20      30      40      50      60      70

          40      50      60      70      80
AAD-12 GYGM DTTATPLRPLVKVHPETGRPSLLIGRHAHAI PGMDAAESERFLE
          :  :  :
gi+AHw-527 ITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AAAEKLGG LAQKRVAGA
          80      90      100      110      120
    
```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 init1: 47 opt: 59 Z-score: 92.2 bits: 23.8 E(): 3.7
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (7-44:198-242)

```

                                10      20      30
AAD-12      TRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                ::.  ::.  ::.  :   :   :   .
gi+AHw-303  LVQHTASDLNQLDQNP RHF FLAGNIQRSQKQ RGER YGLRGGQQILADNVFKGFNMEALAD
              170      180      190      200      210      220

```

```

                                40      50      60      70      80
AAD-12  YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE
              ::.  ::.  ::.  :   :   :   .
gi+AHw-303  VLFGMDTETARKVRGEDDQRGHIVRVEQGLKVI RPPRIREELEQQEGGGYNGLEETICS
              230      240      250      260      270      280

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 init1: 52 opt: 56 Z-score: 89.7 bits: 22.9 E(): 5.1
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (29-80:25-73)

```

                                10      20      30      40      50
AAD-12  TRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPET-GRPSLL
                                .:  ::.  :  ::.  :  .  .  :  .  .  .
gi+AHw-249  MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-
              10      20      30      40      50

```

```

                                60      70      80
AAD-12  IGRHAHAIP-GMDAAESERFLE
              ::.  :  ::.  ::.  :
gi+AHw-249  ----PAAVPSGKATTEEQK LIEKINAGFKAAVAAA AVPPADKYKTFVETFGTATNKAFV
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 init1: 43 opt: 43 Z-score: 85.6 bits: 19.0 E(): 8.6
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (22-42:5-25)

```

                                10      20      30      40      50      60
AAD-12  TRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLI
                                ::.  ::.  ::.  .  ::.  :
gi+AHw-462  AITCGQVSSALSSCLGYLKN GGAVPPGSSCGIKNLNSA
              10      20      30

```

```

                                70      80
AAD-12  GRHAHAIPGMDAAESERFLE

```

+AD4APg-gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen
 +AFs-Blomia (875 aa)
 initn: 33 init1: 33 opt: 58 Z-score: 85.3 bits: 23.5 E(): 8.9

Smith-Waterman score: 58+ADs- 34.783+ACU- identity (60.870+ACU- similar)
in 46 aa overlap (8-52:4-44)

```

                10         20         30         40         50
AAD-12  TRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTA-TPLRPLVKVHPETGRPSLL
                .....  ::      ..  :  ::  :  :  :  :  :  :  :
gi+AHw-219  MAARSAKY--MYQSSRAGH---GGDISIEYGTDLGALTRLEDKIRLLSEDLSESERE
                10         20         30         40         50

                60         70         80
AAD-12  IGRHAHAIPGMDDAAESERFLE

gi+AHw-219  LRQRVEREKSDITVQLMNLTERLEETEGSSSESVTEMNKKRDSELAKLRKLLLEDVHMESEE
                60         70         80         90         100         110

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:22 2010 done: Fri Feb 5 12:56:22 2010
Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 153 - 232 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      2      8:+AD0- +ACo-
      34      2      21:+AD0- +ACo-
      36      36      44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38      52      72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      40      53      101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-

```



```

114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.79300.00323+ADs- mu+AD0- 4.9259
0.167
mean+AF8-var+AD0-33.7462 7.960, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.220781
Kolmogorov-Smirnov statistic: 0.0951 (N+AD0-27) at 50

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

```

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080

```

The best scores are: opt bits E(1471)

```

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  67 26.4  0.52
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  54 22.4  2.6
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)  59 23.9  3.6
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.9  5
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38)  43 19.0  8.7
gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (
875)  58 23.5  8.7
gi+AHw-21751+AHw-emb+AHw-CAA31396.1+AHw- high molecular weight glu ( 648)
56 22.9  9.9

```

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 67 Z-score: 107.5 bits: 26.4 E(): 0.52
Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)
in 67 aa overlap (5-68:327-393)

```

```

                                10      20      30
AAD-12                        RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
                                : ..: ..: ..      : . :. ... :
gi+AHw-113 IGGSASPTILSQGNRFCAPDERSKKNVLGRHGEEAAAESMKWNWRTNKDVLENGAI FVASG
                                300      310      320      330      340      350

                                40      50      60      70      80
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEG
                                .: . :. .      . : . :. .      : .. :.
gi+AHw-113 VDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
                                360      370      380      390

```

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 init1: 45 opt: 54 Z-score: 94.9 bits: 22.4 E(): 2.6
Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)
in 36 aa overlap (6-37:42-77)

```

```

                                10          20          30
AAD-12          RALVHQRSARHS----LVYSQSKLGHVQQAGSAYI
                   : : : : : : : : : : : : : : : : : :
gi+AHw-527  QKLLSSTTYVVVDFADWCPPCKAIAPVYEQSLTKHSVPDVLAFKVNVDHVQDAAQQYG
                   20          30          40          50          60          70

                   40          50          60          70          80
AAD-12  GYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
                   . : .
gi+AHw-527  ITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGLAQKRVAGA
                   80          90          100         110         120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 init1: 47 opt: 59 Z-score: 92.4 bits: 23.9 E(): 3.6
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (6-43:198-242)

```

                                10          20
AAD-12          RALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                   : : : : : : : : : : : : : : :
gi+AHw-303  LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                   170         180         190         200         210         220

                   30          40          50          60          70          80
AAD-12  YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
                   . : : : : : : : : : : :
gi+AHw-303  VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVI RPPRIREELEQQEGGGYNGLEETICS
                   230         240         250         260         270         280

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 init1: 52 opt: 56 Z-score: 89.9 bits: 22.9 E(): 5
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (28-79:25-73)

```

                                10          20          30          40          50
AAD-12  RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET-GRPSLLI
                   . : : : : : : : : : : : : : :
gi+AHw-249  MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT--
                   10          20          30          40          50

                   60          70          80
AAD-12  GRHAHAIP-GMDAAESERFLEG
                   . : : : : : : : : :
gi+AHw-249  ---PAAVPSGKATTEEQK LIEKINAGFKA AVAAA VPPADKYKTFVETFGTATNKAFVE
                   60          70          80          90          100         110

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 init1: 43 opt: 43 Z-score: 85.5 bits: 19.0 E(): 8.7
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (21-41:5-25)

```

          10          20          30          40          50          60
AAD-12 RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG
          :.:.:. .: .: .: .:
gi+AHw-462 AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLNSA
          10          20          30

```

```

          70          80
AAD-12 RHAHAIPGMDAAESERFLEG

```

+AD4APg-gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen
+AFs-Blomia (875 aa)
initn: 33 initl: 33 opt: 58 Z-score: 85.5 bits: 23.5 E(): 8.7
Smith-Waterman score: 58+ADs- 34.783+ACU- identity (60.870+ACU- similar)
in 46 aa overlap (7-51:4-44)

```

          10          20          30          40          50
AAD-12 RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTA-TPLRPLVKVHPETGRPSLLI
          :.:. .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-219 MAARSAKY--MYQSSRAGH---GGDISIEYGTDLGALTRLEDKIRLLSEDLSESEREL
          10          20          30          40          50

```

```

          60          70          80
AAD-12 GRHAHAIPGMDAAESERFLEG

```

```

gi+AHw-219 RQRVEREKSDITVQLMNLTERLEETEGSSESVMNKKRDSELAKLRKLLLEDVHMESEET
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-21751+AHw-emb+AHw-CAA31396.1+AHw- high molecular weight
gluteni (648 aa)
initn: 54 initl: 54 opt: 56 Z-score: 84.5 bits: 22.9 E(): 9.9
Smith-Waterman score: 56+ADs- 27.778+ACU- identity (63.889+ACU- similar)
in 36 aa overlap (6-41:539-574)

```

          10          20          30
AAD-12 RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
          :.:. .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-217 QGGYYPTSPQQPGQGGQGGQGGHCHPTSPQQSGQAQQPGQGGQIGQVQQPGQGGQGGYYP
          510          520          530          540          550          560

```

```

          40          50          60          70          80
AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
          .. .:
gi+AHw-217 TSVQQPGQGGQGGQGGQGGHQPQGGQGGQGGQGGYDQSPYHVSAEQQAASPMVAKAQQP
          570          580          590          600          610          620

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:22 2010 done: Fri Feb 5 12:56:22 2010
Total Scan time: 0.080 Total Display time: 0.010


```

62 49 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
64 44 32:+AD0-+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
66 36 25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
68 25 20:+AD0APQA9AD0APQA9ACoAPQA9-
70 19 16:+AD0APQA9AD0APQAqAD0-
72 15 12:+AD0APQA9ACoAPQ-
74 20 10:+AD0APQA9ACoAPQA9AD0-
76 16 7:+AD0APQAqAD0APQA9-
78 10 6:+AD0AKgA9AD0-
80 10 4:+AD0AKgA9AD0-
82 5 3:+ACoAPQ-
84 6 3:+ACoAPQ-
86 0 2:+ACo-
88 1 2:+ACo- inset +AD0- represents 1 library sequences
90 2 1:+ACo-
92 0 1:+ACo- :+ACo-
94 1 1:+ACo- :+ACo-
96 0 1:+ACo- :+ACo-
98 0 0: +ACo-
100 0 0: +ACo-
102 0 0: +ACo-
104 0 0: +ACo-
106 1 0:+AD0- +ACoAPQ-
108 0 0: +ACo-
110 0 0: +ACo-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.83550.00322+ADs- mu+AD0- 4.8730
0.166
mean+AF8-var+AD0-34.3130 8.271, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.218950
Kolmogorov-Smirnov statistic: 0.0876 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are: opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 67 26.3 0.57
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 54 22.3 2.8
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465) 59 23.7 3.9
gi+AHw-21215170+AHw-gb+AHw-AAM43909.1+AHw-AF464911+AF8-1 large subunit (
392) 57 23.1 5.1
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339) 56 22.8 5.4
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38) 43 18.9 9.2

```

gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (875) 58 23.4 9.5
 gi+AHw-83305621+AHw-sp+AHw-Q8NKF4.2+AHw-RL3+AF8-ASPFU RecName: Full+AD0-60 (392) 54 22.2 9.8

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 65 init1: 65 opt: 67 Z-score: 106.7 bits: 26.3 E(): 0.57
 Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)
 in 67 aa overlap (3-66:327-393)

```

                                10      20      30
AAD-12                        LVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
                                :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-113 IGGSASPTILSQGNRFCA PDERSKKNV LGRHG EAAAESMKWNWRTNKDVL ENGAI FVASG
                300      310      320      330      340      350

                40      50      60      70      80
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEGLV
                . : . : . : . : : : . : . : : :
gi+AHw-113 VDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSQPGAPC
                360      370      380      390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 45 init1: 45 opt: 54 Z-score: 94.3 bits: 22.3 E(): 2.8
 Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)
 in 36 aa overlap (4-35:42-77)

```

                                10      20
AAD-12                        LVHQRSARHS----LVYSQSKLGHVQQAGSAYI
                                : : : : : : : : : : : :
gi+AHw-527 QKLLSSTTYVVVDF FADWC PPKAIAPVYEQ LSTKH SVPDVLAF AKVNV DHDVQDAAQQYG
                20      30      40      50      60      70

                30      40      50      60      70      80
AAD-12 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAI PGMDAAESERFLEGLV
                . : :
gi+AHw-527 ITAMPTFMFFKEGKQVAVNGQAVIKGADPRTL GAAA EKLGGLAQKR VAGA
                80      90      100      110      120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholletia (465 aa)
 initn: 47 init1: 47 opt: 59 Z-score: 91.7 bits: 23.7 E(): 3.9
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (4-41:198-242)

```

                                10      20
AAD-12                        LVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                : : : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHF FLAGNIQR SQKQRGER YGLRGGQQILADNVFKGF NMEALAD
                170      180      190      200      210      220

                30      40      50      60      70      80

```

AAAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV

..... :: ..

gi+AHw-303 VLGFQMDTETARKVVRGDDQRGHIVRVEQGLKVIKPPRIREELEQQEGGGYNGLEETICS
230 240 250 260 270 280

+AD4APg-gi+AHw-21215170+AHw-gb+AHw-AAM43909.1+AHw-AF464911+AF8-1 large subunit rib (392 aa)

initn: 34 initl: 34 opt: 57 Z-score: 89.7 bits: 23.1 E(): 5.1
Smith-Waterman score: 57+ADs- 36.538+ACU- identity (59.615+ACU- similar)
in 52 aa overlap (1-47:17-68)

AAAD-12 LVHQRSARH-SLVYSQSKLGHVQQAG-SAYIGY--GMDTTATPL
: : : : : . . .: : : : : :
gi+AHw-212 MSHRKYEAPRHGSLAFLPRKRAARHRGKVKVSPKYDPKPKVHLTASMGYKAGMTTVVRDL
10 20 30 40 50 60

AAAD-12 -RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
:: ...:
gi+AHw-212 DRPGAKMHKKEIVEAVTIIETPPLVAVGVVGYIETPRGLRSLTTVWAEHLSDEVKRRFYK
70 80 90 100 110 120

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-Major (339 aa)
initn: 52 initl: 52 opt: 56 Z-score: 89.2 bits: 22.8 E(): 5.4
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (26-77:25-73)

AAAD-12 LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET-GRPSLLIGR
.: :. : : : : . . : : . :.
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT----
10 20 30 40 50

AAAD-12 HAHAIP-GMDAAESERFLEGLV
.: : ..::
gi+AHw-249 -PAAVPSGKATTEEQKLEIKINAGFKA AVAAA VVPPADKYKTFVETFGTATNKAFVEGL
60 70 80 90 100 110

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-Non-sp (38 aa)
initn: 43 initl: 43 opt: 43 Z-score: 85.1 bits: 18.9 E(): 9.2
Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
in 21 aa overlap (19-39:5-25)

AAAD-12 LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH
:..... :. :. : . :. :
gi+AHw-462 AITCGQVSSALSSCLGYLKNNGAVPPGSSCGIKNLNSA
10 20 30

70 80

AAAD-12 AHAI PGMDAAESERFLEGLV

+AD4APg-gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-Blomia (875 aa)

initn: 33 init1: 33 opt: 58 Z-score: 84.8 bits: 23.4 E(): 9.5 Smith-Waterman score: 58+ADs- 34.783+ACU- identity (60.870+ACU- similar) in 46 aa overlap (5-49:4-44)

10 20 30 40 50
AAAD-12 LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTA-TPLRPLVKVHPETGRPSLLIGR
gi+AHw-219 MAARSAKY--MYQSSRAGH---GGDISIEYGTDLGALTRLEDKIRLLSEDLSESERELRQ

60 70 80
AAAD-12 HAHAI PGMDAAESERFLEGLV

gi+AHw-219 RVEREKSDITVQLMNLTERLEETE GSSSVTEMNKKRDSELA KLRKLL EDVHMESEETAH
60 70 80 90 100 110

+AD4APg-gi+AHw-83305621+AHw-sp+AHw-Q8NKF4.2+AHw-RL3+AF8-ASPFU RecName: Full+AD0-60S ri (392 aa)
initn: 34 init1: 34 opt: 54 Z-score: 84.6 bits: 22.2 E(): 9.8
Smith-Waterman score: 54+ADs- 36.538+ACU- identity (59.615+ACU- similar)
in 52 aa overlap (1-47:17-68)

10 20 30 40
AAAD-12 LVHQRSARH-SLVYSQSKLGHVQQAG-SAYIGY--GMDTTATPL
gi+AHw-833 MSHRKYEAPRHGSLAFLPRKRAARHRGKVKSPKDDPKKPVHLTASMGYKAGMTTVVRDL

50 60 70 80
AAAD-12 -RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
gi+AHw-833 DRPGAKMHKKEIVEAVTIIETPPLVAVGVVGYIETPRGLRSLTTVWAEHLSDEVKRRFYK

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:23 2010 done: Fri Feb 5 12:56:23 2010
Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

70    13    16:+AD0APQA9AD0APQAq-
72    12    12:+AD0APQA9ACo-
74    27    10:+AD0APQA9ACoAPQA9AD0APQA9-
76    13    7:+AD0APQAqAD0APQ-
78     8    6:+AD0AKgA9-
80    10    4:+AD0AKgA9AD0-
82     5    3:+ACoAPQ-
84     3    3:+ACo-
86     0    2:+ACo-
88     1    2:+ACo-          inset +AD0- represents 1 library sequences
90     1    1:+ACo-
92     1    1:+ACo-          :+ACo-
94     1    1:+ACo-          :+ACo-
96     0    1:+ACo-          :+ACo-
98     0    0:              +ACo-
100    0    0:              +ACo-
102    0    0:              +ACo-
104    0    0:              +ACo-
106    1    0:+AD0-          +ACoAPQ-
108    0    0:              +ACo-
110    0    0:              +ACo-
112    0    0:              +ACo-
114    0    0:              +ACo-
116    0    0:              +ACo-
118    0    0:              +ACo-
+AD4-120    0    0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.47630.00321+ADs- mu+AD0- 6.9927
0.166
mean+AF8-var+AD0-34.8658 8.647, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.217207
Kolmogorov-Smirnov statistic: 0.0850 (N+AD0-27) at 52

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   67 26.2   0.61
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   56 22.7   2.6
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   54 22.1   3.2
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.7    4
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)   56 22.7   5.7
gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (
875)   58 23.4   9.2

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 67 Z-score: 106.3 bits: 26.2 E(): 0.61

```

Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)
in 67 aa overlap (2-65:327-393)

```

                                10      20      30
AAD-12                        VHQRSARHSLVYSQSKLGHVQQAGSAYIGY
                                :  . . .  . . .  . . .  . . .  . . .  . . .
gi+AHw-113 IGGASPTILSQGNRFCDPERSKKNVLRHGEAAAESMKWNWRTNKDVLNGAIFVASG
                300      310      320      330      340      350

```

```

                40      50      60      70      80
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEGLVD
                . : . : : . . : : . : : . : . : :
gi+AHw-113 VDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
                360      370      380      390

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 49 initl: 49 opt: 56 Z-score: 95.0 bits: 22.7 E(): 2.6
Smith-Waterman score: 56+ADs- 41.026+ACU- identity (61.538+ACU- similar)
in 39 aa overlap (46-80:79-116)

```

                20      30      40      50      60      70
AAD-12 KLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                                . . . . : : : : : : . . . .
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50      60      70      80      90      100

```

```

                80
AAD-12 ERFLEGLVD
                . : . : :
gi+AHw-121 EEFRASLVDYLSHHLDWNMTMKSTWDLALNNMFFYILHALEVAQ
                110      120      130      140      150

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 initl: 45 opt: 54 Z-score: 93.3 bits: 22.1 E(): 3.2
Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)
in 36 aa overlap (3-34:42-77)

```

                                10      20
AAD-12                        VHQRSARHS----LVYSQSKLGHVQQAGSAYI
                                :  . . . . : . . . . . : . . . . . :
gi+AHw-527 QKLLSSTTYVVVDFADWCPPCKAIAPVYEQSLTKHSVPDVLAFKVNVDHVQDAAQQYG
                20      30      40      50      60      70

```

```

                30      40      50      60      70      80
AAD-12 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIIPGMDAAESERFLEGLVD
                . : . :
gi+AHw-527 ITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AAAEKLGLAQKR VAGA
                80      90      100      110      120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 initl: 47 opt: 59 Z-score: 91.5 bits: 23.7 E(): 4

Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (3-40:198-242)

```

                                10          20
AAD-12          VHQRSARHSLVYSQSKL-----GHVQQAGSA
                                ... ..: ... :   : ... .
gi+AHw-303 LVQHTASDLNQLDQNP RHF FLAGNIQRSQKQ RGERYGLRGGQQILADNVFKGFNMEALAD
          170      180      190      200      210      220

```

```

          30      40      50      60      70      80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
          ..... : :
gi+AHw-303 VLGFMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
          230      240      250      260      270      280

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 init1: 52 opt: 56 Z-score: 88.8 bits: 22.7 E(): 5.7
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (25-76:25-73)

```

          10      20      30      40      50
AAD-12 VHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET-GRPSLLIGRH
                                .: ... : ::: : . . : : . :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
          10      20      30      40      50

```

```

          60      70      80
AAD-12 AHAIP-GMDAAESERFLEGLVD
          .: : .: .: .: .:
gi+AHw-249 PAAVPSGKATTEEQK LIEKINAGFKA AVAAA AVVPPADKYKTFVETFGTATNKAFVEGLA
          60      70      80      90      100      110

```

+AD4APg-gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen
+AFs-Blomia (875 aa)
initn: 33 init1: 33 opt: 58 Z-score: 85.0 bits: 23.4 E(): 9.2
Smith-Waterman score: 58+ADs- 34.783+ACU- identity (60.870+ACU- similar)
in 46 aa overlap (4-48:4-44)

```

          10      20      30      40      50
AAD-12 VHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTA-TPLRPLVKVHPETGRPSLLIGRH
          ..... : : .: : : : : : : : :
gi+AHw-219 MAARSAKY--MYQSSRAGH---GGDISIEYGTDLGALTRLEDKIRLLSEDLSESERELRQR
          10      20      30      40      50

```

```

          60      70      80
AAD-12 AHAIPGMDAAESERFLEGLVD
          ..... : : .: : : : : : : : :
gi+AHw-219 VEREKSDITVQLMNLTERLEETEGSSES SVTEMNKKRDSELAKLRKLLLEDVHMESEETAHH
          60      70      80      90      100      110

```

80 residues in 1 query sequences

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 58 23.3 1.7
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 54 22.1 3.2
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 23.7 4.1
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.7 5.8
 gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (875)
 58 23.3 9.7

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 65 initl: 65 opt: 67 Z-score: 106.1 bits: 26.2 E(): 0.62
 Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)
 in 67 aa overlap (1-64:327-393)

```

                                10      20      30
AAD-12                        HQR SARHSLVYSQSKLGHVQQAGSAYIGYG
                                :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-113 IGGSASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FV ASG
                300          310          320          330          340          350

                                40      50      60      70      80
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEGLVDW
                :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-113 VDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSQPGAPC
                360          370          380          390
    
```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 initl: 50 opt: 58 Z-score: 98.4 bits: 23.3 E(): 1.7
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (45-80:79-117)

```

                                20      30      40      50      60      70
AAD-12 KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                                :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50          60          70          80          90          100

                                80
AAD-12 ERFLEGLVDW
                :  :  :  :  :
gi+AHw-121 EEFRASLVDYLSHHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                110          120          130          140          150
    
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 45 initl: 45 opt: 54 Z-score: 93.3 bits: 22.1 E(): 3.2
 Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)
 in 36 aa overlap (2-33:42-77)

mean+AF8-var+AD0-35.1853 8.887, 0's: 2 Z-trim: 2 B-trim: 69 in 1/42
 Lambda+AD0- 0.216219
 Kolmogorov-Smirnov statistic: 0.0919 (N+AD0-27) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
 Scan time: 0.080

The best scores are: opt bits E(1471)
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 58 23.3 1.7
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 54 22.1 3.2
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 59 23.7 3.5
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465) 59 23.7 4.1
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.7 5.7
 gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (875) 58 23.4 9.4

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 init1: 50 opt: 58 Z-score: 98.3 bits: 23.3 E(): 1.7
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (44-79:79-117)

	20	30	40	50	60
AAD-12	KLGHVQQAGSAYIGYGM	DTTATPLRPLVKVHPETGRPSL	--LIGRHA--	HAI	PGMDAAES
			
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALK	TLIDGLASSHKARGIEKAQF			
	50	60	70	80	90
	70	80			
AAD-12	ERFLEGLVDWA				
	::			
gi+AHw-121	EEFRASLVVDYLSHHL	DWNTMKSTWDLALNNMFFYILHALEVAQ			
	110	120	130	140	150

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 45 init1: 45 opt: 54 Z-score: 93.2 bits: 22.1 E(): 3.2
 Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)
 in 36 aa overlap (1-32:42-77)

				10	20
AAD-12				QRSARHS----	LVYSQSKLGHVQQAGSAYI
				:
gi+AHw-527	QKLLSSTTYVVVDF	FADWCPPCKAIAPVYEQLSTKHSVPDVLAF	AKVNV	DHVQDAAQQYG	
	20	30	40	50	60
	30	40	50	60	80
AAD-12	GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAI	PGMDAAESERFLEGLVDWA			

```

      .: .
gi+AHw-527 ITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQKRVAGA
              80          90          100          110          120

```

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
  initn: 55 init1: 55 opt: 59 Z-score: 92.6 bits: 23.7 E(): 3.5
Smith-Waterman score: 59+ADs- 21.875+ACU- identity (51.562+ACU- similar)
in 64 aa overlap (3-63:330-393)

```

```

                                10          20          30
AAD-12                        QRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
                                .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-113 SASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNKDVLENGAI FVASGVDP
              300          310          320          330          340          350

```

```

                40          50          60          70          80
AAD-12 TATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWA
          .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-113 VLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
              360          370          380          390

```

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
  initn: 47 init1: 47 opt: 59 Z-score: 91.4 bits: 23.7 E(): 4.1
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (1-38:198-242)

```

```

                                10          20
AAD-12                        QRSARHSLVYSQSKL-----GHVQQAGSA
                                .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
              170          180          190          200          210          220

```

```

                30          40          50          60          70          80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA
          .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
              230          240          250          260          270          280

```

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
  initn: 52 init1: 52 opt: 56 Z-score: 88.7 bits: 22.7 E(): 5.7
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (23-74:25-73)

```

```

                10          20          30          40          50
AAD-12 QRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPET-GRPSLLIGRH
          .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
              10          20          30          40          50

```

```

                60          70          80
AAD-12 AHAIP-GMDAAESERFLEGLVDWA

```

```

      :: :   :: :   :: :
gi+AHw-249 PAAVPSGKATTEEQKLIIEKINAGFKA AVAAA VVPPADKYKTFVETFGTATNKAFVEGLA
           60           70           80           90           100          110
    
```

+AD4APg-gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen
+AFs-Blomia (875 aa)
initn: 33 initl: 33 opt: 58 Z-score: 84.9 bits: 23.4 E(): 9.4
Smith-Waterman score: 58+ADs- 34.783+ACU- identity (60.870+ACU- similar)
in 46 aa overlap (2-46:4-44)

```

           10           20           30           40           50
AAD-12   QRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTA-TPLRPLVKVHPETGRPSLLIGRH
      :::: . . . . . :: . . . : : : : : . . . :
gi+AHw-219 MAARSAKY--MYQSSRAGH---GGDISIEYGTDLGALTRLEDKIRLLSEDLSESERELRQR
           10           20           30           40           50
    
```

```

           60           70           80
AAD-12   AHAIPGMDAAESERFLEGLVDWA
    
```

```

gi+AHw-219 VEREKSDITVQLMNLTERLEETEGSSES SVTEMNKKRDSELAKLRKILLEDVHMESEETAHH
           60           70           80           90           100          110
    
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:23 2010 done: Fri Feb 5 12:56:23 2010
Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 159 - 238 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      0      8: +ACo-
      34      17     21:+AD0APQA9AD0APQA9ACo-
    
```


108 0 0: +ACo-
 110 0 0: +ACo-
 112 0 0: +ACo-
 114 0 0: +ACo-
 116 0 0: +ACo-
 118 0 0: +ACo-
 +AD4-120 0 0: +ACo-
 331323 residues in 1471 sequences
 Expectation+AF8-n fit: rho(ln(x))+AD0- 4.30330.00317+ADs- mu+AD0- 7.8350
 0.165
 mean+AF8-var+AD0-34.2788 8.796, 0's: 2 Z-trim: 2 B-trim: 69 in 1/42
 Lambda+AD0- 0.219059
 Kolmogorov-Smirnov statistic: 0.0925 (N+AD0-26) at 52

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 58 23.4 1.6
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 59 23.8 3.1
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.9 5.2
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 50 20.9 7.4
 gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (
 875) 58 23.6 8.3

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)

initn: 50 init1: 50 opt: 58 Z-score: 98.8 bits: 23.4 E(): 1.6
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (43-78:79-117)

	20	30	40	50	60
AAD-12	KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGM DAAES				
			
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF				
	50	60	70	80	90
					100

	70	80
AAD-12	ERFLEGLVDWAC	

gi+AHw-121	EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
	110 120 130 140 150

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)

initn: 55 init1: 55 opt: 59 Z-score: 93.4 bits: 23.8 E(): 3.1
 Smith-Waterman score: 59+ADs- 21.875+ACU- identity (51.562+ACU- similar)
 in 64 aa overlap (2-62:330-393)

```

                                10      20      30
AAD-12      RSARHSLVYSQSKLGHVQQAGSAYIGYGM
                                .: .:. . . : . . . .:
gi+AHw-113 SASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNKDVL
300          310          320          330          340          350

```

```

                                40      50      60      70      80
AAD-12      TATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWAC
                                .: . . . : .: .: . : . . :
gi+AHw-113 VLTPEQSAGMIPAEPPGESALSLSAGVLSQPGAPC
360          370          380          390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-Major (339 aa)
 initn: 52 init1: 52 opt: 56 Z-score: 89.4 bits: 22.9 E(): 5.2
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (22-73:25-73)

```

                                10      20      30      40      50
AAD-12      RSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET-GRPSLLIGRH
                                .: .:. : .:. : . . : . .
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
10          20          30          40          50

```

```

                                60      70      80
AAD-12      AHAIP-GMDAAESERFLEGLVDWAC
                                .: . : .: .: .:
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA VPPADKYKTFVETFGTATNKAFVEGLA
60          70          80          90          100          110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 45 init1: 45 opt: 50 Z-score: 86.8 bits: 20.9 E(): 7.4
 Smith-Waterman score: 50+ADs- 32.353+ACU- identity (67.647+ACU- similar)
 in 34 aa overlap (2-31:44-77)

```

                                10      20
AAD-12      RSARHS----LVYSQSKLGHVQQAGSAYIGY
                                .: .: .: .: .: .:
gi+AHw-527 LLSSTTYVVVDFADWCPPCKAIAPVYEQSLSTKHSVPDVLAFKVNVDHVQDAAQQYGIT
20          30          40          50          60          70

```

```

                                30      40      50      60      70      80
AAD-12      GMDTTATPLRPLVKVHPETGRPSLLIGRHAHAI PGMDAAESERFLEGLVDWAC
                                .: .
gi+AHw-527 AMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AAAEKLGGLAQKRVAGA
80          90          100          110          120

```

+AD4APg-gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-Blomia (875 aa)
 initn: 33 init1: 33 opt: 58 Z-score: 85.9 bits: 23.6 E(): 8.3
 Smith-Waterman score: 58+ADs- 34.783+ACU- identity (60.870+ACU- similar)
 in 46 aa overlap (1-45:4-44)

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 4.24530.00313+ADs- mu+AD0- 8.0930
0.163

mean+AF8-var+AD0-33.7205 8.747, 0's: 2 Z-trim: 2 B-trim: 69 in 1/42

Lambda+AD0- 0.220865

Kolmogorov-Smirnov statistic: 0.0931 (N+AD0-27) at 52

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
(151) 58 23.5 1.5

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 59 23.9 2.9

gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
(339) 56 22.9 4.9

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 50 20.9 7.1

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)

initn: 50 init1: 50 opt: 58 Z-score: 99.3 bits: 23.5 E(): 1.5
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (42-77:79-117)

	20	30	40	50	60
AAD-12	KLGHVQQAGSAYIGYGM	DTTATPLRPLVKVHPETGR	PSL--LIGRHA--HAIPGMDAAES		
			
gi+AHw-121	DLDSIKDSADFAVHSGRIV	GFFSEVIGLIGNPEN-RP	ALKTLIDGLASSHKARGIE	KAQF	
	50	60	70	80	90

	70	80
AAD-12	ERFLEGLVDWACQ	

gi+AHw-121	EEFRASLVVDYLSHHL	DWNTMKSTWDLALNNMFF
	110	120

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 55 init1: 55 opt: 59 Z-score: 93.9 bits: 23.9 E(): 2.9
Smith-Waterman score: 59+ADs- 21.875+ACU- identity (51.562+ACU- similar)
in 64 aa overlap (1-61:330-393)

		10	20	30
AAD-12		SARHSLVYSQSKLGHVQQ	AGSAYIGYGM	DT
	
gi+AHw-113	SASPTILSQGNRFCAP	DERSKKNVLRHGEEAAES	MKWNWRTNKDVL	ENGAI
	300	310	320	330

	40	50	60	70	80
AAD-12	TATPLRPLVKVHPETGR	PSLLIGRHAHAI---	PGMDAAE	ESERFLEGLVDWACQ	

gi+AHw-113 VLTPEQSAGMIPAEFPGESALSLSAGVLSCQPGAPC
 360 370 380 390

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 init1: 52 opt: 56 Z-score: 89.9 bits: 22.9 E(): 4.9
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (21-72:25-73)

10 20 30 40 50
 AAD-12 SARHSLVYSQSKLGHVQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
 ..::: : . . : . : .
 gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
 10 20 30 40 50

60 70 80
 AAD-12 AHAIP-GMDAAESERFLEGLVDWACQ
 ::: : ..: . . . :
 gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFVEGLA
 60 70 80 90 100 110

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 45 init1: 45 opt: 50 Z-score: 87.1 bits: 20.9 E(): 7.1
 Smith-Waterman score: 50+ADs- 32.353+ACU- identity (67.647+ACU- similar)
 in 34 aa overlap (1-30:44-77)

10 20
 AAD-12 SARHS----LVYSQSKLGHVQAGSAYIGY
 ..::: : . . : . : . :
 gi+AHw-527 LLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVNVDHVQDAAQQYGIT
 20 30 40 50 60 70

30 40 50 60 70 80
 AAD-12 GMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQ
 . : :
 gi+AHw-527 AMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AAAEKLGGLAQKRVAGA
 80 90 100 110 120

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:23 2010 done: Fri Feb 5 12:56:24 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

72    14    12:+AD0APQA9ACoAPQ-
74    13    10:+AD0APQA9ACoAPQ-
76    20    7:+AD0APQAqAD0APQA9AD0-
78    10    6:+AD0AKgA9AD0-
80     8    4:+AD0AKgA9-
82     7    3:+ACoAPQA9-
84     1    3:+ACo-
86     0    2:+ACo-
88     0    2:+ACo-          inset +AD0- represents 1 library sequences
90     1    1:+ACo-
92     1    1:+ACo-          :+ACo-
94     0    1:+ACo-          :+ACo-
96     0    1:+ACo-          :+ACo-
98     1    0:+AD0-          +ACoAPQ-
100    0    0:              +ACo-
102    0    0:              +ACo-
104    0    0:              +ACo-
106    0    0:              +ACo-
108    0    0:              +ACo-
110    0    0:              +ACo-
112    0    0:              +ACo-
114    0    0:              +ACo-
116    0    0:              +ACo-
118    0    0:              +ACo-
+AD4-120    0    0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.27780.00312+ADs- mu+AD0- 8.0118
0.162
mean+AF8-var+AD0-33.4410 8.797, 0's: 2 Z-trim: 2 B-trim: 69 in 1/42
Lambda+AD0- 0.221786
Kolmogorov-Smirnov statistic: 0.0890 (N+AD0-27) at 52

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.5      1.5
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  58 23.6      3.7
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.9      5

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 50 init1: 50 opt: 58 Z-score: 99.3 bits: 23.5 E(): 1.5
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (41-76:79-117)

                20          30          40          50          60
AAD-12 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                .... :... :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF

```

```

50          60          70          80          90          100
      70          80
AAD-12 ERFLEGLVDWACQA
      ::  ::::
gi+AHw-121 EEFRASLVDYLSHLLDWNMTMKSTWDLALNNMFFYILHALEVAQ
      110          120          130          140          150

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 55 init1: 55 opt: 58 Z-score: 92.2 bits: 23.6 E(): 3.7
Smith-Waterman score: 58+ADs- 22.222+ACU- identity (50.794+ACU- similar)
in 63 aa overlap (1-60:331-393)

```

                                10          20          30
AAD-12                          ARHSLVYSQSKLGHVQQAGSAYIGYGMDDT
                                :  ::  ..          :  ::  ...  :::
gi+AHw-113 ASPTILSQGNRFCDPERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPV
              310          320          330          340          350          360

```

```

              40          50          60          70          80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQA
      :: . . . : :: : . . : .. ::
gi+AHw-113 LTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
              370          380          390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 init1: 52 opt: 56 Z-score: 89.9 bits: 22.9 E(): 5
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (20-71:25-73)

```

              10          20          30          40          50
AAD-12      ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET-GRPSLLIGRH
              ::  :::  : :::  : . . : : . ::
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
              10          20          30          40          50

```

```

              60          70          80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQA
      ::: :  :::  ::::
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA AVVPPADKYKTFVETFGTATNKAFVEGLA
              60          70          80          90          100          110

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:24 2010 done: Fri Feb 5 12:56:24 2010
Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-


```

60 55 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62 52 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
64 45 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
66 47 25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0-
68 38 20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-
70 14 16:+AD0APQA9AD0APQAq-
72 15 12:+AD0APQA9ACoAPQ-
74 21 10:+AD0APQA9ACoAPQA9AD0-
76 14 7:+AD0APQAqAD0APQ-
78 10 6:+AD0AKgA9AD0-
80 9 4:+AD0AKgA9-
82 5 3:+ACoAPQ-
84 1 3:+ACo-
86 1 2:+ACo-
88 0 2:+ACo- inset +AD0- represents 1 library sequences
90 2 1:+ACo-
92 0 1:+ACo- :+ACo-
94 0 1:+ACo- :+ACo-
96 0 1:+ACo- :+ACo-
98 1 0:+AD0- +ACoAPQ-
100 0 0: +ACo-
102 0 0: +ACo-
104 0 0: +ACo-
106 0 0: +ACo-
108 0 0: +ACo-
110 0 0: +ACo-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.42650.00311+ADs- mu+AD0- 7.3117
0.162
mean+AF8-var+AD0-33.3830 8.825, 0's: 2 Z-trim: 2 B-trim: 69 in 1/42
Lambda+AD0- 0.221979
Kolmogorov-Smirnov statistic: 0.0919 (N+AD0-28) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are: opt bits E(1471)
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 58 23.5 1.5
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 57 23.2 4.8
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339) 56 22.9 5.1
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 55 22.6 8.2

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)

```

initn: 50 init1: 50 opt: 58 Z-score: 99.3 bits: 23.5 E(): 1.5
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (40-75:79-117)

```

      10      20      30      40      50      60
AAD-12 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      70      80
AAD-12 ERFLEGLVDWACQAP
      . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-121 EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
      110     120     130     140     150

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)

initn: 55 init1: 55 opt: 57 Z-score: 90.2 bits: 23.2 E(): 4.8
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
 in 49 aa overlap (14-59:345-393)

```

      10      20      30      40
AAD-12          RHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET
      . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP
      320     330     340     350     360     370

```

```

      50      60      70      80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAP
      . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-113 GESALSLSAGVLSLSCQPGAPC
      380     390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)

initn: 52 init1: 52 opt: 56 Z-score: 89.6 bits: 22.9 E(): 5.1
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (19-70:25-73)

```

      10      20      30      40      50
AAD-12          RHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET-GRPSLLIGRH
      . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPATPAT-----
      10      20      30      40      50

```

```

      60      70      80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAP
      . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA AVPPADKYKTFVETFGTATNKAFVEGLA
      60      70      80      90      100     110

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)

Expectation+AF8-n fit: rho(ln(x))+AD0- 4.66650.00303+ADs- mu+AD0- 6.2752
0.158

mean+AF8-var+AD0-35.3205 9.283, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43

Lambda+AD0- 0.215805

Kolmogorov-Smirnov statistic: 0.0803 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
(151) 58 23.2 1.8

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 57 22.9 6

gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
(339) 56 22.6 6.4

gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (160)
52 21.3 7.1

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)

initn: 50 init1: 50 opt: 58 Z-score: 97.6 bits: 23.2 E(): 1.8

Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (39-74:79-117)

```

      10      20      30      40      50      60
AAD-12 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      .....::: : : : ..:
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      70      80
AAD-12 ERFLEGLVDWACQAPR
      ..: .:..:
gi+AHw-121 EEFRASLVLDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 55 init1: 55 opt: 57 Z-score: 88.4 bits: 22.9 E(): 6

Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (13-58:345-393)

```

      10      20      30      40
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET
      : . : . . . : . : . : . :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP
      320      330      340      350      360      370

```

```

      50      60      70      80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPR
      : . : . : : : :
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC

```

380 390

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 initl: 52 opt: 56 Z-score: 87.9 bits: 22.6 E(): 6.4
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (18-69:25-73)

```

                10      20      30      40      50
AAD-12      HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET-GRPSLLIGRH
                .:  :.  :  ::  :  .  :  :  .  :.
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                10      20      30      40      50
```

```

                60      70      80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPR
                ::  :  .:  .:  .:
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA VVPPADKYKTFVETFGTATNKAFVEGLA
                60      70      80      90      100      110
```

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein
+AFs-Oryza s (160 aa)
initn: 36 initl: 36 opt: 52 Z-score: 87.1 bits: 21.3 E(): 7.1
Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (8-80:89-154)

```

                10      20      30
AAD-12      HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVK
                :  :.  .:  :  :  .  .  .:
gi+AHw-139 HGAPGGAVDEQLRQDCCRQLAAVDDSWCRCALNHM--VGGIYRELGATDVG---HPMAE
                60      70      80      90      100      110
```

```

                40      50      60      70      80
AAD-12  VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR
                :  :  :  :  :  .:  .:  .:
gi+AHw-139 VFPGCRRGDL--ERAAASLPAFCNVNDIPNGTGGVCYWLGYTPRTPRTGH
                120      130      140      150      160
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:24 2010 done: Fri Feb 5 12:56:24 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

74    21    10:+AD0APQA9ACoAPQA9AD0-
76    12    7:+AD0APQAqAD0-
78     7    6:+AD0AKgA9-
80     8    4:+AD0AKgA9-
82     4    3:+ACoAPQ-
84     1    3:+ACo-
86     0    2:+ACo-
88     3    2:+ACo-          inset +AD0- represents 1 library sequences
90     0    1:+ACo-
92     0    1:+ACo-          :+ACo-
94     0    1:+ACo-          :+ACo-
96     0    1:+ACo-          :+ACo-
98     1    0:+AD0-          +ACoAPQ-
100    0    0:                +ACo-
102    0    0:                +ACo-
104    0    0:                +ACo-
106    0    0:                +ACo-
108    0    0:                +ACo-
110    0    0:                +ACo-
112    0    0:                +ACo-
114    0    0:                +ACo-
116    0    0:                +ACo-
118    0    0:                +ACo-

```

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 4.63200.00301+ADs- mu+AD0- 6.4630
0.157

mean+AF8-var+AD0-34.5747 9.121, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43

Lambda+AD0- 0.218120

Kolmogorov-Smirnov statistic: 0.0830 (N+AD0-28) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
(151) 58 23.3 1.7

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 57 23.0 5.7

gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
(339) 56 22.7 6

gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (
160) 52 21.4 6.8

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
(439) 55 22.3 9.7

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)

initn: 50 init1: 50 opt: 58 Z-score: 98.1 bits: 23.3 E(): 1.7

Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (38-73:79-117)

10

20

30

40

50

60

AAD-12 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES

 gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
 50 60 70 80 90 100

AAD-12 ERFLEGLVDWACQAPRV
 ..
 gi+AHw-121 EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
 110 120 130 140 150

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 88.8 bits: 23.0 E(): 5.7
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
 in 49 aa overlap (12-57:345-393)

AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET

 gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP
 320 330 340 350 360 370

AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRV
 ..
 gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
 380 390

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 initl: 52 opt: 56 Z-score: 88.4 bits: 22.7 E(): 6
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (17-68:25-73)

AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET-GRPSLLIGRH
 ..
 gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
 10 20 30 40 50

AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRV
 ..
 gi+AHw-249 PAAVPSGKATTEEQK LIEKINAGFKA AVAAA AVVPPADKYKTFVETFGTATNKAFVEGLA
 60 70 80 90 100 110

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein
 +AFs-Oryza s (160 aa)
 initn: 36 initl: 36 opt: 52 Z-score: 87.5 bits: 21.4 E(): 6.8
 Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)
 in 73 aa overlap (7-79:89-154)

```

AAD-12                               SLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVK
                                     : :.:. .:. : : .. :.:.
gi+AHw-139 HGAPGGAVDEQLRQDCRQLAAVDDSWCRCSALNHM--VGGIYRELGATDVG---HPMAE
        60          70          80          90          100          110
    
```

```

AAD-12 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRV
        : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-139 VFPGCRRGDL--ERAAASLPAFCNVNDIPNGTGGVVCYWLGYTPRTPRGTGH
        120          130          140          150          160
    
```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 55 initl: 55 opt: 55 Z-score: 84.6 bits: 22.3 E(): 9.7
 Smith-Waterman score: 55+ADs- 42.857+ACU- identity (61.905+ACU- similar)
 in 21 aa overlap (58-78:246-266)

```

        30          40          50          60          70          80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRV
                                     : : : : : : : : : : : :
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKPNNSDKSKWIT
        220          230          240          250          260          270
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
        280          290          300          310          320          330
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:24 2010 done: Fri Feb 5 12:56:24 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 165 - 244 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

        opt      E()
+ADw- 20      2      0:+AD0-
        22      0      0:          one +AD0- represents 3 library sequences
        24      0      0:
        26      0      0:
    
```



```

98      1      0:+AD0-      +ACoAPQ-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120  0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.59340.00302+ADs- mu+AD0- 6.6270
0.158
mean+AF8-var+AD0-34.3439 9.071, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.218852
Kolmogorov-Smirnov statistic: 0.0858 (N+AD0-28) at 48

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.3  1.7
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  57 23.0  5.5
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.7  5.9
gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (
160)  52 21.4  6.6
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  55 22.4  9.5

```

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 50 init1: 50 opt: 58 Z-score: 98.3 bits: 23.3 E(): 1.7
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (37-72:79-117)

```

```

      10      20      30      40      50      60
AAD-12 KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      ..... : : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

      70      80
AAD-12 ERFLEGLVDWACQAPRVH
      : : : : :
gi+AHw-121 EEFRASLVDYLSHHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 55 init1: 55 opt: 57 Z-score: 89.1 bits: 23.0 E(): 5.5
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (11-56:345-393)

```

                                10      20      30      40
AAD-12                          LVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET
                                : . . . . . : : . . . . . :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLNENGAIFVASGVDPVLTPEQSAGMIPAEP
                                320      330      340      350      360      370

```

```

                                50      60      70      80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVH
                                : . . . . . : . . . . . :
gi+AHw-113 GESALSLTSSAGVLSQPGAPC
                                380      390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 init1: 52 opt: 56 Z-score: 88.6 bits: 22.7 E(): 5.9
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (16-67:25-73)

```

                                10      20      30      40      50
AAD-12                          LVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET-GRPSLLIGRH
                                : . . . . . : : : : : : : : : : :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                                10      20      30      40      50

```

```

                                60      70      80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVH
                                : : : : : : : : : : :
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKAAVAAAAVVPPADKYKTFVETFGTATNKAFVEGLA
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein
+AFs-Oryza s (160 aa)
initn: 36 init1: 36 opt: 52 Z-score: 87.6 bits: 21.4 E(): 6.6
Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (6-78:89-154)

```

                                10      20      30
AAD-12                          LVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVK
                                : : : . . . : : : . . . : : . . .
gi+AHw-139 HGAPGGAVDEQLRQDCCRQLAAVDDSWCRCSALNHM--VGGIYRELGATDVG---HPMAE
                                60      70      80      90      100      110

```

```

                                40      50      60      70      80
AAD-12 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
                                : : : : : : : : : : :
gi+AHw-139 VFPGCRRGDL--ERAAASLPAFCNVDIPNGTGGVVCYWLGYTPRTPRTGH
                                120      130      140      150      160

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 55 init1: 55 opt: 55 Z-score: 84.9 bits: 22.4 E(): 9.5
 Smith-Waterman score: 55+ADs- 42.857+ACU- identity (61.905+ACU- similar)
 in 21 aa overlap (57-77:246-266)

```

      30      40      50      60      70      80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
      :::: :: . ::: : . :
gi+AHw-370 APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT
      220      230      240      250      260      270
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330
  
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:24 2010 done: Fri Feb 5 12:56:24 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 166 - 245 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      0      2:+ACo-
      32      2      8:+AD0- +ACo-
      34      15     21:+AD0APQA9AD0APQ- +ACo-
      36      35     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38      44     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      40      70
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
  
```



```

116      0      0:          +ACo-
118      0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.61490.00297+ADs- mu+AD0- 6.4884
0.155
mean+AF8-var+AD0-33.8874 9.002, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.220321
Kolmogorov-Smirnov statistic: 0.0844 (N+AD0-28) at 48

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.4    1.6
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  57 23.1    5.3
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.8    5.6
gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (
160)   52 21.5    6.4
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  55 22.4    9.2

```

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 50 init1: 50 opt: 58 Z-score: 98.7 bits: 23.4 E(): 1.6
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (36-71:79-117)

```

```

          10          20          30          40          50          60
AAD-12  KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDDAAES
          .... : : : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
          50          60          70          80          90          100

```

```

          70          80
AAD-12  ERFLEGLVDWACQAPRVHA
          .. : : : :
gi+AHw-121 EEFRASLVLDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
          110          120          130          140          150

```

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 55 init1: 55 opt: 57 Z-score: 89.4 bits: 23.1 E(): 5.3
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (10-55:345-393)

```

```

          10          20          30
AAD-12  VYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET
          : . : . . . : : . : : . . :
gi+AHw-113 PDERSKKNVLGRHGEEAAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP

```

```

          320          330          340          350          360          370
    40          50          60          70          80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVHA
      :. .: . : .. :
gi+AHw-113 GESALSLTSSAGVLSQPGAPC
          380          390

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
  initn: 52 init1: 52 opt: 56 Z-score: 88.9 bits: 22.8 E(): 5.6
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (15-66:25-73)

          10          20          30          40
AAD-12          VYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
          .: :.. : ::: : . . : : . :.
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
          10          20          30          40          50

          50          60          70          80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHA
      ::: : ..: .....:
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA VVPADKYKTFVETFGTATNKAFVEGLA
          60          70          80          90          100          110

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein
+AFs-Oryza s (160 aa)
  initn: 36 init1: 36 opt: 52 Z-score: 87.9 bits: 21.5 E(): 6.4
Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (5-77:89-154)

          10          20          30
AAD-12          VYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVK
          : :.. .: : : .. :....
gi+AHw-139 HGAPGGAVDEQLRQDCRQLAAVDDSWCRCRSALNHM--VGGIYRELGATDVG---HPMAE
          60          70          80          90          100          110

          40          50          60          70          80
AAD-12 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-139 VFPGCRRGDL--ERAAASLPAFCNVDIPNGTGGVCYWLGYTPRTPRTGH
          120          130          140          150          160

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
  initn: 55 init1: 55 opt: 55 Z-score: 85.1 bits: 22.4 E(): 9.2
Smith-Waterman score: 55+ADs- 42.857+ACU- identity (61.905+ACU- similar)
in 21 aa overlap (56-76:246-266)

          30          40          50          60          70          80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHA
          :::: : : . : : : : : : : : : : :
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT

```


join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 58 23.2 1.8
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 57 22.9 6.1
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.6 6.4
 gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (
 160) 52 21.4 7
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.6 8.6

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 initl: 50 opt: 58 Z-score: 97.7 bits: 23.2 E(): 1.8
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (35-70:79-117)

	10	20	30	40	50	60
AAD-12	KLGHVQQAGSAYIGYGM	DTTATPLRPLVKVHPET	GRPSL--LIGRHA--	HAI	PGMDAAES	
				::	: : :
gi+AHw-121	DLDSIKDSADFAVHSGR	IVGFFSEVIGLIGNPEN	-RPALK	T	LIDGLASSHKARGIEKAQF	
	50	60	70	80	90	100
		70	80			
AAD-12	ERFLEGLVDWACQAPRV	HAH				
	::				
gi+AHw-121	EEFRASLVDYLSHHL	DWNTMKSTWDLALNNM	FFYLH	HALEVAQ		
	110	120	130	140	150	

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 88.3 bits: 22.9 E(): 6.1
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
 in 49 aa overlap (9-54:345-393)

		10	20	30	
AAD-12		YSQSKLGHVQQAGSAY	IGYGM	DTTATPLRPLVKVHPET	
		:	::	: : :
gi+AHw-113	PDERSKKNVLRHGEAAA	ESMKWNWRTNKDVLENGA	IFVASGVDPVLTPEQS	SAGMIPAEP	
	320	330	340	350	360 370
	40	50	60	70	80
AAD-12	GRPSLLIGRHAHAI---	PGMDAAESERFLEGL	VDWACQAPRVHAH		
	::	:	::	
gi+AHw-113	GESALS	LTSSAGVLSCQPGAPC			
	380	390			

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 initl: 52 opt: 56 Z-score: 87.9 bits: 22.6 E(): 6.4

Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (14-65:25-73)

```

                10      20      30      40
AAD-12      YSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
                .:  .:.  :  :::  :  .  .  :  .  .:
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12      AHAIP-GMDAAESERFLEGLVDWACQAPRVHAH
                :::  :  .:  .:  .:
gi+AHw-249 PAAVPSGKATTEEQKLIIEKINAGFKA AVAAA VVPPADKYKTFVETFGTATNKAFVEGLA
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein
+AFs-Oryza s (160 aa)
initn: 36 initl: 36 opt: 52 Z-score: 87.2 bits: 21.4 E(): 7
Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (4-76:89-154)

```

                10      20      30
AAD-12      YSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVK
                :  .:  .:  :  :  .  .  .:
gi+AHw-139 HGAPGGAVDEQLRQDCRQLAAVDDSWCRCSALNHM--VGGIYRELGATDVG---HPMAE
                60      70      80      90      100     110

```

```

                40      50      60      70      80
AAD-12      VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH
                :  :  :  .:  :  .:  .:  .:  .:
gi+AHw-139 VFPGCRRGDL--ERAAASLPAFCNVDIPNGTGGVCYWLGYTPRTPRTGH
                120     130     140     150     160

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 initl: 37 opt: 56 Z-score: 85.6 bits: 22.6 E(): 8.6
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (26-80:46-108)

```

                10      20      30      40
AAD-12      YSQSKLGHVQQAGSAYIGYGMDDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                :  .:  .:  :  :  .:  .:  .:
gi+AHw-253 IEEPemiAPTppGQFPHQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                20      30      40      50      60      70

```

```

                50      60      70      80
AAD-12      -AHAIPGMDAAESERFLEGLVDWACQAPRVHAH
                .:  .:  .:  .:  .:  .:
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
                80      90      100     110     120     130

```

```

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPHLEHSS
                140     150     160     170     180     190

```


gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 57 22.8 6.2
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.5 6.5
 gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (160)
 52 21.3 7.1
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.5 8.7

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 initl: 50 opt: 58 Z-score: 97.5 bits: 23.2 E(): 1.9
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (34-69:79-117)

```

                10         20         30         40         50
AAD-12  KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                ....  ::  :  :  :  :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50         60         70         80         90         100

                60         70         80
AAD-12  ERFLEGLVDWACQAPRVHAHQ
                ::  ::::
gi+AHw-121 EEFRASLVDYLSHHLDWNMTMKSTWDLALNNMFFYILHALEVAQ
                110        120        130        140        150
    
```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 88.2 bits: 22.8 E(): 6.2
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
 in 49 aa overlap (8-53:345-393)

```

                10         20         30
AAD-12  SQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET
                : . : . . . : : . : : . . :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP
                320        330        340        350        360        370

                40         50         60         70         80
AAD-12  GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQ
                : . : . : . : :
gi+AHw-113 GESALS LTSSAGVLSCQPGAPC
                380        390
    
```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 initl: 52 opt: 56 Z-score: 87.7 bits: 22.5 E(): 6.5
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (13-64:25-73)

```

                10         20         30         40
AAD-12  SQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET-GRPSLLIGRH
                ..  ...  :  :::  :  .  .  :  :  .  .  .
    
```



```

58      73
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
60      61
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
62      42      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      47      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
66      34      25:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
68      23      20:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
70      11      16:+AD0APQA9AD0- +ACo-
72      17      12:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
74      18      10:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
76      10      7:+AD0APQA9AD0-
78      10      6:+AD0AKgA9AD0-
80      2      4:+AD0AKg-
82      4      3:+ACoAPQ-
84      1      3:+ACo-
86      3      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      1      1:+ACo-
92      3      1:+ACo-          :+ACoAPQA9-
94      1      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     1      0:+AD0-          +ACoAPQ-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120  0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.68030.00306+ADs- mu+AD0- 6.1866
0.160
mean+AF8-var+AD0-36.903910.119, 0's: 2 Z-trim: 2 B-trim: 5 in 1/42
Lambda+AD0- 0.211124
Kolmogorov-Smirnov statistic: 0.0796 (N+AD0-28) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 66 25.5 1.1 opt bits E(1471)
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 58 23.0 2.1
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 22.4 2.4
gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (
838) 64 24.9 3.2

```

gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 22.4 3.3
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 22.4 3.3
 gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
 (440) 59 23.3 4.9
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 57 22.7 6.7
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.4 7.1
 gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (160)
 52 21.2 7.8
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.4 9.4

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 101.6 bits: 25.5 E(): 1.1
 Smith-Waterman score: 66+ADs- 35.714+ACU- identity (53.571+ACU- similar)
 in 28 aa overlap (53-80:246-273)

	30	40	50	60	70	80
AAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW					
				::: :: . :: :	. :	::
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
	220	230	240	250	260	270

gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK					
	280	290	300	310	320	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 init1: 50 opt: 58 Z-score: 96.6 bits: 23.0 E(): 2.1
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (33-68:79-117)

	10	20	30	40	50	
AAD-12	KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES					
				::: ::: :: :	: : : .. ::	
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF					
	50	60	70	80	90	100

	60	70	80		
AAD-12	ERFLEGLVDWACQAPRVHAHQW				
	::: .:::.				
gi+AHw-121	EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ				
	110	120	130	140	150

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alt e (115 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 95.4 bits: 22.4 E(): 2.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (64-80:68-86)

```

      40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQW
      : . . . . : : : . . . : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40          50          60          70          80          90

```

```

gi+AHw-219 SFSDRSGLLLKQKVSDE
      100          110

```

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aestivum+AF0- (838 aa)
 initn: 43 initl: 43 opt: 64 Z-score: 93.3 bits: 24.9 E(): 3.2
 Smith-Waterman score: 64+ADs- 34.286+ACU- identity (60.000+ACU- similar)
 in 35 aa overlap (5-39:140-171)

```

                                10          20          30
AAD-12                                QSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP
                                : . : : : . . : : . . : : . :
gi+AHw-736 RYYPVTSPPQQVSYYPGQASPPQRPQGQQPGQGGQSGQGGQGY---YPTSPQQPGWQQP
      110          120          130          140          150          160

```

```

      40          50          60          70          80
AAD-12 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW
      : : :
gi+AHw-736 EQGQPGYYPTSPQQPGQLQQPAQGGQQPGQGGQGRQPGQGGPYPTSSQLQPGQLQQPAQ
      170          180          190          200          210          220

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 93.0 bits: 22.4 E(): 3.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (64-80:68-86)

```

      40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQW
      : . . . . : : : . . . : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
      40          50          60          70          80          90

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 93.0 bits: 22.4 E(): 3.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (64-80:68-86)

```

      40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQW
      : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40          50          60          70          80          90

```

gi+AHw-184 SFSDSRGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 59 initl: 59 opt: 59 Z-score: 90.0 bits: 23.3 E(): 4.9
Smith-Waterman score: 59+ADs- 32.143+ACU- identity (53.571+ACU- similar)
in 28 aa overlap (53-80:247-274)

30 40 50 60 70 80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW
::: :: . : . : . :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPKWLK
220 230 240 250 260 270

gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
280 290 300 310 320 330

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 55 initl: 55 opt: 57 Z-score: 87.6 bits: 22.7 E(): 6.7
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (7-52:345-393)

10 20 30
AAD-12 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET
: . : . . . : : . : . :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAIFVASGVDPVLTPEQSAGMIPAEP
320 330 340 350 360 370

40 50 60 70 80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQW
:. : . : . :
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
380 390

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 initl: 52 opt: 56 Z-score: 87.1 bits: 22.4 E(): 7.1
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (12-63:25-73)

10 20 30 40
AAD-12 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
.: : . : : : . : . :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
10 20 30 40 50

50 60 70 80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQW
::: : . : . :
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA AVVPPADKYKTFVETFGTATNKAFVEGLA
60 70 80 90 100 110

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein

+AFs-Oryza s (160 aa)

initn: 36 initl: 36 opt: 52 Z-score: 86.3 bits: 21.2 E(): 7.8
 Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)
 in 73 aa overlap (2-74:89-154)

```

                                10      20      30
AAD-12                        QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVK
                                : :.:. .:. : : .. :.:.
gi+AHw-139 HGAPGGAVDEQLRQDCRQLAAVDDSWCRCALNHM--VGGIYRELGATDVG---HPMAE
        60      70      80      90      100     110

```

```

                40      50      60      70      80
AAD-12 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW
        : : : .: : : :.:. .: : : :.:.
gi+AHw-139 VFPGCRRGDL--ERAAASLP AFCNVNDIPNGTGGVVCYWLGYTPRTPRTGH
        120     130     140     150     160

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protein +AFs-F (450 aa)

initn: 37 initl: 37 opt: 56 Z-score: 84.9 bits: 22.4 E(): 9.4
 Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
 in 63 aa overlap (24-78:46-108)

```

                                10      20      30      40
AAD-12                        QSKLGHVQQAGSAYIGYGMDDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                                : :.:. .:. : :.:. : :.:.
gi+AHw-253 IEEP EMIAPT PPGQ FPHQQ PISSPNR T SRNTPLRPESTEIETHHHANHPPALPVLGMQLP
        20      30      40      50      60      70

```

```

                50      60      70      80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW
        : : : .: : : :.:. .: : : :.:.
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
        80      90      100     110     120     130

```

```

gi+AHw-253 GLPPTGFASHLPASSGPVSLGWNMYHVPNHLNANQFNFEVPGHMNVSGHPHLEHSS
        140     150     160     170     180     190

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:25 2010 done: Fri Feb 5 12:56:25 2010

Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

72      17      12:+AD0APQA9ACoAPQA9-
74      20      10:+AD0APQA9ACoAPQA9AD0-
76      9       7:+AD0APQAq-
78      10      6:+AD0AKgA9AD0-
80      3       4:+AD0AKg-
82      3       3:+ACo-
84      1       3:+ACo-
86      3       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      1       1:+ACo-
92      3       1:+ACo-          :+ACoAPQA9-
94      1       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     1       0:+AD0-        +ACoAPQ-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120  0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.62860.00309+ADs- mu+AD0- 6.4242
0.162
mean+AF8-var+AD0-37.169310.164, 0's: 2 Z-trim: 2 B-trim: 5 in 1/42
Lambda+AD0- 0.210369
Kolmogorov-Smirnov statistic: 0.0796 (N+AD0-28) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  66 25.5      1.1
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.0      2.1
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 22.4      2.5
gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (
838)   64 24.9      3.2
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4      3.4
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4      3.4
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  59 23.3      4.9
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  57 22.7      6.7

```

gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.4 7.1
 gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (160)
 52 21.2 7.9
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.4 9.4

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 101.5 bits: 25.5 E(): 1.1
 Smith-Waterman score: 66+ADs- 35.714+ACU- identity (53.571+ACU- similar)
 in 28 aa overlap (52-79:246-273)

```

                30         40         50         60         70         80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA
                :::: :: . ::: : . : .:
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
                220         230         240         250         260         270

```

```

gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280         290         300         310         320         330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 init1: 50 opt: 58 Z-score: 96.5 bits: 23.0 E(): 2.1
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (32-67:79-117)

```

                10         20         30         40         50
AAD-12 KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                .... :::: :: : : ... ::
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50         60         70         80         90         100

```

```

                60         70         80
AAD-12 ERFLEGLVDWACQAPRVHAHQWA
                :: .:::.
gi+AHw-121 EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
                110         120         130         140         150

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt al
 +AFs-Alte (115 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 95.3 bits: 22.4 E(): 2.5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (63-79:68-86)

```

                40         50         60         70         80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWA
                : .:::. :: ... :::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                40         50         60         70         80         90

```

```

gi+AHw-219 SFSDRSGLLLKQKVSDE
                100         110

```

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aestivum+AF0- (838 aa)
 initn: 43 initl: 43 opt: 64 Z-score: 93.3 bits: 24.9 E(): 3.2
 Smith-Waterman score: 64+ADs- 34.286+ACU- identity (60.000+ACU- similar)
 in 35 aa overlap (4-38:140-171)

```

                                10      20      30
AAD-12                        SKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHP
                                :. :.:.:. :. :. :. :.
gi+AHw-736 RYYPSTVSPQQVSYYPGQASPQRPGQGGQGGQGGQGGQGGY---YPTSPQQPGQWQQP
          110      120      130      140      150      160

```

```

          40      50      60      70      80
AAD-12 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA
          : : :
gi+AHw-736 EQGQPGYIPTSPQQPGQLQQPAQGGQGGQGGQGGQGGQGGYIPTSSQLQPGQLQQPAQ
          170      180      190      200      210      220

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (63-79:68-86)

```

          40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWA
                                : :.:. :. :. :.
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
          40      50      60      70      80      90

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (63-79:68-86)

```

          40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWA
                                : :.:. :. :. :.
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
          40      50      60      70      80      90

```

```

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100      110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 59 initl: 59 opt: 59 Z-score: 90.0 bits: 23.3 E(): 4.9
 Smith-Waterman score: 59+ADs- 32.143+ACU- identity (53.571+ACU- similar)
 in 28 aa overlap (52-79:247-274)


```

                                : : : . . . : : : . . . : : :
gi+AHw-139 HGAPGGAVDEQLRQDCCRQLAAVDDSWCRCRSALNHM--VGGIYRELGATDVG---HPMAE
           60          70          80          90          100          110

                   40          50          60          70          80
AAD-12 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA
       : :   : . :   : : : . . . . . . . .   : . :   : : :
gi+AHw-139 VFPGCRRGDL--ERAAASLPAFCNVNDIPNGTGGVVCYWLGYTPRTPRTGH
           120          130          140          150          160
    
```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protein +AFs-F (450 aa)
 initn: 37 initl: 37 opt: 56 Z-score: 84.9 bits: 22.4 E(): 9.4
 Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar) in 63 aa overlap (23-77:46-108)

```

                   10          20          30          40
AAD-12          SKLGHVQQAGSAYIGYGMTTATPLRPL---VKVHPETGRPSLL--IGRH--
                                : : : :   . . . : . . . : : . .
gi+AHw-253 IEEPEMIAPTTPPGQFPHQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
           20          30          40          50          60          70

                   50          60          70          80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA
       . . : . . . . . : . :   : : :   : :
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
           80          90          100          110          120          130

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNHLNANQFNFEVPGHMNVSGHPTHLEHSS
           140          150          160          170          180          190
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:25 2010 done: Fri Feb 5 12:56:25 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 171 - 250 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

 94      1      1:+ACo-      :+ACo-
 96      1      1:+ACo-      :+ACo-
 98      0      0:          +ACo-
100      0      0:          +ACo-
102      1      0:+AD0-      +ACoAPQ-
104      0      0:          +ACo-
106      0      0:          +ACo-
108      0      0:          +ACo-
110      0      0:          +ACo-
112      0      0:          +ACo-
114      0      0:          +ACo-
116      0      0:          +ACo-
118      0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.61290.00309+ADs- mu+AD0- 6.4472
0.162
mean+AF8-var+AD0-37.329710.188, 0's: 2 Z-trim: 2 B-trim: 5 in 1/42
Lambda+AD0- 0.209917
Kolmogorov-Smirnov statistic: 0.0803 (N+AD0-28) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  66 25.5    1.1
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.0    2.1
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 22.4    2.5
gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (
838)   64 24.9    3.2
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4    3.4
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4    3.4
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  59 23.3    4.8
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  57 22.7    6.7
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.4    7.1
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.4    9.3

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 66 init1: 66 opt: 66 Z-score: 101.5 bits: 25.5 E(): 1.1
Smith-Waterman score: 66+ADs- 35.714+ACU- identity (53.571+ACU- similar)
in 28 aa overlap (51-78:246-273)

```

30

40

50

60

70

80

```

AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      . . . . .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
      220      230      240      250      260      270

gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330
    
```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Globin (151 aa)
 initn: 50 initl: 50 opt: 58 Z-score: 96.5 bits: 23.0 E(): 2.1
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (31-66:79-117)

```

      10      20      30      40      50
AAD-12 KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      . . . . .
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAA
      . . . . .
gi+AHw-121 EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150
    
```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 95.3 bits: 22.4 E(): 2.5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (62-78:68-86)

```

      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAA
      . . . . .
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100      110
    
```

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aestivum+AF0- (838 aa)
 initn: 43 initl: 43 opt: 64 Z-score: 93.4 bits: 24.9 E(): 3.2
 Smith-Waterman score: 64+ADs- 34.286+ACU- identity (60.000+ACU- similar)
 in 35 aa overlap (3-37:140-171)

```

      10      20      30
AAD-12 KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP
      . . . . .
gi+AHw-736 RYYPSVTSPQQVSYYPGQASPORPGQQQPGQQGQQSGQQQGY---YPTSPQQPGWQQP
      110      120      130      140      150      160

      40      50      60      70      80
    
```


Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (5-50:345-393)

```

                                10      20      30
AAD-12                        KLGHVQQAGSAYIGYGMTTATPLRPLVKVHPET
                                : . . . . . : : . . . . . :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP
                                320      330      340      350      360      370

```

```

                                40      50      60      70      80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :. .: . . : . . : :
gi+AHw-113 GESALSLTSSAGVLSQPGAPC
                                380      390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 init1: 52 opt: 56 Z-score: 87.1 bits: 22.4 E(): 7.1
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (10-61:25-73)

```

                                10      20      30      40
AAD-12                        KLGHVQQAGSAYIGYGMTTATPLRPLVKVHPET-GRPSLLIGRH
                                .: .: .: .: .: .: .: .:
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :: : .: .: .: .:
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA AVVPPADKYKTFVETFGTATNKAFVEGLA
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 init1: 37 opt: 56 Z-score: 85.0 bits: 22.4 E(): 9.3
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (22-76:46-108)

```

                                10      20      30      40
AAD-12                        KLGHVQQAGSAYIGYGMTTATPLRPL---VKVHPETGRPSLL--IGRH--
                                : : : : : . . . . . : : . . . . .
gi+AHw-253 IEEPEMIAPTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                                20      30      40      50      60      70

```

```

                                50      60      70      80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                .: .: .: .: .: .: .: .:
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
                                80      90      100      110      120      130

```

```

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPHLEHSS
                                140      150      160      170      180      190

```


gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
 (439) 73 27.6 0.26
 gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
 (440) 66 25.5 1.1
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 58 23.0 2.1
 gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
 56 22.4 2.4
 gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (838)
 64 24.9 3.2
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 22.4 3.3
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 22.4 3.3
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 57 22.7 6.7
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.4 7.1
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.4 9.4

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 113.0 bits: 27.6 E(): 0.26
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (50-80:246-276)

	20	30	40	50	60	70
AAAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
			
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
	220	230	240	250	260	270

	80
AAAD-12	G
:	
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
	280 290 300 310 320 330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 101.5 bits: 25.5 E(): 1.1
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (50-80:247-277)

	20	30	40	50	60	70
AAAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
			
gi+AHw-232	APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS					
	220	230	240	250	260	270

	80
AAAD-12	G
:	

gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
 280 290 300 310 320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 initl: 50 opt: 58 Z-score: 96.6 bits: 23.0 E(): 2.1
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (30-65:79-117)

10 20 30 40 50
 AAD-12 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDDAAES
 :: : : ... :.
 gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
 50 60 70 80 90 100

60 70 80
 AAD-12 ERFLEGLVDWACQAPRVHAHQWAAG
 :.: .:..:
 gi+AHw-121 EEFRASLVDYLSHHLDWNMTKSTWDLALNNMFFYILHALEVAQ
 110 120 130 140 150

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 95.4 bits: 22.4 E(): 2.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (61-77:68-86)

40 50 60 70 80
 AAD-12 PETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAG
 : .:..: :. .: :.
 gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

gi+AHw-219 SFDSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum
 aestivum+AF0- (838 aa)
 initn: 43 initl: 43 opt: 64 Z-score: 93.3 bits: 24.9 E(): 3.2
 Smith-Waterman score: 64+ADs- 34.286+ACU- identity (60.000+ACU- similar)
 in 35 aa overlap (2-36:140-171)

10 20 30
 AAD-12 LGHVQQAGSAYIGYGMDDTATPLRPLVKVHP
 .. :.:. .: :. :.
 gi+AHw-736 RYYPVTSPPQVSYYPGQASPPRPGQGQPGQGGQSGQGQGY---YPTSPQQPGWQQP
 110 120 130 140 150 160

40 50 60 70 80
 AAD-12 ETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAG
 : :.:
 gi+AHw-736 EQGQPGYYPTSPQQPGQLQQPAQGGQPGQGGQGRQPGQGPYYPTSSQLQPGQLQQPAQ
 170 180 190 200 210 220

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 93.0 bits: 22.4 E(): 3.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (61-77:68-86)

```

                40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAG
                : . . . . : : : . . . : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
                40          50          60          70          80          90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                100         110         120         130         140         150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 93.0 bits: 22.4 E(): 3.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (61-77:68-86)

```

                40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAG
                : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
                40          50          60          70          80          90

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                100         110         120         130         140         150

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 55 init1: 55 opt: 57 Z-score: 87.6 bits: 22.7 E(): 6.7
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
 in 49 aa overlap (4-49:345-393)

```

                                10          20          30
AAD-12                                LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET
                                : . . . . . : : . . . . : . :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLNENGAIFVASGVDPVLTPEQSAGMIPAEP
                320         330         340         350         360         370

```

```

                40          50          60          70          80
AAD-12 GRPSLLIGRHAHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQWAAG
                : . . . . : : . . . : :
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
                380         390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 init1: 52 opt: 56 Z-score: 87.1 bits: 22.4 E(): 7.1
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (9-60:25-73)

```

                10      20      30      40
AAD-12          LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
                ..  ...  :  :::  :  .  .  .  .  .  .
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAG
                :::  :  ...  ....:
gi+AHw-249 PAAVPSGKATTEEQKLIIEKINAGFKA AVAAA VVPPADKYKTFVETFGTATNKAFVEGLA
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protein +AFs-F (450 aa)
 initn: 37 initl: 37 opt: 56 Z-score: 84.9 bits: 22.4 E(): 9.4
 Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar) in 63 aa overlap (21-75:46-108)

```

                10      20      30      40
AAD-12          LGHVQQAGSAYIGYGMDDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                :::::  ....:  ....:  :  .  .
gi+AHw-253 IEEPemiAPTppGQFPHQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                20      30      40      50      60      70

```

```

                50      60      70      80
AAD-12  -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG
                ...  .  ...  ..  .:  ...  .:
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
                80      90      100     110     120     130

```

```

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNHLNANQFNFEVPGHMNVSGHPTHLEHSS
                140     150     160     170     180     190

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:25 2010 done: Fri Feb 5 12:56:25 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 173 - 252 80 aa - 80 aa


```

82      4      3:+ACoAPQ-
84      1      3:+ACo-
86      2      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      3      1:+ACo-          :+ACoAPQA9-
94      1      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     1      0:+AD0-        +ACoAPQ-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     1      0:+AD0-        +ACoAPQ-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.76120.00306+ADs- mu+AD0- 5.7931
0.160
mean+AF8-var+AD0-37.371210.173, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.209800
Kolmogorov-Smirnov statistic: 0.0766 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.5    0.27
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.4    1.2
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.0    2.2
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 22.4    2.5
gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (
838)   64 24.8    3.4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4    3.4
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4    3.4
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)  52 21.1    5.6
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  57 22.7    7
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.4    7.4
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.4    9.8

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 112.5 bits: 27.5 E(): 0.27
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (49-79:246-276)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . ::: : . : ::.
gi+AHw-370 APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT
      220      230      240      250      260      270

```

```

      80
AAD-12 GD
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 101.1 bits: 25.4 E(): 1.2
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (49-79:247-277)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . ::: : . ::.
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKPNPESDPKWLK
      220      230      240      250      260      270

```

```

      80
AAD-12 GD
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDWAVHFFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 58 Z-score: 96.3 bits: 23.0 E(): 2.2
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (29-64:79-117)

```

      10      20      30      40      50
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      :::: ::: :: : : : .. ::
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGD
      :: .:::.
gi+AHw-121 EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 95.2 bits: 22.4 E(): 2.5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (60-76:68-86)

```

      30          40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGD
      :  . . . . :  ::  . . .  ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40          50          60          70          80          90

```

```

gi+AHw-219 SFSDRSGLLLKQKVSDE
      100          110

```

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum
 aestivum+AF0- (838 aa)
 initn: 43 init1: 43 opt: 64 Z-score: 92.8 bits: 24.8 E(): 3.4
 Smith-Waterman score: 64+ADs- 34.286+ACU- identity (60.000+ACU- similar)
 in 35 aa overlap (1-35:140-171)

```

                                10          20          30
AAD-12                                GHVQQAGSAYIGYGMDDTATPLRPLVKVHP
                                :  . . . . .  ::  . . :  :  . :
gi+AHw-736 RYYPSVTSPQQVSYYPGQASPPQRPGQQPGQGGQSGQQQGY---YPTSPQQPGQWQQP
      110          120          130          140          150          160

```

```

      40          50          60          70          80
AAD-12 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD
      :  ::
gi+AHw-736 EQGQPGYYPTSPQQPGQLQQPAQGGQQPGQGGQRQPGQGGPYPTSSQLQPGQLQQPAQ
      170          180          190          200          210          220

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 92.7 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (60-76:68-86)

```

      30          40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGD
      :  . . . . :  ::  . . .  ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40          50          60          70          80          90

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 92.7 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (60-76:68-86)

```

      30          40          50          60          70          80
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGD
      : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40          50          60          70          80          90

```

```

gi+AHw-184 SFSDSRGSLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100         110         120         130         140         150

```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
 Full+AD0-60S ac (110 aa)
 initn: 47 initl: 47 opt: 52 Z-score: 89.0 bits: 21.1 E(): 5.6
 Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
 in 68 aa overlap (14-80:19-84)

```

      10          20          30          40          50
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
      : : : : : . . . . . : : : : :
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
      10          20          30          40          50

```

```

      60          70          80
AAD-12  RFLE-GLVDWACQAPRVHAHQWAAGD
      : : : : : : : : : :
gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEKKEEEEKEESDEDMGFGLFD
      60          70          80          90          100         110

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 87.2 bits: 22.7 E(): 7
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
 in 49 aa overlap (3-48:345-393)

```

      10          20          30
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET
      : . . . . : : : . . . : :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP
      320         330         340         350         360         370

```

```

      40          50          60          70          80
AAD-12  GRPSLLIGRHAHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD
      : . : . : : : : : :
gi+AHw-113 GESALSLSAGVLSLSCQPGAPC
      380         390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 initl: 52 opt: 56 Z-score: 86.8 bits: 22.4 E(): 7.4
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (8-59:25-73)

```

      10          20          30          40
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH

```

```

      .:  .:.  :  :::  :  . .  :  :  .  .
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
              10          20          30          40          50

```

```

      50          60          70          80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAGD
      .:  :  .:  .:  .:  .:

```

```

gi+AHw-249 PAAVPSGKATTEEQKLEKINAGFKA AVAAA VVPPADKYKTFVETFGTATNKAFVEGLA
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protein +AFs-F (450 aa)
 initn: 37 initl: 37 opt: 56 Z-score: 84.5 bits: 22.4 E(): 9.8
 Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar) in 63 aa overlap (20-74:46-108)

```

              10          20          30          40
AAD-12          GHVQQAGSAYIGYGMTTATPLRPL---VKVHPETGRPSLL--IGRH--
              .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-253 IEEPemiAptPPGQFPHQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
              20          30          40          50          60          70

```

```

      50          60          70          80
AAD-12  -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD
      .:  .  .:  .:  .:  .:  .:  .:
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
              80          90          100          110          120          130

```

```

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNHLNANQFNFEVPGHMNVSGHPTHLEHSS
              140          150          160          170          180          190

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:25 2010 done: Fri Feb 5 12:56:25 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 174 - 253 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

86      1      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      1      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      2      1:+ACo-          :+ACoAPQ-
96      2      1:+ACo-          :+ACoAPQ-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     1      0:+AD0-        +ACoAPQ-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     1      0:+AD0-        +ACoAPQ-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.85830.00311+ADs- mu+AD0- 5.3847
0.162
mean+AF8-var+AD0-35.7748 9.793, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.214430
Kolmogorov-Smirnov statistic: 0.0739 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.7    0.24
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.5    1.1
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.1    1.9
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 22.5    2.2
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.5    3.1
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.5    3.1
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)  52 21.3    5
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  57 22.8    6.6
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.5    6.9
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.4    9.3
gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (
838)   59 23.3    9.3

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 113.6 bits: 27.7 E(): 0.24
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (48-78:246-276)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . .:: : . : .::
gi+AHw-370 APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT
      220      230      240      250      260      270

```

```

      80
AAD-12 GDV
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 101.9 bits: 25.5 E(): 1.1
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (48-78:247-277)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . .: : . : .::
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

```

```

      80
AAD-12 GDV
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDVAWVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 58 Z-score: 97.2 bits: 23.1 E(): 1.9
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (28-63:79-117)

```

      10      20      30      40      50
AAD-12 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      :::: ::: : : : : . . . .
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDV
      :: .:::
gi+AHw-121 EEFRASLVDYLSHHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```


gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
 10 20 30 40 50

60 70 80
 AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDV
 .:. : : .. :. :.

gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEKKKEEKEESDEDMGFGLFD
 60 70 80 90 100 110

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 87.7 bits: 22.8 E(): 6.6
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
 in 49 aa overlap (2-47:345-393)

10 20 30
 AAD-12 HVQQAGSAYIGYGMDDTATPLRPLVKVHPET
 : . :. . . :. :. : . : . :
 gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP
 320 330 340 350 360 370

40 50 60 70 80
 AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV
 :. :. : : .. :.
 gi+AHw-113 GESALSLTSSAGVLSQPGAPC
 380 390

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 initl: 52 opt: 56 Z-score: 87.3 bits: 22.5 E(): 6.9
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (7-58:25-73)

10 20 30 40
 AAD-12 HVQQAGSAYIGYGMDDTATPLRPLVKVHPET-GRPSLLIGRH
 .: :. : :. : . : . : . :.
 gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
 10 20 30 40 50

50 60 70 80
 AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV
 :. : : .. : . . . :
 gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA AVVPPADKYKTFVETFGTATNKAFVEGLA
 60 70 80 90 100 110

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
 protein +AFs-F (450 aa)
 initn: 37 initl: 37 opt: 56 Z-score: 85.0 bits: 22.4 E(): 9.3
 Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
 in 63 aa overlap (19-73:46-108)

10 20 30 40
 AAD-12 HVQQAGSAYIGYGMDDTATPLRPL---VKVHPETGRPSLL--IGRH--
 :. :. : . : . : . : . : . : . : . : .


```

90      0      1:+ACo-
92      2      1:+ACo-      :+ACoAPQ-
94      1      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     1      0:+AD0-      +ACoAPQ-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     1      0:+AD0-      +ACoAPQ-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120  0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.72780.00337+ADs- mu+AD0- 6.0498
0.176
mean+AF8-var+AD0-36.3164 9.871, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.212825
Kolmogorov-Smirnov statistic: 0.0674 (N+AD0-29) at 48

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.7  0.24
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.5  1.1
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.1  2
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 22.4  2.4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4  3.2
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4  3.2
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)  52 21.2  5.3
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  57 22.7  6.6
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.4  7
gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (
838)  59 23.4  9.2
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.4  9.3

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)

initn: 73 init1: 73 opt: 73 Z-score: 113.4 bits: 27.7 E(): 0.24

Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (47-77:246-276)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      . . . . .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
      220      230      240      250      260      270

```

```

      80
AAD-12 GDVV
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 init1: 66 opt: 66 Z-score: 101.7 bits: 25.5 E(): 1.1
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (47-77:247-277)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      . . . . .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

```

```

      80
AAD-12 GDVV
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDWAVHFFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 58 Z-score: 96.8 bits: 23.1 E(): 2
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (27-62:79-117)

```

      10      20      30      40      50
AAD-12 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      . . . . .
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVV
      . . . . .
gi+AHw-121 EEFRASLVDYLSHHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 95.7 bits: 22.4 E(): 2.4

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (58-74:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVV
      : . . . . :  :: . . . . :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-219 SFSDRSGLLLKQKVSDE
      100      110
    
```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 93.2 bits: 22.4 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (58-74:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVV
      : . . . . :  :: . . . . :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150
    
```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 93.2 bits: 22.4 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (58-74:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVV
      : . . . . :  :: . . . . :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150
    
```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
Full+AD0-60S ac (110 aa)

initn: 47 init1: 47 opt: 52 Z-score: 89.4 bits: 21.2 E(): 5.3
Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (12-78:19-84)

```

      10      20      30      40      50
AAD-12      VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAESE
      : : : : . . . . . : : : : :
gi+AHw-135 MSTSELATSYAALILADDGVDITADKQLSRIKAAKIEEVEPIWTTLFAKALEGKDV--KD
      10      20      30      40      50
    
```

```

        60          70          80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVV
      .:. : : :.:. :.:. :.:.
gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEKKKEEKEEESDEDMGFGLFD
        60          70          80          90          100          110
    
```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 55 init1: 55 opt: 57 Z-score: 87.6 bits: 22.7 E(): 6.6
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
 in 49 aa overlap (1-46:345-393)

```

                                10          20          30
AAD-12                                VQQAGSAYIGYGMDDTATPLRPLVKVHPET
                                : . :. . . . :.:. :.:. : . :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEP
        320          330          340          350          360          370
    
```

```

        40          50          60          70          80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
      .. :. : : .. :.:. :.:.
gi+AHw-113 GESALSLTSSAGVLSQPGAPC
        380          390
    
```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 init1: 52 opt: 56 Z-score: 87.2 bits: 22.4 E(): 7
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (6-57:25-73)

```

                                10          20          30          40
AAD-12                                VQQAGSAYIGYGMDDTATPLRPLVKVHPET-GRPSLLIGRH
                                .: :.:. : :.:. : :.:. : :.:.
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
        10          20          30          40          50
    
```

```

        50          60          70          80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
      :.:. : :.:. :.:. :.:. :.:.
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA AVVPPADKYKTFVETFGTATNKAFVEGLA
        60          70          80          90          100          110
    
```

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum
 aestivum+AF0- (838 aa)
 initn: 43 init1: 43 opt: 59 Z-score: 85.1 bits: 23.4 E(): 9.2
 Smith-Waterman score: 59+ADs- 34.375+ACU- identity (59.375+ACU- similar)
 in 32 aa overlap (2-33:143-171)

```

                                10          20          30
AAD-12                                VQQAGSAYIGYGMDDTATPLRPLVKVHPETG
                                :.:. :.:. :.:. :.:. :.:. :.:.
gi+AHw-736 PSVTSPQQVSYYPGQAS PQRPQGQGPQGQGSQGGQQGY---YPTSPQQPGQWQQPEQG
        120          130          140          150          160
    
```

```

                40          50          60          70          80
AAD-12 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
      .:
gi+AHw-736 QPGYYPTSPQQPGQLQQPAQGGQQPGQQGRQPGQGQPGYYPTSSQLQPGQLQQPAQGGQ
      170          180          190          200          210          220
    
```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protein +AFs-F (450 aa)
 initn: 37 initl: 37 opt: 56 Z-score: 85.0 bits: 22.4 E(): 9.3
 Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar) in 63 aa overlap (18-72:46-108)

```

                10          20          30          40
AAD-12          VQQAGSAYIGYGMTTATPLRPL---VKVHPETGRPSLL--IGRH--
      :::::      ...:  ....:  :  .:
gi+AHw-253 IEEPEMIAPTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
      20          30          40          50          60          70
    
```

```

                50          60          70          80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
      ..:  .:..:  .:  .:  .:
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
      80          90          100          110          120          130
    
```

```

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPTHLEHSS
      140          150          160          170          180          190
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:25 2010 done: Fri Feb 5 12:56:25 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 176 - 255 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
    
```



```
96      1      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     1      0:+AD0-      +ACoAPQ-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     1      0:+AD0-      +ACoAPQ-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120 0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.91590.00346+ADs- mu+AD0- 4.9447
0.180
mean+AF8-var+AD0-37.304310.079, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.209988
Kolmogorov-Smirnov statistic: 0.0795 (N+AD0-29) at 42
```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB	RecName: Full+AD0-En
(439) 73 27.5 0.27	
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL	RecName: Full+AD0-Eno
(440) 66 25.4 1.2	
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH	RecName: Full+AD0-Glo
(151) 58 23.0 2.1	
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs-	(
115) 56 22.4 2.4	
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1	(157)
56 22.4 3.4	
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s	(157)
56 22.4 3.4	
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL	RecName: Full+AD0-60
(110) 52 21.2 5.4	
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR	RecName: Full+AD0-M
(339) 56 22.4 7.5	
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei	(450)
56 22.3 10	

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 112.5 bits: 27.5 E(): 0.27
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (46-76:246-276)

```
20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . ::: : . : . : .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
```

```

      220      230      240      250      260      270
AAD-12  GDVVV
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 init1: 66 opt: 66 Z-score: 101.0 bits: 25.4 E(): 1.2
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (46-76:247-277)

```

      20      30      40      50      60      70
AAD-12  ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

```

```

      80
AAD-12  GDVVV
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 58 Z-score: 96.5 bits: 23.0 E(): 2.1
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (26-61:79-117)

```

      10      20      30      40      50
AAD-12  QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      : : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      60      70      80
AAD-12  ERFLEGLVDWACQAPRVHAHQWAAGDVVV
      : : : :
gi+AHw-121 EEFRASLVVDYLSHHLDWNMTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 95.4 bits: 22.4 E(): 2.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (57-73:68-86)

```

      30      40      50      60      70      80
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVV
      : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF

```

40 50 60 70 80 90

gi+AHw-219 SFSDRSGLLLKQKVSDE
100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (57-73:68-86)

30 40 50 60 70 80
AAD-12 PETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVV
: : : : . . . : :

gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
40 50 60 70 80 90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (57-73:68-86)

30 40 50 60 70 80
AAD-12 PETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVV
: : : : . . . : :

gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
Full+AD0-60S ac (110 aa)

initn: 47 init1: 47 opt: 52 Z-score: 89.2 bits: 21.2 E(): 5.4
Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (11-77:19-84)

10 20 30 40 50
AAD-12 QQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAESE
: : : : : :

gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
10 20 30 40 50

60 70 80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVVV
. . . : : . . . : : . . .

gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWAADAAPAAEKKKEEKEESDEDMGFGLFD
60 70 80 90 100 110

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 initl: 52 opt: 56 Z-score: 86.7 bits: 22.4 E(): 7.5
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (5-56:25-73)

```

                                10      20      30
AAD-12                      QQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
                                .:  :.  :  ::  :  .  :  :  .  :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                                10      20      30      40      50
  
```

```

    40      50      60      70      80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
        ::: :  .:  .:  .:  .:
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKAAVAAAAVVPPADKYKTFVETFGTATNKAFVEGLA
        60      70      80      90     100     110
  
```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
 protein +AFs-F (450 aa)
 initn: 37 initl: 37 opt: 56 Z-score: 84.4 bits: 22.3 E(): 10
 Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
 in 63 aa overlap (17-71:46-108)

```

                                10      20      30
AAD-12                      QQAGSAYIGYGMDDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                                ::::  .:  .:  .:  :  .:  .
gi+AHw-253 IEEPemiAptPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
        20      30      40      50      60      70
  
```

```

    40      50      60      70      80
AAD-12  -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
        .:  .:  .:  .:  .:  .:  .:
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
        80      90     100     110     120     130
  
```

```

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPNNLHLNANQFNFEVPGHMNVSGHPHLEHSS
        140     150     160     170     180     190
  
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:25 2010 done: Fri Feb 5 12:56:26 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

84      1      3:+ACo-
86      2      2:+ACo-
88      1      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      2      1:+ACo-      :+ACoAPQ-
94      1      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      0      0:          +ACo-
100     1      0:+AD0-      +ACoAPQ-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     1      0:+AD0-      +ACoAPQ-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120  0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.92120.00341+ADs- mu+AD0- 4.8674
0.178
mean+AF8-var+AD0-37.454010.121, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.209568
Kolmogorov-Smirnov statistic: 0.0827 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.5    0.28
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.4    1.2
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.0    2.1
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 22.4    2.4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4    3.4
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4    3.4
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)  52 21.2    5.4
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.4    7.5
gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-Penicillium ci (
228)   54 21.8    7.5
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.3    10

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)

initn: 40 init1: 40 opt: 56 Z-score: 95.4 bits: 22.4 E(): 2.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (56-72:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVVW
      : . . . . : : : . . . : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-219 SFSDRSGLLLKQKVSDE
      100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (56-72:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVVW
      : . . . . : : : . . . : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (56-72:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVVW
      : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
 Full+AD0-60S ac (110 aa)

initn: 47 init1: 47 opt: 52 Z-score: 89.2 bits: 21.2 E(): 5.4
 Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
 in 68 aa overlap (10-76:19-84)

```

      10      20      30      40      50
AAD-12      QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE
      : : : : : . . . . : : : . . . : :
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
      10      20      30      40      50

```

```

                60          70          80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVVVW
      .:. : : :. :. :. :. :.
gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEKKKEEKEEESDEDMGFGLFD
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 init1: 52 opt: 56 Z-score: 86.7 bits: 22.4 E(): 7.5
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (4-55:25-73)

```

                                10          20          30
AAD-12                                QAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
                                .: :. : :. : :. : . : . : . :.
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                                10          20          30          40          50

```

```

                40          50          60          70          80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW
      .:. : .: :. :. :.
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA VVPPADKYKTFVETFGTATNKAFVEGLA
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-
Penicillium citrin (228 aa)
initn: 54 init1: 54 opt: 54 Z-score: 86.6 bits: 21.8 E(): 7.5
Smith-Waterman score: 54+ADs- 20.253+ACU- identity (51.899+ACU- similar)
in 79 aa overlap (2-80:74-152)

```

                                10          20          30
AAD-12                                QAGSAYIGYGMDDTTATPLRPLVKVHPETGRP
                                :. :. :. :. :. :. :. :.
gi+AHw-383 SPDAEKYPHVARWYKHIASYESEFPTLPGDASKAFTAYGPEGSEASANPKDKPAEEEEEE
                                50          60          70          80          90          100

```

```

                40          50          60          70          80
AAD-12 SLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW
      .:. . :. : :. :. :. :. :. :. :. :.
gi+AHw-383 DLFASDSEDEDPAVVAERNKNLEEYK K K K K A A K G P K P A A K S L V T L E V K P W D D E T N L E E L E A
                110          120          130          140          150          160

```

```

gi+AHw-383 NVRAIEMDGLVWGASKFVAVGFGIKKLQINLVVEDEKVVSTDELQAQIEEDEDHVQSTDVA
                170          180          190          200          210          220

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 init1: 37 opt: 56 Z-score: 84.4 bits: 22.3 E(): 10
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (16-70:46-108)

```

                                10          20          30
AAD-12                                QAGSAYIGYGMDDTTATPLRPL---VKVHPETGRPSLL--IGRH--

```


331323 residues in 1471 sequences
 Expectation+AF8-n fit: rho(ln(x))+AD0- 4.86640.00332+ADs- mu+AD0- 5.1505
 0.174
 mean+AF8-var+AD0-36.8902 9.934, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
 Lambda+AD0- 0.211163
 Kolmogorov-Smirnov statistic: 0.0814 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
 Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB	RecName: Full+AD0-En
(439) 73 27.6 0.26	
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH	RecName: Full+AD0-Glo
(151) 64 24.9 0.57	
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL	RecName: Full+AD0-Eno
(440) 66 25.4 1.1	
gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-Penicillium ci	(228)
62 24.3 1.3	
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs-	(115)
56 22.5 2.4	
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1	(157)
56 22.4 3.2	
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s	(157)
56 22.4 3.2	
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL	RecName: Full+AD0-60
(110) 52 21.2 5.2	
gi+AHw-71153243+AHw-sp+AHw-Q39547.1+AHw-CUCM1+AF8-CUCME	RecName: Full+AD0-
(731) 60 23.6 6.8	
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR	RecName: Full+AD0-M
(339) 56 22.4 7.1	
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei	(450)
56 22.4 9.6	

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 113.0 bits: 27.6 E(): 0.26
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (44-74:246-276)

	20	30	40	50	60	70
AAAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
				::: :: . ::: : . :		:: .
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
	220	230	240	250	260	270
	80					
AAAD-12	GDVVVWD					
	:					
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK					
	280	290	300	310	320	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 106.7 bits: 24.9 E(): 0.57
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (24-80:79-133)

```

                10      20      30      40
AAD-12      AGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDDAAES
                ....  ....  ::  :  :  ...  ..
gi+AHw-121  DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50      60      70      80      90      100

                50      60      70      80
AAD-12  ERFLEGLVDWACQAPRVHAHQWAAGDVVVWD
                ::  .....  :  .:  ...
gi+AHw-121  EEFRASLVDYLS-----HHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
                110      120      130      140      150
  
```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 101.4 bits: 25.4 E(): 1.1
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (44-74:247-277)

```

                20      30      40      50      60      70
AAD-12  ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAA
                ....  ::  .  .:  :  .  .  .  .  .
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270

                80
AAD-12  GDVVVWD
                :
gi+AHw-232  GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330
  
```

+AD4APg-gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-
 Penicillium citrin (228 aa)
 initn: 62 init1: 62 opt: 62 Z-score: 100.1 bits: 24.3 E(): 1.3
 Smith-Waterman score: 62+ADs- 21.250+ACU- identity (52.500+ACU- similar)
 in 80 aa overlap (1-80:74-153)

```

                10      20      30
AAD-12      AGSAYIGYGMDDTATPLRPLVKVHPETGRP
                .....  .:  .  .  :  :  :  .
gi+AHw-383  SPDAEKYPHVARWYKHIASESEFPTLPGDASKAFTAYGPEGSEASANPKDKPAEEEEEE
                50      60      70      80      90      100

                40      50      60      70      80
AAD-12  SLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWD
                .:  .  :  .:  :  .:  :  .:  .:  .:  .:
gi+AHw-383  DLFASDSEDEDPAVVAERNKNLEEYKKKKAAKGPKPAKSLVTLEVKPWDETNLEELEA
                110      120      130      140      150      160
  
```

gi+AHw-383 NVRAIEMDGLVWGASKFVAVGFGIKKLQINLVVEDEKVVSTDELQAQIEEDEDHVQSTDVA
 170 180 190 200 210 220

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)

initn: 40 init1: 40 opt: 56 Z-score: 95.7 bits: 22.5 E(): 2.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (55-71:68-86)

30 40 50 60 70 80
 AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWD
 : : : : . . . : :
 gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

gi+AHw-219 SFSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 93.2 bits: 22.4 E(): 3.2
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (55-71:68-86)

30 40 50 60 70 80
 AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWD
 : : : : . . . : :
 gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
 40 50 60 70 80 90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 93.2 bits: 22.4 E(): 3.2
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (55-71:68-86)

30 40 50 60 70 80
 AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWD
 : : : : . . . : :
 gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
 Full+AD0-60S ac (110 aa)

initn: 47 init1: 47 opt: 52 Z-score: 89.5 bits: 21.2 E(): 5.2
 Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
 in 68 aa overlap (9-75:19-84)

Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (15-69:46-108)

```

                10         20         30
AAD-12          AGSAYIGYGMDDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                :::::   ...:   ....:   :   .:
gi+AHw-253 IEEPemiAptPPGQfPhQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                20         30         40         50         60         70

                40         50         60         70         80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWD
                ..:   .:..:   .:   .:   ..:   .:
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
                80         90         100        110        120        130

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPHLEHSS
                140        150        160        170        180        190

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:26 2010 done: Fri Feb 5 12:56:26 2010
Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 179 - 258 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      1      2:+ACo-
      32      3      8:+AD0- +ACo-
      34     11     21:+AD0APQA9AD0- +ACo-
      36     24     44:+AD0APQA9AD0APQA9AD0APQ- +ACo-
      38     53     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-

```



```

112      1      0:+AD0-          +ACoAPQ-
114      0      0:              +ACo-
116      0      0:              +ACo-
118      0      0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.97720.00329+ADs- mu+AD0- 4.6011
0.172
mean+AF8-var+AD0-37.2608 9.980, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.210111
Kolmogorov-Smirnov statistic: 0.0834 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.5  0.27
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.8  0.6
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.4  1.2
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 22.4  2.4
gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-Penicillium ci (
228)  59 23.3  2.6
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4  3.3
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4  3.3
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)  52 21.2  5.3
gi+AHw-71153243+AHw-sp+AHw-Q39547.1+AHw-CUCM1+AF8-CUCME RecName: Full+AD0-
( 731)  60 23.5  7.2
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.4  7.5

```

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 112.4 bits: 27.5 E(): 0.27
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (43-73:246-276)

```

```

                20          30          40          50          60          70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                ::: :: . ::: : . : .: .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
                220          230          240          250          260          270

                80
AAD-12 GDVVVWDN
                :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK

```


+AD4APg-gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-
 Penicillium citrin (228 aa)
 initn: 59 init1: 59 opt: 59 Z-score: 94.8 bits: 23.3 E(): 2.6
 Smith-Waterman score: 59+ADs- 20.513+ACU- identity (51.282+ACU- similar)
 in 78 aa overlap (3-80:77-154)

```

                                10      20      30
AAD-12                          GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                                :. .:: . . . : : : . .::
gi+AHw-383 AEKYPHVARWYKHIASYESEFPTLPGDASKAFTAYGPEGSEASANPKDKPAEEEEEDLF
                   50          60          70          80          90          100

```

```

                   40          50          60          70          80
AAD-12 IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDN
                   .   :.. : ... . :   : ...: ... .. : :..
gi+AHw-383 ASDSEDEDPAVVAERNKNLEEYKKKKAAGKPKPAKSLVTLEVKPWDDETNLLEELEANVR
                   110         120         130         140         150         160

```

```

gi+AHw-383 AIEMDGLVWGASKFVAVGFGIKKLQINLVVEDEKVVSTDELQAQIEEDEDHVQSTDVAAMQ
                   170         180         190         200         210         220

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 93.0 bits: 22.4 E(): 3.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (54-70:68-86)

```

                   30          40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDN
                                : .::: : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
                   40          50          60          70          80          90

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                   100         110         120         130         140         150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 93.0 bits: 22.4 E(): 3.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (54-70:68-86)

```

                   30          40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDN
                                : .::: : : : : : : : : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
                   40          50          60          70          80          90

```

```

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                   100         110         120         130         140         150

```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
 Full+AD0-60S ac (110 aa)
 initn: 47 init1: 47 opt: 52 Z-score: 89.3 bits: 21.2 E(): 5.3

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
 (439) 73 27.6 0.26
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 64 24.9 0.56
 gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
 (440) 66 25.4 1.1
 gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
 56 22.5 2.3
 gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-Penicillium ci (228)
 59 23.4 2.5
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 22.5 3.2
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 22.5 3.2
 gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
 (110) 52 21.3 5.1
 gi+AHw-71153243+AHw-sp+AHw-Q39547.1+AHw-CUCM1+AF8-CUCME RecName: Full+AD0-
 (731) 60 23.6 7
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.4 7.2
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.4 9.7

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 113.0 bits: 27.6 E(): 0.26
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (42-72:246-276)

	20	30	40	50	60	70
AAAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAI	PGMDAAESERFLEGLVDWACQAPRVHAHQWAA				
				::: :: . ::: : . :		:: .
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT					
	220	230	240	250	260	270
	80					
AAAD-12	GDVVVDNR					
	:					
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK					
	280	290	300	310	320	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 106.9 bits: 24.9 E(): 0.56
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (22-78:79-133)

		10	20	30	40
AAAD-12	SAYIGYGMDDTATPLRPLVKVHPETGRPSL	--LIGRHA--	HAI	PGMDAAES	
				::: ::: :: : : : .. ::	
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN	RPALKTLIDGLASSHKARGIEKAQF			
	50	60	70	80	90
					100
	50	60	70	80	

AAAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR

```

      ::  ::::  :  ::  :::
gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      110          120          130          140          150
  
```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 101.4 bits: 25.4 E(): 1.1
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (42-72:247-277)

```

      20          30          40          50          60          70
AAAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      ::::  ::  .  ::  :  .  ::  .  ::
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
      220          230          240          250          260          270
  
```

```

      80
AAAD-12 GDVVVWDNR
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280          290          300          310          320          330
  
```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 95.9 bits: 22.5 E(): 2.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (53-69:68-86)

```

      30          40          50          60          70          80
AAAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :  ::::  ::  ...  ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40          50          60          70          80          90
  
```

```

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100          110
  
```

+AD4APg-gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs- Penicillium citrin (228 aa)
 initn: 59 initl: 59 opt: 59 Z-score: 95.2 bits: 23.4 E(): 2.5
 Smith-Waterman score: 59+ADs- 20.513+ACU- identity (51.282+ACU- similar)
 in 78 aa overlap (2-79:77-154)

```

      10          20          30
AAAD-12 SAYIGYGMDDTATPLRPLVKVHPETGRPSLL
      ..  ::  .  .  .  :  :  :  .  .  .
gi+AHw-383 AEKYPHVARWYKHIASYESEFPTLPGDASKAFTAYGPEGSEASANPKDKPAEEEEEEEDLF
      50          60          70          80          90          100
  
```

```

      40          50          60          70          80
AAAD-12 IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR
      .  ::  :  ...  .  :  :  ::::  ...  .  .  :  ::
gi+AHw-383 ASDSEDEDPAVVAERNKNLEEYKMKKAAKGPKPAKSLVTLEVKPWDDETNLLEELEANVR
  
```


+AD4APg-gi+AHw-71153243+AHw-sp+AHw-Q39547.1+AHw-CUCM1+AF8-CUCME RecName:
 Full+AD0-Cucu (731 aa)
 initn: 35 init1: 35 opt: 60 Z-score: 87.2 bits: 23.6 E(): 7
 Smith-Waterman score: 60+ADs- 29.412+ACU- identity (52.941+ACU- similar)
 in 85 aa overlap (2-78:548-631)

```

                                10      20      30
AAD-12                          SAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                                : : .. : : : : . . : . :
gi+AHw-711 FNIISGTSMSCPHITGIATYVKTYNPTWSPAAIKSALMTTASPMNARFNPQAEFAYGSGH
                520          530          540          550          560          570
    
```

```

                40          50          60          70          80
AAD-12 IGRHAHAIPGM--DAAESE--RFLEGLVDWACQAPRVHAHQWAA---GDV-VVWDNR
                .. . : : . : : . : : : . : : : . : : : : : : : : : : : : : :
gi+AHw-711 VNPLKAVRPGLVYDANESDYVKFLCGQ-GYNTQAVRRITGDYSACTSGNTGRVWDLNYP
                580          590          600          610          620          630
    
```

```

gi+AHw-711 FGLSVSPSQTFNQYFNRTLTSVAPQASTYRAMISAPQGLTISVNPVLSFNGLGDRKSFT
                640          650          660          670          680          690
    
```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 init1: 52 opt: 56 Z-score: 87.0 bits: 22.4 E(): 7.2
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (1-52:25-73)

```

                                10      20      30
AAD-12                          SAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
                                . : : : : : : : : : : : : : : : :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                10          20          30          40          50
    
```

```

                40          50          60          70          80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNR
                : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKAAVAAAAVVPPADKYKTFVETFGTATNKAFVEGLA
                60          70          80          90          100          110
    
```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
 protein +AFs-F (450 aa)
 initn: 37 init1: 37 opt: 56 Z-score: 84.6 bits: 22.4 E(): 9.7
 Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
 in 63 aa overlap (13-67:46-108)

```

                                10      20      30
AAD-12                          SAYIGYGMDDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                                : : : : : : : : : : : : : : : : : :
gi+AHw-253 IEEPEMIAPTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                20          30          40          50          60          70
    
```

```

                40          50          60          70          80
AAD-12 -AHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNR
                . : : . : : : : . : : . : : . :
    
```


FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.3  0.31
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.7  0.67
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.2  1.3
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 22.3  2.6
gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-Penicillium ci (
228)  59 23.1  2.9
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.3  3.7
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.3  3.7
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)  52 21.1  5.8
gi+AHw-71153243+AHw-sp+AHw-Q39547.1+AHw-CUCM1+AF8-CUCME RecName: Full+AD0-
( 731)  60 23.4  7.9
gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve
( 206)  53 21.4  9
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  55 21.9  10

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 111.5 bits: 27.3 E(): 0.31
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (41-71:246-276)

```

                20          30          40          50          60          70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                :::: :: . ::: : . : . : .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
                220          230          240          250          260          270

```

```

                80
AAD-12 GDVVVWDNRC
                :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280          290          300          310          320          330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 64 Z-score: 105.5 bits: 24.7 E(): 0.67
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (21-77:79-133)

```

                10          20          30          40
AAD-12 AYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES

```

```

gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
          50          60          70          80          90          100

```

```

          50          60          70          80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRC
      :.: .:..: .: .: .:

```

```

gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
          110          120          130          140          150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 initl: 66 opt: 66 Z-score: 100.1 bits: 25.2 E(): 1.3
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (41-71:247-277)

```

          20          30          40          50          60          70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
          :.: .:..: .: .: .: .: .: .: .:
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
          220          230          240          250          260          270

```

```

          80
AAD-12 GDVVVVDNRC
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFFERVGDKIQIVGDDLTVTNPTRIKT
          280          290          300          310          320          330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 94.8 bits: 22.3 E(): 2.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (52-68:68-86)

```

          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVVDNRC
          : .:..: .: .: .: .:
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

```

          80
AAD-12 C
gi+AHw-219 SFSDRSGLLLKQKVSDE
          100          110

```

+AD4-+AD4-gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-
Penicillium citrin (228 aa)
initn: 59 initl: 59 opt: 59 Z-score: 94.1 bits: 23.1 E(): 2.9
Smith-Waterman score: 59+ADs- 20.513+ACU- identity (51.282+ACU- similar)
in 78 aa overlap (1-78:77-154)

```

          10          20          30
AAD-12 AYIGYGMDDTATPLRPLVKVHPETGRPSLL

```

```

                                :. .:: . . . : : : . .:
gi+AHw-383 AEKYPHVARWYKHIASYESEFPTLPGDASKAFTAYGPEGSEASANPKDKPAEEEEEEEDLF
          50          60          70          80          90          100

```

```

          40          50          60          70          80
AAD-12 IGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRC
.          :.. : ... . :          : ..: .:.. .: : :

```

```

gi+AHw-383 ASDSEDEDPAVVAERNKNLEEYKKKKAAGPKPAKSLVTLEVKPWDDETNLLEELEANVR
          110          120          130          140          150          160

```

```

gi+AHw-383 AIEMDGLVWGASKFVAVGFGIKKLQINLVVEDEKVVSTDELQAQIEEDEDHVQSTDVAAAMQ
          170          180          190          200          210          220

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 92.3 bits: 22.3 E(): 3.7
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (52-68:68-86)

```

          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                : .::: : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90

```

80
 AAD-12 C

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 92.3 bits: 22.3 E(): 3.7
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (52-68:68-86)

```

          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                : .::: : : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

80
 AAD-12 C

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
 Full+AD0-60S ac (110 aa)
 initn: 47 init1: 47 opt: 52 Z-score: 88.7 bits: 21.1 E(): 5.8
 Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
 in 68 aa overlap (6-72:19-84)

initn: 51 init1: 51 opt: 55 Z-score: 84.4 bits: 21.9 E(): 10
 Smith-Waterman score: 55+ADs- 30.189+ACU- identity (52.830+ACU- similar)
 in 53 aa overlap (1-51:26-73)

```

                                10      20      30
AAD-12                          AYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
                                :  ::  :  ::  :  .  :  :  .  ::
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRC
                                ::  :  ::  ....:
gi+AHw-249 PAAVPSGKATTEEQKLIIEKINAGFKA AVAAA VVPPADKYKTFVETFGTATNKAFVEGLA
                                60      70      80      90      100     110
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:26 2010 done: Fri Feb 5 12:56:26 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 182 - 261 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	1	0:+AD0-	
30	0	2:+ACo-	
32	3	8:+AD0- +ACo-	
34	15	21:+AD0APQA9AD0APQ- +ACo-	
36	19	44:+AD0APQA9AD0APQA9AD0- +ACo-	
38	49	72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-	
+ACo-			
40	54	101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-	
+ACo-			


```

116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.01210.00313+ADs- mu+AD0- 4.5390
0.164
mean+AF8-var+AD0-37.1168 9.823, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.210518
Kolmogorov-Smirnov statistic: 0.0834 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.5  0.28
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.8  0.6
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.3  1.2
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 22.4  2.4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4  3.4
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4  3.4
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)  52 21.2  5.4
gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-Penicillium ci (
228)  54 21.7  7.6
gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve
( 206)  53 21.4  8.5

```

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 112.3 bits: 27.5 E(): 0.28
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (40-70:246-276)

```

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . ::: : . : .: .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
      220      230      240      250      260      270

```

```

      70      80
AAD-12 GDVVVWDNRCL
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)

```

initn: 51 init1: 51 opt: 64 Z-score: 106.3 bits: 24.8 E(): 0.6
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (20-76:79-133)

```

                10      20      30      40
AAD-12          YIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                ....  ::  :  :  ...  .
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50      60      70      80      90      100
    
```

```

                50      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL
                ::  .....  :  :  ...
gi+AHw-121 EEFRASLVDYLS-----HHLDWNMTMKSTWDLALNNMFFYILHALEVAQ
                110      120      130      140      150
    
```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 100.8 bits: 25.3 E(): 1.2
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (40-70:247-277)

```

                10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                ....  ::  .  :  .  .  .  .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270
    
```

```

                70      80
AAD-12 GDVVVWDNRCL
                :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330
    
```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 95.4 bits: 22.4 E(): 2.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (51-67:68-86)

```

                30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                :  ....  ::  ...  ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGNFKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
                40      50      60      70      80      90
    
```

```

                80
AAD-12 CL
                :
gi+AHw-219 SFSDRSGLLLKQKVSDE
                100      110
    
```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (51-67:68-86)

```

                30         40         50         60         70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . : : : . . . : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
                40         50         60         70         80         90
    
```

80
 AAD-12 CL

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                100         110         120         130         140         150
    
```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (51-67:68-86)

```

                30         40         50         60         70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
                40         50         60         70         80         90
    
```

80
 AAD-12 CL

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                100         110         120         130         140         150
    
```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60S ac (110 aa)

initn: 47 initl: 47 opt: 52 Z-score: 89.2 bits: 21.2 E(): 5.4
 Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
 in 68 aa overlap (5-71:19-84)

```

                10         20         30         40
AAD-12                YIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
                : : : : : . : : : : : : : :
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
                10         20         30         40         50
    
```

```

                50         60         70         80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVVVWDNRCL
                . . . : : . . . : : : :
gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWAADAAPAAEKKKEEKEEEDMGMGFLFD
                60         70         80         90         100         110
    
```

+AD4APg-gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs- Penicillium citrin (228 aa)

initn: 51 initl: 51 opt: 54 Z-score: 86.5 bits: 21.7 E(): 7.6
 Smith-Waterman score: 54+ADs- 19.481+ACU- identity (50.649+ACU- similar)
 in 77 aa overlap (1-77:78-154)

```

                                10      20      30
AAD-12      YIGYGMDDTATPLRPLVKVHPETGRPSLLI
              . . . . . : : : . . .
gi+AHw-383  EKYPHVARWYKHIASYESEFPTLPGDASKAFTAYGPEGSEASANPKDKPAEEEEEEEDLFA
              50      60      70      80      90      100

              40      50      60      70      80
AAD-12  GRHAHAIPGMDDAERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL
              . . . : . . . : . . . : . . . : . . .
gi+AHw-383  SDESEDDPAVVAERNKNLEEYKKAAGPKPAKSLVTLEVKPWDDETNLEEELEANVRA
              110     120     130     140     150     160

gi+AHw-383  IEMDGLVWGASKFVAVGFGIKKLQINLVEDEKVVSTDELQAQIEEDEDHVQSTDVAAMQK
              170     180     190     200     210     220
    
```

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
 Full+AD0-Venom (206 aa)
 initn: 34 initl: 34 opt: 53 Z-score: 85.7 bits: 21.4 E(): 8.5
 Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
 in 55 aa overlap (25-79:54-104)

```

                                10      20      30      40      50
AAD-12      YIGYGMDDTATPLRPLVKVHPETGRPSLLI GRHAHAIPGMDDAERFLEGLVD
              : . . : . . . : . . : . . : . . . : . . .
gi+AHw-250  PSKNCAGKVIKSVGPTEEEEKLLIVEEHNRFQKVAQGLETRGNPGPQPAASN--MNNLV-
              30      40      50      60      70      80

              60      70      80
AAD-12  WACQAPRVHAHQWAAGDVVVWDNRCL
              : . . : . . : . . : . . : . . : . . : . . : . .
gi+AHw-250  WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPVTKLIQLWENEV
              90      100     110     120     130
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:26 2010 done: Fri Feb 5 12:56:26 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

76      15      7:+AD0APQAqAD0APQ-
78      10      6:+AD0AKgA9AD0-
80       3      4:+AD0AKg-
82       7      3:+ACoAPQA9-
84       1      3:+ACo-
86       1      2:+ACo-
88       1      2:+ACo-          inset +AD0- represents 1 library sequences
90       0      1:+ACo-
92       2      1:+ACo-          :+ACoAPQ-
94       1      1:+ACo-          :+ACo-
96       0      1:+ACo-          :+ACo-
98       0      0:          +ACo-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     1      0:+AD0-          +ACoAPQ-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     1      0:+AD0-          +ACoAPQ-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-

```

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 5.04940.0031+ADs- mu+AD0- 4.3569
0.163

mean+AF8-var+AD0-37.1029 9.772, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43

Lambda+AD0- 0.210557

Kolmogorov-Smirnov statistic: 0.0843 (N+AD0-29) at 40

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
(439) 73 27.5 0.28

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
(151) 64 24.8 0.6

gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
(440) 66 25.3 1.2

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 22.4 2.4

gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
56 22.4 3.4

gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
56 22.4 3.4

gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
(110) 52 21.2 5.4

gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve
(206) 53 21.4 8.5

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)

initn: 73 init1: 73 opt: 73 Z-score: 112.3 bits: 27.5 E(): 0.28
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (39-69:246-276)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . .:: : . : .: .
gi+AHw-370 APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
      220      230      240      250      260      270

```

```

      70      80
AAD-12 GDVVVWDNRCLL
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 106.3 bits: 24.8 E(): 0.6
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (19-75:79-133)

```

      10      20      30      40
AAD-12 IGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      :::: ::: : : : : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      50      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLL
      :: : : : : : : : :
gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNMFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-EN01+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 100.7 bits: 25.3 E(): 1.2
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (39-69:247-277)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . .: : . : .: .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGGYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

```

```

      70      80
AAD-12 GDVVVWDNRCLL
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDVAWVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)

initn: 40 init1: 40 opt: 56 Z-score: 95.4 bits: 22.4 E(): 2.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (50-66:68-86)

```

      20          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . :  :: . . .  ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
            40          50          60          70          80          90
  
```

80
 AAD-12 CLL

gi+AHw-219 SFSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (50-66:68-86)

```

      20          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . :  :: . . .  ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
            40          50          60          70          80          90
  
```

80
 AAD-12 CLL

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (50-66:68-86)

```

      20          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . :  :: . . .  ::
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
            40          50          60          70          80          90
  
```

80
 AAD-12 CLL

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
 Full+AD0-60S ac (110 aa)

initn: 47 init1: 47 opt: 52 Z-score: 89.3 bits: 21.2 E(): 5.4
 Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
 in 68 aa overlap (4-70:19-84)

```

                10      20      30      40
AAD-12          IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE
                :: ::  . :.:. . . . . . . . . . . . . . . .
gi+AHw-135 MSTSELATSYAALILADDGVDITADKQLSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
                10      20      30      40      50

                50      60      70      80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVVVWDNRCLL
                .:. :  :  :..  .: :.:.
gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWAADAAPAAEKKEEEEKEESDEDMGFGLFD
                60      70      80      90      100     110
    
```

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
 Full+AD0-Venom (206 aa)
 initn: 34 init1: 34 opt: 53 Z-score: 85.7 bits: 21.4 E(): 8.5
 Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
 in 55 aa overlap (24-78:54-104)

```

                10      20      30      40      50
AAD-12          IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAESERFLEGLVD
                : . . : . . . . : . : . . . . :
gi+AHw-250 PSKNCAGKVIKSVGPTEEEEKKLIVEEHNRFQKVAQGLETRGNPGPQPAASN--MNNLV-
                30      40      50      60      70      80

                60      70      80
AAD-12 WACQAPRVHAHQWAAGDVVVWDNRCLL
                : . . . : . . . :
gi+AHw-250 WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPSVTKLIQLWENEV
                90      100     110     120     130
    
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:26 2010 done: Fri Feb 5 12:56:26 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```
82      7      3:+ACoAPQA9-
84      2      3:+ACo-
86      1      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      1      1:+ACo-
92      1      1:+ACo-          :+ACo-
94      1      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     1      0:+AD0-          +ACoAPQ-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     1      0:+AD0-          +ACoAPQ-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.08150.00309+ADs- mu+AD0- 4.2168
0.162
mean+AF8-var+AD0-36.1527 9.323, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.213306
Kolmogorov-Smirnov statistic: 0.0854 (N+AD0-28) at 44
```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are: opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
(439) 73 27.6 0.26
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
(151) 64 24.9 0.55
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
(440) 66 25.4 1.1
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 22.5 2.3
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
56 22.5 3.2
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
56 22.5 3.2
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
(110) 52 21.3 5
gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve
(206) 53 21.5 8.1
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
56 22.4 9.9

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 113.0 bits: 27.6 E(): 0.26

Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (38-68:246-276)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      . . . . .
gi+AHw-370 APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT
      220      230      240      250      260      270

```

```

      70      80
AAD-12 GDVVVWDNRCLLH
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 64 Z-score: 107.0 bits: 24.9 E(): 0.55
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (18-74:79-133)

```

      10      20      30      40
AAD-12          YGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      . . . . .
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      50      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLH
      . . . . .
gi+AHw-121 EEFRASLV DYLS-----HHLWDNDTMKSTWDLALNMFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-EN01+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 init1: 66 opt: 66 Z-score: 101.3 bits: 25.4 E(): 1.1
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (38-68:247-277)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      . . . . .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

```

```

      70      80
AAD-12 GDVVVWDNRCLLH
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDVAWVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 96.0 bits: 22.5 E(): 2.3

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (49-65:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :  . . . . :  ::  . . .  ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

80
AAD-12 CLLH

gi+AHw-219 SFSDRSGLLLKQKVSDE
100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 93.4 bits: 22.5 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (49-65:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :  . . . . :  ::  . . .  ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

```

80
AAD-12 CLLH

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 93.4 bits: 22.5 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (49-65:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :  . . . . :  ::  . . .  ::
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

80
AAD-12 CLLH

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
Full+AD0-60S ac (110 aa)

initn: 47 init1: 47 opt: 52 Z-score: 89.7 bits: 21.3 E(): 5

Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (3-69:19-84)

```

                10      20      30      40
AAD-12          GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
                ::: ::  :  ::::  .  ::::  :  :  ..
gi+AHw-135 MSTSELATSYAALILADDGVDITADKQLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
                10      20      30      40      50

                50      60      70      80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH
                .:: :  :  :..  .:  :::
gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWAADAAPAAEKKEEEEKEESEDEDMGFGLFD
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
Full+AD0-Venom (206 aa)
initn: 34 init1: 34 opt: 53 Z-score: 86.1 bits: 21.5 E(): 8.1
Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
in 55 aa overlap (23-77:54-104)

```

                10      20      30      40      50
AAD-12          GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
                :  .  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-250 PSKNCAGKVIKSVGPTEEEEKLVIVEEHNRFQKVAQGLETRGNPGPQPAASN--MNNLV-
                30      40      50      60      70      80

                60      70      80
AAD-12 WACQAPRVHAHQWAAGDVVVWDNRCLLH
                :  .  .  .  :  ::  .  .  :  :
gi+AHw-250 WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPSVTKLIQLWENEV
                90      100      110      120      130

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 init1: 37 opt: 56 Z-score: 84.5 bits: 22.4 E(): 9.9
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (9-63:46-108)

```

                10      20      30
AAD-12          GYGMDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                :::::  ...:  ....:  :  :  :
gi+AHw-253 IEEPemiAptPPGQFPHQQPissPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                20      30      40      50      60      70

                40      50      60      70      80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH
                .::  .  ::::  :  .  :  :::  :
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
                80      90      100      110      120      130

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPHLEHSS
                140      150      160      170      180      190

```


52 115 106:+AD0APQ-
 +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
 D0APQA9AD0APQA9ACoAPQA9AD0-
 54 79
 91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
 A9- +ACo-
 56 67
 76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
 58 82
 62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
 A9AD0-
 60 56 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
 62 44 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
 64 45 32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
 66 28 25:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
 68 31 20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
 70 15 16:+AD0APQA9AD0APQA9-
 72 14 12:+AD0APQA9ACoAPQ-
 74 8 10:+AD0APQA9ACo-
 76 17 7:+AD0APQA9AD0APQA9-
 78 4 6:+AD0AKg-
 80 7 4:+AD0AKgA9-
 82 5 3:+ACoAPQ-
 84 3 3:+ACo-
 86 2 2:+ACo-
 88 0 2:+ACo- inset +AD0- represents 1 library sequences
 90 1 1:+ACo-
 92 0 1:+ACo- :+ACo-
 94 2 1:+ACo- :+ACoAPQ-
 96 1 1:+ACo- :+ACo-
 98 0 0: +ACo-
 100 0 0: +ACo-
 102 1 0:+AD0- +ACoAPQ-
 104 0 0: +ACo-
 106 0 0: +ACo-
 108 1 0:+AD0- +ACoAPQ-
 110 0 0: +ACo-
 112 0 0: +ACo-
 114 1 0:+AD0- +ACoAPQ-
 116 0 0: +ACo-
 118 0 0: +ACo-
 +AD4-120 0 0: +ACo-
 331323 residues in 1471 sequences
 Expectation+AF8-n fit: rho(ln(x))+AD0- 4.73490.00304+ADs- mu+AD0- 6.0962
 0.160
 mean+AF8-var+AD0-34.8254 9.215, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
 Lambda+AD0- 0.217333
 Kolmogorov-Smirnov statistic: 0.0752 (N+AD0-28) at 44

 FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1
 join: 42, opt: 30, open/ext: -10/-2, width: 32
 Scan time: 0.080
 The best scores are: opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
 (439) 73 27.9 0.21
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 64 25.1 0.49
 gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
 (440) 66 25.7 0.96
 gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
 56 22.6 2.1
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 22.6 2.9
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 22.6 2.9
 gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
 (110) 52 21.4 4.8
 gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve
 (206) 53 21.6 7.4
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.5 8.6

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 114.6 bits: 27.9 E(): 0.21
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (37-67:246-276)

	10	20	30	40	50	60
AAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAI	PGMDAAESERFLEGLVDWACQAPRVHAHQWAA				
				::: :: . ::: : . : :: .		
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKPNPSDKSKWIT					
	220	230	240	250	260	270
	70	80				
AAD-12	GDVVVWDNRCLLHR					
	:					
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK					
	280	290	300	310	320	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 107.9 bits: 25.1 E(): 0.49
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (17-73:79-133)

		10	20	30	40	
AAD-12		YGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES				
			::: ::: :: : : : .. ::			
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF					
	50	60	70	80	90	100
	50	60	70	80		
AAD-12	ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHR					
	::: ::: :: : : : :::					
gi+AHw-121	EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ					
	110	120	130	140	150	

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 init1: 66 opt: 66 Z-score: 102.7 bits: 25.7 E(): 0.96
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (37-67:247-277)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

```

```

      70      80
AAD-12 GDVVVWDNRCLLHR
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 96.5 bits: 22.6 E(): 2.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (48-64:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

```

      80
AAD-12 CLLHR
gi+AHw-219 SFSDRSGLLLKQKVSDE
      100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 94.0 bits: 22.6 E(): 2.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (48-64:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

```

```

      80
AAD-12 CLLHR
gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 94.0 bits: 22.6 E(): 2.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (48-64:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

80
AAD-12 CLLHR

```

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
Full+AD0-60S ac (110 aa)
initn: 47 init1: 47 opt: 52 Z-score: 90.1 bits: 21.4 E(): 4.8
Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (2-68:19-84)

```

      10      20      30      40
AAD-12          YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
      : : : . : : : . : : : : : : :
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
      : : : : : : : : : :
gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEKKKEEKEESDEDMGFGLFD
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
Full+AD0-Venom (206 aa)
initn: 34 init1: 34 opt: 53 Z-score: 86.7 bits: 21.6 E(): 7.4
Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
in 55 aa overlap (22-76:54-104)

```

      10      20      30      40      50
AAD-12          YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
      : . : : . . . : : : : : : :
gi+AHw-250 PSKNCAGKVIKSVGPTEEEKKLIVEEHNRFQKVAQGLETRGNPGPQPAASN--MNNLV-
      30      40      50      60      70      80

```

```

      60      70      80
AAD-12 WACQAPRVHAHQWAAGDVVVWDNRCLLHR
      : . . . : : : . . . :
gi+AHw-250 WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPVTKLIQLWENEV
      90      100      110      120      130

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
 protein +AFs-F (450 aa)
 initn: 37 initl: 37 opt: 56 Z-score: 85.5 bits: 22.5 E(): 8.6
 Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
 in 63 aa overlap (8-62:46-108)

```

                                10          20          30
AAD-12          YGMDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                                :::::   ...:  ....:  :  ..
gi+AHw-253  IEEPemiAptPPGQFPHQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                20          30          40          50          60          70

                                40          50          60          70          80
AAD-12  -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
                ..:  .  :::.  :.  .:  .::  .:
gi+AHw-253  VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRRHRAHSAQSSA
                80          90          100         110         120         130

gi+AHw-253  GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPHLEHSS
                140         150         160         170         180         190
  
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:27 2010 done: Fri Feb 5 12:56:27 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 186 - 265 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	0	0:	
30	0	2:+ACo-	
32	3	8:+AD0- +ACo-	
34	19	21:+AD0APQA9AD0APQA9ACo-	


```

106      0      0:      +ACo-
108      1      0:+AD0-      +ACoAPQ-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      1      0:+AD0-      +ACoAPQ-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.83680.00305+ADs- mu+AD0- 5.4607
0.161
mean+AF8-var+AD0-34.8181 9.243, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.217356
Kolmogorov-Smirnov statistic: 0.0807 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 27.9 0.21
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 64 25.1 0.48
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 25.7 0.96
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 22.7 2.1
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.6 2.8
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.6 2.8
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110) 52 21.4 4.7
gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve
( 206) 53 21.7 7.3
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.6 8.6

```

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 114.6 bits: 27.9 E(): 0.21
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (36-66:246-276)

```

```

          10          20          30          40          50          60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
          ::: :: . ::: : . : .: .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
          220          230          240          250          260          270

          70          80
AAD-12 GDVVVWDNRCLLHRA
:
```

gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
280 290 300 310 320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 64 Z-score: 108.1 bits: 25.1 E(): 0.48
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (16-72:79-133)

AAD-12 10 20 30 40
GMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
.... :: : : ... :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
50 60 70 80 90 100

AAD-12 50 60 70 80
ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA
:: : : : :
gi+AHw-121 EEFRASLVDYLS-----HHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
110 120 130 140 150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 init1: 66 opt: 66 Z-score: 102.7 bits: 25.7 E(): 0.96
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (36-66:247-277)

AAD-12 10 20 30 40 50 60
ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
:::: :: . : : . : . :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
220 230 240 250 260 270

AAD-12 70 80
GDVVVWDNRCLLHRA
:
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDVAWVHFFERVGDKIQIVGDDLTVTNPTRIKT
280 290 300 310 320 330

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 96.8 bits: 22.7 E(): 2.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (47-63:68-86)

AAD-12 20 30 40 50 60 70
PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
: :: ... ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

80
AAD-12 CLLHRA

gi+AHw-219 SFDSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 94.2 bits: 22.6 E(): 2.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (47-63:68-86)

	20	30	40	50	60	70
AAD-12	PETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR					
	: : : : . . . : :					
gi+AHw-456	YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF					
	40	50	60	70	80	90

80
 AAD-12 CLLHRA

	100	110	120	130	140	150
gi+AHw-456	SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS					

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 94.2 bits: 22.6 E(): 2.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (47-63:68-86)

	20	30	40	50	60	70
AAD-12	PETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR					
	: : : : . . . : :					
gi+AHw-184	YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF					
	40	50	60	70	80	90

80
 AAD-12 CLLHRA

	100	110	120	130	140	150
gi+AHw-184	SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS					

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
 Full+AD0-60S ac (110 aa)

initn: 47 init1: 47 opt: 52 Z-score: 90.3 bits: 21.4 E(): 4.7
 Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
 in 68 aa overlap (1-67:19-84)

		10	20	30	40
AAD-12		GMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESE			
		: : : : : : . . . : :			
gi+AHw-135		MSTSELATSYAALILADDGVDITADKLSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD			
		10	20	30	40

	50	60	70	80
AAD-12	RFLE-GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA			
	. . . : : . . . : : . . .			


```

66      33      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
68      45      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
70      15      16:+AD0APQA9AD0APQAq-
72      11      12:+AD0-+AD0APQAq-
74      18      10:+AD0APQA9ACoAPQA9-
76      8       7:+AD0APQAq-
78      9       6:+AD0AKgA9-
80      4       4:+AD0AKg-
82      4       3:+ACoAPQ-
84      4       3:+ACoAPQ-
86      1       2:+ACo-
88      4       2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      2       1:+ACo-          :+ACoAPQ-
96      1       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     1       0:+AD0-          +ACoAPQ-
106     0       0:          +ACo-
108     1       0:+AD0-          +ACoAPQ-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     1       0:+AD0-          +ACoAPQ-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.88450.00306+ADs- mu+AD0- 5.1693
0.162
mean+AF8-var+AD0-33.7186 9.451, 0's: 2 Z-trim: 4 B-trim: 44 in 1/42
Lambda+AD0- 0.220871
Kolmogorov-Smirnov statistic: 0.0807 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:          opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 28.1  0.18
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 25.3  0.42
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.8  0.86
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 22.8  1.8
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.8  2.6
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.8  2.6

```


+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:

Full+AD0-Enolase (440 aa)

initn: 66 init1: 66 opt: 66 Z-score: 103.6 bits: 25.8 E(): 0.86

Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)

in 31 aa overlap (35-65:247-277)

```

          10          20          30          40          50          60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
          :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
          220          230          240          250          260          270

```

```

          70          80
AAD-12 GDVVVWDNRCLLHRAE
          :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFFERVGDKIQIVGDDLTVTNPTRIKT
          280          290          300          310          320          330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)

initn: 40 init1: 40 opt: 56 Z-score: 97.6 bits: 22.8 E(): 1.8

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)

in 19 aa overlap (46-62:68-86)

```

          20          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

```

          80
AAD-12 CLLHRAE
          :
gi+AHw-219 SFSDRSGLLLKQKVSDE
          100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 95.0 bits: 22.8 E(): 2.6

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)

in 19 aa overlap (46-62:68-86)

```

          20          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90

```

```

          80
AAD-12 CLLHRAE
          :
gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 95.0 bits: 22.8 E(): 2.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (46-62:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : ..... :: ... ::
gi+AHw-184 YVWKISEFYGRKPEGTYNSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

80
AAD-12 CLLHRAE

```

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 89.2 bits: 22.1 E(): 5.4
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (66-80:122-138)

```

      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAE
      : ..... :: ...
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

```

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
      160      170      180      190      200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 89.1 bits: 22.1 E(): 5.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (66-80:122-138)

```

      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAE
      : ..... :: ...
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

```

```

gi+AHw-124 RKELAAVSDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 89.1 bits: 22.1 E(): 5.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (66-80:122-138)

```

      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAE
      : . . . . . : . . .
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

```

```

gi+AHw-209 RKELAAVSVDCEYKPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
 Full+AD0-Venom (206 aa)
 initn: 34 initl: 34 opt: 53 Z-score: 87.6 bits: 21.8 E(): 6.7
 Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
 in 55 aa overlap (20-74:54-104)

```

      10      20      30      40
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
      : . . : . . . . : : . : . . . . :
gi+AHw-250 PSKNCAGKVIKSVGPTEEEEKLVIEEHNRFQKVAQGLETRGNPGPQAASN--MNNLV-
      30      40      50      60      70      80

```

```

      50      60      70      80
AAD-12 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
      : . . . : . . . : . . . :
gi+AHw-250 WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPSVTKLIQLWENEV
      90      100      110      120      130

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
 protein +AFs-F (450 aa)
 initn: 37 initl: 37 opt: 56 Z-score: 86.1 bits: 22.7 E(): 8
 Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
 in 63 aa overlap (6-60:46-108)

```

      10      20
AAD-12 MDTTATPLRPL---VKVHPETGRPSLL--IGRH--
      : : : : : : : : : : : :
gi+AHw-253 IEEPemiAPTppGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
      20      30      40      50      60      70

```

```

      30      40      50      60      70      80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
      . . : . . . : . . : . . : . .
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
      80      90      100      110      120      130

```

```

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPHLEHSS
      140      150      160      170      180      190

```

+AD4APg-gi+AHw-51093377+AHw-gb+AHw-AAT95010.1+AHw- allergen Pol d 5
 precursor (227 aa)
 initn: 34 initl: 34 opt: 52 Z-score: 85.0 bits: 21.5 E(): 9.3
 Smith-Waterman score: 52+ADs- 23.636+ACU- identity (60.000+ACU- similar)
 in 55 aa overlap (20-74:75-125)

```

                10      20      30      40
AAD-12      MDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
                : .. : .... :: . : . . . . .
gi+AHw-510  PSKNCAGKLIKSVGPTEEEKKLIVEEHNRFQKVAKGLETRGNPGPQPAASN--MNNLV-
                50      60      70      80      90      100

```

```

                50      60      70      80
AAD-12      WACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
                : . .. :. :. . . . .
gi+AHw-510  WNDELAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPSVTKLIQLWENEV
                110     120     130     140     150     160

```

+AD4APg-gi+AHw-170708+AHw-gb+AHw-AAA34274.1+AHw- gamma-gliadin B precursor
+AFs-Tr (291 aa)
initn: 53 init1: 53 opt: 53 Z-score: 84.6 bits: 21.8 E(): 9.7
Smith-Waterman score: 53+ADs- 43.750+ACU- identity (62.500+ACU- similar)
in 16 aa overlap (46-61:27-42)

```

                20      30      40      50      60      70
AAD-12      PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL
                : :: : : . . ::
gi+AHw-170  MKTLLILITILAMAITIATANMQADPSGQVQWFPQQPFLQPHQPFSSQQPQQIFFPQPQ
                10      20      30      40      50

```

```

                80
AAD-12      LHRAE
gi+AHw-170  QTFPHQPQQQFPQPQQPQQQFLQPRQFPFPQQPQQPYPQQPQQPFPQTQQPQQPFPQSKQP
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein
+AFs-Oryza s (160 aa)
initn: 36 init1: 36 opt: 50 Z-score: 84.5 bits: 20.9 E(): 9.9
Smith-Waterman score: 50+ADs- 25.532+ACU- identity (51.064+ACU- similar)
in 47 aa overlap (10-56:110-154)

```

                10      20      30
AAD-12      MDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAE
                : . . . : : : : . . . . .
gi+AHw-139  AVDDSWCRCRSALNHMVGGIYRELGATDVGHMAEVFPGCRRGDLE--RAAASLPAFCNVD
                80      90      100     110     120     130

```

```

                40      50      60      70      80
AAD-12      SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
                : . : : . . .
gi+AHw-139  IPNGTGGVCYWLGYTPRTPRTGH
                140     150     160

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:27 2010 done: Fri Feb 5 12:56:27 2010


```

56      65
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
58      67
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60      42      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9--AD0APQ- +ACo-
62      58      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
64      41      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      44      25:+AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
68      21      20:+AD0APQA9AD0APQA9ACo-
70      13      16:+AD0APQA9AD0APQAq-
72      15      12:+AD0APQA9ACoAPQ-
74      26      10:+AD0APQA9ACoAPQA9AD0APQA9-
76      14      7:+AD0APQAqAD0APQ-
78      5       6:+AD0AKg-
80      6       4:+AD0AKg-
82      4       3:+ACoAPQ-
84      3       3:+ACo-
86      3       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      1       1:+ACo-
92      2       1:+ACo-          :+ACoAPQ-
94      1       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:          +ACo-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:          +ACo-
104     1       0:+AD0-          +ACoAPQ-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     1       0:+AD0-          +ACoAPQ-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.60980.00317+ADs- mu+AD0- 6.7431
0.168
mean+AF8-var+AD0-38.252110.902, 0's: 2 Z-trim: 4 B-trim: 15 in 1/42
Lambda+AD0- 0.207370
Kolmogorov-Smirnov statistic: 0.0814 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
(439) 73 27.4 0.3

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
(151) 64 24.6 0.7

gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
(440) 66 25.3 1.3

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115) 56 22.2 2.8
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157) 56 22.2 3.8
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157) 56 22.2 3.8
 gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se (608) 61 23.8 4.9
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus (208) 54 21.6 7.5
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.6 7.6
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo (210) 54 21.6 7.6
 gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve (206) 53 21.3 9.2

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 111.8 bits: 27.4 E(): 0.3
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar) in 31 aa overlap (34-64:246-276)

	10	20	30	40	50	60
AAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
				...	:	:
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
	220	230	240	250	260	270
	70	80				
AAD-12	GDVVVWDNRCLLHRAEP					
	:					
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK					
	280	290	300	310	320	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 105.2 bits: 24.6 E(): 0.7
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar) in 61 aa overlap (14-70:79-133)

		10	20	30		
AAD-12	DTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES					
			...	:	:	:
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF					
	50	60	70	80	90	100
	40	50	60	70	80	
AAD-12	ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEP					
	:	:
gi+AHw-121	EEFRASLVDYLS-----HHLWDNDTMKSTWDLALNNMFFYILHALEVAQ					
	110	120	130	140	150	

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:

Full+AD0-Enolase (440 aa)

initn: 66 init1: 66 opt: 66 Z-score: 100.4 bits: 25.3 E(): 1.3
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (34-64:247-277)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
      220      230      240      250      260      270
  
```

```

      70      80
AAD-12 GDVVVWDNRCLLHRAEP
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330
  
```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)

initn: 40 init1: 40 opt: 56 Z-score: 94.3 bits: 22.2 E(): 2.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (45-61:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90
  
```

```

      80
AAD-12 CLLHRAEP
gi+AHw-219 SFSDRSGLLLKQKVSDE
      100      110
  
```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 92.0 bits: 22.2 E(): 3.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (45-61:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90
  
```

```

      80
AAD-12 CLLHRAEP
gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150
  
```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 92.0 bits: 22.2 E(): 3.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (45-61:68-86)

```

                20         30         40         50         60         70
AAD-12 PETGRPSLLIGRHAHAIPGMDAEESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                40         50         60         70         80         90

```

```

                80
AAD-12 CLLHRAEP

```

```

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
                100         110         120         130         140         150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)
initn: 43 init1: 43 opt: 61 Z-score: 89.9 bits: 23.8 E(): 4.9
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (16-80:424-492)

```

                10         20         30         40
AAD-12          DTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
                : : . . : . . . . : . . . : :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEGYGFQNALLVRYTKKVPQVSTPTLVEVSRS
                400         410         420         430         440         450

```

```

                50         60         70         80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEP
                : . . : : . . . . : : : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
                460         470         480         490         500         510

```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
                520         530         540         550         560         570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 86.6 bits: 21.6 E(): 7.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (65-79:122-138)

```

                40         50         60         70         80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEP
                : : : : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100         110         120         130         140         150

```

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
                160         170         180         190         200

```



```

56      65      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
58      65
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
60      44      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
62      59      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
64      49      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
66      41      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
68      16      20:+AD0APQA9AD0APQA9ACo-
70      11      16:+AD0APQA9AD0- +ACo-
72      15      12:+AD0APQA9ACoAPQ-
74      14      10:+AD0APQA9ACoAPQ-
76      20      7:+AD0APQAqAD0APQA9AD0-
78      11      6:+AD0AKgA9AD0-
80      5       4:+AD0AKg-
82      5       3:+ACoAPQ-
84      3       3:+ACo-
86      1       2:+ACo-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      2       1:+ACo-
92      1       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     1       0:+AD0-          +ACoAPQ-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     1       0:+AD0-          +ACoAPQ-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.68580.00312+ADs- mu+AD0- 6.3795
0.166
mean+AF8-var+AD0-40.198211.205, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.202288
Kolmogorov-Smirnov statistic: 0.0916 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
(439) 73 27.1 0.37

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
(151) 64 24.3 0.83

gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
(440) 66 25.0 1.5

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115) 56 22.0 3.2
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157) 56 22.0 4.4
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157) 56 22.0 4.4
 gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se (608) 61 23.6 5.7
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus (208) 54 21.5 8.5
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.5 8.6
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo (210) 54 21.5 8.6

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 110.1 bits: 27.1 E(): 0.37
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (33-63:246-276)

	10	20	30	40	50	60
AAAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
				::: :: . :: :	. :	:: .
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
	220	230	240	250	260	270
		70	80			
AAAD-12	GDVVVDNRCLLHRAEPW					
	:					
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK					
	280	290	300	310	320	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 103.8 bits: 24.3 E(): 0.83
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (13-69:79-133)

		10	20	30		
AAAD-12		TTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES				
			::: ::: :: :	: :	: . . .	
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF					
	50	60	70	80	90	100
		40	50	60	70	80
AAAD-12	ERFLEGLVDWACQAPRVHAHQWAAAGDVVVDNRCLLHRAEPW					
	:: . ::: . :	: . :	::: .			
gi+AHw-121	EEFRASLVYLS----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ					
	110	120	130	140	150	

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 99.1 bits: 25.0 E(): 1.5

Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (33-63:247-277)

```

          10          20          30          40          50          60
AAD-12  ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
          : : : : : : : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
          220          230          240          250          260          270

```

```

          70          80
AAD-12  GDVVVWDNRCLLHRAEPW
          :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
          280          290          300          310          320          330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 93.2 bits: 22.0 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (44-60:68-86)

```

          20          30          40          50          60          70
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : : : : : : : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSEFMDF
          40          50          60          70          80          90

```

```

          80
AAD-12  CLLHRAEPW
          :
gi+AHw-219 SFSDRSGLLLKQKVSDE
          100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 90.9 bits: 22.0 E(): 4.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (44-60:68-86)

```

          20          30          40          50          60          70
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSEFMNF
          40          50          60          70          80          90

```

```

          80
AAD-12  CLLHRAEPW
          :
gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 90.9 bits: 22.0 E(): 4.4

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (44-60:68-86)

```

                20          30          40          50          60          70
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                40          50          60          70          80          90
    
```

```

                80
AAD-12  CLLHRAEPW
    
```

```

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
                100          110          120          130          140          150
    
```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)
initn: 43 init1: 43 opt: 61 Z-score: 88.8 bits: 23.6 E(): 5.7
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (15-79:424-492)

```

                10          20          30          40
AAD-12          TTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
                : : . . : . . . . : . . . : :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEGYGFQNALLVRYTKKVPQVSTPTLVEVSRS
                400          410          420          430          440          450
    
```

```

                50          60          70          80
AAD-12  LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPW
                : . . : : . . . . : : : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
                460          470          480          490          500          510
    
```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
                520          530          540          550          560          570
    
```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 85.7 bits: 21.5 E(): 8.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (64-78:122-138)

```

                40          50          60          70          80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPW
                : : : : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100          110          120          130          140          150
    
```

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVEENGLTLTLSHFGKC
                160          170          180          190          200
    
```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 85.6 bits: 21.5 E(): 8.6

Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (64-78:122-138)

```

          40          50          60          70          80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPW
          : .....: ...
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
          100          110          120          130          140          150

gi+AHw-209 RKELAAVSVDCSEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
          160          170          180          190          200          210

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.6 bits: 21.5 E(): 8.6
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (64-78:122-138)

```

          40          50          60          70          80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPW
          : .....: ...
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
          100          110          120          130          140          150

gi+AHw-124 RKELAAVSVDCSEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
          160          170          180          190          200          210

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:27 2010 done: Fri Feb 5 12:56:27 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 190 - 269 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:

```



```

  96      0      1:+ACo-      :+ACo-
  98      1      0:+AD0-      +ACoAPQ-
100      0      0:          +ACo-
102      0      0:          +ACo-
104      1      0:+AD0-      +ACoAPQ-
106      0      0:          +ACo-
108      0      0:          +ACo-
110      1      0:+AD0-      +ACoAPQ-
112      0      0:          +ACo-
114      0      0:          +ACo-
116      0      0:          +ACo-
118      0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.68230.00311+ADs- mu+AD0- 6.4235
0.166
mean+AF8-var+AD0-39.864211.089, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.203134
Kolmogorov-Smirnov statistic: 0.0922 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 27.1 0.36
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 64 24.4 0.81
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 25.0 1.5
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 22.0 3.2
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.0 4.3
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.0 4.3
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608) 61 23.6 5.6
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208) 54 21.5 8.4
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
210) 54 21.5 8.5
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210) 54 21.5 8.5
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91) 50 20.2 8.6

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 110.3 bits: 27.1 E(): 0.36
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (32-62:246-276)

```

```

          10          20          30          40          50          60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
          :::: :: . .:: : . : .: .
gi+AHw-370 APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT
          220          230          240          250          260          270

```

```

          70          80
AAD-12 GDVVVWDNRCLLHRAEPWD
          :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
          280          290          300          310          320          330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 64 Z-score: 104.0 bits: 24.4 E(): 0.81
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (12-68:79-133)

```

          10          20          30
AAD-12 TATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
          :::: :: : : : .. ::
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
          50          60          70          80          90          100

```

```

          40          50          60          70          80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEPWD
          :: .::: : : : :
gi+AHw-121 EEFRASLVDYLS-----HHLDWNMTMKSTWDLALNNMFFYILHALEVAQ
          110          120          130          140          150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 init1: 66 opt: 66 Z-score: 99.2 bits: 25.0 E(): 1.5
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (32-62:247-277)

```

          10          20          30          40          50          60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
          :::: :: . .: : . : .: .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGYDLDFKPNPESDPSKWLS
          220          230          240          250          260          270

```

```

          70          80
AAD-12 GDVVVWDNRCLLHRAEPWD
          :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
          280          290          300          310          320          330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 93.3 bits: 22.0 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (43-59:68-86)

```

                20          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . : : : . . . : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                40          50          60          70          80          90

```

```

                80
AAD-12 CLLHRAEPWD

```

```

gi+AHw-219 SFSDRSGLLLKQKVSDE
                100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 91.0 bits: 22.0 E(): 4.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (43-59:68-86)

```

                20          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . : : : . . . : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
                40          50          60          70          80          90

```

```

                80
AAD-12 CLLHRAEPWD

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 91.0 bits: 22.0 E(): 4.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (43-59:68-86)

```

                20          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . : : : . . . : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                40          50          60          70          80          90

```

```

                80
AAD-12 CLLHRAEPWD

```

```

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                100          110          120          130          140          150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Serum (608 aa)

initn: 43 init1: 43 opt: 61 Z-score: 88.9 bits: 23.6 E(): 5.6
 Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
 in 69 aa overlap (14-78:424-492)

```

                10         20         30         40
AAD-12          TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
                : : . :. :... .: ... .: :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFKELGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
                400         410         420         430         440         450

```

```

                50         60         70         80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWD
                : . . : :... . : . : :: :... :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSERVTKCTESLVNRRPCFS
                460         470         480         490         500         510

```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
                520         530         540         550         560         570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus gal (208 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 85.8 bits: 21.5 E(): 8.4
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (63-77:122-138)

```

                40         50         60         70         80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWD
                : :...: :...
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100         110         120         130         140         150

```

```

gi+AHw-162 RKELAAVDCSEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTTLSHFGKC
                160         170         180         190         200

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gallus+AF0- (210 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 85.7 bits: 21.5 E(): 8.5
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (63-77:122-138)

```

                40         50         60         70         80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWD
                : :...: :...
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100         110         120         130         140         150

```

```

gi+AHw-209 RKELAAVSDCSEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTTLSHFGKC
                160         170         180         190         200         210

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovomuco (210 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 85.7 bits: 21.5 E(): 8.5
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (63-77:122-138)

```

                40         50         60         70         80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWD
                : :...: :...

```

gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
 100 110 120 130 140 150

gi+AHw-124 RKELAAVSVDCSEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
 160 170 180 190 200 210

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
 Full+AD0-Chiti (91 aa)
 initn: 40 initl: 40 opt: 50 Z-score: 85.6 bits: 20.2 E(): 8.6
 Smith-Waterman score: 50+ADs- 31.429+ACU- identity (45.714+ACU- similar)
 in 35 aa overlap (46-80:29-59)

20 30 40 50 60 70
 AAD-12 GRPSELLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
 : ::: : .. : .. :: : .
 gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAY
 10 20 30 40 50

80
 AAD-12 AEPWD
 ::
 gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
 60 70 80 90

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:27 2010 done: Fri Feb 5 12:56:27 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 191 - 270 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
	22	0	0: one +AD0- represents 3 library sequences
	24	0	0:
	26	0	0:
	28	0	0:
	30	0	2:+ACo-


```

100 0 0: +ACo-
102 1 0:+AD0- +ACoAPQ-
104 0 0: +ACo-
106 0 0: +ACo-
108 1 0:+AD0- +ACoAPQ-
110 0 0: +ACo-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.64370.00312+ADs- mu+AD0- 6.6954
0.166
mean+AF8-var+AD0-41.382311.924, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.199373
Kolmogorov-Smirnov statistic: 0.0936 (N+AD0-27) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 26.9 0.42
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 64 24.2 0.94
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 24.9 1.7
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 21.8 3.6
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.9 4.8
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.9 4.8
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608) 61 23.5 6.2
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208) 54 21.3 9.3
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
210) 54 21.3 9.4
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210) 54 21.3 9.4
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91) 50 20.1 9.6

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)

initn: 73 init1: 73 opt: 73 Z-score: 109.1 bits: 26.9 E(): 0.42

Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (31-61:246-276)

```

10 20 30 40 50 60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA

```

```

gi+AHw-370 APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
          220      230      240      250      260      270

```

```

          70      80
AAD-12 GDVVVWDNRCLLHRAEPWDF
:
```

```

gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
          280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 initl: 51 opt: 64 Z-score: 102.9 bits: 24.2 E(): 0.94
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (11-67:79-133)

```

          10      20      30
AAD-12 ATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDDAAES
          .... : : : : : : : : : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
          50      60      70      80      90      100

```

```

          40      50      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF
          .. : : : : : : : : : : : :
gi+AHw-121 EEFRASLVDYLS-----HHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
          110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 initl: 66 opt: 66 Z-score: 98.3 bits: 24.9 E(): 1.7
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (31-61:247-277)

```

          10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAA
          .... : : : : : : : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
          220      230      240      250      260      270

```

```

          70      80
AAD-12 GDVVVWDNRCLLHRAEPWDF
:
```

```

gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFFERVGDKIQIVGDDLTVTNPTRIKT
          280      290      300      310      320      330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 92.4 bits: 21.8 E(): 3.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (42-58:68-86)

```

          20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR

```

```

          : . . . . : :: . . . . :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

```

          70          80
AAD-12 CLLHRAEPWDF

```

```

gi+AHw-219 SFDSDRSGLLLKQKVSDE
          100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (42-58:68-86)

```

          20          30          40          50          60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : . . . . : :: . . . . :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90

```

```

          70          80
AAD-12 CLLHRAEPWDF

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (42-58:68-86)

```

          20          30          40          50          60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : . . . . : :: . . . . :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

```

          70          80
AAD-12 CLLHRAEPWDF

```

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
 Full+AD0-Serum (608 aa)

initn: 43 init1: 43 opt: 61 Z-score: 88.1 bits: 23.5 E(): 6.2
 Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
 in 69 aa overlap (13-77:424-492)

```

          10          20          30
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF

```

```

                                : : . :. :... .: ... .: :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLG EYGFQNALLVRYTKKVPQVSTPTLVEVSRS
              400           410           420           430           440           450

```

```

      40           50           60           70           80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDF
      : . . : :... . : . : :: :... :

```

```

gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSERVTKCTESLVNRRPCFS
              460           470           480           490           500           510

```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQLKTVMG
              520           530           540           550           560           570

```

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
  initn: 49 initl: 49 opt: 54 Z-score: 85.0 bits: 21.3 E(): 9.3
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (62-76:122-138)

```

```

      40           50           60           70           80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDF

```

```

                                : :...: :...
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100           110           120           130           140           150

```

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160           170           180           190           200

```

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
  initn: 49 initl: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.4
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (62-76:122-138)

```

```

      40           50           60           70           80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDF

```

```

                                : :...: :...
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100           110           120           130           140           150

```

```

gi+AHw-209 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160           170           180           190           200           210

```

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
  initn: 49 initl: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.4
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (62-76:122-138)

```

```

      40           50           60           70           80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDF

```

```

                                : :...: :...
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100           110           120           130           140           150

```

gi+AHw-124 RKELAAVSVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
 160 170 180 190 200 210

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
 Full+AD0-Chiti (91 aa)
 initn: 40 initl: 40 opt: 50 Z-score: 84.8 bits: 20.1 E(): 9.6
 Smith-Waterman score: 50+ADs- 31.429+ACU- identity (45.714+ACU- similar)
 in 35 aa overlap (45-79:29-59)

20 30 40 50 60 70
 AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
 : ::: : .. : .. :: : .
 gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAY
 10 20 30 40 50

80
 AAD-12 AEPWDF
 ::
 gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
 60 70 80 90

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:27 2010 done: Fri Feb 5 12:56:27 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 192 - 271 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	0	0:	
30	0	2:+ACo-	
32	0	8: +ACo-	
34	8	21:+AD0APQA9-	+ACo-


```

102      1      0:+AD0-          +ACoAPQ-
104      0      0:              +ACo-
106      0      0:              +ACo-
108      1      0:+AD0-          +ACoAPQ-
110      0      0:              +ACo-
112      0      0:              +ACo-
114      0      0:              +ACo-
116      0      0:              +ACo-
118      0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.50980.00322+ADs- mu+AD0- 7.4479
0.172
mean+AF8-var+AD0-42.743112.786, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.196174
Kolmogorov-Smirnov statistic: 0.0936 (N+AD0-27) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.7  0.47
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.0  1.1
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.7  1.8
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 21.7   4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.7   5.3
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.7   5.3
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  61 23.4  6.6

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 108.3 bits: 26.7 E(): 0.47
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (30-60:246-276)

```

                10          20          30          40          50
AAD-12  TPLRPLVKVHPETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAA
                :::  ::  .  :::  :  .  :  .  :
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
                220          230          240          250          260          270

                60          70          80
AAD-12  GDVVVWDNRCLLHRAEPWDFK
                :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280          290          300          310          320          330

```


+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:

Full+AD0-Enolase (440 aa)

initn: 66 init1: 66 opt: 66 Z-score: 97.5 bits: 24.7 E(): 1.9
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (29-59:247-277)

```

          10          20          30          40          50
AAD-12  PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
          :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
          220          230          240          250          260          270

```

```

          60          70          80
AAD-12  GDVVVWDNRCLLHRAEPWDFKL
          :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
          280          290          300          310          320          330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)

initn: 40 init1: 40 opt: 56 Z-score: 91.5 bits: 21.7 E(): 4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (40-56:68-86)

```

          10          20          30          40          50          60
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

```

          70          80
AAD-12  CLLHRAEPWDFKL

```

```

gi+AHw-219 SFSDRSGLLLKQKVSDE
          100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 89.3 bits: 21.7 E(): 5.3
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (40-56:68-86)

```

          10          20          30          40          50          60
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90

```

```

          70          80
AAD-12  CLLHRAEPWDFKL

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 89.3 bits: 21.7 E(): 5.3
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (40-56:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

      70      80
AAD-12 CLLHRAEPWDFKL

```

```

gi+AHw-184 SFSDSRGSLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)
initn: 43 init1: 43 opt: 61 Z-score: 87.6 bits: 23.4 E(): 6.6
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (11-75:424-492)

```

      10      20      30
AAD-12          PLRPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
      : : . . : . . . . : . . . : :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEGYGFQNALLVRYTKKVPQVSTPTLVEVSRS
      400      410      420      430      440      450

      40      50      60      70      80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKL
      : . . : . . . . : . . : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
      460      470      480      490      500      510

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
      520      530      540      550      560      570

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:28 2010 done: Fri Feb 5 12:56:28 2010
Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

72    12    12:+AD0APQA9ACo-
74    10    10:+AD0APQA9ACo-
76    18    7:+AD0APQAqAD0APQA9-
78    23    6:+AD0AKgA9AD0APQA9AD0APQ-
80     9    4:+AD0AKgA9-
82     2    3:+ACo-
84     3    3:+ACo-
86     0    2:+ACo-
88     3    2:+ACo-          inset +AD0- represents 1 library sequences
90     2    1:+ACo-
92     0    1:+ACo-          :+ACo-
94     0    1:+ACo-          :+ACo-
96     0    1:+ACo-          :+ACo-
98     1    0:+AD0-          +ACoAPQ-
100    0    0:              +ACo-
102    1    0:+AD0-          +ACoAPQ-
104    0    0:              +ACo-
106    0    0:              +ACo-
108    1    0:+AD0-          +ACoAPQ-
110    0    0:              +ACo-
112    0    0:              +ACo-
114    0    0:              +ACo-
116    0    0:              +ACo-
118    0    0:              +ACo-
+AD4-120    0    0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.46070.0032+ADs- mu+AD0- 7.5062
0.171
mean+AF8-var+AD0-43.244912.899, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.195032
Kolmogorov-Smirnov statistic: 0.1059 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.7    0.47
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.0    1.1
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.8    1.8
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 21.7    4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.7    5.2
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.7    5.2
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)  53 20.8    5.9
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  61 23.4    6.4

```

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.2 9.9
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.2 10
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.2 10

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 108.3 bits: 26.7 E(): 0.47
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (28-58:246-276)

```

                10         20         30         40         50
AAD-12      LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                ::: : . : : . :
gi+AHw-370  APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
                220         230         240         250         260         270
    
```

```

                60         70         80
AAD-12  GDVVVWDNRCLLHRAEPWDFKLP
                :
gi+AHw-370  GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280         290         300         310         320         330
    
```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 101.9 bits: 24.0 E(): 1.1
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (8-64:79-133)

```

                10         20         30
AAD-12      LRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                ::: : : : :
gi+AHw-121  DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50         60         70         80         90         100
    
```

```

                40         50         60         70         80
AAD-12  ERFLEGLVDWACQAPRVHAHQWAAAGDVVVVWDNRCLLHRAEPWDFKLP
                :: : : : : :
gi+AHw-121  EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                110         120         130         140         150
    
```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 97.7 bits: 24.8 E(): 1.8
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (28-58:247-277)

```

                10         20         30         40         50
AAD-12      LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                ::: : . : : . :
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220         230         240         250         260         270
    
```

60 70 80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLP

:
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
280 290 300 310 320 330

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)

initn: 40 initl: 40 opt: 56 Z-score: 91.6 bits: 21.7 E(): 4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (39-55:68-86)

10 20 30 40 50 60
AAD-12 PETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR

: : :: :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

70 80
AAD-12 CLLHRAEPWDFKLP

gi+AHw-219 SFSDRSGLLLKQKVSDE
100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 89.4 bits: 21.7 E(): 5.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (39-55:68-86)

10 20 30 40 50 60
AAD-12 PETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR

: : :: :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
40 50 60 70 80 90

70 80
AAD-12 CLLHRAEPWDFKLP

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 89.4 bits: 21.7 E(): 5.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (39-55:68-86)

10 20 30 40 50 60
AAD-12 PETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR

: : :: :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90


```

: .....: ...
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRDHGGC
          100          110          120          130          140          150

```

```

gi+AHw-162 RKELAAVDCSEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
          160          170          180          190          200

```

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
  initn: 49 initl: 49 opt: 54 Z-score: 84.4 bits: 21.2 E(): 10
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (59-73:122-138)

```

```

          30          40          50          60          70          80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLP

```

```

: .....: ...
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRDHGGC
          100          110          120          130          140          150

```

```

gi+AHw-124 RKELAAVSDCSEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
          160          170          180          190          200          210

```

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
  initn: 49 initl: 49 opt: 54 Z-score: 84.4 bits: 21.2 E(): 10
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (59-73:122-138)

```

```

          30          40          50          60          70          80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLP

```

```

: .....: ...
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRDHGGC
          100          110          120          130          140          150

```

```

gi+AHw-209 RKELAAVSDCSEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
          160          170          180          190          200          210

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:28 2010 done: Fri Feb 5 12:56:28 2010
Total Scan time: 0.090 Total Display time: 0.010

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```
84      3      3:+ACo-
86      0      2:+ACo-
88      2      2:+ACo-      inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      1      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      1      0:+AD0-      +ACoAPQ-
100     0      0:      +ACo-
102     1      0:+AD0-      +ACoAPQ-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     1      0:+AD0-      +ACoAPQ-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120 0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.54970.00323+ADs- mu+AD0- 7.0204
0.172
mean+AF8-var+AD0-42.564813.042, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.196584
Kolmogorov-Smirnov statistic: 0.1072 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.8  0.44
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.1  1
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.8  1.8
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 21.8  3.8
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.8  5
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.8  5
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91)  53 20.9  5.5
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  61 23.4  6.3
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)  54 21.3  9.5
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210)  54 21.3  9.6
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
210)  54 21.3  9.6
```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 108.7 bits: 26.8 E(): 0.44
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (27-57:246-276)

```

      10      20      30      40      50
AAD-12  RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      . . . . .
gi+AHw-370 APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
      220      230      240      250      260      270

      60      70      80
AAD-12  GDVVVWDNRCLLHRAEPWDFKLPR
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 102.3 bits: 24.1 E(): 1
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (7-63:79-133)

```

      10      20      30
AAD-12  RPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      . . . . .
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

      40      50      60      70      80
AAD-12  ERFLEGLVDWACQAPRVHAHQWAAGDVVVVWDNRCLLHRAEPWDFKLPR
      . . . . .
gi+AHw-121 EEFRASLV DYLS-----HHLDWNDTMKSTWDLALNMFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 98.0 bits: 24.8 E(): 1.8
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (27-57:247-277)

```

      10      20      30      40      50
AAD-12  RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      . . . . .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

      60      70      80
AAD-12  GDVVVWDNRCLLHRAEPWDFKLPR
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDVAWVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 92.0 bits: 21.8 E(): 3.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (38-54:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . :  :: ...  ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

      70      80
AAD-12 CLLHRAEPWDFKLPR

gi+AHw-219 SFSDRSGLLLKQKVSDE
      100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 89.8 bits: 21.8 E(): 5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (38-54:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . :  :: ...  ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

      70      80
AAD-12 CLLHRAEPWDFKLPR

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 89.8 bits: 21.8 E(): 5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (38-54:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . :  :: ...  ::
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

      70      80
AAD-12 CLLHRAEPWDFKLPR

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:

Full+AD0-Chiti (91 aa)

initn: 43 init1: 43 opt: 53 Z-score: 89.0 bits: 20.9 E(): 5.5
 Smith-Waterman score: 53+ADs- 30.769+ACU- identity (43.590+ACU- similar)
 in 39 aa overlap (41-79:29-63)

```

                20         30         40         50         60         70
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
                :   :::   : .. : ..   :: : .
gi+AHw-323  QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAY
                10         20         30         40         50

```

```

                80
AAD-12 AEPWDFKLPR
                :: :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
                60         70         80         90

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:

Full+AD0-Serum (608 aa)

initn: 43 init1: 43 opt: 61 Z-score: 88.0 bits: 23.4 E(): 6.3
 Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
 in 69 aa overlap (9-73:424-492)

```

                                10         20         30
AAD-12                                RPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
                                : : . : . : . . . : . . . : : :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEGYGFQNALLVRYTKKVPQVSTPTLVEVSRS
                400         410         420         430         440         450

```

```

                40         50         60         70         80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPR
                : . . : : . . . : : : : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
                460         470         480         490         500         510

```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
                520         530         540         550         560         570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid

+AFs-Gallus gal (208 aa)

initn: 49 init1: 49 opt: 54 Z-score: 84.8 bits: 21.3 E(): 9.5
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (58-72:122-138)

```

                30         40         50         60         70         80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPR
                : : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100         110         120         130         140         150

```

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
                160         170         180         190         200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
 Full+AD0-Ovomuco (210 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 84.7 bits: 21.3 E(): 9.6
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (58-72:122-138)

```

      30          40          50          60          70          80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPR
      : .....: ...:
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100          110          120          130          140          150

gi+AHw-124 RKELAAVSVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
      160          170          180          190          200          210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
 gallus+AF0- (210 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 84.7 bits: 21.3 E(): 9.6
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (58-72:122-138)

```

      30          40          50          60          70          80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPR
      : .....: ...:
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100          110          120          130          140          150

gi+AHw-209 RKELAAVSVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
      160          170          180          190          200          210

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:28 2010 done: Fri Feb 5 12:56:28 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 196 - 275 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

opt E()

```

+ADw- 20      2      0:+AD0-
 22      0      0:          one +AD0- represents 4 library sequences
 24      0      0:
 26      0      0:
 28      0      0:
 30      0      2:+ACo-
 32      1      8:+AD0AKg-
 34      2      21:+AD0-      +ACo-
 36      24     44:+AD0APQA9AD0APQA9-      +ACo-
 38      34     72:+AD0APQA9AD0APQA9AD0APQA9-      +ACo-
 40      73    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
 42      96
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
 44      120
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9-      +ACo-
 46      182
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0-
 48      168
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-
 50      143
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACoAPQA9AD0APQA9-
 52      121
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QAqAD0APQA9AD0-
 54      91
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
 56      61     76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-      +ACo-
 58      61     62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
 60      48     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
 62      53     40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
 64      38     32:+AD0APQA9AD0APQA9AD0AKgA9AD0-
 66      37     25:+AD0APQA9AD0APQA9ACoAPQA9AD0-
 68      19     20:+AD0APQA9AD0AKg-
 70      11     16:+AD0APQA9ACo-
 72      12     12:+AD0APQAq-
 74      9      10:+AD0APQAq-
 76      15     7:+AD0AKgA9AD0-
 78      26     6:+AD0AKgA9AD0APQA9AD0-
 80      7      4:+ACoAPQ-
 82      5      3:+ACoAPQ-
 84      4      3:+ACo-
 86      0      2:+ACo-
 88      2      2:+ACo-          inset +AD0- represents 1 library sequences
 90      2      1:+ACo-
 92      1      1:+ACo-          :+ACo-
 94      0      1:+ACo-          :+ACo-
 96      0      1:+ACo-          :+ACo-
 98      1      0:+AD0-          +ACoAPQ-

```

```

100      0      0:      +ACo-
102      1      0:+AD0-      +ACoAPQ-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      1      0:+AD0-      +ACoAPQ-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.58960.00324+ADs- mu+AD0- 6.7803
0.172
mean+AF8-var+AD0-42.573413.035, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.196564
Kolmogorov-Smirnov statistic: 0.1065 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.070

The best scores are:

opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.8  0.44
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.1  1
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.8  1.8
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 21.8  3.8
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.8  5
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.8  5
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91)  53 20.9  5.5
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  61 23.4  6.3
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)  54 21.3  9.5
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210)  54 21.3  9.6
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
210)  54 21.3  9.6

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)

initn: 73 init1: 73 opt: 73 Z-score: 108.7 bits: 26.8 E(): 0.44

Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (26-56:246-276)

```

                                10          20          30          40          50
AAD-12      PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA

```



```

                                : . . . . : :: . . . . :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
           40           50           60           70           80           90

```

```

           70           80
AAD-12 CLLHRAEPWDFKLPRV

```

```

gi+AHw-219 SFDSDRSGLLLKQKVSDE
           100           110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 89.9 bits: 21.8 E(): 5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (37-53:68-86)

```

           10           20           30           40           50           60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                : . . . . : :: . . . . :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
           40           50           60           70           80           90

```

```

           70           80
AAD-12 CLLHRAEPWDFKLPRV

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
           100           110           120           130           140           150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 89.9 bits: 21.8 E(): 5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (37-53:68-86)

```

           10           20           30           40           50           60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                : . . . . : :: . . . . :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
           40           50           60           70           80           90

```

```

           70           80
AAD-12 CLLHRAEPWDFKLPRV

```

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
           100           110           120           130           140           150

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-Chiti (91 aa)

initn: 43 init1: 43 opt: 53 Z-score: 89.1 bits: 20.9 E(): 5.5
 Smith-Waterman score: 53+ADs- 30.769+ACU- identity (43.590+ACU- similar)
 in 39 aa overlap (40-78:29-63)

```

           10           20           30           40           50           60
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR

```

```

                                : ::: : .. : .. :: : .
gi+AHw-323  QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAY
                                10          20          30          40          50

```

```

    70          80
AAD-12  AEPWDFKLPRV

```

```

    :: :
gi+AHw-323  CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
            60          70          80          90

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)
initn: 43 initl: 43 opt: 61 Z-score: 88.0 bits: 23.4 E(): 6.3
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (8-72:424-492)

```

                                10          20          30
AAD-12                                PLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
                                : : . : . : . . . : . . . : : :
gi+AHw-135  YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEGYGFQNALLVRYTKKVPQVSTPTLVEVSRS
            400          410          420          430          440          450

```

```

    40          50          60          70          80
AAD-12  LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRV

```

```

    : . . : : . . . : : : : : : : : : :
gi+AHw-135  LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
            460          470          480          490          500          510

```

```

gi+AHw-135  ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
            520          530          540          550          560          570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 initl: 49 opt: 54 Z-score: 84.8 bits: 21.3 E(): 9.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (57-71:122-138)

```

    30          40          50          60          70          80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRV

```

```

    : : : : : : : : : : : : :
gi+AHw-162  MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
            100          110          120          130          140          150

```

```

gi+AHw-162  RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
            160          170          180          190          200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 84.8 bits: 21.3 E(): 9.6
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (57-71:122-138)

```

    30          40          50          60          70          80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRV

```



```

118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.67290.00321+ADs- mu+AD0- 6.2279
0.171
mean+AF8-var+AD0-42.208112.937, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.197413
Kolmogorov-Smirnov statistic: 0.1202 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 26.9 0.43
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 64 24.2 0.94
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 24.9 1.7
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 21.9 3.6
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.9 4.7
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.9 4.7
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91) 53 21.0 5.2
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608) 61 23.5 6.2
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208) 54 21.4 9.1
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210) 54 21.4 9.2
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
210) 54 21.4 9.2

```

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 109.0 bits: 26.9 E(): 0.43
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (25-55:246-276)

```

```

          10          20          30          40          50
AAD-12      LVKVHPETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAA
                ::: :: . ::: : . : .: .
gi+AHw-370  APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
          220          230          240          250          260          270

          60          70          80
AAD-12  GDVVVWDNRCLLHRAEPWDFKLPVVM
:
gi+AHw-370  GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
          280          290          300          310          320          330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 102.8 bits: 24.2 E(): 0.94
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (5-61:79-133)

```

                                10          20          30
AAD-12                        LVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                                ....  ::  :  :  ...  .
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                   50          60          70          80          90          100

```

```

                   40          50          60          70          80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM
                   ::  .....  :  .:  .::
gi+AHw-121 EEFRASLVDYLS-----HHLDWNMTMKSTWDLALNNMFFYILHALEVAQ
                   110          120          130          140          150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 98.2 bits: 24.9 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (25-55:247-277)

```

                                10          20          30          40          50
AAD-12                        LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                ....  ::  .  :  :  .  .  .  .  .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                   220          230          240          250          260          270

```

```

                   60          70          80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPRVM
                   :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDWAVHFFERVGDKIQIVGDDLTVTNPTRIKT
                   280          290          300          310          320          330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 92.5 bits: 21.9 E(): 3.6
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (36-52:68-86)

```

                                10          20          30          40          50          60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                :  ....  ::  ...  .::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                   40          50          60          70          80          90

```

```

                   70          80
AAD-12 CLLHRAEPWDFKLPRVM

gi+AHw-219 SFSDRSGLLLKQKVSDE
                   100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.2 bits: 21.9 E(): 4.7
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (36-52:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

```

```

      70      80
AAD-12 CLLHRAEPWDFKLPRVM

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.2 bits: 21.9 E(): 4.7
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (36-52:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

```

      70      80
AAD-12 CLLHRAEPWDFKLPRVM

```

```

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)

initn: 43 init1: 43 opt: 53 Z-score: 89.5 bits: 21.0 E(): 5.2
Smith-Waterman score: 53+ADs- 30.769+ACU- identity (43.590+ACU- similar)
in 39 aa overlap (39-77:29-63)

```

      10      20      30      40      50      60
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
      : : : : : : : . . : . . : : : .
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAY
      10      20      30      40      50

```

```

      70      80
AAD-12 AEPWDFKLPRVM

```

```

      : : :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
      60      70      80      90

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
 Full+AD0-Serum (608 aa)
 initn: 43 init1: 43 opt: 61 Z-score: 88.2 bits: 23.5 E(): 6.2
 Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
 in 69 aa overlap (7-71:424-492)

```

                                10      20      30
AAD-12                        LVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
                                : : . : . : . . . : . . . : . : :
gi+AHw-135 YAHVFDEFKPLVEEPPHNLVKTNCELFEKLGGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
           400      410      420      430      440      450

```

```

           40      50      60      70      80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVM
           : . . : : . . . . : . : : : : . . . :
gi+AHw-135 LGKVGSKCCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
           460      470      480      490      500      510

```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQQLKTMG
           520      530      540      550      560      570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
 +AFs-Gallus gal (208 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 85.1 bits: 21.4 E(): 9.1
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (56-70:122-138)

```

           30      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVM
                                : : : : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
           100      110      120      130      140      150

```

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
           160      170      180      190      200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
 Full+AD0-Ovomuco (210 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 85.1 bits: 21.4 E(): 9.2
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (56-70:122-138)

```

           30      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVM
                                : : : : : : : : : : : :
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
           100      110      120      130      140      150

```

```

gi+AHw-124 RKELAAVSVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
           160      170      180      190      200      210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
 gallus+AF0- (210 aa)

Lambda+AD0- 0.196027

Kolmogorov-Smirnov statistic: 0.1236 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.070

The best scores are: opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB	RecName: Full+AD0-En
(439) 73 26.8 0.44	
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH	RecName: Full+AD0-Glo
(151) 64 24.1 0.98	
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL	RecName: Full+AD0-Eno
(440) 66 24.8 1.8	
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA	RecName: Full+AD0-C
(91) 55 21.5 3.6	
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs-	(
115) 56 21.8 3.7	
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1	(157)
56 21.9 4.9	
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s	(157)
56 21.9 4.9	
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA	RecName: Full+AD0-Se
(608) 61 23.4 6.3	
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus	
(208) 54 21.3 9.3	
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK	RecName: Full+AD0-Ovo
(210) 54 21.3 9.4	
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall	(
210) 54 21.3 9.4	

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 108.7 bits: 26.8 E(): 0.44
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (24-54:246-276)

	10	20	30	40	50
AAD-12	VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA				
			::: :: . :: :	. :	:: .
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT				
	220	230	240	250	260 270
	60	70	80		
AAD-12	GDVVVWDNRCLLHRAEPWDFKLPRVMW				
	:				
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK				
	280	290	300	310	320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 64 Z-score: 102.5 bits: 24.1 E(): 0.98
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (4-60:79-133)

```

                                10          20
AAD-12                        VKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                                ....  ::  :  :  :  :  :  :  :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                                50          60          70          80          90          100

```

```

                                30          40          50          60          70          80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMW
                                ::  ::  :  :  :  :  :
gi+AHw-121 EEFRASLVDYLS-----HHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
                                110         120         130         140         150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 98.0 bits: 24.8 E(): 1.8
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (24-54:247-277)

```

                                10          20          30          40          50
AAD-12                        VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                ::  ::  .  :  :  .  :  :  :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                                220         230         240         250         260         270

```

```

                                60          70          80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPVMMW
                                :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWAUVHFFFERVGDKIQIVGDDLTVTNPTRIKT
                                280         290         300         310         320         330

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
 Full+AD0-Chiti (91 aa)
 initn: 43 init1: 43 opt: 55 Z-score: 92.3 bits: 21.5 E(): 3.6
 Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
 in 46 aa overlap (38-80:29-70)

```

                                10          20          30          40          50          60
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
                                :  ::  :  .  :  .  :  :  :
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAY
                                10          20          30          40          50

```

```

                                70          80
AAD-12 AEPWDFKLP---RVMW
                                ::  :  :  :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
                                60          70          80          90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 92.2 bits: 21.8 E(): 3.7
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (35-51:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

```

      70      80
AAD-12 CLLHRAEPWDFKLPRVMW

```

```

gi+AHw-219 SFSDRSGLLLKQKVSDE
      100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.0 bits: 21.9 E(): 4.9
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (35-51:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

```

```

      70      80
AAD-12 CLLHRAEPWDFKLPRVMW

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.0 bits: 21.9 E(): 4.9
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (35-51:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

```

      70      80
AAD-12 CLLHRAEPWDFKLPRVMW

```

```

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
 Full+AD0-Serum (608 aa)

initn: 43 init1: 43 opt: 61 Z-score: 88.0 bits: 23.4 E(): 6.3
 Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
 in 69 aa overlap (6-70:424-492)

```

                                10      20      30
AAD-12      VKVHPETGRPSSLIGRHAHAIPGMDA---AESERF
                                : : . : . : . : . : . : . :
gi+AHw-135  YAHVFDEFKPLVEEPHNLVKTNCELFEKLGGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
            400      410      420      430      440      450
```

```

                40      50      60      70      80
AAD-12  LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMMW
                : . . : : . . . : . : : : : : . :
gi+AHw-135  LGKVGSKCCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSERVTKCTESLVNRRPCFS
            460      470      480      490      500      510
```

```

gi+AHw-135  ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
            520      530      540      550      560      570
```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.3
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (55-69:122-138)

```

                30      40      50      60      70      80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVMMW
                                : : : : : : : : : :
gi+AHw-162  MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
            100      110      120      130      140      150
```

```

gi+AHw-162  RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTTLSHFGKC
            160      170      180      190      200
```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.4
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (55-69:122-138)

```

                30      40      50      60      70      80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVMMW
                                : : : : : : : : : :
gi+AHw-124  MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
            100      110      120      130      140      150
```

```

gi+AHw-124  RKELAAVSVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTTLSHFGKC
            160      170      180      190      200      210
```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.4
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (55-69:122-138)

```

                30      40      50      60      70      80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVMMW
```

```

                                : .....: ...
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100          110          120          130          140          150

```

```

gi+AHw-209 RKELAAVSVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
                160          170          180          190          200          210

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:28 2010 done: Fri Feb 5 12:56:28 2010
Total Scan time: 0.070 Total Display time: 0.010

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

1+AD4APgA+-AAD-12: 199 - 278 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      0      8: +ACo-
      34      3      21:+AD0-      +ACo-
      36      33     44:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38      25     72:+AD0APQA9AD0APQA9AD0-      +ACo-
      40      70    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      42      90
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      44      110    136:+AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
      46      185
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
      48      185
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-

```


gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
 (439) 73 26.7 0.47
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 64 24.0 1
 gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
 (440) 66 24.8 1.8
 gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
 (91) 55 21.4 3.8
 gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
 56 21.8 3.8
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 21.8 5.1
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 21.8 5.1
 gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
 (608) 61 23.4 6.5
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.3 9.6
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.7
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
 54 21.3 9.7

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 108.3 bits: 26.7 E(): 0.47
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (23-53:246-276)

	10	20	30	40	50	
AAAD-12	KVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
			::: :: . ::: : . :		:: .	
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT					
	220	230	240	250	260	270
	60	70	80			
AAAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWH					
	:					
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK					
	280	290	300	310	320	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 102.1 bits: 24.0 E(): 1
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (3-59:79-133)

		10		20		
AAAD-12		KVHPETGRPSL--LIGRHA--HAIPGMDAAES				
		::: ::: : :		: : : . .		
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF					
	50	60	70	80	90	100
	30	40	50	60	70	80

AAAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVVMWH

```

      ::  ::::  :  ::  :::
gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      110          120          130          140          150
  
```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 97.7 bits: 24.8 E(): 1.8
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (23-53:247-277)

```

      10          20          30          40          50
AAAD-12      KVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      ::::  ::  .  .:  :  .  .:  .:
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
      220          230          240          250          260          270
  
```

```

      60          70          80
AAAD-12 GDVVVWDNRCLLHRAEPWDFKLPVVMWH
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280          290          300          310          320          330
  
```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
 Full+AD0-Chiti (91 aa)
 initn: 43 initl: 43 opt: 55 Z-score: 92.0 bits: 21.4 E(): 3.8
 Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
 in 46 aa overlap (37-79:29-70)

```

      10          20          30          40          50          60
AAAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
      :  :::  :  .  .:  .:  .:
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAY
      10          20          30          40          50
  
```

```

      70          80
AAAD-12 AEPWDFKLP---RVMWH
      ::  :  :  :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
      60          70          80          90
  
```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt al
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 91.9 bits: 21.8 E(): 3.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (34-50:68-86)

```

      10          20          30          40          50          60
AAAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :  ::::  ::  ...  ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40          50          60          70          80          90
  
```

70 80

AAD-12 CLLHRAEPWDFKLPRVMWH

gi+AHw-219 SFDSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (34-50:68-86)

10 20 30 40 50 60
 AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
 : : : : . . . : :
 gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
 40 50 60 70 80 90

70 80
 AAD-12 CLLHRAEPWDFKLPRVMWH

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (34-50:68-86)

10 20 30 40 50 60
 AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
 : : : : . . . : :
 gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

70 80
 AAD-12 CLLHRAEPWDFKLPRVMWH

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
 Full+AD0-Serum (608 aa)

initn: 43 init1: 43 opt: 61 Z-score: 87.8 bits: 23.4 E(): 6.5
 Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
 in 69 aa overlap (5-69:424-492)

10 20 30
 AAD-12 KVHPETGRPSLLIGRHAHAIPGMDA---AESERF
 : : . : : : . . . : :
 gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
 400 410 420 430 440 450
 40 50 60 70 80

AAAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVVDNR-CLLHRAEPWDFKLPVMMWH
: . . : :... . : . : :: :... :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSERVTKCTESLVNRRPCFS
460 470 480 490 500 510

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQLKTVMG
520 530 540 550 560 570

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.7 bits: 21.3 E(): 9.6
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (54-68:122-138)

30 40 50 60 70 80
AAAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCLL--HRAEPWDFKLPVMMWH
: :...: :...:
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
100 110 120 130 140 150

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
160 170 180 190 200

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.6 bits: 21.3 E(): 9.7
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (54-68:122-138)

30 40 50 60 70 80
AAAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCLL--HRAEPWDFKLPVMMWH
: :...: :...:
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
100 110 120 130 140 150

gi+AHw-124 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
160 170 180 190 200 210

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.6 bits: 21.3 E(): 9.7
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (54-68:122-138)

30 40 50 60 70 80
AAAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCLL--HRAEPWDFKLPVMMWH
: :...: :...:
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
100 110 120 130 140 150

gi+AHw-209 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
160 170 180 190 200 210


```

56      66      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
58      63      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
60      46      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62      58      40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
64      43      32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      39      25:+AD0APQA9AD0APQA9ACoAPQA9AD0-
68      19      20:+AD0APQA9AD0AKg-
70      14      16:+AD0APQA9ACo-
72      10      12:+AD0APQAq-
74      9       10:+AD0APQAq-
76      15      7:+AD0AKgA9AD0-
78      24      6:+AD0AKgA9AD0APQA9-
80      7       4:+ACoAPQ-
82      6       3:+ACoAPQ-
84      3       3:+ACo-
86      0       2:+ACo-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      2       1:+ACo-
92      2       1:+ACo-          :+ACoAPQ-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:          +ACo-
102     1       0:+AD0-          +ACoAPQ-
104     0       0:          +ACo-
106     0       0:          +ACo-
108     1       0:+AD0-          +ACoAPQ-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0 0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.56650.0033+ADs- mu+AD0- 6.6904
0.175
mean+AF8-var+AD0-43.585313.347, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.194269
Kolmogorov-Smirnov statistic: 0.1174 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:          opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 26.7 0.46
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 64 24.0 1
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 24.8 1.8
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91) 55 21.4 3.8

```

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115) 56 21.7 3.8
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157) 56 21.8 5.1
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157) 56 21.8 5.1
 gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se (608) 61 23.4 6.4
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus (208) 54 21.3 9.6
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo (210) 54 21.3 9.7
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.3 9.7

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 108.4 bits: 26.7 E(): 0.46
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (22-52:246-276)

	10	20	30	40	50
AAD-12	VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA				
			::: :: . ::: :	. :	:: .
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT				
	220	230	240	250	260
		60	70	80	
AAD-12	GDVVVWDNRCLLHRAEPWDFKLPVVMWHS				
	:				
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK				
	280	290	300	310	320
					330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 102.1 bits: 24.0 E(): 1
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (2-58:79-133)

		10		20	
AAD-12		VHPETGRPSL--LIGRHA--HAIPGMDAAES			
		::: ::: :: :	:	:	::: ::
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF				
	50	60	70	80	90
					100
	30	40	50	60	70
AAD-12	ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHS				
	::: ::: :: :	:	:	::: ::	
gi+AHw-121	EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ				
	110	120	130	140	150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 97.7 bits: 24.8 E(): 1.8

Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (22-52:247-277)

```

                10      20      30      40      50
AAD-12      VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                : : : : :
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270
    
```

```

                60      70      80
AAD-12  GDVVVWDNRCLLHRAEPWDFKLPVMMWHS
                :
gi+AHw-232  GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330
    
```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 init1: 43 opt: 55 Z-score: 92.0 bits: 21.4 E(): 3.8
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (36-78:29-70)

```

                10      20      30      40      50      60
AAD-12  GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVVWDNRCLLHR
                : : : : :
gi+AHw-323  QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAY
                10      20      30      40      50
    
```

```

                70      80
AAD-12  AEPWDFKLP---RVMWHS
                : : : :
gi+AHw-323  CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
                60      70      80      90
    
```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 91.9 bits: 21.7 E(): 3.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (33-49:68-86)

```

                10      20      30      40      50      60
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVVWDNR
                : : : : :
gi+AHw-219  YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSEFMDF
                40      50      60      70      80      90
    
```

```

                70      80
AAD-12  CLLHRAEPWDFKLPVMMWHS

gi+AHw-219  SFSDRSGLLLKQKVSDE
                100      110
    
```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (33-49:68-86)

```

                10         20         30         40         50         60
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . :  ::  ...  ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
                40         50         60         70         80         90
    
```

```

                70         80
AAD-12  CLLHRAEPWDFKLPRVMWHS

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                100        110        120        130        140        150
    
```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (33-49:68-86)

```

                10         20         30         40         50         60
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . :  ::  ...  ::
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
                40         50         60         70         80         90
    
```

```

                70         80
AAD-12  CLLHRAEPWDFKLPRVMWHS

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                100        110        120        130        140        150
    
```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Serum (608 aa)

initn: 43 initl: 43 opt: 61 Z-score: 87.9 bits: 23.4 E(): 6.4
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (4-68:424-492)

```

                10         20         30
AAD-12  VHPETGRPSLLIGRHAHAIPGMDA---AESERF
                : :  .  . : . . . . :  ::  ...  . :  :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEGYGFQNALLVRYTKKVPQVSTPTLVEVSRS
                400        410        420        430        440        450
    
```

```

                40         50         60         70         80
AAD-12  LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHS
                :  .  .  :  . . . .  . :  . :  ::  . . . .  :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
                460        470        480        490        500        510
    
```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKKTVMG
                520        530        540        550        560        570
    
```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
 +AFs-Gallus gal (208 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 84.7 bits: 21.3 E(): 9.6
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (53-67:122-138)

```

          30          40          50          60          70          80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCLL--HRAEPWDFKLPVMMWHS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
          100          110          120          130          140          150

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
          160          170          180          190          200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
 Full+AD0-Ovomuco (210 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 84.7 bits: 21.3 E(): 9.7
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (53-67:122-138)

```

          30          40          50          60          70          80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCLL--HRAEPWDFKLPVMMWHS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
          100          110          120          130          140          150

gi+AHw-124 RKELAAVSDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
          160          170          180          190          200          210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
 gallus+AF0- (210 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 84.7 bits: 21.3 E(): 9.7
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (53-67:122-138)

```

          30          40          50          60          70          80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCLL--HRAEPWDFKLPVMMWHS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
          100          110          120          130          140          150

gi+AHw-209 RKELAAVSDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
          160          170          180          190          200          210

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:29 2010 done: Fri Feb 5 12:56:29 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

```
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 201 - 280 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

      opt      E()
+ADw- 20      2      0:+AD0-
22     0      0:          one +AD0- represents 4 library sequences
24     0      0:
26     0      0:
28     0      0:
30     0      2:+ACo-
32     1      8:+AD0AKg-
34     20     21:+AD0APQA9AD0APQAq-
36     17     44:+AD0APQA9AD0APQ-      +ACo-
38     25     72:+AD0APQA9AD0APQA9AD0-      +ACo-
40     72     101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42     99
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
44     104    136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9-      +ACo-
46     189
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
48     188
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
50     135
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACoAPQA9AD0-
52     128
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QAqAD0APQA9AD0APQ-
54     62     91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-      +ACo-
56     65     76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
58     61     62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
60     50     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62     55     40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
64     46     32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
66     42     25:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
68     20     20:+AD0APQA9AD0AKg-
70     14     16:+AD0APQA9ACo-
72     8      12:+AD0APQAq-
```

```

74      5      10:+AD0APQAq-
76     14      7:+AD0AKgA9AD0-
78     25      6:+AD0AKgA9AD0APQA9AD0-
80      7      4:+ACoAPQ-
82      5      3:+ACoAPQ-
84      4      3:+ACo-
86      0      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:              +ACo-
102     1      0:+AD0-          +ACoAPQ-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     1      0:+AD0-          +ACoAPQ-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.58200.0033+ADs- mu+AD0- 6.6331
0.175
mean+AF8-var+AD0-42.776013.219, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.196098
Kolmogorov-Smirnov statistic: 0.1147 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.8    0.44
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.1    0.98
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.8    1.7
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)  55 21.5    3.6
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 21.8    3.7
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.9    4.8
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.9    4.8
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  61 23.5    6.1
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)  54 21.3    9.2

```

gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.3
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.3 9.3

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 108.8 bits: 26.8 E(): 0.44
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (21-51:246-276)

```

                                10      20      30      40      50
AAD-12      HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :::: :: . :: : . : . :
gi+AHw-370  APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
                220      230      240      250      260      270

```

```

                                60      70      80
AAD-12  GDVVVWDNRCLLHRAEPWDFKLPVVMWHSR
:
gi+AHw-370  GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 102.6 bits: 24.1 E(): 0.98
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (1-57:79-133)

```

                                10      20
AAD-12      HPETGRPSL--LIGRHA--HAIPGMDAAES
                                .... :: : : ... ::
gi+AHw-121  DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50      60      70      80      90      100

```

```

                30      40      50      60      70      80
AAD-12  ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSR
                :: .::: . : . ::
gi+AHw-121  EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 98.1 bits: 24.8 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (21-51:247-277)

```

                                10      20      30      40      50
AAD-12      HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :::: :: . :: : . : . :
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270

```

```

                60      70      80

```

AAD-12 GDVVVWDNRCLLHRAEPWDFKLPVVMWHSR

```

:
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
          280          290          300          310          320          330

```

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
  initn: 43 initl: 43 opt: 55 Z-score: 92.3 bits: 21.5 E(): 3.6
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (35-77:29-70)

```

```

          10          20          30          40          50          60
AAD-12 GRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
          :   :::   : .. : ..   :: : .
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYPNQNN--WDLRAVSAY
          10          20          30          40          50

```

```

          70          80
AAD-12 AEPWDFKLP---RVMWHSR
          :: : : :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
          60          70          80          90

```

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
  initn: 40 initl: 40 opt: 56 Z-score: 92.2 bits: 21.8 E(): 3.7
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (32-48:68-86)

```

```

          10          20          30          40          50
AAD-12 PETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          :   .:::   :: ... ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

```

          60          70          80
AAD-12 CLLHRAEPWDFKLPVVMWHSR
          :
gi+AHw-219 SFDSDRSGLLLKQKVSDE
          100          110

```

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
  initn: 40 initl: 40 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (32-48:68-86)

```

```

          10          20          30          40          50
AAD-12 PETGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          :   .:::   :: ... ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90

          60          70          80

```

AAD-12 CLLHRAEPWDFKLPVMMWHSR

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
           100           110           120           130           140           150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (32-48:68-86)

```

           10           20           30           40           50
AAD-12 PETGRPSLLIGRHAHAIPGMDAEESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
           : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYNSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
           40           50           60           70           80           90

```

```

           60           70           80
AAD-12 CLLHRAEPWDFKLPVMMWHSR

```

```

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
           100           110           120           130           140           150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Serum (608 aa)

initn: 43 init1: 43 opt: 61 Z-score: 88.2 bits: 23.5 E(): 6.1
 Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
 in 69 aa overlap (3-67:424-492)

```

           10           20
AAD-12 HPETGRPSLLIGRHAHAIPGMDA---AESERF
           : : . . : . . . : : . . : :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEGYGFQNALLVRYTKKVPQVSTPTLVEVSRS
           400           410           420           430           440           450

```

```

           30           40           50           60           70           80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMMWHSR
           : . . : : . . . : : : : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
           460           470           480           490           500           510

```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
           520           530           540           550           560           570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus gal (208 aa)

initn: 49 init1: 49 opt: 54 Z-score: 85.0 bits: 21.3 E(): 9.2
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (52-66:122-138)

```

           30           40           50           60           70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVMMWHS
           : : . . . . : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC

```



```
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 202 - 281 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

      opt      E()
+ADw- 20      2      0:+AD0-
22     0      0:          one +AD0- represents 4 library sequences
24     0      0:
26     0      0:
28     0      0:
30     0      2:+ACo-
32     0      8: +ACo-
34     21     21:+AD0APQA9AD0APQAq-
36     17     44:+AD0APQA9AD0APQ-      +ACo-
38     24     72:+AD0APQA9AD0APQA9-      +ACo-
40     73     101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
42     97
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
44     112
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0-      +ACo-
46     182
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0-
48     188
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
50     141
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACoAPQA9AD0APQA9-
52     123
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QAqAD0APQA9AD0-
54     63     91:+AD0APQA9AD0APQA9AD0APQ-+AD0APQA9AD0APQA9AD0APQ-
+ACo-
56     66     76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
58     64     62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
60     47     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62     53     40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
64     49     32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
66     39     25:+AD0APQA9AD0APQA9ACoAPQA9AD0-
68     20     20:+AD0APQA9AD0AKg-
```

```

70      14      16:+AD0APQA9ACo-
72      7       12:+AD0APQAq-
74      6       10:+AD0APQAq-
76     14       7:+AD0AKgA9AD0-
78     24       6:+AD0AKgA9AD0APQA9-
80      7       4:+ACoAPQ-
82      6       3:+ACoAPQ-
84      4       3:+ACo-
86      0       2:+ACo-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      2       1:+ACo-
92      2       1:+ACo-          :+ACoAPQ-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     1       0:+AD0-          +ACoAPQ-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120  0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.57120.00334+ADs- mu+AD0- 6.6678
0.177
mean+AF8-var+AD0-42.451213.163, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.196847
Kolmogorov-Smirnov statistic: 0.1106 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.9    0.42
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  63 23.9    1.2
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.9    1.7
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)  55 21.5    3.5
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 21.9    3.6
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.9    4.7
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.9    4.7
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  61 23.5    6

```

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.4 9
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.4 9.1
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.4 9.1

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 109.1 bits: 26.9 E(): 0.42
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (20-50:246-276)

```

                                10      20      30      40
AAD-12      PETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAA
                                ::: : . : . :
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
                220      230      240      250      260      270
    
```

```

                50      60      70      80
AAD-12      GDVVVWDNRCLLHRAEPWDFKLPVMMWHSRL
                :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280      290      300      310      320      330
    
```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 63 Z-score: 101.3 bits: 23.9 E(): 1.2
 Smith-Waterman score: 63+ADs- 33.333+ACU- identity (50.000+ACU- similar)
 in 60 aa overlap (1-56:80-133)

```

                                10      20
AAD-12      PETGRPSL--LIGRHA--HAIPGMDDAAESE
                                :: : : : : : :
gi+AHw-121 LDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQFE
                50      60      70      80      90      100
    
```

```

                30      40      50      60      70      80
AAD-12      RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRL
                .: : : : . : : :
gi+AHw-121 EFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                110      120      130      140      150
    
```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 98.4 bits: 24.9 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (20-50:247-277)

```

                                10      20      30      40
AAD-12      PETGRPSLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAA
                                ::: : . : . :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270
    
```

```

      50          60          70          80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPVMMWHSRL
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280          290          300          310          320          330

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 init1: 43 opt: 55 Z-score: 92.5 bits: 21.5 E(): 3.5
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (34-76:29-70)

```

      10          20          30          40          50          60
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
      :   :::   : .. : ..   :: : .
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAY
      10          20          30          40          50

```

```

      70          80
AAD-12 AEPWDFKLP---RVMWHSRL
      :: : : :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
      60          70          80          90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 92.4 bits: 21.9 E(): 3.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (31-47:68-86)

```

      10          20          30          40          50
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : :: . . . ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40          50          60          70          80          90

```

```

      60          70          80
AAD-12 CLLHRAEPWDFKLPVMMWHSRL
gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 90.2 bits: 21.9 E(): 4.7
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (31-47:68-86)

```

      10          20          30          40          50
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : :: . . . ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
      40          50          60          70          80          90

```

60 70 80
AAD-12 CLLHRAEPWDFKLPVMMWHSRL

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.2 bits: 21.9 E(): 4.7
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (31-47:68-86)

10 20 30 40 50
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
: : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

60 70 80
AAD-12 CLLHRAEPWDFKLPVMMWHSRL

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)

initn: 43 init1: 43 opt: 61 Z-score: 88.4 bits: 23.5 E(): 6
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (2-66:424-492)

10 20
AAD-12 PETGRPSLLIGRHAHAIPGMDA---AESERF
: : . . : : : . . . : :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
400 410 420 430 440 450

30 40 50 60 70 80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMMWHSRL
: . . : : . . . : : : : : : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
460 470 480 490 500 510

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
520 530 540 550 560 570

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)

initn: 49 init1: 49 opt: 54 Z-score: 85.2 bits: 21.4 E(): 9
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (51-65:122-138)

30 40 50 60 70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVMMWHS

```
          : ..... :  
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC  
          100      110      120      130      140      150
```

80
AAD-12 RL

```
gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC  
          160      170      180      190      200
```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
 initn: 49 initl: 49 opt: 54 Z-score: 85.1 bits: 21.4 E(): 9.1
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (51-65:122-138)

```
          30      40      50      60      70  
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLRVMWHS  
          : ..... :  
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC  
          100      110      120      130      140      150
```

80
AAD-12 RL

```
gi+AHw-124 RKELAAVSVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC  
          160      170      180      190      200      210
```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
 initn: 49 initl: 49 opt: 54 Z-score: 85.1 bits: 21.4 E(): 9.1
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (51-65:122-138)

```
          30      40      50      60      70  
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLRVMWHS  
          : ..... :  
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC  
          100      110      120      130      140      150
```

80
AAD-12 RL

```
gi+AHw-209 RKELAAVSVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC  
          160      170      180      190      200      210
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:29 2010 done: Fri Feb 5 12:56:29 2010
Total Scan time: 0.080 Total Display time: 0.010


```

70    13    16:+AD0APQA9ACo-
72    11    12:+AD0APQAq-
74     7    10:+AD0APQAq-
76    13    7:+AD0AKgA9AD0-
78    25    6:+AD0AKgA9AD0APQA9AD0-
80     8    4:+ACoAPQ-
82     4    3:+ACo-
84     4    3:+ACo-
86     0    2:+ACo-
88     1    2:+ACo-          inset +AD0- represents 1 library sequences
90     2    1:+ACo-
92     2    1:+ACo-          :+ACoAPQ-
94     1    1:+ACo-          :+ACo-
96     0    1:+ACo-          :+ACo-
98     1    0:+AD0-          +ACoAPQ-
100    0    0:              +ACo-
102    0    0:              +ACo-
104    0    0:              +ACo-
106    0    0:              +ACo-
108    1    0:+AD0-          +ACoAPQ-
110    0    0:              +ACo-
112    0    0:              +ACo-
114    0    0:              +ACo-
116    0    0:              +ACo-
118    0    0:              +ACo-
+AD4-120    0    0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.43670.00337+ADs- mu+AD0- 7.3394
0.179
mean+AF8-var+AD0-43.006113.196, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.195573
Kolmogorov-Smirnov statistic: 0.1065 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.8    0.43
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.9    1.7
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  59 22.7    2.6
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)  55 21.5    3.7
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 21.8    3.7
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.8    4.9
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.8    4.9
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  61 23.5    6

```

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.3 9.2
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.3
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.3 9.3

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 109.0 bits: 26.8 E(): 0.43
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar) in 31 aa overlap (19-49:246-276)

```

                10      20      30      40
AAD-12          ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                :::: :: . :: : . : .: .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
                220      230      240      250      260      270
    
```

```

                50      60      70      80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLA
                :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280      290      300      310      320      330
    
```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 98.3 bits: 24.9 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar) in 31 aa overlap (19-49:247-277)

```

                10      20      30      40
AAD-12          ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                :::: :: . : : . : .: .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270
    
```

```

                50      60      70      80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLA
                :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDVAWVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330
    
```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 59 Z-score: 94.8 bits: 22.7 E(): 2.6
 Smith-Waterman score: 59+ADs- 32.143+ACU- identity (48.214+ACU- similar) in 56 aa overlap (4-55:83-133)

```

                10      20
AAD-12          ETGRPSL--LIGRHA--HAIPGMDAAESERFLE
                :::: :: : : : . . : .:
gi+AHw-121 IKDSADFAVHSGRIVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEEFRA
                60      70      80      90      100      110
    
```

```

      30          40          50          60          70          80
AAD-12  GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA
      .:..: : : : :
gi+AHw-121  SLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                  120          130          140          150

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 initl: 43 opt: 55 Z-score: 92.2 bits: 21.5 E(): 3.7
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (33-75:29-70)

```

      10          20          30          40          50          60
AAD-12  GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
                  : : : : :
gi+AHw-323  QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAY
                  10          20          30          40          50

```

```

      70          80
AAD-12  AEPWDFKLP---RVMWHSRLA
      :: : : :
gi+AHw-323  CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
                  60          70          80          90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 92.1 bits: 21.8 E(): 3.7
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (30-46:68-86)

```

      10          20          30          40          50
AAD-12  ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                  : : : : :
gi+AHw-219  YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                  40          50          60          70          80          90

```

```

      60          70          80
AAD-12  CLLHRAEPWDFKLPRVMWHSRLA
      : : :
gi+AHw-219  SFDSDRSGLLLKQKVSDE
                  100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 90.0 bits: 21.8 E(): 4.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (30-46:68-86)

```

      10          20          30          40          50
AAD-12  ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                  : : : : :
gi+AHw-456  YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
                  40          50          60          70          80          90

```


gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
100 110 120 130 140 150

80
AAD-12 RLA

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
160 170 180 190 200

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.0 bits: 21.3 E(): 9.3
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (50-64:122-138)

20 30 40 50 60 70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLRVMWHS

gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
100 110 120 130 140 150

80
AAD-12 RLA

gi+AHw-124 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
160 170 180 190 200 210

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.0 bits: 21.3 E(): 9.3
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (50-64:122-138)

20 30 40 50 60 70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLRVMWHS

gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
100 110 120 130 140 150

80
AAD-12 RLA

gi+AHw-209 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
160 170 180 190 200 210

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:29 2010 done: Fri Feb 5 12:56:29 2010
Total Scan time: 0.080 Total Display time: 0.000


```

68    18    20:+AD0APQA9AD0AKg-
70    13    16:+AD0APQA9ACo-
72    12    12:+AD0APQAq-
74     7    10:+AD0APQAq-
76    16     7:+AD0AKgA9AD0-
78    22     6:+AD0AKgA9AD0APQA9-
80     8     4:+ACoAPQ-
82     3     3:+ACo-
84     3     3:+ACo-
86     0     2:+ACo-
88     0     2:+ACo-          inset +AD0- represents 1 library sequences
90     3     1:+ACo-
92     1     1:+ACo-          :+ACo-
94     1     1:+ACo-          :+ACo-
96     0     1:+ACo-          :+ACo-
98     1     0:+AD0-          +ACoAPQ-
100    0     0:              +ACo-
102    0     0:              +ACo-
104    0     0:              +ACo-
106    0     0:              +ACo-
108    1     0:+AD0-          +ACoAPQ-
110    0     0:              +ACo-
112    0     0:              +ACo-
114    0     0:              +ACo-
116    0     0:              +ACo-
118    0     0:              +ACo-
+AD4-120    0     0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.38670.00339+ADs- mu+AD0- 7.5819
0.180
mean+AF8-var+AD0-43.897513.052, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.193577
Kolmogorov-Smirnov statistic: 0.1086 (N+AD0-26) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.7    0.46
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.8    1.8
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  59 22.6    2.8
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)  55 21.4    3.9
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 21.7    3.9
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.8    5.1
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.8    5.1

```

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.3 9.6
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
 210) 54 21.3 9.7
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.7

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 108.5 bits: 26.7 E(): 0.46
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (18-48:246-276)

```

                                10      20      30      40
AAD-12      TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :::: :: . :: : . : .: .
gi+AHw-370  APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
                220      230      240      250      260      270
    
```

```

                    50      60      70      80
AAD-12  GDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG
:
gi+AHw-370  GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280      290      300      310      320      330
    
```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 97.9 bits: 24.8 E(): 1.8
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (18-48:247-277)

```

                                10      20      30      40
AAD-12      TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :::: :: . : : . : .: .
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270
    
```

```

                    50      60      70      80
AAD-12  GDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG
:
gi+AHw-232  GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330
    
```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 59 Z-score: 94.4 bits: 22.6 E(): 2.8
 Smith-Waterman score: 59+ADs- 32.143+ACU- identity (48.214+ACU- similar)
 in 56 aa overlap (3-54:83-133)

```

                                10      20
AAD-12      TGRPSL--LIGRHA--HAIPGMDAAESERFLE
                                :::: :: : : : . . : .:
gi+AHw-121  IKDSADFAVHSGRIVGFFSEVIGLIGNPENRPAKTLIDGLASSHKARGIEKAQFEEFRA
                60      70      80      90      100      110
    
```

```

      30          40          50          60          70          80
AAD-12  GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG
      .:..: .: .: .:
gi+AHw-121  SLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
              120          130          140          150

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 initl: 43 opt: 55 Z-score: 91.7 bits: 21.4 E(): 3.9
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (32-74:29-70)

```

      10          20          30          40          50          60
AAD-12  GRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
              : ::: : .. : .. :: : .
gi+AHw-323  QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAY
              10          20          30          40          50

```

```

      70          80
AAD-12  AEPWDFKLP---RVMWHSRLAG
      :: : : :
gi+AHw-323  CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
              60          70          80          90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 91.7 bits: 21.7 E(): 3.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (29-45:68-86)

```

      10          20          30          40          50
AAD-12  TGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
              : .:..: : : .: .:
gi+AHw-219  YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
              40          50          60          70          80          90

```

```

      60          70          80
AAD-12  CLLHRAEPWDFKLPRVMWHSRLAG
gi+AHw-219  SFDSDRSGLLLKQKVSDE
              100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 89.6 bits: 21.8 E(): 5.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (29-45:68-86)

```

      10          20          30          40          50
AAD-12  TGRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
              : .:..: : : .: .:
gi+AHw-456  YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
              40          50          60          70          80          90

```



```

112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.39680.00337+ADs- mu+AD0- 7.5565
0.179
mean+AF8-var+AD0-41.635212.859, 0's: 2 Z-trim: 3 B-trim: 44 in 1/42
Lambda+AD0- 0.198767
Kolmogorov-Smirnov statistic: 0.0984 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.0  0.38
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.0  1.5
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  59 22.8  2.4
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)  55 21.6  3.4
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 21.9  3.4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.0  4.5
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.0  4.5
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)  54 21.4  8.6
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
210)  54 21.4  8.7
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210)  54 21.4  8.7

```

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 110.0 bits: 27.0 E(): 0.38
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (17-47:246-276)

```

```

                                10      20      30      40
AAD-12      GRPSLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :::  :: .  :::  :  .  :  :: .
gi+AHw-370  APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
                220      230      240      250      260      270

                50      60      70      80
AAD-12  GDVVVDNRCLLHRAEPWDFKLPVMMWHSRLAGR
:
gi+AHw-370  GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK

```

280 290 300 310 320 330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 init1: 66 opt: 66 Z-score: 99.1 bits: 25.0 E(): 1.5
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (17-47:247-277)

```

                10      20      30      40
AAD-12          GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                :::: :: . .: : . :. .: .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPFSKWS
                220      230      240      250      260      270

                50      60      70      80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAGR
                :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330
    
```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 59 Z-score: 95.5 bits: 22.8 E(): 2.4
Smith-Waterman score: 59+ADs- 32.143+ACU- identity (48.214+ACU- similar)
in 56 aa overlap (2-53:83-133)

```

                                10      20
AAD-12                          GRPSL--LIGRHA--HAIPGMDAAESERFLE
                                :::: :: : : : .. :: :::
gi+AHw-121 IKDSADFAVHSGRIVGFFSEVIGLIGNPENRPAKTLIDGLASSHKARGIEKAQFEFRA
                                60      70      80      90      100     110

                30      40      50      60      70      80
AAD-12 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAGR
                ::::. : .: .::
gi+AHw-121 SLVDYLS-----HHLDWNMTMKSTWDLALNNMFFYILHALEVAQ
                120      130      140      150
    
```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 init1: 43 opt: 55 Z-score: 92.8 bits: 21.6 E(): 3.4
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (31-73:29-70)

```

                10      20      30      40      50      60
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHR
                : :::: : .. : .. :: : .
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAY
                10      20      30      40      50

                70      80
AAD-12 AEPWDFKLP---RVMWHSRLAGR
                :: : : :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
    
```

60 70 80 90

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)

initn: 40 init1: 40 opt: 56 Z-score: 92.7 bits: 21.9 E(): 3.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (28-44:68-86)

```

          10      20      30      40      50
AAD-12   GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          :  . . . . :  ::  . . .  ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40      50      60      70      80      90

```

```

          60      70      80
AAD-12   CLLHRAEPWDFKLPRVMWHSRLAGR

```

```

gi+AHw-219 SFSDRSGLLLKQKVSDE
          100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.6 bits: 22.0 E(): 4.5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (28-44:68-86)

```

          10      20      30      40      50
AAD-12   GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          :  . . . . :  ::  . . .  ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
          40      50      60      70      80      90

```

```

          60      70      80
AAD-12   CLLHRAEPWDFKLPRVMWHSRLAGR

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.6 bits: 22.0 E(): 4.5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (28-44:68-86)

```

          10      20      30      40      50
AAD-12   GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          :  . . . . :  ::  . . .  ::
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40      50      60      70      80      90

```

```

          60      70      80
AAD-12   CLLHRAEPWDFKLPRVMWHSRLAGR

```

```

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS

```

100 110 120 130 140 150

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
 +AFs-Gallus gal (208 aa)
 initn: 49 initl: 49 opt: 54 Z-score: 85.6 bits: 21.4 E(): 8.6
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (48-62:122-138)

20 30 40 50 60 70
 AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVVMWHS
 : :
 gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
 100 110 120 130 140 150

80
 AAD-12 RLAGR

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
 160 170 180 190 200

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
 gallus+AF0- (210 aa)
 initn: 49 initl: 49 opt: 54 Z-score: 85.5 bits: 21.4 E(): 8.7
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (48-62:122-138)

20 30 40 50 60 70
 AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVVMWHS
 : :
 gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
 100 110 120 130 140 150

80
 AAD-12 RLAGR

gi+AHw-209 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
 160 170 180 190 200 210

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
 Full+AD0-Ovomuco (210 aa)
 initn: 49 initl: 49 opt: 54 Z-score: 85.5 bits: 21.4 E(): 8.7
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (48-62:122-138)

20 30 40 50 60 70
 AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVVMWHS
 : :
 gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
 100 110 120 130 140 150

80
 AAD-12 RLAGR

gi+AHw-124 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 59 22.6 2.7
 gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
 (608) 64 24.3 3.4
 gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
 (91) 55 21.4 3.8
 gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
 56 21.7 3.8
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 21.8 5
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 21.8 5
 gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName: Full+AD0-Se
 (607) 60 23.2 7.3
 gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin +AFs-B (607)
 60 23.2 7.3
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.3 9.4
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.5
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
 54 21.3 9.5

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 108.7 bits: 26.8 E(): 0.44
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (16-46:246-276)

	10	20	30	40
AAD-12	RPSLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAA			
		
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT			
	220	230	240	250
				260
				270
	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRP			
	:			
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK			
	280	290	300	310
				320
				330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 98.1 bits: 24.8 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (16-46:247-277)

	10	20	30	40
AAD-12	RPSLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAA			
		
gi+AHw-232	APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS			
	220	230	240	250
				260
				270
	50	60	70	80

AAAD-12 GDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAGRP

```

:
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
          280          290          300          310          320          330
    
```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 59 Z-score: 94.6 bits: 22.6 E(): 2.7
 Smith-Waterman score: 59+ADs- 32.143+ACU- identity (48.214+ACU- similar)
 in 56 aa overlap (1-52:83-133)

```

                                10          20
AAAD-12                        RPSL--LIGRHA--HAIPGMDAAESERFLE
                                ::: : : : : : : : :
gi+AHw-121 IKDSADFAVHSGRIVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEEFRA
          60          70          80          90          100          110
    
```

```

          30          40          50          60          70          80
AAAD-12 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAGRP
          : : : : : :
gi+AHw-121 SLVDYLS-----HHLDWNMTMKSTWDLALNNMFFYILHALEVAQ
          120          130          140          150
    
```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
 Full+AD0-Serum (608 aa)
 initn: 53 init1: 53 opt: 64 Z-score: 92.9 bits: 24.3 E(): 3.4
 Smith-Waterman score: 64+ADs- 23.750+ACU- identity (53.750+ACU- similar)
 in 80 aa overlap (5-80:431-510)

```

                                10          20          30
AAAD-12                        RPSLLIGRHAHAIPGMDA---AESERFLEGLVDW
                                .. :... : : ... : : : .
gi+AHw-135 FKPLVEEPHNLVKTNCELFEKLGEGYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSK
          410          420          430          440          450          460
    
```

```

          40          50          60          70          80
AAAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMMWHSRLAGRP
          : :... : : : : : : : : : : : : : : : :
gi+AHw-135 CCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSEKTKCTESLVNRRPCFSALQVDET
          470          480          490          500          510          520
    
```

```

gi+AHw-135 YVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKTVMGDFGFSVD
          530          540          550          560          570          580
    
```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
 Full+AD0-Chiti (91 aa)
 initn: 43 init1: 43 opt: 55 Z-score: 91.9 bits: 21.4 E(): 3.8
 Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
 in 46 aa overlap (30-72:29-70)

```

          10          20          30          40          50          60
AAAD-12 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA
          : : : : : : : : : : : :
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCS PDNQCQATY-HYYNPAQNN---WDLRAVSAYC
    
```

```

                10          20          30          40          50
                70          80
AAD-12 EPWDFKLP---RVMWHSRLAGRP
      :: : : :
gi+AHw-323 STWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
      60          70          80          90

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
  initn: 40 initl: 40 opt: 56 Z-score: 91.9 bits: 21.7 E(): 3.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (27-43:68-86)

```

```

                10          20          30          40          50
AAD-12 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : :: . . . ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40          50          60          70          80          90

                60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRP

gi+AHw-219 SFSDRSGLLLKQKVSDE
      100          110

```

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
  initn: 40 initl: 40 opt: 56 Z-score: 89.8 bits: 21.8 E(): 5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (27-43:68-86)

```

```

                10          20          30          40          50
AAD-12 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : :: . . . ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40          50          60          70          80          90

                60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRP

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100          110          120          130          140          150

```

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
  initn: 40 initl: 40 opt: 56 Z-score: 89.8 bits: 21.8 E(): 5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (27-43:68-86)

```

```

                10          20          30          40          50
AAD-12 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : :: . . . ::
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF

```

40 50 60 70 80 90

60 70 80
AAD-12 CLLHRAEPWDFKLPVMWHSRLAGRP

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName:
Full+AD0-Serum (607 aa)
initn: 51 initl: 51 opt: 60 Z-score: 86.8 bits: 23.2 E(): 7.3
Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (5-80:430-509)

10 20 30
AAD-12 RPSLLIGRHAHAIPGMDA---AESERFLEGLVDW
:: :... .:: : : .
gi+AHw-135 LKHLVDEPQNLIKQNCQDFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
400 410 420 430 440 450

40 50 60 70 80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMWHSRLAGRP
: :. :: :... : . : . . : :
gi+AHw-135 CCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALTPDET
460 470 480 490 500 510

gi+AHw-135 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD
520 530 540 550 560 570

+AD4APg-gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin
+AFs-Bos t (607 aa)
initn: 51 initl: 51 opt: 60 Z-score: 86.8 bits: 23.2 E(): 7.3
Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (5-80:430-509)

10 20 30
AAD-12 RPSLLIGRHAHAIPGMDA---AESERFLEGLVDW
:: :... .:: : : .
gi+AHw-333 LKHLVDEPQNLIKQNCQDFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
400 410 420 430 440 450

40 50 60 70 80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMWHSRLAGRP
: :. :: :... : . : . . : :
gi+AHw-333 CCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALTPDET
460 470 480 490 500 510

gi+AHw-333 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD
520 530 540 550 560 570

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 initl: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.4

Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (47-61:122-138)

```

      20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVVMWHS
      : .....: ...
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

```

80
AAD-12 RLAGRP

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTTLSHFGKC
      160      170      180      190      200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 84.8 bits: 21.3 E(): 9.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (47-61:122-138)

```

      20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVVMWHS
      : .....: ...
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

```

80
AAD-12 RLAGRP

```

gi+AHw-124 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTTLSHFGKC
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 84.8 bits: 21.3 E(): 9.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (47-61:122-138)

```

      20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVVMWHS
      : .....: ...
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

```

80
AAD-12 RLAGRP

```

gi+AHw-209 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTTLSHFGKC
      160      170      180      190      200      210

```

80 residues in 1 query sequences


```

58      56      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
60      47      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-+AD0AKg-
62      53      40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
64      40      32:+AD0APQA9AD0APQA9AD0AKgA9AD0-
66      36      25:+AD0APQA9AD0APQA9ACoAPQA9-
68      21      20:+AD0APQA9AD0AKgA9-
70      14      16:+AD0APQA9ACo-
72      12      12:+AD0APQAq-
74      7       10:+AD0APQAq-
76      17      7:+AD0AKgA9AD0APQ-
78      23      6:+AD0AKgA9AD0APQA9-
80      8       4:+ACoAPQ-
82      3       3:+ACo-
84      4       3:+ACo-
86      2       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      4       1:+ACo-
92      2       1:+ACo-          :+ACoAPQ-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     0       0:          +ACo-
108     1       0:+AD0-          +ACoAPQ-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.34930.00345+ADs- mu+AD0- 7.8131
0.183
mean+AF8-var+AD0-43.607913.006, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.194219
Kolmogorov-Smirnov statistic: 0.0956 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.8    0.45
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.8    1.7
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  64 24.3    3.4
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)  55 21.4    3.9
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 21.7    3.9

```

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 57 22.1 4.1
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 21.8 5.1
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 21.8 5.1
 gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName: Full+AD0-Se
 (607) 60 23.2 7.3
 gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin +AFs-B (607)
 60 23.2 7.3
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.3 9.5
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.6
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
 54 21.3 9.6

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 108.6 bits: 26.8 E(): 0.45
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (15-45:246-276)

	10	20	30	40
AAD-12	PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA			
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT			
	220	230	240	250
	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPE			
	:			
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK			
	280	290	300	310
	280	290	300	310

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 98.0 bits: 24.8 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (15-45:247-277)

	10	20	30	40
AAD-12	PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA			
gi+AHw-232	APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS			
	220	230	240	250
	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPE			
	:			
gi+AHw-232	GPQLADLYEQLISEYPIVSIEDPFAEDDWDVAWVHFFERVGDKIQIVGDDLTVTNPTRIKT			
	280	290	300	310
	280	290	300	310

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
 Full+AD0-Serum (608 aa)
 initn: 53 init1: 53 opt: 64 Z-score: 92.9 bits: 24.3 E(): 3.4
 Smith-Waterman score: 64+ADs- 23.750+ACU- identity (53.750+ACU- similar)
 in 80 aa overlap (4-79:431-510)

```

                                10          20          30
AAD-12          PSLLIGRHAHAIPGMDA---AESERFLEGLVDW
                   :. :... .: ... .: : : .
gi+AHw-135 FKPLVEEPHNLVKTNCELFEKLGEGYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSK
                   410          420          430          440          450          460

                   40          50          60          70          80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMMWHSRLAGRPE
                   : :... . : . : :: :... : . . . . : : : :
gi+AHw-135 CCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSEKTKCCTESLVNRRPCFSALQVDET
                   470          480          490          500          510          520

gi+AHw-135 YVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMGDFGFSFVD
                   530          540          550          560          570          580
    
```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
 Full+AD0-Chiti (91 aa)
 initn: 43 init1: 43 opt: 55 Z-score: 91.7 bits: 21.4 E(): 3.9
 Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
 in 46 aa overlap (29-71:29-70)

```

                                10          20          30          40          50          60
AAD-12 PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
                   : :: : : .. : .. : : : .
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYPNPAQNN---WDLRAVSAYCS
                   10          20          30          40          50

                   70          80
AAD-12 PWDFKLP---RVMWHSRLAGRPE
                   :: : : :
gi+AHw-323 TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
                   60          70          80          90
    
```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 91.7 bits: 21.7 E(): 3.9
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (26-42:68-86)

```

                                10          20          30          40          50
AAD-12          PSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                   : :... : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
                   40          50          60          70          80          90

                   60          70          80
AAD-12 CLLHRAEPWDFKLPVMMWHSRLAGRPE
    
```

gi+AHw-219 SFSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 57 Z-score: 91.4 bits: 22.1 E(): 4.1
 Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
 in 43 aa overlap (9-51:96-133)

 10 20 30
 AAD-12 PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
 .: .. :. .: .: .: .: .: .:
 gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEEFRASLVDYLS-----H
 70 80 90 100 110 120

 40 50 60 70 80
 AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPE
 .: .:
 gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
 130 140 150

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (26-42:68-86)

 10 20 30 40 50
 AAD-12 PSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
 : .: .: .: .: .: .: .:
 gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
 40 50 60 70 80 90

 60 70 80
 AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPE

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (26-42:68-86)

 10 20 30 40 50
 AAD-12 PSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
 : .: .: .: .: .: .: .:
 gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

 60 70 80
 AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPE

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName:
Full+AD0-Serum (607 aa)
initn: 51 init1: 51 opt: 60 Z-score: 86.8 bits: 23.2 E(): 7.3
Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (4-79:430-509)

AAD-12 PSLIIGRHAHAIPGMDA---AESERFLEGLVDW
:: :... .:: : : .
gi+AHw-135 LKHLVDEPQNLIKQNCDFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
400 410 420 430 440 450

AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPE
: :. :: :... : . : . . :. : ::
gi+AHw-135 CCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALTPDET
460 470 480 490 500 510

gi+AHw-135 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD
520 530 540 550 560 570

+AD4APg-gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin
+AFs-Bos t (607 aa)
initn: 51 init1: 51 opt: 60 Z-score: 86.8 bits: 23.2 E(): 7.3
Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (4-79:430-509)

AAD-12 PSLIIGRHAHAIPGMDA---AESERFLEGLVDW
:: :... .:: : : .
gi+AHw-333 LKHLVDEPQNLIKQNCDFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
400 410 420 430 440 450

AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPE
: :. :: :... : . : . . :. : ::
gi+AHw-333 CCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALTPDET
460 470 480 490 500 510

gi+AHw-333 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD
520 530 540 550 560 570

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.8 bits: 21.3 E(): 9.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (46-60:122-138)

AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
: :...: :...: :...: :...:


```

72    12    12:+AD0APQAq-
74    7     10:+AD0APQAq-
76    17    7:+AD0AKgA9AD0APQ-
78    24    6:+AD0AKgA9AD0APQA9-
80    7     4:+ACoAPQ-
82    4     3:+ACo-
84    4     3:+ACo-
86    2     2:+ACo-
88    0     2:+ACo-          inset +AD0- represents 1 library sequences
90    3     1:+ACo-
92    3     1:+ACo-          :+ACoAPQA9-
94    0     1:+ACo-          :+ACo-
96    0     1:+ACo-          :+ACo-
98    1     0:+AD0-          +ACoAPQ-
100   0     0:              +ACo-
102   0     0:              +ACo-
104   0     0:              +ACo-
106   0     0:              +ACo-
108   1     0:+AD0-          +ACoAPQ-
110   0     0:              +ACo-
112   0     0:              +ACo-
114   0     0:              +ACo-
116   0     0:              +ACo-
118   0     0:              +ACo-
+AD4-120    0     0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.30810.00343+ADs- mu+AD0- 8.0127
0.182
mean+AF8-var+AD0-43.495412.979, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.194470
Kolmogorov-Smirnov statistic: 0.0959 (N+AD0-28) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.8    0.44
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.8    1.7
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  64 24.4    3.3
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)  55 21.4    3.9
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 21.7    3.9
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  57 22.1    4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.8    5.1
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.8    5.1

```

gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName: Full+AD0-Se
 (607) 60 23.2 7.2
 gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin +AFs-B (
 607) 60 23.2 7.2
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.3 9.4
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.5
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
 210) 54 21.3 9.5

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 108.8 bits: 26.8 E(): 0.44
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (14-44:246-276)

	10	20	30	40
AAD-12	SLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAA			
		:::	::	. .:: :
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT			
	220	230	240	250
	260	270		
	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPET			
	:			
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK			
	280	290	300	310
	320	330		

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 98.2 bits: 24.8 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (14-44:247-277)

	10	20	30	40
AAD-12	SLLIGRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAA			
		:::	::	. .:: :
gi+AHw-232	APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKPNPESDPSKWLS			
	220	230	240	250
	260	270		
	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPET			
	:			
gi+AHw-232	GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT			
	280	290	300	310
	320	330		

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
 Full+AD0-Serum (608 aa)
 initn: 53 init1: 53 opt: 64 Z-score: 93.0 bits: 24.4 E(): 3.3
 Smith-Waterman score: 64+ADs- 23.750+ACU- identity (53.750+ACU- similar)
 in 80 aa overlap (3-78:431-510)

```

AAD-12          SLLIGRHAHAIPGMDA---AESERFLEGLVDW
                :. .... .: ... .: : : .
gi+AHw-135 FKPLVEEPHNLVKTNCLELFEKLGEGYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSK
                410          420          430          440          450          460

```

```

          30          40          50          60          70          80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMMWHSRLAGRPET
          : :... . : . : :: :... : . . . . : : . :
gi+AHw-135 CCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFSALQVDET
                470          480          490          500          510          520

```

```

gi+AHw-135 YVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMGDFGFSFVD
                530          540          550          560          570          580

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 initl: 43 opt: 55 Z-score: 91.8 bits: 21.4 E(): 3.9
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (28-70:29-70)

```

          10          20          30          40          50
AAD-12 SLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
                : ::: : .. : .. : : .
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAYCS
                10          20          30          40          50

```

```

          60          70          80
AAD-12 PWDFKLP---RVMWHSRLAGRPET
          :: : : :
gi+AHw-323 TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
          60          70          80          90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 91.8 bits: 21.7 E(): 3.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (25-41:68-86)

```

          10          20          30          40          50
AAD-12 SLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : . . . . : : . . : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                40          50          60          70          80          90

```

```

          60          70          80
AAD-12 CLLHRAEPWDFKLPVMMWHSRLAGRPET

gi+AHw-219 SFDSDRSGLLLKQKVSDE
          100          110

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 initl: 51 opt: 57 Z-score: 91.5 bits: 22.1 E(): 4

Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
in 43 aa overlap (8-50:96-133)

```

                                10      20      30
AAD-12                          SLLIGRHAHAIPGMDDAAESERFLEGLVDWACQAPRVH
                                .:  ...  .:  .:  .:  .:  .:
gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEEFRASLVDYLS-----H
                                70      80      90      100     110     120

```

```

                                40      50      60      70      80
AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPET
                                .:  ...  .:  .:  .:
gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                                130     140     150

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (25-41:68-86)

```

                                10      20      30      40      50
AAD-12                          SLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                :  .:  .:  .:  .:  .:
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSEFMNF
                                40      50      60      70      80      90

```

```

                                60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPET

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                                100     110     120     130     140     150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (25-41:68-86)

```

                                10      20      30      40      50
AAD-12                          SLLIGRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                :  .:  .:  .:  .:  .:
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSEFMDF
                                40      50      60      70      80      90

```

```

                                60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPET

```

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                                100     110     120     130     140     150

```

+AD4APg-gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName:
Full+AD0-Serum (607 aa)

initn: 51 init1: 51 opt: 60 Z-score: 87.0 bits: 23.2 E(): 7.2

Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (3-78:430-509)

```

                                10          20
AAD-12          SLLIGRHAHAIPGMDA---AESERFLEGLVDW
                   :: :... .: ... .: : : .
gi+AHw-135 LKHLVDEPQNLIKQNCDFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
           400          410          420          430          440          450

           30          40          50          60          70          80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMMWHSRLAGRPET
           : :. . . . . :: :... : . : . . : : . ::
gi+AHw-135 CCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTCCTESLVNRRPCFSALTPDET
           460          470          480          490          500          510

gi+AHw-135 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD
           520          530          540          550          560          570

```

+AD4APg-gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin
+AFs-Bos t (607 aa)
initn: 51 init1: 51 opt: 60 Z-score: 87.0 bits: 23.2 E(): 7.2
Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (3-78:430-509)

```

                                10          20
AAD-12          SLLIGRHAHAIPGMDA---AESERFLEGLVDW
                   :: :... .: ... .: : : .
gi+AHw-333 LKHLVDEPQNLIKQNCDFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
           400          410          420          430          440          450

           30          40          50          60          70          80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMMWHSRLAGRPET
           : :. . . . . :: :... : . : . . : : . ::
gi+AHw-333 CCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTCCTESLVNRRPCFSALTPDET
           460          470          480          490          500          510

gi+AHw-333 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD
           520          530          540          550          560          570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.4
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (45-59:122-138)

```

           20          30          40          50          60          70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVMMWHS
                   : :...: :...
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
           100          110          120          130          140          150

           80
AAD-12 RLAGRPET

```



```

82      4      3:+ACo-
84      4      3:+ACo-
86      2      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      4      1:+ACo-          :+ACoAPQA9AD0-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     1      0:+AD0-          +ACoAPQ-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.41700.00341+ADs- mu+AD0- 7.4795
0.181
mean+AF8-var+AD0-42.761712.729, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.196131
Kolmogorov-Smirnov statistic: 0.0972 (N+AD0-27) at 42

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.9    0.42
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.9    1.7
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  64 24.4    3.3
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)  55 21.5    3.7
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 21.8    3.7
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  57 22.1    3.9
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.9    4.9
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.9    4.9
gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName: Full+AD0-Se
( 607)  60 23.3    7.2
gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin +AFs-B (
607)   60 23.3    7.2
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)  54 21.3    9.2

```

gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.2
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.3 9.2

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 109.1 bits: 26.9 E(): 0.42
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (13-43:246-276)

```

                                10      20      30      40
AAD-12      L L I G R H A H A I P G M D A A E S E R F L E G L V D W A C Q A P R V H A H Q W A A
                                . . . . .
gi+AHw-370  A P D I K T A K E A L D L I V S A I E A A G Y T G Q V D I A M D V A S S E F Y K D G L Y D L D F K N P N S D K S K W I T
                220      230      240      250      260      270

```

```

                                50      60      70      80
AAD-12  G D V V V W D N R C L L H R A E P W D F K L P R V M W H S R L A G R P E T E
:
gi+AHw-370  G P Q L A E L Y E Q L L N E Y P I V S I E D P F A E D D W E A W S H F F S K V E G K T Q I V G D D L T V T N P I R I K K
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 98.4 bits: 24.9 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (13-43:247-277)

```

                                10      20      30      40
AAD-12      L L I G R H A H A I P G M D A A E S E R F L E G L V D W A C Q A P R V H A H Q W A A
                                . . . . .
gi+AHw-232  A P D I K T P K E A L D L I M D A I D K A G Y K G K V G I A M D V A S S E F Y K D G K Y D L D F K N P E S D P S K W L S
                220      230      240      250      260      270

```

```

                                50      60      70      80
AAD-12  G D V V V W D N R C L L H R A E P W D F K L P R V M W H S R L A G R P E T E
:
gi+AHw-232  G P Q L A D L Y E Q L I S E Y P I V S I E D P F A E D D W D A W V H F F E R V G D K I Q I V G D D L T V T N P T R I K T
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Serum (608 aa)
 initn: 53 init1: 53 opt: 64 Z-score: 93.1 bits: 24.4 E(): 3.3
 Smith-Waterman score: 64+ADs- 23.750+ACU- identity (53.750+ACU- similar)
 in 80 aa overlap (2-77:431-510)

```

                                10      20
AAD-12      L L I G R H A H A I P G M D A --- A E S E R F L E G L V D W
                                . . . . .
gi+AHw-135  F K P L V E E P H N L V K T N C E L F E K L G E Y G F Q N A L L V R Y T K K V P Q V S T P T L V E V S R S L G K V G S K
                410      420      430      440      450      460

```

```

30      40      50      60      70      80

```



```

      70          80          90          100          110          120
AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETE
      ..      ...
gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
          130          140          150
  
```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 90.0 bits: 21.9 E(): 4.9
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (24-40:68-86)

```

          10          20          30          40          50
AAD-12      LLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : . . . . : : : . . . : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90
  
```

```

          60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETE

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150
  
```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 90.0 bits: 21.9 E(): 4.9
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (24-40:68-86)

```

          10          20          30          40          50
AAD-12      LLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90
  
```

```

          60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETE

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150
  
```

+AD4APg-gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName: Full+AD0-Serum (607 aa)
 initn: 51 init1: 51 opt: 60 Z-score: 87.0 bits: 23.3 E(): 7.2
 Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
 in 80 aa overlap (2-77:430-509)

```

          10          20
AAD-12      LLIGRHAHAIPGMDA---AESERFLEGLVDW
          : : . . . . : : . . . . : : : :
gi+AHw-135 LKHLVDEPQNLIKQNCQFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
  
```

```

400      410      420      430      440      450
      30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMMWHSRLAGRPETE
      :  : . . . . . : : : : : : . . . . . : : . . . : :
gi+AHw-135 CCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALTPDET
      460      470      480      490      500      510

```

```

gi+AHw-135 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD
      520      530      540      550      560      570

```

+AD4APg-gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin
+AFs-Bos t (607 aa)
initn: 51 initl: 51 opt: 60 Z-score: 87.0 bits: 23.3 E(): 7.2
Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (2-77:430-509)

```

                                10      20
AAD-12                                LLIGRHAHAIPGMDA---AESERFLEGLVDW
                                : : : . . . : . . . : : : .
gi+AHw-333 LKHLVDEPQNLIKQNCQDFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
      400      410      420      430      440      450

```

```

      30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMMWHSRLAGRPETE
      :  : . . . . . : : : : : : . . . . . : : . . . : :
gi+AHw-333 CCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALTPDET
      460      470      480      490      500      510

```

```

gi+AHw-333 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD
      520      530      540      550      560      570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.1 bits: 21.3 E(): 9.2
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (44-58:122-138)

```

                20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVMMWHS
                : : : : : : : : : : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100      110      120      130      140      150

```

```

      80
AAD-12 RLAGRPETE

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
                160      170      180      190      200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.0 bits: 21.3 E(): 9.2

Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (44-58:122-138)

```

      20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
      : : : : : : : : : : : : : : : : : :
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

```

```

      80
AAD-12 RLAGRPEETE

```

```

gi+AHw-124 RKELAAVSVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)

initn: 49 initl: 49 opt: 54 Z-score: 85.0 bits: 21.3 E(): 9.2
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (44-58:122-138)

```

      20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
      : : : : : : : : : : : : : : : : : :
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

```

```

      80
AAD-12 RLAGRPEETE

```

```

gi+AHw-209 RKELAAVSVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
      160      170      180      190      200      210

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:32 2010 done: Fri Feb 5 12:56:32 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 210 - 289 80 aa - 80 aa


```

  94      0      1:+ACo-      :+ACo-
  96      0      1:+ACo-      :+ACo-
  98      1      0:+AD0-      +ACoAPQ-
100      0      0:          +ACo-
102      0      0:          +ACo-
104      0      0:          +ACo-
106      0      0:          +ACo-
108      0      0:          +ACo-
110      1      0:+AD0-      +ACoAPQ-
112      0      0:          +ACo-
114      0      0:          +ACo-
116      0      0:          +ACo-
118      0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.42160.00335+ADs- mu+AD0- 7.3913
0.178
mean+AF8-var+AD0-42.071412.335, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.197734
Kolmogorov-Smirnov statistic: 0.1000 (N+AD0-28) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.0    0.39
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.0    1.6
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  64 24.5    3.1
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)  55 21.6    3.5
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 21.9    3.5
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  57 22.2    3.6
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.9    4.6
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.9    4.6
gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName: Full+AD0-Se
( 607)  60 23.3    6.8
gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin +AFs-B (
607)  60 23.3    6.8
gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis familiar (
608)  60 23.3    6.8
gi+AHw-3319897+AHw-emb+AHw-CAA76841.1+AHw- albumin +AFs-Canis familiar (
585)  59 23.0     8
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)  54 21.4    8.7
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210)  54 21.4    8.8

```

gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.4 8.8

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 109.7 bits: 27.0 E(): 0.39
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (12-42:246-276)

```

                                10      20      30      40
AAD-12                        LIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                ::: :: . ::: : . : .::
gi+AHw-370 APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNPSDKSKWIT
                220      230      240      250      260      270
    
```

```

                    50      60      70      80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAGRPETEG
          :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280      290      300      310      320      330
    
```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 98.9 bits: 25.0 E(): 1.6
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (12-42:247-277)

```

                                10      20      30      40
AAD-12                        LIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                ::: :: . .: : . : .::
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270
    
```

```

                    50      60      70      80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAGRPETEG
          :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330
    
```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Serum (608 aa)
 initn: 53 init1: 53 opt: 64 Z-score: 93.6 bits: 24.5 E(): 3.1
 Smith-Waterman score: 64+ADs- 23.750+ACU- identity (53.750+ACU- similar)
 in 80 aa overlap (1-76:431-510)

```

                                10      20
AAD-12                        LIGRHAHAIPGMDA---AESERFLEGLVDW
                                .. :... .: ... .: : : .
gi+AHw-135 FKPLVEEPHNLVKTNCELFEKLGEGYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSK
                410      420      430      440      450      460
    
```

```

                30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAAGDVVVWDNR-CLLHRAEPWDFKLPVVMWHSRLAGRPETEG
          : :... . : . : :: :... : . . . .: . ::
    
```



```

      40          50          60          70          80
AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEG
      .:          .::
gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
          130          140          150

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 90.5 bits: 21.9 E(): 4.6
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (23-39:68-86)

```

          10          20          30          40          50
AAD-12          LIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : . . . . : : : . . . : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90

```

```

          60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEG

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 90.5 bits: 21.9 E(): 4.6
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (23-39:68-86)

```

          10          20          30          40          50
AAD-12          LIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

```

          60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEG

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName: Full+AD0-Serum (607 aa)
 initn: 51 init1: 51 opt: 60 Z-score: 87.4 bits: 23.3 E(): 6.8
 Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
 in 80 aa overlap (1-76:430-509)

```

          10          20
AAD-12          LIGRHAHAIPGMDA---AESERFLEGLVDW
          : : . . . . : : . . . . : : : :
gi+AHw-135 LKHLVDEPQNLIKQNCQFEKLG EYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
          400          410          420          430          440          450

```

```

      30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETEG
      :  : . . . . . : : : : : : . . . . . : : . . . . . : :
gi+AHw-135 CCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTCCCTESLVNRRPCFSALTPDET
      460      470      480      490      500      510

```

```

gi+AHw-135 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKLTVMENFVAFVD
      520      530      540      550      560      570

```

+AD4APg-gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin +AFs-Bos t (607 aa)
 initn: 51 initl: 51 opt: 60 Z-score: 87.4 bits: 23.3 E(): 6.8
 Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
 in 80 aa overlap (1-76:430-509)

```

                                10      20
AAD-12                                LIGRHAHAIPGMDA---AESERFLEGLVDW
                                : : : . . . : . . . . : : : .
gi+AHw-333 LKHLVDEPQNLIKQNCQDFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
      400      410      420      430      440      450

```

```

      30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETEG
      :  : . . . . . : : : : : : . . . . . : : . . . . . : :
gi+AHw-333 CCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTCCCTESLVNRRPCFSALTPDET
      460      470      480      490      500      510

```

```

gi+AHw-333 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKLTVMENFVAFVD
      520      530      540      550      560      570

```

+AD4APg-gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis familiaris+AF0- (608 aa)
 initn: 54 initl: 54 opt: 60 Z-score: 87.4 bits: 23.3 E(): 6.8
 Smith-Waterman score: 60+ADs- 23.810+ACU- identity (50.000+ACU- similar)
 in 84 aa overlap (1-80:431-514)

```

                                10      20
AAD-12                                LIGRHAHAIPGMDA---AESERFLEGLVDW
                                : : : . . . : . . . . : : : .
gi+AHw-668 FKPLVDEPQNLVKTNCELFEKLGEYGFQNALLVRYTKKAPQVSTPTLVEVSRKLGKVGTK
      410      420      430      440      450      460

```

```

      30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETEG
      :  : . . . . . : : : : : : . . . . . : : . . . . . : :
gi+AHw-668 CCKKPESERMSCAEDFLSVVLNRLCVLHEKTPVSEKVTCCCTESLVNRRPCFSGLEVDDET
      470      480      490      500      510      520

```

```

gi+AHw-668 YVPKEFNAETFTFHADLCTLPPEAEKQVKKQTALVELLKHKPKATDEQKLTVMGDFGAFVE
      530      540      550      560      570      580

```

+AD4APg-gi+AHw-3319897+AHw-emb+AHw-CAA76841.1+AHw- albumin +AFs-Canis familiaris+AF0- (585 aa)
 initn: 54 initl: 54 opt: 59 Z-score: 86.1 bits: 23.0 E(): 8

Smith-Waterman score: 59+ADs- 23.810+ACU- identity (50.000+ACU- similar)
in 84 aa overlap (1-80:408-491)

```

                                10          20
AAD-12          LIGRHAHAIPGMDA---AESERFLEGLVDW
                :. :... : ...  .: : : .
gi+AHw-331 FKPLVDEPQNLVKTNCELFEKLG EYGFQNALLVRYTKKAPQVSTPTLVEVSRKLGKVGTK
                380      390      400      410      420      430

                30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMWHSRLAGRPETEG
                :. :. . . : . : :: :... : . . . . :. : :: :
gi+AHw-331 CCKKPESERMSCADDFLSVVLNRLCVLHEKTPVSEKTKCCSESLVNRRCPCFSGLEVDET
                440      450      460      470      480      490

gi+AHw-331 YVPKEFNAETFTFHADLCTLP EAKQVKKQTALVELLKHKPKATDEQLKTVMGDFGAFVE
                500      510      520      530      540      550

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 85.5 bits: 21.4 E(): 8.7
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (43-57:122-138)

```

                20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVMWHS
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100      110      120      130      140      150

                80
AAD-12 RLAGRPETEG

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTTLSHFGKC
                160      170      180      190      200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 85.4 bits: 21.4 E(): 8.8
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (43-57:122-138)

```

                20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVMWHS
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100      110      120      130      140      150

                80
AAD-12 RLAGRPETEG

gi+AHw-124 RKELAAVSDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTTLSHFGKC
                160      170      180      190      200      210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gallus+AF0- (210 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 85.4 bits: 21.4 E(): 8.8
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (43-57:122-138)

```

                20          30          40          50          60          70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVVDNRCLL--HRAEPWDFKLPVMMWHS
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100          110          120          130          140          150
  
```

```

                80
AAD-12 RLAGRPETEG

gi+AHw-209 RKELAAVSVDCSEYKPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLLTSLSHFGKC
                160          170          180          190          200          210
  
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:32 2010 done: Fri Feb 5 12:56:32 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 211 - 290 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 4 library sequences
24	0	0:	
26	0	0:	
28	0	0:	
30	0	2:+ACo-	
32	1	8:+AD0AKg-	
34	18	21:+AD0APQA9AD0APQAq-	
36	22	44:+AD0APQA9AD0APQA9-	+ACo-
38	26	72:+AD0APQA9AD0APQA9AD0-	+ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 4.45710.00337+ADs- mu+AD0- 7.2131 0.179

mean+AF8-var+AD0-42.182212.320, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42

Lambda+AD0- 0.197474

Kolmogorov-Smirnov statistic: 0.0972 (N+AD0-29) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0- ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En (439) 73 26.9 0.4

gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno (440) 66 25.0 1.6

gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C (91) 55 21.5 3.5

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115) 56 21.9 3.5

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo (151) 57 22.2 3.7

gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157) 56 21.9 4.6

gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157) 56 21.9 4.6

gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se (608) 61 23.6 5.7

gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis familiar (608) 59 23.0 8.4

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus (208) 54 21.4 8.8

gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo (210) 54 21.4 8.9

gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.4 8.9

gi+AHw-3319897+AHw-emb+AHw-CAA76841.1+AHw- albumin +AFs-Canis familiar (585) 58 22.7 9.9

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)

initn: 73 init1: 73 opt: 73 Z-score: 109.5 bits: 26.9 E(): 0.4

Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar) in 31 aa overlap (11-41:246-276)

Sequence alignment showing AAD-12 and gi+AHw-370 sequences with positions 10, 20, 30, 40, 50, 60, 70, 80 marked.

Sequence alignment showing AAD-12 and gi+AHw-370 sequences with positions 50, 60, 70, 80 marked.

:

gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFFSKVEGKTQIVGDDLTVTNPIRIKK
280 290 300 310 320 330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 initl: 66 opt: 66 Z-score: 98.7 bits: 25.0 E(): 1.6
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (11-41:247-277)

AAD-12 IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
: : : : : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
220 230 240 250 260 270

AAD-12 GDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAGRPETEGA
:
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFFERVGDKIQIVGDDLTVTNPTRIKT
280 290 300 310 320 330

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 initl: 43 opt: 55 Z-score: 92.6 bits: 21.5 E(): 3.5
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (25-67:29-70)

AAD-12 IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVVWDNRCLLHRAE
: : : : : : : : :
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCS PDNQCQATY-HYYPNQNN--WDLRAVSAYCS
10 20 30 40 50

AAD-12 PWDFKLP---RVMWHSRLAGRPETEGA
: : : :
gi+AHw-323 TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
60 70 80 90

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 92.6 bits: 21.9 E(): 3.5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (22-38:68-86)

AAD-12 IGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVVWDNR
: : : : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

AAD-12 CLLHRAEPWDFKLPVVMWHSRLAGRPETEGA

gi+AHw-219 SFDSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 57 Z-score: 92.2 bits: 22.2 E(): 3.7
 Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
 in 43 aa overlap (5-47:96-133)

```

                                10      20      30
AAD-12                        IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
                                .:  ...  .:  .:.  .:..  .:
gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEEFRASLVDYLS-----H
                   70      80      90      100     110     120

                   40      50      60      70      80
AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGA
                   .:  ...  .:
gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                   130     140     150

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 90.4 bits: 21.9 E(): 4.6
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (22-38:68-86)

```

                                10      20      30      40
AAD-12                        IGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                :  .:..:  ::  ...  .:
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
                   40      50      60      70      80      90

                   50      60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEGA

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                   100     110     120     130     140     150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 90.4 bits: 21.9 E(): 4.6
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (22-38:68-86)

```

                                10      20      30      40
AAD-12                        IGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                :  .:..:  ::  ...  .:
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                   40      50      60      70      80      90

                   50      60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEGA

```


FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB	RecName: Full+AD0-En
(439) 73 27.0 0.39	
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL	RecName: Full+AD0-Eno
(440) 66 25.0 1.6	
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA	RecName: Full+AD0-C
(91) 55 21.6 3.4	
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs-	(115) 56 21.9 3.5
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH	RecName: Full+AD0-Glo
(151) 57 22.2 3.6	
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1	(157) 56 21.9 4.6
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s	(157) 56 21.9 4.6
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA	RecName: Full+AD0-Se
(608) 61 23.6 5.6	
gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis familiar	(608) 59 23.0 8.3
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus	(208) 54 21.4 8.7
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK	RecName: Full+AD0-Ovo
(210) 54 21.4 8.8	
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall	(210) 54 21.4 8.8
gi+AHw-3319897+AHw-emb+AHw-CAA76841.1+AHw- albumin +AFs-Canis familiar	(585) 58 22.7 9.8

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 109.7 bits: 27.0 E(): 0.39
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (10-40:246-276)

	10	20	30	
AAD-12	GRHAHAIPGMDDAESERFLEGLVDWACQAPRVHAHQWAA			
	:	:	:	:
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT			
	220	230	240	250 260 270
	40	50	60	70 80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA			
	:			
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK			
	280	290	300	310 320 330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 init1: 66 opt: 66 Z-score: 98.8 bits: 25.0 E(): 1.6

Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (10-40:247-277)

```

                                10      20      30
AAD-12      GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                : : : : : : : : : :
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270

```

```

                40      50      60      70      80
AAD-12  GDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAGRPETEGAA
                :
gi+AHw-232  GPQLADLYEQLISEYPIVSIEDPFAEDDWDWVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 init1: 43 opt: 55 Z-score: 92.7 bits: 21.6 E(): 3.4
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (24-66:29-70)

```

                                10      20      30      40      50
AAD-12      GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVVWDNRCLLHRAE
                                : : : : : : : : : :
gi+AHw-323  QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAYCS
                10      20      30      40      50

```

```

                60      70      80
AAD-12  PWDFKLP---RVMWHSRLAGRPETEGAA
                : : : :
gi+AHw-323  TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
                60      70      80      90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 92.7 bits: 21.9 E(): 3.5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (21-37:68-86)

```

                                10      20      30      40
AAD-12      GRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVVWDNR
                                : : : : : : : : : :
gi+AHw-219  YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                40      50      60      70      80      90

```

```

                50      60      70      80
AAD-12  CLLHRAEPWDFKLPVMMWHSRLAGRPETEGAA

gi+AHw-219  SFSDRSGLLLKQKVSDE
                100      110

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 57 Z-score: 92.3 bits: 22.2 E(): 3.6

Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
in 43 aa overlap (4-46:96-133)

```

                                10      20      30
AAD-12                          GRHAHAIPGMDDAAESERFLEGLVDWACQAPRVH
                                .:   ...  .:  .:  .:  .:  .:  .:
gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEEFRASLVDYLS-----H
                   70      80      90      100     110     120

                   40      50      60      70      80
AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA
                   .:   ...  .:  .:  .:  .:  .:  .:
gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                   130     140     150

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.5 bits: 21.9 E(): 4.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (21-37:68-86)

```

                                10      20      30      40
AAD-12                          GRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                :  .:  .:  .:  .:  .:  .:  .:
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSEFMNF
                   40      50      60      70      80      90

                   50      60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                   100     110     120     130     140     150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.5 bits: 21.9 E(): 4.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (21-37:68-86)

```

                                10      20      30      40
AAD-12                          GRHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                :  .:  .:  .:  .:  .:  .:  .:
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSEFMDF
                   40      50      60      70      80      90

                   50      60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA

gi+AHw-184 SFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                   100     110     120     130     140     150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)

initn: 53 init1: 53 opt: 61 Z-score: 88.9 bits: 23.6 E(): 5.6

Smith-Waterman score: 61+ADs- 23.377+ACU- identity (53.247+ACU- similar)
in 77 aa overlap (2-74:434-510)

```

                                10          20
AAD-12          GRHAHAIPGMDA---AESERFLEGLVDWACQ
                   :... .: ... .: : : . . :
gi+AHw-135  LVEEPHNLVKTNCELFEKLG EYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSKCCT
                   410          420          430          440          450          460

                   30          40          50          60          70          80
AAD-12  APRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA
                   :... . : . : :: :... : . . . . : : . ::
gi+AHw-135  HPEAERLSCAEDYLSVVLNRLCVLHEKTPVSEKVTCCCTESLVNRRPCFSALQVDETYVP
                   470          480          490          500          510          520

gi+AHw-135  KEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMGDFGFSFVDKCC
                   530          540          550          560          570          580

```

+AD4APg-gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis familiaris+AF0- (608 aa)
initn: 54 init1: 54 opt: 59 Z-score: 85.8 bits: 23.0 E(): 8.3
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (50.943+ACU- similar)
in 53 aa overlap (27-78:462-514)

```

                                10          20          30          40          50
AAD-12          GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAE
                                   :. . . . : . : :: :...
gi+AHw-668  LVRYTKKAPQVSTPTLVEVSRKLGKVGTKCCKKPESEKMSCAEDFLSVVLNRLCVLHEKT
                   440          450          460          470          480          490

                   60          70          80
AAD-12  PWDFKLPRVMWHSRLAGRPETEGAA
                   : . . . . : : . : :
gi+AHw-668  PVSEKVTCCSESLVNRRPCFSGLEVDETYVPKEFNAETFTFHADLCTLPEAEKQVKKQT
                   500          510          520          530          540          550

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 85.5 bits: 21.4 E(): 8.7
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (41-55:122-138)

```

                                20          30          40          50          60
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
                                   : : : : : : : : : : :
gi+AHw-162  MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                   100          110          120          130          140          150

                   70          80
AAD-12  RLAGRPETEGAA

gi+AHw-162  RKELAAVDCSEYKPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
                   160          170          180          190          200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:

Full+AD0-Ovomuco (210 aa)

initn: 49 initl: 49 opt: 54 Z-score: 85.4 bits: 21.4 E(): 8.8

Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)

in 17 aa overlap (41-55:122-138)

```

                20         30         40         50         60
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
                : : : : : : : : : : : : : : : : : :
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100         110         120         130         140         150

```

```

                70         80
AAD-12 RLAGRPETEGAA

```

```

gi+AHw-124 RKELAAVSVDCSEYKPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLLTSLHFGKC
                160         170         180         190         200         210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gallus+AF0- (210 aa)

initn: 49 initl: 49 opt: 54 Z-score: 85.4 bits: 21.4 E(): 8.8

Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)

in 17 aa overlap (41-55:122-138)

```

                20         30         40         50         60
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
                : : : : : : : : : : : : : : : : : :
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100         110         120         130         140         150

```

```

                70         80
AAD-12 RLAGRPETEGAA

```

```

gi+AHw-209 RKELAAVSVDCSEYKPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLLTSLHFGKC
                160         170         180         190         200         210

```

+AD4APg-gi+AHw-3319897+AHw-emb+AHw-CAA76841.1+AHw- albumin +AFs-Canis familiaris+AF0- (585 aa)

initn: 54 initl: 54 opt: 58 Z-score: 84.6 bits: 22.7 E(): 9.8

Smith-Waterman score: 58+ADs- 26.415+ACU- identity (50.943+ACU- similar)

in 53 aa overlap (27-78:439-491)

```

                10         20         30         40         50
AAD-12 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAE
                : . : . . : . : : : : : :
gi+AHw-331 LVRYTKKAPQVSTPTLVEVSRKLGKVGTKCKKPESERMSCADDFLSVVLNRLCVLHEKT
                410         420         430         440         450         460

```

```

                60         70         80
AAD-12 PWDFKLPRVMWHSRLAGRPETEGAA
                : . . . . : : : :

```

```

gi+AHw-331 PVSERVTKCCSESLVNRRCFSGLEVDETYVPKEFNAETFTFHADLCTLPEAEKQVKKQT
                470         480         490         500         510         520

```



```

54      84
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
56      61      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
58      60      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
60      46      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62      47      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-+AD0APQ-
64      35      32:+AD0APQA9AD0APQA9AD0AKgA9-
66      34      25:+AD0APQA9AD0APQA9ACoAPQA9-
68      14      20:+AD0APQA9AD0AKg-
70      19      16:+AD0APQA9ACoAPQ-
72      11      12:+AD0APQAq-
74      7       10:+AD0APQAq-
76      15      7:+AD0AKgA9AD0-
78      21      6:+AD0AKgA9AD0APQA9-
80      10      4:+ACoAPQA9-
82      5       3:+ACoAPQ-
84      3       3:+ACo-
86      2       2:+ACo-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      2       1:+ACo-
92      3       1:+ACo-          :+ACoAPQA9-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:          +ACo-
102     0       0:          +ACo-
104     0       0:          +ACo-
106     0       0:          +ACo-
108     0       0:          +ACo-
110     1       0:+AD0-          +ACoAPQ-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.38820.00339+ADs- mu+AD0- 7.5941
0.180
mean+AF8-var+AD0-41.508612.074, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.199070
Kolmogorov-Smirnov statistic: 0.0870 (N+AD0-29) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 27.0 0.37
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 25.0 1.5
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91) 55 21.6 3.4

```

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115) 56 21.9 3.4
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo (151) 57 22.3 3.5
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157) 56 22.0 4.5
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157) 56 22.0 4.5
 gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se (608) 61 23.7 5.4
 gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis familiar (608) 59 23.1 8
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus (208) 54 21.5 8.5
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo (210) 54 21.5 8.6
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.5 8.6
 gi+AHw-3319897+AHw-emb+AHw-CAA76841.1+AHw- albumin +AFs-Canis familiar (585) 58 22.8 9.5

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 110.1 bits: 27.0 E(): 0.37
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar) in 31 aa overlap (9-39:246-276)

```

                                10      20      30
AAD-12      RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                ::: :: . :: : . : .: .
gi+AHw-370  APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGlyDLDFKNPNsDKSKWIT
                220      230      240      250      260      270

                40      50      60      70      80
AAD-12  GDVVVWdNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL
:
gi+AHw-370  GPQLAELyEQLLNEYPivsIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 99.2 bits: 25.0 E(): 1.5
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar) in 31 aa overlap (9-39:247-277)

```

                                10      20      30
AAD-12      RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                ::: :: . :: : . : .: .
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPEsDPSKWLS
                220      230      240      250      260      270

                40      50      60      70      80
AAD-12  GDVVVWdNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL
:

```

gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
 280 290 300 310 320 330

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
 Full+AD0-Chiti (91 aa)
 initn: 43 initl: 43 opt: 55 Z-score: 92.9 bits: 21.6 E(): 3.4
 Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
 in 46 aa overlap (23-65:29-70)

10 20 30 40 50
 AAD-12 RHAHAIPGMDDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
 : ::: : .. : .. :: : .
 gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAYCS
 10 20 30 40 50

60 70 80
 AAD-12 PWDFKLP---RVMWHSRLAGRPETEGAAL
 :: : : :
 gi+AHw-323 TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
 60 70 80 90

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt al
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 92.8 bits: 21.9 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (20-36:68-86)

10 20 30 40
 AAD-12 RHAHAIPGMDDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
 : :...: :: ... ::
 gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

50 60 70 80
 AAD-12 CLLHRAEPWDFKLPVVMWHSRLAGRPETEGAAL
 gi+AHw-219 SFDSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 initl: 51 opt: 57 Z-score: 92.5 bits: 22.3 E(): 3.5
 Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
 in 43 aa overlap (3-45:96-133)

10 20 30
 AAD-12 RHAHAIPGMDDAAESERFLEGLVDWACQAPRVH
 .: :.. :. :: :... :
 gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEFRASLVDYLS-----H
 70 80 90 100 110 120

40 50 60 70 80
 AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPVVMWHSRLAGRPETEGAAL
 .: :... :

gi+AHw-135 HPEAERLSCAEDYLSVVLNRLCVLHEKTPVSERVTKCCTESLVNRRPCFSAEQVDETYVP
470 480 490 500 510 520

gi+AHw-135 KEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMGDFGFSFVDKCC
530 540 550 560 570 580

+AD4APg-gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis
familiaris+AF0- (608 aa)
initn: 54 init1: 54 opt: 59 Z-score: 86.1 bits: 23.1 E(): 8
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (50.943+ACU- similar)
in 53 aa overlap (26-77:462-514)

10 20 30 40 50
AAD-12 RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNR-CLLHRAE
: : . : :: :. . . .
gi+AHw-668 LVRYTKKAPQVSTPTLVEVSRKLGKVGTKCCKKPESERMSCAEDFLSVVLNRLCVLHEKT
440 450 460 470 480 490

60 70 80
AAD-12 PWDFKLPRVMWHSRLAGRPETEGAAL
: : . : :
gi+AHw-668 PVSERVTKCCSESLVNRRPCFSGLEVEDETYVPKEFNAETFTFHADLCTLPEAEKQVKKQT
500 510 520 530 540 550

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 85.7 bits: 21.5 E(): 8.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (40-54:122-138)

10 20 30 40 50 60
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLL--HRAEPWDFKLPRVMWHS
: : . : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
100 110 120 130 140 150

70 80
AAD-12 RLAGRPETEGAAL
gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
160 170 180 190 200

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 85.6 bits: 21.5 E(): 8.6
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (40-54:122-138)

10 20 30 40 50 60
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLL--HRAEPWDFKLPRVMWHS
: : . : :
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
100 110 120 130 140 150


```

74    10    10:+AD0APQAq-
76    9     7:+AD0AKgA9-
78    19    6:+AD0AKgA9AD0APQ-
80    18    4:+ACoAPQA9AD0APQ-
82    7     3:+ACoAPQ-
84    1     3:+ACo-
86    4     2:+ACo-
88    1     2:+ACo-          inset +AD0- represents 1 library sequences
90    0     1:+ACo-
92    2     1:+ACo-          :+ACoAPQ-
94    3     1:+ACo-          :+ACoAPQA9-
96    0     1:+ACo-          :+ACo-
98    0     0:              +ACo-
100   1     0:+AD0-        +ACoAPQ-
102   0     0:              +ACo-
104   0     0:              +ACo-
106   0     0:              +ACo-
108   0     0:              +ACo-
110   0     0:              +ACo-
112   1     0:+AD0-        +ACoAPQ-
114   0     0:              +ACo-
116   0     0:              +ACo-
118   0     0:              +ACo-
+AD4-120  0     0:              +ACo-

```

331323 residues in 1471 sequences

Expectation+AF8-n fit: $\rho(\ln(x))+AD0-$ 4.32680.00338+ADs- $\mu+AD0-$ 7.8660
0.179

mean+AF8-var+AD0-39.030511.909, 0's: 2 Z-trim: 3 B-trim: 59 in 2/41

Lambda+AD0- 0.205292

Kolmogorov-Smirnov statistic: 0.0823 (N+AD0-29) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
(439) 73 27.4 0.29

gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
(440) 66 25.4 1.2

gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(91) 55 21.8 2.8

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 22.2 2.9

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
(151) 57 22.5 3

gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
56 22.2 3.8

gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
56 22.2 3.8

gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis familiar (
608) 59 23.3 6.8

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
(208) 54 21.7 7.3


```

          60          70          80
AAD-12 PWDFKLP---RVMWHSRLAGRPETEGAALV
      ::  :  :  :
gi+AHw-323 TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
          60          70          80          90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 94.2 bits: 22.2 E(): 2.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (19-35:68-86)

```

          10          20          30          40
AAD-12          HAHAIIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          :  . . . . :  ::  . . .  ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

```

          50          60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAALV

gi+AHw-219 SFDSDRSGLLLKQKVSDE
          100          110

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 initl: 51 opt: 57 Z-score: 93.9 bits: 22.5 E(): 3
Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
in 43 aa overlap (2-44:96-133)

```

          10          20          30
AAD-12          HAHAIIPGMDAAESERFLEGLVDWACQAPRVH
          .:  . . . . :  ::  . . . . :
gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEEFRASLVDYLS-----H
          70          80          90          100          110          120

```

```

          40          50          60          70          80
AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAALV
      .:  . . . . :
gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
          130          140          150

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 92.0 bits: 22.2 E(): 3.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (19-35:68-86)

```

          10          20          30          40
AAD-12          HAHAIIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          :  . . . . :  ::  . . .  ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90

```



```
          60          70          80
AAD-12 PWDFKLPVMMWHSRLAGRPETEGAALV
      : . . . . . : : : :
gi+AHw-331 PVSERVTKCCSESLVNRRPCFSGLEVDETYVPKEFNAETFTFHADLCTLPEAEKQVKKQT
      470          480          490          500          510          520
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:34 2010 done: Fri Feb 5 12:56:34 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-