

SUMMARY

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STUDY TITLE

Bioinformatics Analysis of Soybean Event DAS-68416-4 Insert and Its Flanking Border
Sequences

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N/A

AUTHOR(S)

P. Song

STUDY COMPLETED ON

28 – June – 2010

PERFORMING LABORATORY

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Bioinformatics Analysis of Soybean Event DAS-68416-4 Insert and Its Flanking Border Sequences

SUMMARY

A plant-optimized aryloxyalkanoate dioxygenase gene (*aad-12*), originally from the soil bacterium *Delftia acidovorans*, was integrated into soybean (*Glycine max*) by *Agrobacterium*-mediated transformation of a variety “Maverick” with plasmid pDAB4468 to produce event DAS-68416-4. The aryloxyalkanoate dioxygenase-12 (AAD-12 protein), encoded by the *aad-12* gene, provides tolerance to the herbicide 2,4-dichlorophenoxyacetic acid (2,4-D). Molecular characterization indicated that event DAS-68416-4 contained a single insert including two intact expression cassettes, AAD-12 and PAT. DNA sequences flanking the insert in event DAS-68416-4 soybean were also cloned and characterized. The DNA sequence of the insert is identical to the corresponding portion in the T-DNA insert of plasmid pDAB4468 except for an extra 9 bp insertion at the 3’ junction.

To update the characterization of the soybean genomic DNA sequences surrounding the insert location of event DAS-68416-4 soybean, the sequences of the flanking borders and parental locus were analyzed using BLAST search algorithms along with up-to-date GenBank nucleotide collection [Nucleotide collection (nr/nt)], Non-Human and Non-Mouse ESTs (est_others), and protein [Non-redundant protein sequences (nr)] databases. BLASTn and BLASTx analysis of the sequences comprising the insert of DAS-68416-4 and its 5’ and 3’ flanking border regions revealed identities only to soybean derived or pDAB4468 T-DNA derived sequences. The insert of DAS-68416-4 most likely integrated into a locus close to the 3’ end downstream of a putative peroxidase gene in the soybean genome.

STUDY TITLE

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DATA REQUIREMENTS

N/A

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Title: Bioinformatics Analysis of Soybean Event DAS-68416-4 Insert and Its Flanking Border Sequences

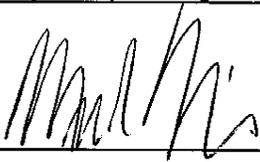
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Border Sequences

Study Initiation Date: 26/04/2010

This report represents data generated after the effective date of the EPA FIFRA Good Laboratory Practice Standards.

United States Environmental Protection Agency
Title 40 Code of Federal Regulations Part 160
FEDERAL REGISTER, August 17, 1989

Organisation for Economic Co-Operation and Development
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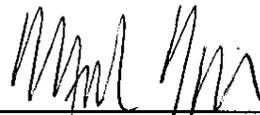
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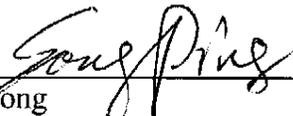
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Dow AgroSciences LLC

24 June 2010

Date



P. Song
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QUALITY ASSURANCE STATEMENT

Compound: Soybean aad-12 event DAS-68416-4

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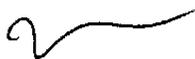
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28 June - 2010
Date



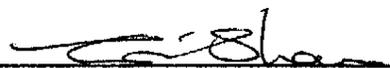
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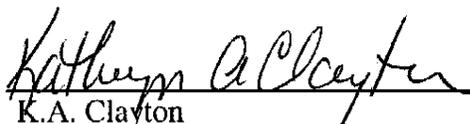
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Bioinformatics Analysis of Soybean Event DAS-68416-4 Insert and Its Flanking Border Sequences

ABSTRACT

A plant-optimized aryloxyalkanoate dioxygenase gene (*aad-12*), originally from the soil bacterium *Delftia acidovorans*, was integrated into soybean (*Glycine max*) by *Agrobacterium*-mediated transformation of a variety “Maverick” with plasmid pDAB4468 to produce event DAS-68416-4. The aryloxyalkanoate dioxygenase-12 (AAD-12 protein), encoded by the *aad-12* gene, provides tolerance to the herbicide 2,4-dichlorophenoxyacetic acid (2,4-D). Molecular characterization indicated that event DAS-68416-4 contained a single insert including two intact expression cassettes, AAD-12 and PAT. DNA sequences flanking the insert in event DAS-68416-4 soybean were also cloned and characterized. The DNA sequence of the insert is identical to the corresponding portion in the T-DNA insert of plasmid pDAB4468 except for an extra 9 bp insertion at the 3’ junction.

To update the characterization of the soybean genomic DNA sequences surrounding the insert location of event DAS-68416-4 soybean, the sequences of the flanking borders and parental locus were analyzed using BLAST search algorithms along with up-to-date GenBank nucleotide collection [Nucleotide collection (nr/nt)], Non-Human and Non-Mouse ESTs (est_others), and protein [Non-redundant protein sequences (nr)] databases. BLASTn and BLASTx analysis of the sequences comprising the insert of DAS-68416-4 and its 5’ and 3’ flanking border regions revealed identities only to soybean derived or pDAB4468 T-DNA derived sequences. The insert of DAS-68416-4 most likely integrated into a locus close to the 3’ end downstream of a putative peroxidase gene in the soybean genome.

INTRODUCTION

A plant-optimized *aad-12* gene, originally from common soil bacterium *Delftia acidovorans*, was integrated into soybean (*Glycine max*) by *Agrobacterium*-mediated transformation of a variety “Maverick” with plasmid pDAB4468 to produce event DAS-68416-4. Aryloxyalkanoate dioxygenase-12 (AAD-12 protein), encoded by the *aad-12* gene, provides tolerance to the herbicide 2,4-dichlorophenoxyacetic acid (2,4-D). Molecular characterization indicated that the event DAS-68416-4 contained a single insert including two intact expression cassettes, AAD-12 and PAT (1). In addition, DNA sequences flanking the insert in event DAS-68416-4 soybean as well as the parental locus have been cloned and characterized (2). The DNA sequence of the insert is identical to the corresponding portion in the T-DNA insert of plasmid pDAB4468 except for an extra 9 bp insertion at the 3’ border junction.

Considering the nature of random integration through conventional *Agrobacterium*-mediated transformation, insertion of an exogenous gene into soybean genome could disrupt an existing gene, open reading frame, or regulatory element. The purpose of this study is to characterize the location of the insert within the soybean genome and the nature of the flanking border sequences using BLASTn and BLASTx algorithms and up-to-date nucleotide and protein databases, thus evaluating if the transgenic insert in soybean event DAS-68416-4 had integrated into an endogenous gene or genetic element.

METHODS

Query Sequence Preparation

The whole insert and its flanking border sequences were divided into 3 regions according to the previous analysis (Figure 1). DNA sequence from Region 2 includes the full-length insert of the T-DNA in pDAB4468, and the rest of the regions represent the flanking borders. The query sequences were prepared in FASTA format for the BLASTn and BLASTx search programs. The

parental locus represents the sequences from the soybean genomic region prior to insertion of the transgene.

Sequence Search and Databases

Query sequences of Region 1, 2, and the parental locus were searched for sequence similarities against the GenBank nucleotide database [Nucleotide collection (nr/nt)] (<http://www.ncbi.nlm.nih.gov>, update to February 12, 2010) and GenBank Non-mouse and Non-human ESTs (est_others) (update to February 12, 2010) using BLASTn (Basic Local Alignment Search Tool, Version 2.2.21). The 6-frame translations of the DNA sequences were also searched against the non-redundant protein dataset (Non-redundant Protein Sequences “nr”) including non-redundant GenBank CDS translation along with protein sequences from SWISS-PROT (<http://www.expasy.org/sprot/>), PIR (<http://pir.georgetown.edu/>), PRF (<http://www.prf.or.jp/aboutdb-e.html>), and PDB (<http://www.wwpdb.org/>) (update to February 12, 2010) using BLASTx (version 2.2.21). BLASTn and BLASTx searches were performed in an internal UNIX computer using the default setting of algorithm parameters (BLASTn: Expect = 10, Gap Costs = Existence: 5, Extension: 2; BLASTx: Expectation = 10, Matrix = BLOSUM 62, Gap Costs: Existence: 11, Extension: 1; Word Size =3).

RESULTS AND DISCUSSION

Sequence similarity search results from BLASTn and BLASTx and descriptions are summarized in Table 1.

Region 1 consists of 2730 bp, representing the 5' border. BLASTn search of Region 1 returned several significant alignments ($E()=0\sim 3\times 10^{-87}$) in a complement orientation with a soybean mRNA sequence (Accession #: BT093225.1; Table 1). These alignments cover Nucleotides (Nt) 508 – 2332 of the 5' border sequence, corresponding the Nt 96 – 1272 in the unknown soybean mRNA. According to the annotation on BT093225.1, its complement strand (Nt 247 – 1209) encodes an unknown protein (Accession #: ACU17608.1). Furthermore, the nucleotides from

508 to 2281 in the 5' border are also aligned in a sense orientation with another soybean mRNA sequences ($E()=0\sim 3\times 10^{-75}$; Accession #: BT093496.1; Table 1) in which the sequence of Nt 61-1023 encodes an unknown soybean protein (Accession #: ACU17865.1). One of the other top scoring alignments is with a peroxidase (PRX1) mRNA from *Medicago truncatula* in a sense orientation (Accession #: EF456703.1; $E()=8\times 10^{-14} \sim 4\times 10^{-40}$; APPENDIX 2). Amino acid sequence alignment of the peroxidase (Accession #: ABO77632) encoded by the mRNA from *Medicago truncatula* and the 2 undefined soybean proteins (Accession ACU17608.1 and ACU17865.1) displays a 78% identity (data not shown); indicating that the unknown function of the soybean proteins might be a peroxidase. Thus, the 5' border sequence possibly contains the coding sequence for a peroxidase gene. Similar to the search of nucleotide database, the search against the EST database returned several identical alignments with soybean cDNAs, including soybean cDNAs (Accession #: CX703225.1; CX709633.1) isolated from the water-stressed (5h and 48h) soybean root libraries, but in a complement orientation (Table 1). Nt 1495 -2332 in the 5' border also displays significant alignments with a soybean mRNA (Accession #: CF807990.1) and other plant cDNAs that may encode a peroxidase. Apparently, the unaligned regions located in the Nt 508 – 2332 of the 5' border presumably represent introns in a gene. The BLASTx search of Region 1 returned significant alignments with unknown soybean proteins (Accession #: ACU17608.1 and ACU17865.1) encoded by the aforementioned unknown mRNAs (Accession #: BT093225.1 and BT093496.1), *Medicago truncatula* peroxidase encoded by the mRNA (Accession #: EF456703.1), and peroxidase from other plant species. The BLASTx search result perfectly matched the BLASTn search results, clearly demonstrating that the 5' border sequence encodes a putative peroxidase gene. Global sequence alignment of the 5' border with GenBank Accession # BT093496.1, BT093225.1 (complement), and EF456703.1 indicates the alignment is terminated at Nt 2416 of the 5' end border, while the match position of the stop codon is located at Nt 2181 (APPENDIX 1), which is far away from the start (Nt 2731) of the transgene insert. Considering the 550 bp distance between the stop codon and the start position of the insert, the insert in DAS-68416-4 is likely located outside of the sequence associated with the putative peroxidase gene.

Region 2 encompasses the T-DNA insert from pDAB4468. As described previously, the promoter, gene, and terminator sequences of the expression cassettes for AAD-12 and PAT are intact, plus a complete MAR element at the 5' end of the insert (Table 1). Further analysis identified a 9 bp short segment located between the 3' end insert and its border. Screening this 9 bp in both orientations through the whole sequence of pDAB4468 failed to identify any matches. Neither did the BLASTn search using GenBank nucleotide database and the available soybean nucleotide database (<http://soybase.org/GlycineBlastPages>).

Region 3 consists of 1082 bp of the 3' border region. BLASTn search of Region 3 returned 2 significant short alignments with the DNA sequence from a soybean genomic clone (Accession #: AC235472.1; APPENDIX 2). The alignments start at Nt 212 of the 3' border and are too short to determine the nature associated with these alignments. In addition, there are no identified coding regions available in Accession # AC235472.1 based on the information available in this GenBank accession. BLASTn search of Region 3 using the EST database only returned no-significant alignments related to sequences from various plant species including soybean. As such, BLASTx search returned nothing but very weak alignments with protein sequences from *Bombyx mori* and fruit fly. These results imply that the sequence in the 3' border is beyond the possible coding regions identified in the 5' border.

As expected, BLAST (BLASTn, BLASTx) search of the parental locus returned a close-to-identical profile as displayed in the BLAST search of the 5' border sequence. Only the portion corresponding to the 5' border showed significant alignments (Table 1), confirming the results from the search of the individual border sequences.

Taking account of all the results from sequence similarity searches using BLAST tools, the insert of DAS-68416-4 was most likely integrated into a locus close to the 3' end downstream of a putative peroxidase gene in soybean. However, the exact coding sequence is not identified due to the lack of information on the transcription as well as the location of introns and exons in this putative peroxidase gene.

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1. Song, P., Cruse, J., Thomas, A., 2009. Molecular Characterization of AAD-12 Soybean Event DAS-68416-4. Dow AgroSciences Study Report 081087.
2. Poorbaugh, J., Zhou, N., Mo, J., 2009. Cloning and Characterization of DNA Sequence in the Insert and the Flanking Border Regions of AAD-2 Soybean Event DAS-68416-4. Dow AgroSciences Study Report 091048.

Table 1. Description of DNA Sequences from the Insert, its Flanking Borders in DAS-68416-4 and the Parental Locus

Region	Location	Size (bp)	% Identity (Location and Orientation) and E-value	Homologue Accession #	Location in Homologous Sequences	Description
1	1-2730	2730	98 (508-784) E($)=1 \times 10^{-145}$	BT093225.1	1272-996 (complement)	Soybean clone JCVI-FLGm-17C9 unknown mRNA (Length = 1274)
			100 (1157-1348) E($)=1 \times 10^{-101}$		996-805 (complement)	
			100 (1478-1645) E($)=3 \times 10^{-87}$		804-637 (complement)	
			99 (1789-2332) E($)=0$		639-96 (complement)	
			100 (1540-1645, E($)=3 \times 10^{-50}$	CX703225	743-638 (complement)	A soybean cDNA isolated from the water-stressed (5h and 48h) soybean root libraries (Length= 743)
			99 (1789-2332) E($)=0$		640-97 (complement)	
			100 (2338-2427) E($)=7 \times 10^{-11}$		40-1 (complement)	
			93 (508-784); E($)=1 \times 10^{-111}$	BT093496.1	2-274	Soybean clone JCVI-FLGm-17I24 unknown mRNA (Length = 1217)
			96(1157-1347); E($)=1 \times 10^{-86}$		274-464	
			97 (1478-1645): E($)=3 \times 10^{-75}$		466-633	
			93(1789-2281); E($)=0$		631-1128	
			100(1495-1645); E($)=4 \times 10^{-77}$	CF807990.1	1-151	psHB031xA07f USDA IFAFS: Expression of <i>Phytophthora sojae</i> genes during infection and propagation <i>Glycine max</i> cDNA clone sHB031A07 5, mRNA sequence (Length = 708)
			99 (1789-2332); E($)=0$		149-693	
			86 (628-784); E($)= 2 \times 10^{-30}$	EF456703.1	64-220	<i>Medicago truncatula</i> peroxidase (PRX1) mRNA, complete cds (Length = 969)
			83 (1157-1342); E($)=6 \times 10^{-24}$		220-405	
			86 (1478-1578); E($)=8 \times 10^{-14}$		412-512	
80 (1795-2170); E($)=4 \times 10^{-40}$	583-958					

Region	Location	Size (bp)	% Identity (Location and Orientation) and E-value	Homologue Accession #	Location in Homologous Sequences	Description
2	2731-9121	6391	100	T-DNA insert in pDAB4468	23-6413	T-DNA insert including complete MAR, aad-12 and pat expression cassettes
	9122-9130	9	N/A	N/A		No sequence identity
3	9131-10212	1082	90 (212-263) E() $=2\times 10^{-6}$	AC235472.1	77662-77713	<i>Glycine max</i> strain Williams 82 clone GM_WBc0099F2 3, complete sequence (Length = 134971)
			87 (216-256) E() $=6.6$		78023-77983 (complement)	
Parental Locus		3867	98 (508-784) E() $=1\times 10^{-145}$	BT093225.1	1272-996 (complement)	Soybean clone JCVI-FLGm-17C9 unknown mRNA (Length = 1274)
			100 (1157-1348) E() $=1\times 10^{-101}$		996-805 (complement)	
			100 (1478-1645) E() $=5\times 10^{-87}$		804-637 (complement)	
			99 (17898-2332) E() $=0$		639-96 (complement)	
			100 (1540-1645) E() $=1\times 10^{-50}$	CX703225	743-638 (complement)	gmrtDrNS01_14-B_M13R_D10_0 74.s2 Water stressed 5h segment 2 gmrtDrNS01 <i>Glycine max</i> cDNA 3', mRNA sequence (Length = 743)
			99 (1789-2332) E() $=0$		640-97 (complement)	
			100 (2338-2427) E() $=1\times 10^{-10}$		40-1 (complement)	
			93 (508-784); E() $=1\times 10^{-111}$	BT093496.1	2-274	Soybean clone JCVI-FLGm-17I24 unknown mRNA (Length = 1217)
			96(1157-1347); E() $=2\times 10^{-86}$		274-464	
			97 (1478-1645): E() $=4\times 10^{-75}$		466-633	
			93(1789-2281); E() $=0$		631-1128	
			100 (1495-1645); E() $=6\times 10^{-77}$	CF807990.1	1-151	psHB031xA07f USDA IFAFS:Expressio n of Phytophthora sojae genes during infection and propagation
			99 (1789-2332); E() $=0$		149-693	

Region	Location	Size (bp)	% Identity (Location and Orientation) and E-value	Homologue Accession #	Location in Homologous Sequences	Description
						<i>Glycine max</i> cDNA clone sHB031A07 5, mRNA sequence (Length = 708)
			86 (628-784); E()= 2×10^{-30}	EF456703.1	64-220	<i>Medicago truncatula</i> peroxidase (PRX1) mRNA, complete cds (Length = 969)
			83 (1157-1342); E()= 8×10^{-24}		220-405	
			86 (1478-1578); E()= 1×10^{-13}		412-512	
			80 (1795-2170); E()= 6×10^{-40}		583-958	

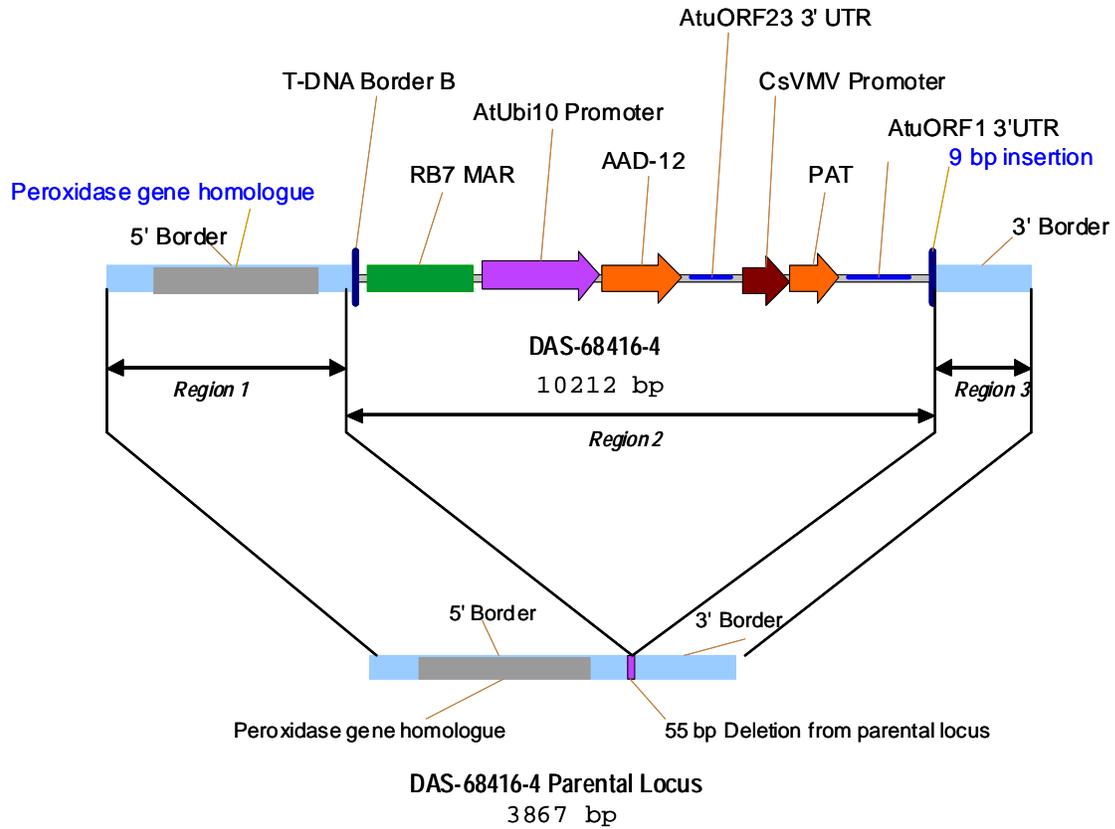


Figure 1. Diagram of the Insert, its Flanking Borders, and Parental Locus in Soybean Event DAS-68416-4

APPENDIX

1. Sequence Alignments of GenBank Accession #: BT093225, BT093496, and EF456703 with the 5' Border of DAS-68416-4

```

        1                               50
68416_5'_Border      (1) CTGTCGTTGGATTACAGAACATTGACGCCAGTTTTCACTTCGTTATCTT
BT093225_complement (1) -----
        BT093496      (1) -----
        EF456703      (1) -----

        51                               100
68416_5'_Border      (51) TGAATTCATTA AAAATCGAATCTCTCACCTATAACCCCCCATTTTTCTAAT
BT093225_complement (1) -----
        BT093496      (1) -----
        EF456703      (1) -----

        101                              150
68416_5'_Border      (101) CCATCATAATCAA AATTCATAAATGAATCAGTTACCATTACCATAATACC
BT093225_complement (1) -----
        BT093496      (1) -----
        EF456703      (1) -----

        151                              200
68416_5'_Border      (151) TTTTTGAAAATGAGTTTGAATAATCAGTATCTTTAGAAA ACTAATTAAGA
BT093225_complement (1) -----
        BT093496      (1) -----
        EF456703      (1) -----

        201                              250
68416_5'_Border      (201) AATTAAATAAAAAATATTTATCATGAAGATGAGTGTAAGAAAAATTATGA
BT093225_complement (1) -----
        BT093496      (1) -----
        EF456703      (1) -----

        251                              300
68416_5'_Border      (251) AAAGTATAACTTTATACATTTCTATAAAAATTATTTTTCTTTTAATTTCT
BT093225_complement (1) -----
        BT093496      (1) -----
        EF456703      (1) -----

        301                              350
68416_5'_Border      (301) TAATTAATATACCTAAGTAAATGAGTTAATATTTATCTTTCAAAAATTCCT
BT093225_complement (1) -----
        BT093496      (1) -----
        EF456703      (1) -----

        351                              400
68416_5'_Border      (351) ATAGTCGCCAATTAATTTTCCCATGCAATGACAACCTTGTCGGTATTCTAC
BT093225_complement (1) -----
        BT093496      (1) -----
        EF456703      (1) -----

        401                              450
68416_5'_Border      (401) GTGGTAGGTTAGGCTACCTGCCGAGACAAATTGCCTTGAGACAAATTC AA
BT093225_complement (1) -----
        BT093496      (1) -----
        EF456703      (1) -----

        451                              500
68416_5'_Border      (451) TAGAGAACCCTTCCAAGGGACCATTATAAATAGAGAACTTTTCATTAACCG
BT093225_complement (1) -----
        BT093496      (1) -----
        EF456703      (1) -----

        501                              550

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68416_5'_Border (501) ATAAGCCACACCCCTTTCAATCAAACCAAACACTTGAAGTACTAAGTTAG
BT093225_complement (1) -----GACACCCCTTTCAATCAAACCAAACACTTGAAGTACTAAGTTAG
BT093496 (1) -----GACACCCCTCTCAAGCAAACCAAACACTTGAAGTACTAAGTTAG
EF456703 (1) -----
551 600
68416_5'_Border (551) TGTGTTTGAGCAAATTAACATATGGCTTCGTT---TTGTTCTAGATTGACA
BT093225_complement (46) TGTGTTTGAGCAAATTAACATATGGCTTCGTT---TTGTTCTAGATTGACA
BT093496 (45) TGTGTTTGAGCAAATTAACATATGGCTTCGTT---TTGTTCTAGATTGACC
EF456703 (1) -----ATGGCTTCGTTAAAATGTTCTAGATTAAAC
601 650
68416_5'_Border (598) ATTT---GTTTGGCTCTGTTTGTCTCATAATGGGGAGTGCCAATGCACA
BT093225_complement (93) ATTT---GTTTGGCTCTGTTTGTCTCATAATGGGGAGTGCCAATGCACA
BT093496 (88) ATTT---GTTTGGCTCTGTTTGTCTCATAATGGGGAGTGCCAATGCCCA
EF456703 (31) ATGATCAATTTAGTTCTATCTGTTCTCATAATAGGGAGTGCCAATGCACA
651 700
68416_5'_Border (645) ACTTTCTACAAACTTTTACTACCAATTCATGTCCAAACCTCTTCTCCTCTG
BT093225_complement (140) ACTTTCTACAAACTTTTACTACCAATTCATGTCCAAACCTCTTCTCCTCTG
BT093496 (135) ACTTTCTACAAACTTTTACTACCAATTCATGTCCAAACCTCTTCTCCTCTG
EF456703 (81) ACTTTCTACAAACTTTTACTCAAATACTGTCCAAACTCTTCTACCAACAG
701 750
68416_5'_Border (695) TGAAATCCACAGTGCAATCTGCCATATCAAGGAGACCCGATGGGTGCT
BT093225_complement (190) TGAAATCCACAGTGCAATCTGCCATATCAAGGAGACCCGATGGGTGCT
BT093496 (185) TGAAATCCACAGTGCAATCTGCCATATCAAGGAGACCCGATGGGTGCT
EF456703 (131) TGAAATCCACAGTGCAATCTGCCATATCAAGGAGACCCGATGGGTGCT
751 800
68416_5'_Border (745) TCTCCTCTCGCTTGTCTTCCACGATTGCTTTGTCAATGTAATTTATTT
BT093225_complement (240) TCTCCTCTCGCTTGTCTTCCACGATTGCTTTGTCAATG-----
BT093496 (235) TCTCCTCTCGCTTGTCTTCCACGATTGCTTTGTCAATG-----
EF456703 (181) TCTATCCTCGCTTGTCTTCCACGATTGCTTTGTCAATG-----
801 850
68416_5'_Border (795) GCACCTTCTCCACTTACATACAAATATGCTAAGCTTACATATAGCTCCT
BT093225_complement (280) -----
BT093496 (275) -----
EF456703 (221) -----
851 900
68416_5'_Border (845) CTTTCTACCACTTGCATGCATCATCTAATTTTGTGAAACAACACTTGT
BT093225_complement (280) -----
BT093496 (275) -----
EF456703 (221) -----
901 950
68416_5'_Border (895) TCCTTTTATTATACACATCATCTTTGATAAAATTTTGTGCTGTGCAACTT
BT093225_complement (280) -----
BT093496 (275) -----
EF456703 (221) -----
951 1000
68416_5'_Border (945) TTTTTTAGTGTGTTAATCAGTTCTATGATGATACTATTAGTTAAGAAATT
BT093225_complement (280) -----
BT093496 (275) -----
EF456703 (221) -----
1001 1050
68416_5'_Border (995) TTAATGCACTTAATAAACCAATTTTAAGTACTTTAACCGTTCAATGATATT
BT093225_complement (280) -----
BT093496 (275) -----
EF456703 (221) -----
1051 1100
68416_5'_Border (1045) ATATATTTAAAGATAATAAATATTTCTGCTTTTGTCTTCTATATTAGTGTA
BT093225_complement (280) -----
BT093496 (275) -----
EF456703 (221) -----
1101 1150
68416_5'_Border (1095) GTTAAGAACCTTCTTACTTCTTAGCTAGCTAAATATTAATGAGTAAACAT

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BT093225_complement (280) -----
  BT093496 (275) -----
  EF456703 (221) -----
                                     1151                                     1200
68416_5'_Border (1145) TAACAAATGCAGG GATGTGATGGT TCAATTCTATT GATGACACATCAAG
BT093225_complement (280) ----- GATGTGATGGT TCAATTCTATT GATGACACATCAAG
  BT093496 (275) ----- GATGTGATGGT TCAATTCTATT GATGACACATCAAG
  EF456703 (221) ----- GATGTGATGGATCAATTCTCTTAGATGACACATCAAG
                                     1201                                     1250
68416_5'_Border (1195) CTT CACCGGAGAGAAGAACGCAAACCC AACAGGAACTCTGCTCGTGGAT
BT093225_complement (317) CTT CACCGGAGAGAAGAACGCAAACCC AACAGGAACTCTGCTCGTGGAT
  BT093496 (312) CTT CACCGGAGAGAAGAACGCAAACCC AACAGGAACTCTGCTCGTGGAT
  EF456703 (258) CTTT ACCGGTGAGAAGAA TGCAAATCCAAATAGAAACTC GCTCGTGGAT
                                     1251                                     1300
68416_5'_Border (1245) TCGAGGTTATTGACAACATTA AATCAGCCGTGGAGAAAGTGTGTCCAGGA
BT093225_complement (367) TCGAGGTTATTGACAACATTA AATCAGCCGTGGAGAAAGTGTGTCCAGGA
  BT093496 (362) ACGAGGTCATTGACAACATTA AATCAGCCGTGGAGAAAGTGTGTCCAGGA
  EF456703 (308) TTGATGTCATCGACAACATA AAGA CAGCCGTAGAGAAAGTATGCCCGGA
                                     1301                                     1350
68416_5'_Border (1295) GTTGTTCCTGCGCAGATATCCTTGCCATCGCTGCCAGAGACTCTGTTCA
BT093225_complement (417) GTTGTTCCTGCGCAGATATCCTTGCCATCGCTGCCAGAGACTCTGTTCA
  BT093496 (412) GTTGTTCCTGCGCAGATATCCTTGCCATAGCTGCCAGAGACTCTGTTCA
  EF456703 (358) GTTGTATCATGTGCTGATATCCTAGCCATGCTGCCGCAGACTCTGTTGC
                                     1351                                     1400
68416_5'_Border (1345) GATTGTAAGTGGTCAAACAACCAACAAAAACACATTA AACTAAATCATT
BT093225_complement (467) GATT-----
  BT093496 (462) GATC-----
  EF456703 (408) AATT-----
                                     1401                                     1450
68416_5'_Border (1395) AATTGTACATATCAAAATTAATTACCAATTTAGTACCACACATGCAATTA
BT093225_complement (471) -----
  BT093496 (466) -----
  EF456703 (412) -----
                                     1451                                     1500
68416_5'_Border (1445) AAGAGAACATTTTGTGATTTTGATCAATATAG CTTGGAGGCCCTACATG
BT093225_complement (471) ----- CTTGGAGGCCCTACATG
  BT093496 (466) ----- CTTGGAGGCCCTAGTTG
  EF456703 (412) ----- CTTGGAGGTCCAACTG
                                     1501                                     1550
68416_5'_Border (1495) GAATGTTAAACTTGGAGAAGAGACGCTAGA AACTGCTAGCCAATCTGCTG
BT093225_complement (488) GAATGTTAAACTTGGAGAAGAGACGCTAGA AACTGCTAGCCAATCTGCTG
  BT093496 (483) GAATGTTAAAGTGGAGAAGAGACGCTAGA AACTGCTAGCCAATCTGCTG
  EF456703 (429) GAATGTTAAACTTGGAGAAGAGATGCTAAACGGCTAGTCAATCCGCTG
                                     1551                                     1600
68416_5'_Border (1545) CTAACAATGGCATCCCTGCACCCACTTCAAACCTTAA CCAACTCATCTCA
BT093225_complement (538) CTAACAATGGCATCCCTGCACCCACTTCAAACCTTAA CCAACTCATCTCA
  BT093496 (533) CTAACAATGGCATCCCTGCACCCACTTCAAACCTTAA CCAACTCATCTCA
  EF456703 (479) CTAACAATGGCATCCCTGCACCAACTTCAAACCTCAA TACTCACTCA
                                     1601                                     1650
68416_5'_Border (1595) AGATTTAGCGCTCTTGGACTTTCCACCAAGGACTTGGTCGCCTTGTCCGG
BT093225_complement (588) AGATTTAGCGCTCTTGGACTTTCCACCAAGGACTTGGTCGCCTTGTCCGG
  BT093496 (583) AGATTCAGCGCTCTTGGACTTTCCACCAAGGACTTGGTCGCCTTGTCCGG
  EF456703 (529) ATGTTTAGCGCCGTTGGTCTTTCTAGCAAAGATTGGTCACTTGTCAAG
                                     1651                                     1700
68416_5'_Border (1645) TACAAAACATATATCACATAATTTTCCAATTAATTACATTTCAATCATAT
BT093225_complement (638) T-----
  BT093496 (633) T-----
  EF456703 (579) T-----
                                     1701                                     1750
68416_5'_Border (1695) AGTAAAATTTCTCAATTAATTAGGAACATGAGAAACTTATAGTCACACGT
BT093225_complement (639) -----

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BT093496 (634) -----
EF456703 (580) -----
1751 1800
68416_5'_Border (1745) TCTTTTGTGAGGAATATTGCATGGTTAATTTTGCATTAGGTGGT
BT093225_complement (639) -----GGT
BT093496 (634) -----GGT
EF456703 (580) -----GCA
1801 1850
68416_5'_Border (1795) CACACAATTGGACAAGCAAGGTGCACAAACTTCAGAGCCCGCATCTACAA
BT093225_complement (642) CACACAATTGGACAAGCAAGGTGCACAAACTTCAGAGCCCGCATCTACAA
BT093496 (637) CACACAATTGGACAAGCAAGGTGCACAAACTTCAGAGCCCGCATCTACAA
EF456703 (583) CACACAATTGGACAAGCAAGGTGTACAAATTTAGGGCAAGCATCTACAA
1851 1900
68416_5'_Border (1845) CGAGACCAACATAGAAACCGCATTTCGCAAGGACTAGGCAGCAAAGCTGCC
BT093225_complement (692) CGAGACCAACATAGAAACCGCATTTCGCAAGGACTAGGCAGCAAAGCTGCC
BT093496 (687) CGAGACCAACATAGAAACCGCATTTCGCAAGGCAAGGCAACAAAGCTGCC
EF456703 (633) CGAGACCAACATAAATGCTGCATTNGCTAGCACGAGGCAATCAAATGCC
1901 1950
68416_5'_Border (1895) CTAGAACATCAGGGTCAGGGGACAACAATCTGGCACCCTTGATCTTCAA
BT093225_complement (742) CTAGAACATCAGGGTCAGGGGACAACAATCTGGCACCCTTGATCTTCAA
BT093496 (737) CAAGAACATCAGGGTCAGGGGACAACAATCTTGCAACGCTTGATCTTCAA
EF456703 (683) CAAGGCATCAGGATCAGGTGACAACAATTTGGCACCTTTGATCTTCA
1951 2000
68416_5'_Border (1945) ACTCCAACCAGCTTTGACAACACTACTTCAAGAACCTCGTTCAGAAAGAA
BT093225_complement (792) ACTCCAACCAGCTTTGACAACACTACTTCAAGAACCTCGTTCAGAAAGAA
BT093496 (787) ACTCCAACCAGATTGACAACACTACTTCAAGAACTTTGTTTCAGAAAGAA
EF456703 (733) ACTCCTAGTTCCTTTGACAACAACACTACTTCAAGAACCTTTGTTTCAGAAAGAA
2001 2050
68416_5'_Border (1995) GGGTCTCCTCCACTCTGATCAGCAACTGTTCAACGGTGGGTCCACCAGCT
BT093225_complement (842) GGGTCTCCTCCACTCTGATCAGCAACTGTTCAACGGTGGGTCCACCAGCT
BT093496 (837) GGGTCTCCTCCACTCTGATCAGCAACTGTTCAATGGTGGGTCCACCAGCT
EF456703 (783) GGGTCTCCTCCATTCAGACCAACAACCTTTTAAACGGCGGGTCCACCAGCT
2051 2100
68416_5'_Border (2045) CCATTGTGCGTGGCTACAGCACCAACCCGGGCACCTTCTCCTCTGATTTTC
BT093225_complement (892) CCATTGTGCGTGGCTACAGCACCAACCCGGGCACCTTCTCCTCTGATTTTC
BT093496 (887) CCATTGTGCGTGGCTACAGCACCAACCCAGCTCCTTCTCCTCTGACTTC
EF456703 (833) CAATAGTGAGTGGTTATAGTACTAGCCCAAGCTCTTTTCTCCTCTGATTTT
2101 2150
68416_5'_Border (2095) GCCGCCGCCATGATCAAGATGGGAGACATTAGTCCTCTCACATGGCTCCAA
BT093225_complement (942) GCCGCCGCCATGATCAAGATGGGAGACATTAGTCCTCTCACATGGCTCCAA
BT093496 (937) GCCGCCGCCATGATCAAGATGGGAGACATTAGTCCTCTCACATGGCTCCAA
EF456703 (883) GCCGCTGCTATGATCAAGATGGGAATATTAACCTCTCACCGGATCAAA
2151 2200
68416_5'_Border (2145) TGGAGAAATCAGGAAGAAATGTAGAAAGATTAACTAAATTTGATTCAAGT
BT093225_complement (992) TGGAGAAATCAGGAAGAAATGTAGAAAGATTAACTAAATTTAATTCAAGT
BT093496 (987) CGGAGAAATCAGGAAGAAATGTAGAAAGATTAACTAAATTTAATTGAGT
EF456703 (933) TGGAGAAATAGGAAGAACTGTAGAAAAACCAACTAA-----
2201 2250
68416_5'_Border (2193) CTTGAATATTAAGGGTCTCTA---CACATACGCAAGCAATTTAATTGTGTT
BT093225_complement (1040) CTTGAATATTAAGGGTCTCTA---CACATACGCAAGCAATTTAATTGTGTT
BT093496 (1037) CTCCAAATATTAAGGGTCTCTACTACACATACGCAAGCAATTTAATTGTGTT
EF456703 (970) -----
2251 2300
68416_5'_Border (2240) TAATAAGTTGTTAAAACATGTTTTGGTTGTATTTGGATTCCCTAGTGTAG
BT093225_complement (1087) TAATAAGTTGTTAAAACATGTTTTGGTTGTATTTGGATTCCCTAGTGTAG
BT093496 (1087) TAATAAGTTGTTAAAACATGTTTTGGTTGTGTTTTGGATTCCCTGTTGGG
EF456703 (970) -----
2301 2350
68416_5'_Border (2290) TTTCGGTGATCAATGCCGTCTACTTTAGTGTGTTCTACTTCCCTTTATTT
BT093225_complement (1137) TTTCGGTGATCAATGCCGTCTACTTTAGTGTGTTCTACTTCCCTTTATTT
BT093496 (1137) TTAATTCCTAGTGTAGTTGCTGTTATCAAAGCCGTTACGTTAGTGT

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EF456703 (970) -----
                2351                                     2400
68416_5'_Border (2340) TTGTTTCTTTTACTTTTCCTTAACTATATTGTAGG-AAAAAAAAAAT
BT093225_complement (1187) TTGTTTCTTTTACTTTTCCTTAACTATATTGTAGGAAAAAAAAAAT
                BT093496 (1187) GTTC TACTT CAAA AAAAAAAAAA AAAAAA -----
                EF456703 (970) -----
                2401                                     2450
68416_5'_Border (2389) CCTTTATCAAGCATTTA TCAAGAA CGGA GTTTGCTTTTAAATTTCCCTT
BT093225_complement (1237) CCTTTATCAAGCATTTA CAAAA AAAAA AAAAAA -----
                BT093496 (1218) -----
                EF456703 (970) -----
                2451                                     2500
68416_5'_Border (2439) CATAACATCCATCAGAATTCAGTTTGTCTTTGCTTCTAAATTACGTTC
BT093225_complement (1275) -----
                BT093496 (1218) -----
                EF456703 (970) -----
                2501                                     2550
68416_5'_Border (2489) AAATCAGGGATGATAATCGGTTAGGTAATATATACAGTACCCCTTGCATA
BT093225_complement (1275) -----
                BT093496 (1218) -----
                EF456703 (970) -----
                2551                                     2600
68416_5'_Border (2539) GTCACGTTTGAAAAATATAATCATACTTAGTTCGGTAACAATTTAAATTA
BT093225_complement (1275) -----
                BT093496 (1218) -----
                EF456703 (970) -----
                2601                                     2650
68416_5'_Border (2589) TCATTCTCGTAATCATTAGCTACTTATGCACTCATATCCGTATCCGTAC
BT093225_complement (1275) -----
                BT093496 (1218) -----
                EF456703 (970) -----
                2651                                     2700
68416_5'_Border (2639) TTGCTCTTGTCGTAAGTCAATAAATTAATATAAAAAAATACTTAAACTT
BT093225_complement (1275) -----
                BT093496 (1218) -----
                EF456703 (970) -----
                2701                                     2742
68416_5'_Border (2689) GTTACAATAAATTAATAAATTTATTTTAAATCATTC AAGCA
BT093225_complement (1275) -----
                BT093496 (1218) -----
                EF456703 (970) -----

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2. BLASTn Search Output of the 5' End Border Sequence in Soybean Event DAS-68416-4 against GenBank Nucleotide Collection (nr/nt)
3. BLASTn Search Output of the 5' End Border Sequence in Soybean Event DAS-68416-4 against GenBank No-mouse and No-human EST s (est_others)
4. BLASTx Search Outputs of the 5' END Border Sequence in Soybean Event DAS-68416-4 against GenBank Non-redundant Protein Sequences "nr"

5. BLASTn Search Output of the 3' End Border Sequence in Soybean Event DAS-68416-4 against GenBank Nucleotide Collection (nr/nt)
6. BLASTn Search Output of the 3' End Border Sequence in Soybean Event DAS-68416-4 against GenBank No-mouse and No-human ESTs (est_others)
7. BLASTx Search Outputs of the 3' End Border Sequence in Soybean Event DAS-68416-4 against GenBank Non-redundant Proteins Sequences "nr"
8. BLASTn Search Output of the DNA sequence at the Parental Locus of Soybean Event DAS-68416-4 against GenBank Nucleotide Collection (nr/nt)
9. BLASTn Search Output of the DNA sequences at the Parental Locus of Soybean Event DAS-68416-4 against GenBank No-mouse and No-human ESTs (est_others)
10. BLASTx Search Outputs of the DNA sequence at the Parental Locus of Soybean Event DAS-68416-4 against GenBank Non-redundant Proteins Sequences "nr"

NOTE: All The BLAST search output files are electronically stored in a secured computer in Dow AgroSciences and available for view in PDF format.

BLASTn Output of the 5' Border Sequence Flanking the Insert in Soybean Event DAS-68416-4 against GenBank Nucleotide Collection (nt/nr)

BLASTN 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Query= 68416_5_border
(2730 letters)

Database: /usr/local/blast/db/blastlibs/nt
10,930,266 sequences; 30,212,464,392 total letters

Searching.....done

Sequences producing significant alignments:	Score	E
	(bits)	Value
gb BT093225.1 Soybean clone JCVI-FLGm-17C9 unknown mRNA	1039	0.0
gb BT093496.1 Soybean clone JCVI-FLGm-17I24 unknown mRNA	731	0.0
gb EF456703.1 Medicago truncatula peroxidase (PRX1) mRNA, compl...	176	4e-40
gb BT098008.1 Soybean clone JCVI-FLGm-22H8 unknown mRNA	174	2e-39
emb CU137662.1 Medicago truncatula chromosome 5 clone mth2-155l...	172	7e-39
emb CR938710.1 Medicago truncatula chromosome 5 clone mth2-170k...	172	7e-39
gb AF149281.1 AF149281 Phaseolus vulgaris clone pBPERB5 peroxida...	163	7e-36
ref XM_002520789.1 Ricinus communis Peroxidase 52 precursor, pu...	129	9e-26
gb BT052838.1 Medicago truncatula clone MTYFH_FI_FJ_FK1G-0-8 un...	111	2e-20
gb AY311597.1 Gossypium hirsutum class III peroxidase (pod7) mR...	105	1e-18
emb FP100639.1 Phyllostachys edulis cDNA clone: bphyem110n02, f...	103	5e-18
emb FP099994.1 Phyllostachys edulis cDNA clone: bphyem210i11, f...	103	5e-18
dbj AB027752.1 Nicotiana tabacum mRNA for peroxidase, complete ...	96	1e-15
gb AY837788.2 Catharanthus roseus clone Prx4 putative secretory...	90	8e-14
gb FJ644943.1 Sesuvium portulacastrum peroxidase 1 (POD1) mRNA,...	88	3e-13
dbj AK242814.1 Oryza sativa Japonica Group cDNA, clone: J090061...	86	1e-12
ref NM_001072100.1 Oryza sativa (japonica cultivar-group) Os1lg...	86	1e-12
tpe BN000659.1 TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	86	1e-12
dbj AB019228.1 Arabidopsis thaliana genomic DNA, chromosome 5, ...	86	1e-12
emb BX000512.1 Oryza sativa chromosome 11, . BAC OSJNBa0025K19 ...	86	1e-12
gb EF661875.2 Catharanthus roseus putative secretory peroxidase...	84	5e-12
ref NM_125225.1 Arabidopsis thaliana peroxidase, putative (AT5G...	80	8e-11
dbj AK117722.1 Arabidopsis thaliana At5g58390 mRNA for putative...	80	8e-11
gb AY085030.1 Arabidopsis thaliana clone 124846 mRNA, complete ...	80	8e-11
gb EZ329073.1 TSA: Artemisia annua strain Madagascar Contig1561...	76	1e-09

ref XM_002450087.1	Sorghum bicolor hypothetical protein, mRNA	76	1e-09
ref XM_002269882.1	PREDICTED: Vitis vinifera hypothetical prote...	76	1e-09
emb AM447728.2	Vitis vinifera contig VV78X018697.9, whole genom...	76	1e-09
ref XM_002278960.1	PREDICTED: Vitis vinifera hypothetical prote...	72	2e-08
gb AY206413.1	Ipomoea batatas anionic peroxidase swpb2 mRNA, co...	72	2e-08
gb EZ399860.1	TSA: Artemisia annua strain Uganda Contig16355, m...	70	7e-08
gb EZ145065.1	TSA: Artemisia annua strain Artemis Contig4471, m...	70	7e-08
gb EZ141680.1	TSA: Artemisia annua strain Artemis Contig1086, m...	70	7e-08
ref XM_002489001.1	Sorghum bicolor hypothetical protein (SORBID...	70	7e-08
ref XM_002441657.1	Sorghum bicolor hypothetical protein, mRNA	70	7e-08
emb AM456467.1	Vitis vinifera, whole genome shotgun sequence, c...	70	7e-08
gb GU230149.1	Ipomoea batatas anionic peroxidase mRNA, complete...	68	3e-07
ref XM_002268223.1	PREDICTED: Vitis vinifera hypothetical prote...	68	3e-07
gb FJ099755.1	Pinus taeda isolate 1286 anonymous locus 2_6350_0...	68	3e-07
emb CU231251.1	Populus EST from mild drought-stressed leaves	68	3e-07
gb AY206412.1	Ipomoea batatas anionic peroxidase swpb1 mRNA, co...	68	3e-07
dbj AK322204.1	Solanum lycopersicum cDNA, clone: LEFL1035AA07, ...	66	1e-06
ref XM_002328955.1	Populus trichocarpa predicted protein, mRNA	66	1e-06
ref XM_002319932.1	Populus trichocarpa predicted protein, mRNA	66	1e-06
gb AC214418.1	Populus trichocarpa clone POP106-D21, complete se...	66	1e-06
gb BT096974.1	Soybean clone JCVI-FLGm-21M8 unknown mRNA	64	5e-06
gb FJ596178.1	Capsicum annuum peroxidase (POD) mRNA, complete cds	64	5e-06
gb EF433455.1	Ipomoea batatas basic peroxidase swpb4 mRNA, comp...	64	5e-06
gb AC235385.1	Glycine max strain Williams 82 clone GM_WBb0113B1...	62	2e-05
gb GQ258782.1	Brassica rapa peroxidase 52 mRNA, partial cds	60	7e-05
gb FJ099770.1	Pinus taeda isolate 1299 anonymous locus 2_6350_0...	60	7e-05
gb FJ099768.1	Pinus taeda isolate 1282 anonymous locus 2_6350_0...	60	7e-05
gb FJ099767.1	Pinus taeda isolate 1292 anonymous locus 2_6350_0...	60	7e-05
gb FJ099766.1	Pinus taeda isolate 1285 anonymous locus 2_6350_0...	60	7e-05
gb FJ099765.1	Pinus taeda isolate 1288 anonymous locus 2_6350_0...	60	7e-05
gb FJ099762.1	Pinus taeda isolate 1298 anonymous locus 2_6350_0...	60	7e-05
gb FJ099761.1	Pinus taeda isolate 1289 anonymous locus 2_6350_0...	60	7e-05
gb FJ099760.1	Pinus taeda isolate 1297 anonymous locus 2_6350_0...	60	7e-05
gb FJ099759.1	Pinus taeda isolate 1283 anonymous locus 2_6350_0...	60	7e-05
gb FJ099758.1	Pinus taeda isolate 1287 anonymous locus 2_6350_0...	60	7e-05
gb FJ099757.1	Pinus taeda isolate 1291 anonymous locus 2_6350_0...	60	7e-05
gb EF433456.1	Ipomoea batatas basic peroxidase swpb5 mRNA, comp...	60	7e-05
gb AC226196.1	Musa acuminata clone BAC MA4-125A12, complete seq...	60	7e-05
ref XM_001754018.1	Physcomitrella patens subsp. patens predicte...	60	7e-05
emb AM449831.1	Vitis vinifera, whole genome shotgun sequence, c...	60	7e-05
gb AY206414.1	Ipomoea batatas anionic peroxidase swpb3 mRNA, co...	60	7e-05
gb AF485265.1	Gossypium hirsutum class III peroxidase (pod3) mR...	60	7e-05
gb EZ328614.1	TSA: Artemisia annua strain Madagascar Contig1516...	58	3e-04
gb EZ256818.1	TSA: Artemisia annua strain Artemis Contig23488, ...	58	3e-04
gb EZ397212.1	TSA: Artemisia annua strain Uganda Contig13707, m...	58	3e-04
dbj AK328734.1	Solanum lycopersicum cDNA, clone: LEFL3035G12, H...	58	3e-04
emb AJ544515.1	Asparagus officinalis partial mRNA for peroxidas...	58	3e-04
ref XM_002521820.1	Ricinus communis Lignin-forming anionic pero...	56	0.001
ref XM_002521805.1	Ricinus communis Lignin-forming anionic pero...	56	0.001

ref XM_002521804.1	Ricinus communis Peroxidase 30 precursor, pu...	56	0.001
gb FJ529216.1	Cucumis sativus 1-aminocyclopropane-1-carboxylate...	56	0.001
ref XM_002450088.1	Sorghum bicolor hypothetical protein, mRNA	56	0.001
gb FJ050772.1	Pinus taeda isolate 4650 anonymous locus 0_13032_...	56	0.001
gb FJ050764.1	Pinus taeda isolate 4651 anonymous locus 0_13032_...	56	0.001
gb FJ050758.1	Pinus taeda isolate 4655 anonymous locus 0_13032_...	56	0.001
gb FJ050757.1	Pinus taeda isolate 4653 anonymous locus 0_13032_...	56	0.001
gb AF149278.1	AF149278 Phaseolus vulgaris peroxidase 3 precursor...	56	0.001
dbj AK320453.1	Solanum lycopersicum cDNA, clone: LEFL1009CA06, ...	54	0.004
dbj AK320190.1	Solanum lycopersicum cDNA, clone: LEFL1006BD07, ...	54	0.004
gb AC235342.1	Glycine max strain Williams 82 clone GM_WBb0088H1...	54	0.004
emb CT832689.1	Oryza sativa (indica cultivar-group) cDNA clone:...	54	0.004
emb CT832688.1	Oryza sativa (indica cultivar-group) cDNA clone:...	54	0.004
emb CT832687.1	Oryza sativa (indica cultivar-group) cDNA clone:...	54	0.004
ref NM_001072503.1	Oryza sativa (japonica cultivar-group) Os12g...	54	0.004
tpe BN000664.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	54	0.004
dbj AK069456.1	Oryza sativa Japonica Group cDNA clone:J023019E0...	54	0.004
emb X91172.1	R. sativus prxK1 gene	54	0.004
emb BX000510.1	Oryza sativa chromosome 12, . BAC OJ1769_D07 of ...	54	0.004
gb EZ315890.1	TSA: Artemisia annua strain Madagascar Contig2436...	52	0.018
gb EZ359220.1	TSA: Artemisia annua strain Uganda Contig6381, mR...	52	0.018
gb EZ166433.1	TSA: Artemisia annua strain Artemis Contig25839, ...	52	0.018
gb BT106781.1	Picea glauca clone GQ03010_F17 mRNA sequence	52	0.018
ref XM_002285606.1	PREDICTED: Vitis vinifera hypothetical prote...	52	0.018
gb AC235417.1	Glycine max strain Williams 82 clone GM_WBb0135A0...	52	0.018
ref XM_002334206.1	Populus trichocarpa predicted protein, mRNA	52	0.018
ref NM_001157951.1	Zea mays peroxidase 2 (LOC100285056), mRNA >...	52	0.018
gb BT044614.1	Arabidopsis thaliana unknown protein (At4g33420) ...	52	0.018
gb FJ099764.1	Pinus taeda isolate 1294 anonymous locus 2_6350_0...	52	0.018
gb FJ099763.1	Pinus taeda isolate 1290 anonymous locus 2_6350_0...	52	0.018
gb BT042071.1	Zea mays full-length cDNA clone ZM_BFb0125B03 mRN...	52	0.018
emb AM450885.2	Vitis vinifera contig VV78X220288.8, whole genom...	52	0.018
ref NM_119496.3	Arabidopsis thaliana peroxidase, putative (AT4G...	52	0.018
emb AM446475.1	Vitis vinifera, whole genome shotgun sequence, c...	52	0.018
emb AM436560.1	Vitis vinifera, whole genome shotgun sequence, c...	52	0.018
emb AM429435.1	Vitis vinifera, whole genome shotgun sequence, c...	52	0.018
ref NM_101322.1	Arabidopsis thaliana anionic peroxidase, putati...	52	0.018
gb AF453791.1	Ipomoea batatas anionic peroxidase (POD) gene, pr...	52	0.018
dbj AB193816.1	Pisum sativum mRNA for peroxidase, complete cds,...	52	0.018
dbj AK176812.1	Arabidopsis thaliana mRNA for peroxidase ATP17a ...	52	0.018
gb AY089094.1	Arabidopsis thaliana clone 32346 mRNA, complete s...	52	0.018
gb AC108072.3	Homo sapiens BAC clone RP11-704A16 from 2, comple...	52	0.018
gb AF451951.1	Arabidopsis thaliana class III peroxidase ATP32 m...	52	0.018
emb AL161583.2	Arabidopsis thaliana DNA chromosome 4, contig fr...	52	0.018
gb AC010657.3	AC010657 Genomic sequence for Arabidopsis thaliana...	52	0.018
emb AL035678.1	Arabidopsis thaliana DNA chromosome 4, BAC clone...	52	0.018
gb AC012188.2	F14L17 Sequence of BAC F14L17 from Arabidopsis tha...	52	0.018
gb EZ395724.1	TSA: Artemisia annua strain Uganda Contig12219, m...	50	0.069
gb EZ362599.1	TSA: Artemisia annua strain Uganda Contig9760, mR...	50	0.069

gb BT066765.1	Zea mays full-length cDNA clone ZM_BFb0066D03 mRN...	50	0.069
gb BT055307.1	Zea mays full-length cDNA clone ZM_BFc0167H14 mRN...	50	0.069
gb EU962146.1	Zea mays clone 240603 mRNA sequence	50	0.069
gb FJ070719.1	Pinus taeda isolate 7938 anonymous locus 0_3458_0...	50	0.069
gb FJ070718.1	Pinus taeda isolate 7947 anonymous locus 0_3458_0...	50	0.069
gb FJ070717.1	Pinus taeda isolate 7943 anonymous locus 0_3458_0...	50	0.069
gb FJ070716.1	Pinus taeda isolate 7950 anonymous locus 0_3458_0...	50	0.069
gb FJ070715.1	Pinus taeda isolate 7940 anonymous locus 0_3458_0...	50	0.069
gb FJ070714.1	Pinus taeda isolate 7948 anonymous locus 0_3458_0...	50	0.069
gb FJ070713.1	Pinus taeda isolate 7949 anonymous locus 0_3458_0...	50	0.069
gb FJ070712.1	Pinus taeda isolate 7952 anonymous locus 0_3458_0...	50	0.069
gb FJ070711.1	Pinus taeda isolate 7941 anonymous locus 0_3458_0...	50	0.069
gb FJ070710.1	Pinus taeda isolate 7951 anonymous locus 0_3458_0...	50	0.069
gb FJ070709.1	Pinus taeda isolate 7942 anonymous locus 0_3458_0...	50	0.069
gb FJ070708.1	Pinus taeda isolate 7953 anonymous locus 0_3458_0...	50	0.069
gb FJ070707.1	Pinus taeda isolate 7937 anonymous locus 0_3458_0...	50	0.069
gb FJ070706.1	Pinus taeda isolate 7946 anonymous locus 0_3458_0...	50	0.069
gb FJ070705.1	Pinus taeda isolate 7945 anonymous locus 0_3458_0...	50	0.069
gb FJ070703.1	Pinus taeda isolate 7939 anonymous locus 0_3458_0...	50	0.069
ref NM_001137528.1	Zea mays hypothetical protein LOC100192105 (...)	50	0.069
gb DQ244260.1	Zea mays clone 3973 mRNA sequence	50	0.069
tpe BN000615.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	50	0.069
dbj AP004731.3	Oryza sativa Japonica Group genomic DNA, chromos...	50	0.069
dbj AB007645.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	50	0.069
emb Y10465.1	S.oleracea mRNA for peroxidase, clone PC44	50	0.069
gb CP000102.1	Methanosphaera stadtmanae DSM 3091, complete genome	50	0.069
emb FP012230.5	Pig DNA sequence from clone CH242-162F1 on chrom...	48	0.27
gb EZ275595.1	TSA: Artemisia annua strain Madagascar Contig1982...	48	0.27
gb EZ286664.1	TSA: Artemisia annua strain Madagascar Contig1305...	48	0.27
gb EZ342046.1	TSA: Artemisia annua strain Uganda Contig9262, mR...	48	0.27
gb EZ321242.1	TSA: Artemisia annua strain Madagascar Contig7788...	48	0.27
gb EZ318330.1	TSA: Artemisia annua strain Madagascar Contig4876...	48	0.27
gb EZ247069.1	TSA: Artemisia annua strain Artemis Contig13739, ...	48	0.27
gb EZ258457.1	TSA: Artemisia annua strain Madagascar Contig1560...	48	0.27
gb EZ396283.1	TSA: Artemisia annua strain Uganda Contig12778, m...	48	0.27
gb EZ220993.1	TSA: Artemisia annua Contig18004	48	0.27
gb EZ366681.1	TSA: Artemisia annua strain Uganda Contig132, mRN...	48	0.27
gb EZ196247.1	TSA: Artemisia annua strain Artemis Contig9804, m...	48	0.27
gb EZ355157.1	TSA: Artemisia annua strain Uganda Contig2318, mR...	48	0.27
gb EZ173232.1	TSA: Artemisia annua strain Artemis Contig32638, ...	48	0.27
gb BT102799.1	Picea glauca clone GQ02016_E21 mRNA sequence	48	0.27
gb BT101612.1	Picea glauca clone GQ01308_P23 mRNA sequence	48	0.27
gb AC212861.3	Pongo abelii BAC clone CH276-236D6 from chromosom...	48	0.27
ref XM_002451803.1	Sorghum bicolor hypothetical protein, mRNA	48	0.27
gb AC235800.1	Solanum lycopersicum chromosome 3 clone C03HBa013...	48	0.27
ref XM_002285687.1	PREDICTED: Vitis vinifera hypothetical prote...	48	0.27
ref XM_002269022.1	PREDICTED: Vitis vinifera hypothetical prote...	48	0.27
dbj AK323976.1	Solanum lycopersicum cDNA, clone: LEFL1068DD08, ...	48	0.27
ref XM_002320381.1	Populus trichocarpa predicted protein, mRNA	48	0.27

gb CP001098.1	Halothermothrix orenii H 168, complete genome	48	0.27
gb EF677600.1	Picea sitchensis clone WS02771_I11 unknown mRNA	48	0.27
gb FJ050773.1	Pinus taeda isolate 4643 anonymous locus 0_13032_...	48	0.27
gb FJ050771.1	Pinus taeda isolate 4657 anonymous locus 0_13032_...	48	0.27
gb FJ050770.1	Pinus taeda isolate 4649 anonymous locus 0_13032_...	48	0.27
gb FJ050769.1	Pinus taeda isolate 4648 anonymous locus 0_13032_...	48	0.27
gb FJ050768.1	Pinus taeda isolate 4659 anonymous locus 0_13032_...	48	0.27
gb FJ050767.1	Pinus taeda isolate 4658 anonymous locus 0_13032_...	48	0.27
gb FJ050766.1	Pinus taeda isolate 4644 anonymous locus 0_13032_...	48	0.27
gb FJ050765.1	Pinus taeda isolate 4645 anonymous locus 0_13032_...	48	0.27
gb FJ050763.1	Pinus taeda isolate 4660 anonymous locus 0_13032_...	48	0.27
gb FJ050762.1	Pinus taeda isolate 4647 anonymous locus 0_13032_...	48	0.27
gb FJ050761.1	Pinus taeda isolate 4654 anonymous locus 0_13032_...	48	0.27
gb FJ050760.1	Pinus taeda isolate 4646 anonymous locus 0_13032_...	48	0.27
gb FJ050759.1	Pinus taeda isolate 4656 anonymous locus 0_13032_...	48	0.27
gb FJ050756.1	Pinus taeda isolate 4652 anonymous locus 0_13032_...	48	0.27
gb EF083074.1	Picea sitchensis clone WS02728_C07 unknown mRNA	48	0.27
gb EU024896.1	Uncultured bacterium clone tgutfos2_Contig107 gen...	48	0.27
emb BX548174.1	Prochlorococcus marinus MED4 complete genome	48	0.27
gb CP000647.1	Klebsiella pneumoniae subsp. pneumoniae MGH 78578...	48	0.27
emb AM454579.2	Vitis vinifera contig VV78X062755.15, whole geno...	48	0.27
emb AM428729.2	Vitis vinifera contig VV78X273545.5, whole genom...	48	0.27
emb AM462968.1	Vitis vinifera, whole genome shotgun sequence, c...	48	0.27
emb AM453059.1	Vitis vinifera, whole genome shotgun sequence, c...	48	0.27
emb AM481723.1	Vitis vinifera contig VV78X090480.3, whole genom...	48	0.27
dbj AP006865.1	Lotus japonicus genomic DNA, chromosome 2, clone...	48	0.27
dbj AB049589.1	Avicennia marina PER mRNA for secretory peroxida...	48	0.27
emb BX828399.1	Arabidopsis thaliana Full-length cDNA Complete s...	48	0.27
emb BX832751.1	Arabidopsis thaliana Full-length cDNA Complete s...	48	0.27
dbj AB010692.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	48	0.27
emb Y10467.1	S. oleracea mRNA for peroxidase, clone PC23	48	0.27
ref XM_670091.1	Plasmodium berghei strain ANKA hypothetical pro...	48	0.27
gb AF109124.1	AF109124 Ipomoea batatas anionic peroxidase swpa2 ...	48	0.27
gb EZ295716.1	TSA: Artemisia annua strain Madagascar Contig1601...	46	1.1
gb EZ256521.1	TSA: Artemisia annua strain Artemis Contig23191, ...	46	1.1
gb EZ360402.1	TSA: Artemisia annua strain Uganda Contig7563, mR...	46	1.1
gb EZ150610.1	TSA: Artemisia annua strain Artemis Contig10016, ...	46	1.1
gb AC239433.3	Solanum lycopersicum strain Heinz 1706 chromosome...	46	1.1
ref NW_003037936.1	Schistosoma mansoni genome sequence supercon...	46	1.1
gb BT095984.1	Soybean clone JCVI-FLGm-20M19 unknown mRNA	46	1.1
gb BT093602.1	Soybean clone JCVI-FLGm-17D17 unknown mRNA	46	1.1
gb AC237089.1	Oryza granulata clone OG_ABa0096023, complete seq...	46	1.1
ref XM_002448761.1	Sorghum bicolor hypothetical protein, mRNA	46	1.1
emb FN357570.1	Schistosoma mansoni genome sequence supercontig ...	46	1.1
emb FN357441.1	Schistosoma mansoni genome sequence supercontig ...	46	1.1
gb BT086529.1	Zea mays full-length cDNA clone ZM_BFc0177005 mRN...	46	1.1
gb EZ053600.1	TSA: Zea mays contig54722, mRNA sequence	46	1.1
emb AL844509.2	Plasmodium falciparum 3D7 chromosome 13	46	1.1
gb AC235371.1	Glycine max strain Williams 82 clone GM_WBb0104B0...	46	1.1

gb AC235196.1	Glycine max strain Williams 82 clone GM_WBb0014G1...	46	1.1
gb AC235187.1	Glycine max strain Williams 82 clone GM_WBb0010C0...	46	1.1
gb AC235182.1	Glycine max strain Williams 82 clone GM_WBb0008C1...	46	1.1
ref XM_002319931.1	Populus trichocarpa predicted protein, mRNA	46	1.1
ref NM_001158468.1	Zea mays peroxidase 52 (LOC100285577), mRNA ...	46	1.1
gb EU954765.1	Zea mays clone 1482328 mRNA sequence	46	1.1
gb EU951047.1	Zea mays clone 687198 mRNA sequence	46	1.1
gb FJ088527.1	Pinus taeda isolate 6658 anonymous locus 2_10243_...	46	1.1
gb FJ088526.1	Pinus taeda isolate 6661 anonymous locus 2_10243_...	46	1.1
gb FJ088525.1	Pinus taeda isolate 6650 anonymous locus 2_10243_...	46	1.1
gb FJ088524.1	Pinus taeda isolate 6653 anonymous locus 2_10243_...	46	1.1
gb FJ088523.1	Pinus taeda isolate 6663 anonymous locus 2_10243_...	46	1.1
gb FJ088522.1	Pinus taeda isolate 6662 anonymous locus 2_10243_...	46	1.1
gb FJ088521.1	Pinus taeda isolate 6654 anonymous locus 2_10243_...	46	1.1
gb FJ088520.1	Pinus taeda isolate 6655 anonymous locus 2_10243_...	46	1.1
gb FJ088519.1	Pinus taeda isolate 6657 anonymous locus 2_10243_...	46	1.1
gb FJ088518.1	Pinus taeda isolate 6664 anonymous locus 2_10243_...	46	1.1
gb FJ088517.1	Pinus taeda isolate 6651 anonymous locus 2_10243_...	46	1.1
gb FJ088516.1	Pinus taeda isolate 6649 anonymous locus 2_10243_...	46	1.1
gb FJ088515.1	Pinus taeda isolate 6666 anonymous locus 2_10243_...	46	1.1
gb FJ088514.1	Pinus taeda isolate 6660 anonymous locus 2_10243_...	46	1.1
gb FJ088513.1	Pinus taeda isolate 6665 anonymous locus 2_10243_...	46	1.1
gb FJ088512.1	Pinus taeda isolate 6656 anonymous locus 2_10243_...	46	1.1
gb FJ088511.1	Pinus taeda isolate 4039 anonymous locus 2_10243_...	46	1.1
gb FJ088510.1	Pinus taeda isolate 4033 anonymous locus 2_10243_...	46	1.1
gb FJ088509.1	Pinus taeda isolate 4024 anonymous locus 2_10243_...	46	1.1
gb FJ088508.1	Pinus taeda isolate 4026 anonymous locus 2_10243_...	46	1.1
gb FJ088507.1	Pinus taeda isolate 4025 anonymous locus 2_10243_...	46	1.1
gb FJ088506.1	Pinus taeda isolate 4031 anonymous locus 2_10243_...	46	1.1
gb FJ088505.1	Pinus taeda isolate 4032 anonymous locus 2_10243_...	46	1.1
gb FJ088504.1	Pinus taeda isolate 4037 anonymous locus 2_10243_...	46	1.1
gb FJ088503.1	Pinus taeda isolate 4022 anonymous locus 2_10243_...	46	1.1
gb FJ088502.1	Pinus taeda isolate 4028 anonymous locus 2_10243_...	46	1.1
gb FJ088501.1	Pinus taeda isolate 4034 anonymous locus 2_10243_...	46	1.1
gb FJ088500.1	Pinus taeda isolate 4038 anonymous locus 2_10243_...	46	1.1
gb FJ088499.1	Pinus taeda isolate 4030 anonymous locus 2_10243_...	46	1.1
gb FJ088498.1	Pinus taeda isolate 4035 anonymous locus 2_10243_...	46	1.1
gb FJ088497.1	Pinus taeda isolate 4036 anonymous locus 2_10243_...	46	1.1
gb FJ088496.1	Pinus taeda isolate 4029 anonymous locus 2_10243_...	46	1.1
gb FJ088495.1	Pinus taeda isolate 4027 anonymous locus 2_10243_...	46	1.1
gb FJ088494.1	Pinus taeda isolate 4023 anonymous locus 2_10243_...	46	1.1
gb AC189631.2	Brassica rapa subsp. pekinensis clone KBrS003K07,...	46	1.1
dbj AP010414.1	Lotus japonicus genomic DNA, chromosome 6, clone...	46	1.1
dbj AP009714.1	Lotus japonicus genomic DNA, clone: Ljt08001, TM...	46	1.1
gb CP001056.1	Clostridium botulinum B str. Eklund 17B, complete...	46	1.1
ref XM_001751456.1	Physcomitrella patens subsp. patens predicte...	46	1.1
gb EF087739.1	Picea sitchensis clone WS02740_P19 unknown mRNA	46	1.1
gb AC213540.1	Populus trichocarpa clone POP053-A08, complete se...	46	1.1
gb EU060241.1	Uncultured bacterium clone LMOABA27ZD09RM1 genomi...	46	1.1

gb EF645823.1	Manihot esculenta cultivar MTAI8 cationic peroxid...	46	1.1
emb AM489166.2	Vitis vinifera contig VV78X028632.7, whole genom...	46	1.1
emb AM444565.2	Vitis vinifera contig VV78X153928.11, whole geno...	46	1.1
emb AM436965.2	Vitis vinifera contig VV78X063704.11, whole geno...	46	1.1
ref NM_117724.3	Arabidopsis thaliana peroxidase 40 (PER40) (P40...	46	1.1
emb BX293980.2	Mycoplasma mycoides subsp. mycoides SC str. PG1,...	46	1.1
ref NM_001097269.1	Xenopus (Silurana) tropicalis hypothetical p...	46	1.1
gb EF055261.1	Sesbania rostrata peroxidase 1 (prx1) mRNA, compl...	46	1.1
ref XM_623898.2	PREDICTED: Apis mellifera similar to Muscle pro...	46	1.1
ref NM_120616.2	Arabidopsis thaliana peroxidase, putative (AT5G...	46	1.1
gb BT017949.1	Zea mays clone ELO1N0522B07.c mRNA sequence	46	1.1
gb BT013033.1	Lycopersicon esculentum clone 114281R, mRNA sequence	46	1.1
gb BT011747.1	Arabidopsis thaliana At4g16270 gene, complete cds	46	1.1
gb AY065270.1	Arabidopsis thaliana putative peroxidase (At5g053...	46	1.1
emb AJ809342.1	Picea abies mRNA for peroxidase (px7 gene)	46	1.1
emb AJ809341.1	Picea abies mRNA for peroxidase (px6 gene)	46	1.1
gb AC084740.5	Homo sapiens BAC clone RP11-423E20 from 4, comple...	46	1.1
gb AC099520.2	Homo sapiens chromosome 5 clone RP11-6N13, comple...	46	1.1
gb AC012602.4	Homo sapiens chromosome 5 clone CTC-328N13, compl...	46	1.1
emb BX005227.12	Zebrafish DNA sequence from clone CH211-286C23 ...	46	1.1
dbj AK175982.1	Arabidopsis thaliana mRNA, complete cds, clone: ...	46	1.1
dbj AK175661.1	Arabidopsis thaliana mRNA, complete cds, clone: ...	46	1.1
emb BX826801.1	Arabidopsis thaliana Full-length cDNA Complete s...	46	1.1
emb BX537286.4	Zebrafish DNA sequence from clone DKEY-28J4 in l...	46	1.1
dbj AP006135.1	Lotus japonicus genomic DNA, chromosome 1, clone...	46	1.1
gb AC008970.4	AC008970 Homo sapiens chromosome 5 clone CTD-2374C...	46	1.1
emb AL161543.2	Arabidopsis thaliana DNA chromosome 4, contig fr...	46	1.1
emb AL132978.1	Arabidopsis thaliana DNA chromosome 3, BAC clone...	46	1.1
emb Z97340.2	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA ...	46	1.1
emb Z82992.1	A. thaliana FCA gene encoding FCA alpha, beta, gamm...	46	1.1
gb AC166091.3	Glycine max clone gmw1-11j16, complete sequence	46	1.1
gb AY108407.1	Zea mays PC0110242 mRNA sequence	46	1.1
emb AL157764.12	Human DNA sequence from clone RP11-562E17 on ch...	46	1.1
gb AF145349.1	AF145349 Glycine max peroxidase (Prx3) mRNA, parti...	46	1.1
gb AF078691.1	AF078691 Manihot esculenta peroxidase gene, partia...	46	1.1
gb AF067188.1	AF067188 Beta vulgaris cell wall peroxidase mRNA, ...	46	1.1
gb L36231.1	SSNPX12A Stylosanthes humilis peroxidase (px12) mRNA...	46	1.1
gb L36110.1	SSNPEROXIA Stylosanthes humilis peroxidase mRNA	46	1.1
emb FN554766.1	Escherichia coli 042 complete genome	44	4.3
gb EZ396827.1	TSA: Artemisia annua strain Uganda Contig13322, m...	44	4.3
gb AC239575.2	Solanum lycopersicum strain Heinz 1706 clone hba-...	44	4.3
ref NG_016144.1	Homo sapiens inositol 1,4,5-triphosphate recept...	44	4.3
gb BT106566.1	Picea glauca clone GQ03005_B15 mRNA sequence	44	4.3
gb FJ415216.1	Gossypium hirsutum clone Ghpox5 class III peroxid...	44	4.3
emb CU633361.7	Pig DNA sequence from clone CH242-1G8 on chromos...	44	4.3
gb AE014187.2	Plasmodium falciparum 3D7 chromosome 14, complete...	44	4.3
gb DQ676955.1	Ipomoea batatas anionic peroxidase (swpa4) gene, ...	44	4.3
emb FP099688.1	Phyllostachys edulis cDNA clone: bphylf045i10, f...	44	4.3
emb FP094559.1	Phyllostachys edulis cDNA clone: bphylf061m22, f...	44	4.3

emb FP093329.1	Phyllostachys edulis cDNA clone: bphyst031i16, f...	44	4.3
emb FP092972.1	Phyllostachys edulis cDNA clone: bphylf025d09, f...	44	4.3
emb FP091819.1	Phyllostachys edulis cDNA clone: bphyem202n22, f...	44	4.3
emb FP101172.1	Phyllostachys edulis cDNA clone: bphyem105e15, f...	44	4.3
ref XM_002442921.1	Sorghum bicolor hypothetical protein, mRNA	44	4.3
ref XM_002455522.1	Sorghum bicolor hypothetical protein, mRNA	44	4.3
ref XM_002455521.1	Sorghum bicolor hypothetical protein, mRNA	44	4.3
ref XM_002432395.1	Pediculus humanus corporis conserved hypothe...	44	4.3
gb EU725468.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	4.3
gb EU725467.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	4.3
gb EU725466.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	4.3
gb EU725465.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	4.3
gb EU725464.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	4.3
gb EU725463.1	Triticum aestivum class III peroxidase (Prx109-A)...	44	4.3
gb AC216032.2	Oryza minuta clone OM_Ba0196N15, complete sequence	44	4.3
gb EZ063624.1	TSA: Zea mays contig64746, mRNA sequence	44	4.3
emb AL844507.2	Plasmodium falciparum 3D7 chromosome 8	44	4.3
dbj AK329676.1	Solanum lycopersicum cDNA, clone: LEFL3153D08, H...	44	4.3
gb AC235246.1	Glycine max strain Williams 82 clone GM_WBb0033G1...	44	4.3
gb AC235231.1	Glycine max strain Williams 82 clone GM_WBb0026L1...	44	4.3
gb AC235115.1	Glycine max strain Williams 82 clone GM_WBa0021N1...	44	4.3
gb AE013600.1	Mus musculus piebald deletion region complete seq...	44	4.3
ref XM_002338588.1	Populus trichocarpa predicted protein, mRNA	44	4.3
ref XM_002336305.1	Populus trichocarpa predicted protein, mRNA	44	4.3
ref XM_002303984.1	Populus trichocarpa predicted protein, mRNA	44	4.3
gb BT061140.1	Zea mays full-length cDNA clone ZM_BFb0114015 mRN...	44	4.3
emb CU928163.2	Escherichia coli UMN026 chromosome, complete genome	44	4.3
emb CU928164.2	Escherichia coli IAI39 chromosome, complete genome	44	4.3
dbj AK245281.1	Glycine max cDNA, clone: GMFL01-25-021	44	4.3
gb EU960147.1	Zea mays clone 222156 mRNA sequence	44	4.3
gb EU945238.1	Zea mays clone 245264 mRNA sequence	44	4.3
gb AC232892.1	Oryza officinalis clone 00_Ba0082D20, complete s...	44	4.3
gb FJ078274.1	Pinus taeda isolate 5928 anonymous locus 0_6659_0...	44	4.3
gb FJ078266.1	Pinus taeda isolate 5925 anonymous locus 0_6659_0...	44	4.3
gb FJ078265.1	Pinus taeda isolate 5919 anonymous locus 0_6659_0...	44	4.3
gb FJ078264.1	Pinus taeda isolate 5914 anonymous locus 0_6659_0...	44	4.3
gb FJ078263.1	Pinus taeda isolate 5916 anonymous locus 0_6659_0...	44	4.3
gb FJ078262.1	Pinus taeda isolate 5915 anonymous locus 0_6659_0...	44	4.3
gb FJ078261.1	Pinus taeda isolate 5922 anonymous locus 0_6659_0...	44	4.3
gb BT038706.1	Zea mays full-length cDNA clone ZM_BFb0310H17 mRN...	44	4.3
gb BT037971.1	Zea mays full-length cDNA clone ZM_BFb0205C16 mRN...	44	4.3
ref NM_001143045.1	Zea mays hypothetical protein LOC100216632 (...)	44	4.3
ref NM_001137329.1	Zea mays hypothetical protein LOC100191905 (...)	44	4.3
gb EU795178.1	Uncultured bacterium HF0010_09016 genomic sequence	44	4.3
gb CP000970.1	Escherichia coli SMS-3-5, complete genome	44	4.3
emb CU570896.5	Zebrafish DNA sequence from clone DKEY-194E13 in...	44	4.3
gb EF444530.1	Oryza sativa Japonica Group putative peroxidase m...	44	4.3
gb AC216704.1	Solanum lycopersicum chromosome 2 clone C02HBa023...	44	4.3
emb CU570678.3	M.truncatula DNA sequence from clone MTH2-16J21 ...	44	4.3

gb AC215650.1	Populus trichocarpa clone POP108-K22, complete se...	44	4.3
gb AC215390.1	Solanum lycopersicum chromosome 2 clone C02HBa012...	44	4.3
gb AC210491.1	Oryza glaberrima clone OG_BBa0088K23, complete se...	44	4.3
ref XM_001553571.1	Botryotinia fuckeliana B05.10 60S ribosomal ...	44	4.3
gb EF533695.1	Glycine max clone BAC GM_WBb098N15, complete sequ...	44	4.3
emb AM483376.2	Vitis vinifera contig VV78X083975.15, whole geno...	44	4.3
emb AM466347.2	Vitis vinifera contig VV78X176098.3, whole genom...	44	4.3
emb AM464800.2	Vitis vinifera contig VV78X220659.11, whole geno...	44	4.3
emb AM445395.2	Vitis vinifera contig VV78X136138.6, whole genom...	44	4.3
emb AM434275.2	Vitis vinifera contig VV78X203901.6, whole genom...	44	4.3
emb CT025903.11	Zebrafish DNA sequence from clone DKEY-66H5 in ...	44	4.3
emb AM432525.2	Vitis vinifera contig VV78X143782.10, whole geno...	44	4.3
emb AM451582.2	Vitis vinifera contig VV78X210575.8, whole genom...	44	4.3
ref XM_001446891.1	Paramecium tetraurelia hypothetical protein ...	44	4.3
ref XM_001428564.1	Paramecium tetraurelia hypothetical protein ...	44	4.3
ref NM_129711.3	Arabidopsis thaliana electron carrier/ heme bin...	44	4.3
ref NM_126037.4	Arabidopsis thaliana peroxidase 72 (PER72) (P72...	44	4.3
gb EF421197.1	Nelumbo nucifera cationic peroxidase (CP) mRNA, c...	44	4.3
emb AM463654.1	Vitis vinifera contig VV78X012147.8, whole genom...	44	4.3
emb AM464677.1	Vitis vinifera contig VV78X194278.8, whole genom...	44	4.3
emb AM475805.1	Vitis vinifera contig VV78X097027.7, whole genom...	44	4.3
gb AE014298.4	Drosophila melanogaster chromosome X, complete se...	44	4.3
gb CP000551.1	Prochlorococcus marinus str. AS9601, complete genome	44	4.3
gb AC120193.5	Homo sapiens chromosome 8, clone RP11-10H17, comp...	44	4.3
gb AC185364.2	Populus trichocarpa clone Pop1-63B23, complete se...	44	4.3
emb CT830771.1	Oryza sativa (indica cultivar-group) cDNA clone:...	44	4.3
emb CT836342.1	Oryza sativa (indica cultivar-group) cDNA clone:...	44	4.3
emb CT828052.1	Oryza sativa (indica cultivar-group) cDNA clone:...	44	4.3
dbj AK243473.1	Oryza sativa Japonica Group cDNA, clone: J100072...	44	4.3
ref NM_001071707.1	Oryza sativa (japonica cultivar-group) Os10g...	44	4.3
ref NM_001071706.1	Oryza sativa (japonica cultivar-group) Os10g...	44	4.3
ref NM_001061107.1	Oryza sativa (japonica cultivar-group) Os05g...	44	4.3
ref NM_001055328.1	Oryza sativa (japonica cultivar-group) Os03g...	44	4.3
ref NM_001052935.1	Oryza sativa (japonica cultivar-group) Os02g...	44	4.3
ref NM_001049442.1	Oryza sativa (japonica cultivar-group) Os01g...	44	4.3
emb AM293547.1	Picea abies mRNA for properoxidase (px17 gene), ...	44	4.3
tpe BN000657.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
tpe BN000656.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
tpe BN000598.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
tpe BN000562.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
tpe BN000559.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
tpe BN000544.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
tpe BN000535.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
dbj AK227717.1	Arabidopsis thaliana mRNA for peroxidase, comple...	44	4.3
gb AY206411.1	Ipomoea batatas anionic peroxidase swpa6 mRNA, co...	44	4.3
gb AY206409.1	Ipomoea batatas anionic peroxidase swpa4 mRNA, co...	44	4.3
gb AC102440.12	Mus musculus chromosome 1, clone RP24-146C18, co...	44	4.3
gb AC087552.3	Oryza sativa Japonica Group chromosome 5 clone PO...	44	4.3
gb AE017263.1	Mesoplasma florum L1 complete genome	44	4.3

gb	AC123834.4	Mus musculus BAC clone RP24-132N9 from chromosome...	44	4.3
gb	AC133523.3	Mus musculus BAC clone RP23-34E20 from 19, comple...	44	4.3
gb	AC126691.3	Mus musculus BAC clone RP23-221H11 from 14, compl...	44	4.3
gb	AC069248.4	Homo sapiens chromosome 3 clone RP11-6I21 map 3p,...	44	4.3
gb	AC113010.10	Mus musculus chromosome 18, clone RP23-172F6, co...	44	4.3
gb	AC155955.2	Xenopus (Silurana) tropicalis clone CH216-151P9, ...	44	4.3
dbj	AP007151.1	Aspergillus oryzae RIB40 DNA, SC005	44	4.3
gb	BT008727.1	Arabidopsis thaliana At2g41480 gene, complete cds	44	4.3
gb	BT008314.1	Arabidopsis thaliana At5g66390 gene, complete cds	44	4.3
emb	BX546477.9	Zebrafish DNA sequence from clone DKEYP-79C5 in ...	44	4.3
emb	BX842700.35	Zebrafish DNA sequence from clone DKEY-2P18 in ...	44	4.3
gb	AC161005.4	Pan troglodytes BAC clone CH251-668M6 from chromo...	44	4.3
gb	AC161283.2	Pan troglodytes BAC clone CH251-354N8 from chromo...	44	4.3
dbj	AK081398.1	Mus musculus 16 days embryo head cDNA, RIKEN ful...	44	4.3
gb	AY139994.1	Arabidopsis thaliana putative peroxidase (At2g414...	44	4.3
gb	AC074196.14	Oryza sativa chromosome 10 BAC OSJNBa0040D23 gen...	44	4.3
gb	AC105363.2	Oryza sativa Japonica Group chromosome 3 clone OJ...	44	4.3
gb	AC004625.3	Arabidopsis thaliana chromosome 2 clone T26J13 ma...	44	4.3
gb	AC021006.7	Homo sapiens chromosome 11, clone RP11-124G5, com...	44	4.3
gb	AC093154.2	Homo sapiens chromosome 1 clone RP3-445010, compl...	44	4.3
gb	AF455807.1	AF455807 Nicotiana tomentosiformis anionic peroxid...	44	4.3
gb	AC024958.8	Homo sapiens, clone RP11-561E1, complete sequence	44	4.3
gb	AC092697.6	Oryza sativa chromosome 10 BAC OSJNBb0060I05 geno...	44	4.3
emb	AL160288.21	Human DNA sequence from clone RP11-160P20 on ch...	44	4.3
gb	AC021956.8	Homo sapiens chromosome 11, clone RP11-447I3, com...	44	4.3
emb	AL121584.24	Human DNA sequence from clone RP11-388K2 on chr...	44	4.3
gb	AC158774.6	Mus musculus chromosome 18, clone RP23-427N16, co...	44	4.3
gb	AC156828.8	Medicago truncatula clone mth2-18j19, complete se...	44	4.3
gb	AC142260.6	Mus musculus BAC clone RP24-508M8 from chromosome...	44	4.3
emb	CR937028.1	Zebrafish DNA sequence from clone DKEYP-79C5 in ...	44	4.3
dbj	AP004358.5	Oryza sativa Japonica Group genomic DNA, chromos...	44	4.3
emb	AL935302.7	Zebrafish DNA sequence from clone DKEY-13N1 in l...	44	4.3
emb	BX629350.6	Zebrafish DNA sequence from clone CH211-155E13 i...	44	4.3
emb	BX571960.6	Zebrafish DNA sequence from clone DKEY-165I8 in ...	44	4.3
emb	BX832014.1	Arabidopsis thaliana Full-length cDNA Complete s...	44	4.3
emb	BX831693.1	Arabidopsis thaliana Full-length cDNA Complete s...	44	4.3
dbj	AP005613.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	4.3
emb	BX323818.8	Zebrafish DNA sequence from clone DKEY-48H7 in l...	44	4.3
dbj	BS000099.1	Pan troglodytes chromosome 22 clone:PTB-047E13, ...	44	4.3
dbj	AK108037.1	Oryza sativa Japonica Group cDNA clone:002-137-C...	44	4.3
dbj	AK105708.1	Oryza sativa Japonica Group cDNA clone:001-201-E...	44	4.3
dbj	AK103660.1	Oryza sativa Japonica Group cDNA clone:J033135H0...	44	4.3
dbj	AK099187.1	Oryza sativa Japonica Group cDNA clone:J023107P1...	44	4.3
dbj	AK073847.1	Oryza sativa Japonica Group cDNA clone:J033069F0...	44	4.3
dbj	AK070715.1	Oryza sativa Japonica Group cDNA clone:J023058L0...	44	4.3
dbj	AK060028.1	Oryza sativa Japonica Group cDNA clone:006-303-F...	44	4.3
dbj	AK059977.1	Oryza sativa Japonica Group cDNA clone:006-212-B...	44	4.3
dbj	AP006427.1	Lotus japonicus genomic DNA, chromosome 1, clone...	44	4.3
emb	AJ544516.1	Asparagus officinalis mRNA for peroxidase (prx3 ...	44	4.3

emb AL596024.5	Zebrafish DNA sequence from clone BUSM1-199M19 i...	44	4.3
gb AC093380.6	Homo sapiens BAC clone RP11-329G2 from 2, complet...	44	4.3
gb AC012373.14	AC012373 Drosophila melanogaster, chromosome X, r...	44	4.3
gb AC012098.9	AC012098 Drosophila melanogaster, chromosome X, re...	44	4.3
dbj AP002971.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	4.3
dbj AP002820.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	4.3
dbj AP002482.1	Oryza sativa Japonica Group genomic DNA, chromos...	44	4.3
dbj AB042103.1	Asparagus officinalis AoPOX1 mRNA for peroxidase...	44	4.3
emb AL115668.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb AL114300.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb AL113536.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb AL113375.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb AL112173.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb AL111555.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb AL111377.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb AL111140.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb AL111098.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb AL110651.1	Botrytis cinerea strain T4 cDNA library	44	4.3
dbj AB013389.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	44	4.3
emb AL021684.1	Arabidopsis thaliana DNA chromosome 5, BAC clone...	44	4.3
dbj AB010075.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	44	4.3
emb X98774.1	A. thaliana mRNA for peroxidase ATP6a, EST clone 15...	44	4.3
emb X98320.1	A. thaliana mRNA for peroxidase, prxr8	44	4.3
emb BX908747.25	Zebrafish DNA sequence from clone DKEY-58J15 in...	44	4.3
gb AC157575.1	Mus musculus BAC clone RP23-16D16 from 9, complet...	44	4.3
gb AC155233.2	Mus musculus BAC clone RP24-381F23 from 12, compl...	44	4.3
gb AY923052.1	Homo sapiens PDZ and LIM domain 1 (elfin) (PDLIM1...	44	4.3
gb AC102393.8	Mus musculus chromosome 18, clone RP24-125H9, com...	44	4.3
emb BX649473.8	Zebrafish DNA sequence from clone CH211-65G16 in...	44	4.3
emb BX548017.3	Mouse DNA sequence from clone RP23-335I21 on chr...	44	4.3
emb AL935181.5	Zebrafish DNA sequence from clone CH211-162K9, c...	44	4.3
emb AL807770.17	Mouse DNA sequence from clone RP23-206L14 on ch...	44	4.3
dbj AP005626.2	Homo sapiens genomic DNA, chromosome 8q24, clone...	44	4.3
gb AY108615.1	Zea mays PC0132912 mRNA sequence	44	4.3

>gb|BT093225.1| Soybean clone JCVI-FLGm-17C9 unknown mRNA

Length = 1274

Score = 1039 bits (524), Expect = 0.0

Identities = 539/544 (99%)

Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848

|||||

Sbjct: 639 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 580

Query: 1849 accaacatagaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtggtttgagcaaatta 567
|||||
Sbjct: 1272 acaccctttcaatcaaacacaaacactcgaagtactaagttagtggttcgagcaaatta 1213

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
|||||
Sbjct: 1212 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 1153

Query: 628 gggagtccaatgcacaactttctacaaacttttactaccattcatgtccaacctcttc 687
|||||
Sbjct: 1152 gggagtccaatgcacaactttctacaaacttttactaccattcatgtccaacctcttc 1093

Query: 688 tcctctgtgaaatccacagtgaatctgccatatctaaggagaccgcatgggtgcttct 747
|||||
Sbjct: 1092 tcctctgtgaaatccgacagtgaatctgccatatctaaggagaccgcatgggtgcttct 1033

Query: 748 ctcttcgcttggttcttcacgattgctttgtcaatg 784
|||||
Sbjct: 1032 ctcttcgcttggttcttcacgattgctttgtcaatg 996

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 996 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 937

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 936 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 877

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 876 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 817

Query: 1337 tctgttcagatt 1348
|||||

Sbjct: 811 tacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgttcaat 870

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagaccaacccgggcaccttctcctct 2088
|||||

Sbjct: 871 ggtgggtccaccgactccattgtgcgtggctacagaccaacccgagctccttctcctct 930

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||

Sbjct: 931 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaacgga 990

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt--tgattcagcttgaatattaagg 2206
|||||

Sbjct: 991 gaaatcaggaagaattgtagaaggattaactaattactaattgagctccaatattaagg 1050

Query: 2207 gtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaacatgtttt 2263
|||

Sbjct: 1051 gtctactacacatacgaagcaatttaattgtgtttaataagttgttaaacatgtttt 1110

Query: 2264 gttgtatgttgattcc 2281
|||||

Sbjct: 1111 gttgtatgttgattcc 1128

Score = 412 bits (208), Expect = e-111
Identities = 260/277 (93%), Gaps = 4/277 (1%)
Strand = Plus / Plus

Query: 508 acacccttcaatcaaacacaaacacttgaagtactaagttagtggtttgagcaaatta 567
|||||

Sbjct: 2 acaccctctcaagcaaacacaaacacttgaagtactaagttagtggtttgagcaa--- 58

Query: 568 actatggcttcgttttgttctagattgacaatttggctctgtttgcctcatatgg 627
|||||

Sbjct: 59 -ctatggcttcgttttgttctagattgaccatttggctctgtttgcctcatattg 117

Query: 628 gggagtgccaatgcacaactttctacaaactttactaccattcatgtccaaacctcttc 687
|||||

Sbjct: 118 gggagtgccaatgcacaactttctacaaactttactaccattcgtgtccaaacctcttc 177

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttct 747
||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 178 tccactgtgaaatccacagtgcaatctgccatatcaaaggagaccgcatgggtgcttct 237

Query: 748 ctctctcgcttgttcttccacgattgctttgtcaatg 784
||||| ||| ||||||||||||||||||||||||||||||||
Sbjct: 238 ctctccgcccgttcttccacgattgctttgtcaatg 274

Score = 331 bits (167), Expect = 1e-86
Identities = 185/191 (96%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 274 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 333

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Sbjct: 334 aacccaacaggaactctgctcgtggatcacgaggtcattgacaacattaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgttctcctgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||||||||| ||||||||||||||||||||| |||||||||
Sbjct: 394 gagaaagcatgtccaggagttgtctcctgcgcagatatccttgccatagctgccagagac 453

Query: 1337 tctgttcagat 1347
|||||||||||
Sbjct: 454 tctgttcagat 464

Score = 293 bits (148), Expect = 3e-75
Identities = 163/168 (97%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||||||| ||||||||| ||||||||||||||||||||| |||||||||
Sbjct: 466 cttggaggccctagttggaatgttaaagtggagaagagacgctagaactgctagccaa 525

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||||||||||||||||| ||||||||||||||||||||| |||||||||

Score = 145 bits (73), Expect = 2e-30
Identities = 136/157 (86%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaacctcttc 687
|||||
Sbjct: 64 gggagtgccaatgcacaactttctacaaacttttactcaaaaacttgtcccaactctct 123

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttct 747
|||
Sbjct: 124 accacagtgaaatccacactgcaaactgccatatcaaaggaggcccgaatgggtgcctct 183

Query: 748 ctctctgcttgttcttccacgattgctttgtcaatg 784
||||
Sbjct: 184 atctctgcttgttcttccacgattgctttgtcaatg 220

Score = 123 bits (62), Expect = 6e-24
Identities = 155/186 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 220 ggatgtgatggatcaattctcttagatgacacatcaagctttaccggtgagaagaatgca 279

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaatcagccgtg 1276
|||
Sbjct: 280 aatccaatagaaactccgctcgtggatttgatgtcatcgacaacataaagacagccgta 339

Query: 1277 gaaaagtgtgtccaggagttgttctgctgagatataccttgccatcgctgccagagac 1336
|||||
Sbjct: 340 gagaacgtatgccccggagttgtatcatgtgctgatataccttagcattgctgccgagac 399

Query: 1337 tctgtt 1342
|||||
Sbjct: 400 tctgtt 405

Score = 89.7 bits (45), Expect = 8e-14
Identities = 87/101 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||||| || || ||||| ||||||||| ||||| ||| ||||| |||
Sbjct: 412 cttggaggtccaacctggaatgtaaaacttgaagaagagatgctaaaacggctagtcaa 471

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacct 1578
|| ||||| || ||||| ||||| ||||| |||||
Sbjct: 472 tccgctgctaacaactgccatcccggcaccaacttcaaacct 512

>gb|BT098008.1| Soybean clone JCVI-FLGm-22H8 unknown mRNA
Length = 1324

Score = 174 bits (88), Expect = 2e-39
Identities = 316/392 (80%)
Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
||||| ||||||||| ||||||||| ||| ||||| ||||||||| |||
Sbjct: 678 ggtcatacaattggacaagcaaggtgcacaacctttagagcccgaatctacaacgagagc 619

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
||||||| | | ||||| | | || | | || | | ||||| ||||| |||
Sbjct: 618 aacatagatagctcttttgcccgcacatgagacaatctaggtgtcccgaacctcaggatca 559

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaaactccaaccagctttgacaactactac 1971
||||||| || ||||| ||||| || ||||| || ||||| ||||| |||||
Sbjct: 558 ggggacaacaaccttgaccattgactttgccactcccactttctttgacaaccactac 499

Query: 1972 ttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacgggt 2031
||||||| ||||||||| ||||| || ||||| || ||||| ||||| |||
Sbjct: 498 ttcaagaacctcattcagaagaagggttcatccattccgaccaagaactcttcaatggt 439

Query: 2032 ggttccaccgactccattgtgctggttacagcaccaaccgggcaccttctctctgat 2091
|| ||||| ||||| | || | ||||||||| ||||| | | |||
Sbjct: 438 ggttccactgactccttagtgggtacctacagcaccaaccggcctcctttttcgccgat 379

Sbjct: 915 aaagtgtgtccgggtgtggtttcttgcgctgacattcttgccatcgctgccagagactct 856

Query: 1340 gttcagat 1347

||| ||||

Sbjct: 855 gttgagat 848

Score = 121 bits (61), Expect = 2e-23
Identities = 85/93 (91%)
Strand = Plus / Minus

Query: 692 ctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttctctcc 751

||||||| ||||||| |||| ||||||||| ||||||||| ||||||||| |||||||||

Sbjct: 1130 ctgtgaaacgcacagtggaatcgccatatcaaaggagaccgcatgggtgcttctctcc 1071

Query: 752 ttcgcttgttcttccacgattgctttgtcaatg 784

| || ||||||||| ||||||||| ||||

Sbjct: 1070 tacgtttgttcttccacgattgctttgttaatg 1038

>emb|CU137662.1| Medicago truncatula chromosome 5 clone mth2-15518, COMPLETE SEQUENCE
Length = 111929

Score = 172 bits (87), Expect = 7e-39
Identities = 150/171 (87%)
Strand = Plus / Plus

Query: 1476 agcttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagcc 1535

||||||| ||||||| |||| ||||||||| ||||||||| || ||||| |||||

Sbjct: 97958 agcttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagta 98017

Query: 1536 aatctgctgctaacaatggcatccctgacccacttcaaaccttaaccaactcatctcaa 1595

|||| ||||| ||||||| ||||||| ||||||||| |||| ||||||||| |||||

Sbjct: 98018 aatcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaa 98077

Query: 1596 gatttagcgctcttggactttccaccaaggacttggctgccttgtccggta 1646

| |||| ||||||| ||||||||| ||||||||| ||||| ||||

Sbjct: 98078 ggtttaatgctcttggctttccaccaaggatttggctgcattgtctggta 98128

Score = 157 bits (79), Expect = 4e-34

Identities = 172/203 (84%)
Strand = Plus / Plus

Query: 1152 tgcagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
|||||
Sbjct: 97540 tgcagggatgtgatggttcaattctctcgtatgacacatcaagcttcaccggagagaaaa 97599

Query: 1212 acgcaaaccacaacaggaactctgctcgtggattcgaggttattgacaacattaaatcag 1271
|||
Sbjct: 97600 ctgccaatcccaacaaaaattcggcccgtggattcgaagtgatcgacaaaatcaaatacag 97659

Query: 1272 ccgtggagaaagtgtgtccaggagttgttctcgcgcagatatccttgccatcgctgcca 1331
|
Sbjct: 97660 cagtggagaaagtgtgtccaggatgcagtttcatgctgacatccttaccatcactgcta 97719

Query: 1332 gagactctgttcagattgtaagt 1354
|||||
Sbjct: 97720 gagactctgttgagatcgtaagt 97742

Score = 119 bits (60), Expect = 9e-23
Identities = 288/364 (79%)
Strand = Plus / Plus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacttacaacg 1846
|||||
Sbjct: 98322 taggggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacg 98381

Query: 1847 agaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcag 1906
|
Sbjct: 98382 actccaacatagatacttctttgctcgcacaaggcaatcagggtgcccgaagacatcgg 98441

Query: 1907 ggtcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaact 1966
|
Sbjct: 98442 gttccggggacaataatttggcacccttgatcttgcaacaccaacatcctttgacaacc 98501

Query: 1967 actacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttca 2026
|
Sbjct: 98502 attacttcaagaacctagttgacagtaagggtactcactccgaccaacaactcttta 98561

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
|||||
Sbjct: 421 tggaatgttaaacttgaagaagagatgctagaactgcaagccttctgctgccaataat 480

Query: 1553 ggcacccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggga 1612
|||||
Sbjct: 481 ggcattccagctccaacttctaacttgaaccaactcatctcaagatttagtgccttggc 540

Query: 1613 ctttc 1617
|||||
Sbjct: 541 ctttc 545

Score = 54.0 bits (27), Expect = 0.004
Identities = 33/35 (94%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatc 1191
|||||
Sbjct: 214 ggatgtgatggttcaattctacttggatgacacatc 248

Score = 50.1 bits (25), Expect = 0.069
Identities = 31/33 (93%)
Strand = Plus / Plus

Query: 752 ttcgcttggttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 182 ttcgcttggttcttccacgactgctttgttaatg 214

Score = 50.1 bits (25), Expect = 0.069
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaa 1823
|||||
Sbjct: 577 cacacaatcggacaagcaaggtgcacaaa 605

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 2103 catgatcaagatgggagacattag 2126
|||||
Sbjct: 879 catgatcaagatgggagacattag 902

>gb|BT052838.1| Medicago truncatula clone MTYFH_FI_FJ_FK1G-0-8 unknown mRNA
Length = 773

Score = 111 bits (56), Expect = 2e-20
Identities = 146/176 (82%)
Strand = Plus / Minus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| | ||||| ||| ||||| ||||| |||
Sbjct: 464 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactccc 405

Query: 1223 aacaggaactctgctcgtggattcgagttattgacaacattaatcagccgtggagaaa 1282
|| | ||||| ||| ||||| || ||||| || | ||| |||||
Sbjct: 404 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 345

Query: 1283 gtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagactc 1338
|| || || ||||| || || || ||||| ||||| |||||
Sbjct: 344 gtatgccccggagttgtatcatgtgtgatatccttgccattgctgccacagactc 289

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Minus

Query: 705 agtgcaatctgcatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
||||| ||||| ||||| || || || ||||| ||||| |||||
Sbjct: 549 agtgcaatccgcatatcaaaggaggcacgaattggtgcttctatcctccgcttgttctt 490

Query: 765 ccacgattgctttgtcaatg 784
|||||
Sbjct: 489 ccacgattgctttgtcaatg 470

Score = 79.8 bits (40), Expect = 8e-11
Identities = 133/164 (81%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| ||||||||||||||||| || | ||||||| |||
Sbjct: 278 cttggtggcccaacctggaatgtaaaacttgaagaagagatgccacaactgctagtcaa 219

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||| ||| |||| || |||||| | || ||||| ||||||| ||||| |||||
Sbjct: 218 tctgatgcgaacactgccatcccaagaccaactccaaccttaataactcacctcaatg 159

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtc 1641
|||| | |||| ||||||||||||||||| ||||| |||||
Sbjct: 158 ttaagaatgttggtctttccaccaaggacttagtcgcattgtc 115

Score = 63.9 bits (32), Expect = 5e-06
Identities = 62/72 (86%)
Strand = Plus / Minus

Query: 1788 agtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcctctacaacga 1847
||||| ||||||||||||||||||| ||||||| || ||| || ||||||| |||
Sbjct: 114 agtgctcacacaattggacaagcaaggtgcacaacatttaggtacgaatctacaatga 55

Query: 1848 gaccaacataga 1859
|||||||||||
Sbjct: 54 gaccaacataga 43

>gb|AY311597.1| Gossypium hirsutum class III peroxidase (pod7) mRNA, complete cds
Length = 1282

Score = 105 bits (53), Expect = 1e-18
Identities = 238/297 (80%), Gaps = 2/297 (0%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaacttggcaccacttgatcttcaaactcc 1949
||||| |||||| |||| ||||||||||||||| ||||||| ||||||| | |||||||
Sbjct: 732 ctgccaagaacaacaggctcaggggacaacaacttggcacccttggatcttcaaactcc 791

Score = 54.0 bits (27), Expect = 0.004
Identities = 78/95 (82%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcccgatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||| ||||||||||||||||||| | | || | || |||||||||||||
Sbjct: 983 gatttcgtggccggcatgatcaagatgggagacgtcacgccgttgacgggctccaatgga 1042

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt 2183
| ||||||||||| || ||||||| |||||||||||
Sbjct: 1043 caggtcaggaagaactgcagaagggttaactaatt 1077

>dbj|AB027752.1| Nicotiana tabacum mRNA for peroxidase, complete cds, clone:tpoxC1
Length = 1356

Score = 95.6 bits (48), Expect = 1e-15
Identities = 111/132 (84%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||||| ||||| ||||||| ||||||||||||||||||| ||||||||||||||||||| |||||||||
Sbjct: 719 ctgccaagaagttcagggtcaggggacaacaatttggcaccacttgatcttcaaactcc 778

Query: 1950 aaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctctccactc 2009
| || ||||||||||| | || ||||||||| || |||| | || ||||||||| || |||||||
Sbjct: 779 taacaaattgacaacaattatttcaagaatcttgttgacaaaagggtctcttccactc 838

Query: 2010 tgatcagcaact 2021
||||||| |||||
Sbjct: 839 tgatcaacaact 850

Score = 54.0 bits (27), Expect = 0.004
Identities = 60/71 (84%)
Strand = Plus / Plus

Query: 1232 tctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291
||||||| | ||||| || ||||||||||||||| || ||||| || ||||||||||||||| ||
Sbjct: 333 tctgctagaggatttgaagttattgacaatatcaaatctgctgtggagaaagtgtgcctc 392

Query: 1292 ggagttgtttc 1302
|| |||||
Sbjct: 393 ggtgtgtttc 403

Score = 50.1 bits (25), Expect = 0.069
Identities = 43/49 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||||| ||||| | ||||| ||||| |||||
Sbjct: 210 atgggtgcttctcttcttctgtctattcttccatgattgcttctgtcaatg 258

Score = 46.1 bits (23), Expect = 1.1
Identities = 104/131 (79%)
Strand = Plus / Plus

Query: 1493 tggaaatgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 465 tggaaatgtaaaattggagaagagattctagaactgcaagtcaaagtgtgccaatagt 524

Query: 1553 ggcattcctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggga 1612
||||| ||| | | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 525 ggcattcctcctgctacttctaaccttaatagactcatctcaagtttcagtgtgttggc 584

Query: 1613 ctttccaccaa 1623
||||| |||||
Sbjct: 585 ctttctaccaa 595

>gb|AY837788.2| Catharanthus roseus clone Prx4 putative secretory peroxidase mRNA,
complete cds
Length = 1055

Score = 89.7 bits (45), Expect = 8e-14
Identities = 126/153 (82%)
Strand = Plus / Plus

Query: 1493 tggaaatgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 459 tggaaatgtgaaacttggagaagagatgcaacaactgcaagccaagtgtgctgctaacaat 518

>gb|FJ644943.1| Sesuvium portulacastrum peroxidase 1 (POD1) mRNA, complete cds
Length = 1293

Score = 87.7 bits (44), Expect = 3e-13
Identities = 71/80 (88%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
|||||
Sbjct: 937 atgatcaagatgggtgacatcaaaccttactggttcaatggagaaattaggaagaat 996

Query: 2164 tgtagaaggattaactaatt 2183
||
Sbjct: 997 tgcagaaggattaactaatt 1016

Score = 61.9 bits (31), Expect = 2e-05
Identities = 61/71 (85%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 457 cttggaggaccaacatgggatgtgaaactaggaagaagagatgccagaacagctaaccaa 516

Query: 1538 tctgctgctaa 1548
|||||
Sbjct: 517 gctgctgctaa 527

Score = 54.0 bits (27), Expect = 0.004
Identities = 51/59 (86%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacttacaacga 1847
|||||
Sbjct: 622 ggtggcactcaataggacaagcaaggtgcacaaatctcagggtcacatatacaacga 680

>dbj|AK242814.1| Oryza sativa Japonica Group cDNA, clone: J090061H15, full insert
sequence
Length = 1215

Score = 85.7 bits (43), Expect = 1e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||| ||||||||| | ||||||||| ||| ||||||| |||||
Sbjct: 662 tcacaccattggacaagcagcatgcacaaacttcagagctcacatatacaacgaaaccaa 721

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaagctgccctagaacatcagggtcagg 1913
||| || | | ||||| | | ||||| | ||||||| | | ||||| |||||
Sbjct: 722 catcgacagtggctttgcatgagcaggcaatcaggctgccctcgtagctcaggctcagg 781

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||||||||||||| | ||||||| | ||||||| || | || ||| |||||
Sbjct: 782 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 841

Query: 1974 caagaacctggtcagaagaagggtctcctccactctgatcag 2016
||||||||||| ||||||| ||||| |||||||||
Sbjct: 842 caagaacctgctcgaagaagggtctcctgcactctgatcag 884

>ref|NM_001072100.1| Oryza sativa (japonica cultivar-group) Os11g0112400 (Os11g0112400)
mRNA, complete cds
Length = 975

Score = 85.7 bits (43), Expect = 1e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||| ||||||||| | ||||||||| ||| ||||||| |||||
Sbjct: 588 tcacaccattggacaagcagcatgcacaaacttcagagctcacatatacaacgaaaccaa 647

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaagctgccctagaacatcagggtcagg 1913
||| || | | ||||| | | ||||| | ||||||| | | ||||| |||||
Sbjct: 648 catcgacagtggctttgcatgagcaggcaatcaggctgccctcgtagctcaggctcagg 707

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||||||||||||| | ||||||| | ||||||| || | || ||| |||||
Sbjct: 708 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 767

Query: 1974 caagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 768 caagaacctcgctgcaagaagggctcctgcactctgatcag 810

>tpe|BN000659.1| TPA: TPA_inf: Oryza sativa (japonica cultivar-group) prx130 gene for
class III peroxidase 130 precursor, exons 1-4
Length = 2195

Score = 85.7 bits (43), Expect = 1e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcactctacaacgagaccaa 1853
||||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1808 tcacaccattggacaagcagatgcacaaacttcagagctcacatatacaacgaaaccaa 1867

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaagctgccctagaacatcagggtcagg 1913
||| ||| | ||||| || || ||||| | ||||| ||||| ||||| |||||
Sbjct: 1868 catcgacagtggctttgcatgagcaggcaatcaggctgccctcgtagctcaggctcagg 1927

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactact 1973
||||||| ||||||| || ||||| || ||||| || || || || |||||
Sbjct: 1928 tgacaacaatctggcacctttgatcttcagacccaaccgtgttcgagaacaactacta 1987

Query: 1974 caagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1988 caagaacctcgctgcaagaagggctcctgcactctgatcag 2030

>dbj|AB019228.1| Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCK7
Length = 87090

Score = 85.7 bits (43), Expect = 1e-12
Identities = 52/55 (94%)
Strand = Plus / Minus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaa 787
||||||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 74225 cgc atgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatgtaa 74171

>emb|BX000512.1| Oryza sativa chromosome 11, . BAC OSJNBa0025K19 of library OSJNBa from

chromosome 11 of cultivar Nipponbare of ssp. japonica of
Oryza sativa (rice), complete sequence
Length = 181322

Score = 85.7 bits (43), Expect = 1e-12
Identities = 178/223 (79%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||| ||||||||| | ||||||||| ||| ||||||| |||||
Sbjct: 158955 tcacaccattggacaagcacgatgcacaaacttcagagctcacatatacaacgaaaccaa 158896

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | | ||||| || ||||| | ||||||| | | ||||| |||||
Sbjct: 158895 catcgacagtggctttgcatgagcaggcaatcaggctgccctcgtagctcaggctcagg 158836

Query: 1914 ggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactactactt 1973
||||||||||| ||| ||||||| || ||||| || || ||| |||||
Sbjct: 158835 tgacaacaatctggcaccttggatcttcagacgccaaccgtgttcgagaacaactacta 158776

Query: 1974 caagaacctcgcttcagaagaagggtctctcactctgatcag 2016
||||||| || ||||| ||||| |||||||||
Sbjct: 158775 caagaacctcgctcgaagaagggtctctcactctgatcag 158733

>gb|EF661875.2| Catharanthus roseus putative secretory peroxidase (Prx3) mRNA,
complete cds
Length = 1233

Score = 83.8 bits (42), Expect = 5e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttgcgccccatgatcaagatgggagacattagtcctctcactggc 2139
|||| ||||||| || ||||||||| ||||||||| ||||||||| | |||||
Sbjct: 924 ttctactctgatttgcgccccatgatcaagatgggagatattagtcctttgactggt 983

Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
|| ||||||| | ||||| ||||||| || |||||
Sbjct: 984 tcaaatggagaggttaggaaaaattgtagaggattaa 1021

Score = 46.1 bits (23), Expect = 1.1
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcaca 1821
|||||
Sbjct: 639 cacacaattgggtcaagcaaggtgcaca 665

>ref|NM_125225.1| Arabidopsis thaliana peroxidase, putative (AT5G58390) mRNA,
complete cds
Length = 1220

Score = 79.8 bits (40), Expect = 8e-11
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 229 cgc atgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 280

>dbj|AK117722.1| Arabidopsis thaliana At5g58390 mRNA for putative peroxidase,
complete cds, clone: RAFL17-40-J20
Length = 656

Score = 79.8 bits (40), Expect = 8e-11
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 226 cgc atgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 277

>gb|AY085030.1| Arabidopsis thaliana clone 124846 mRNA, complete sequence
Length = 1220

Score = 79.8 bits (40), Expect = 8e-11
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 229 cgc atgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 280

>ref|XM_002269882.1| PREDICTED: Vitis vinifera hypothetical protein LOC100257005
(LOC100257005), mRNA
Length = 1180

Score = 75.8 bits (38), Expect = 1e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||||| ||||||||| || ||||||||| || || ||||| |||||||||||||
Sbjct: 754 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 813

Query: 1969 tacttcaagaacct 1982
|||| |||||||||
Sbjct: 814 tactacaagaacct 827

Score = 58.0 bits (29), Expect = 3e-04
Identities = 47/53 (88%)
Strand = Plus / Plus

Query: 732 ccgcatggggtccttctctccttcgcttgcttcttccacgattgctttgtcaatg 784
||||||||| ||||||||||| || | ||||||||| |||||||||||||
Sbjct: 225 ccgcatggggcgttctctcctcctcgtctcttcttccatgattgctttgtcaatg 277

>emb|AM447728.2| Vitis vinifera contig VV78X018697.9, whole genome shotgun sequence
Length = 22220

Score = 75.8 bits (38), Expect = 1e-09
Identities = 65/74 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||||| ||||||||| || ||||||||| || || ||||| |||||||||||||
Sbjct: 11004 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 10945

Query: 1969 tacttcaagaacct 1982
|||| |||||||||
Sbjct: 10944 tactacaagaacct 10931

Score = 65.9 bits (33), Expect = 1e-06
Identities = 51/57 (89%)
Strand = Plus / Minus

Query: 732 ccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaat 788
||||||| ||||||||| || | ||||||| |||||||||
Sbjct: 12714 ccgcatgggcgcttctctcctccgtctcttccatgattgctttgtcaatgtaat 12658

>ref|XM_002278960.1| PREDICTED: Vitis vinifera hypothetical protein LOC100257059
(LOC100257059), mRNA
Length = 966

Score = 71.9 bits (36), Expect = 2e-08
Identities = 101/120 (84%), Gaps = 2/120 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagcttt-gacaacta 1967
||||||| |||| | | ||||||| || ||||| || || |
Sbjct: 694 tcaggggacaacaacttggccctctggatcttcaactcctac-agcttttgagaaca 752

Query: 1968 ctacttcaagaacctggtcagaagaagggtctcctcactctgatcagcaactgttcaa 2027
||||| ||||||| | ||||||| || | ||||||| |||||||
Sbjct: 753 ctactacaagaacctgatcaagaagaagggtctcctcactctgatcagcagctgttcaa 812

Score = 67.9 bits (34), Expect = 3e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaac 1854
||||||| ||||||||| ||||| ||||||| ||||| ||||| |||
Sbjct: 580 cacacaattgggcaagcaaggtgcacatccttcagggccgcataataatgagacaac 639

Query: 1855 at 1856
||
Sbjct: 640 at 641

Score = 65.9 bits (33), Expect = 1e-06
Identities = 129/161 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| |||| | |||| | || ||||| | ||||| | | | | |||||
Sbjct: 409 cttggaggccctagctggaacgtaaaacttggcggaagagacgcccgaccgcaagccag 468

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
||||||| |||| | ||||| | | ||||| ||||| ||||| ||||| |||||
Sbjct: 469 gctgctgcaacaacagcatccctcctccaacttcaaactgaaccaactaatctctaga 528

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgcctt 1638
|| | ||||| || | | ||||| |||||
Sbjct: 529 ttccaagctcttggcctctcaaccaggacttggttgcctt 569

Score = 58.0 bits (29), Expect = 3e-04
Identities = 59/69 (85%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||||| ||||| || | | ||||| | | ||||| | | |||||
Sbjct: 889 atgatcaagatgggagatatcagccactcactggatcaaatggagagattaggaagaac 948

Query: 2164 tgtagaagg 2172
|| |||||
Sbjct: 949 tgcagaagg 957

>gb|AY206413.1| Ipomoea batatas anionic peroxidase swpb2 mRNA, complete cds
Length = 1263

Score = 71.9 bits (36), Expect = 2e-08
Identities = 57/64 (89%)
Strand = Plus / Plus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaaga 2161
||||||| |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 989 ccatgatcaagatggccaacatttcgctctcactggctccaaggagaaatcaggaaga 1048

Query: 2162 attg 2165
|||
Sbjct: 1049 attg 1052

>gb|EZ399860.1| TSA: Artemisia annua strain Uganda Contig16355, mRNA sequence
Length = 1170

Score = 69.9 bits (35), Expect = 7e-08
Identities = 56/63 (88%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| |||||||||||| |||||||||| ||||||| || ||||| |||||||||
Sbjct: 518 ctgccaagaacctcagggtcaggagacaacaatttggcaccgctagatctcaaactcc 459

Query: 1950 aac 1952
|||
Sbjct: 458 aac 456

>gb|EZ145065.1| TSA: Artemisia annua strain Artemis Contig4471, mRNA sequence
Length = 1332

Score = 69.9 bits (35), Expect = 7e-08
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| |||||||||||| |||||||||| ||||||| || ||||| |||||||||
Sbjct: 713 ctgccaagaacctcagggtcaggagacaacaatttggcaccgctagatctcaaactcc 772

Query: 1950 aac 1952
|||
Sbjct: 773 aac 775

Score = 58.0 bits (29), Expect = 3e-04
Identities = 44/49 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgcttcttccacgattgctttgtcaatg 784
||||| |||||||||||||| ||| |||||| |||||||||||||||||
Sbjct: 207 atgggcgcttctctccttcgcttgcttccatgattgctttgtcaatg 255

Score = 48.1 bits (24), Expect = 0.27
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgggaaga 1513
||||||| ||||||||||||| ||||| |||||
Sbjct: 447 cttggaggacctacatggaatgtgaaactgggaaga 482

>gb|EZ141680.1| TSA: Artemisia annua strain Artemis Contig1086, mRNA sequence
Length = 456

Score = 69.9 bits (35), Expect = 7e-08
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||||||||| ||||||||| ||||||| || ||||| |||||||
Sbjct: 224 ctgccaagaacctcagggtcagggagacaacaatttggcaccgctagatctcaaactcc 283

Query: 1950 aac 1952
|||
Sbjct: 284 aac 286

>ref|XM_002489001.1| Sorghum bicolor hypothetical protein (SORBIDRAFT_0246s002010) mRNA,
complete cds
Length = 1045

Score = 69.9 bits (35), Expect = 7e-08
Identities = 200/255 (78%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||| ||||| || || ||||| | ||||| ||||||||| || |||||||||
Sbjct: 653 ggtgctcacacataggccaagcacgctgcaccaacttcagagaccacatctacaacgac 712

Query: 1849 accaacatagaaacgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
||||| | || || ||||||||||| ||||| | | || ||||| || |||||
Sbjct: 713 accaacgtcgacggagcctttgaaggacaaggcaatcaggttgctcctagcacctcagga 772

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

|| |||||
Sbjct: 15564 tgcagaagg 15572

>gb|GU230149.1| Ipomoea batatas anionic peroxidase mRNA, complete cds
Length = 1125

Score = 67.9 bits (34), Expect = 3e-07
Identities = 46/50 (92%)
Strand = Plus / Plus

Query: 730 acccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgt 779
|||||
Sbjct: 289 acccgcatgggtgcttccctcattcgttgttcttccatgactgctttgt 338

>ref|XM_002268223.1| PREDICTED: Vitis vinifera hypothetical protein LOC100263665
(LOC100263665), mRNA
Length = 1002

Score = 67.9 bits (34), Expect = 3e-07
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttc 1827
|||||
Sbjct: 516 tcacacaattggacaagcaaggtgcacaaacttc 549

>gb|FJ099755.1| Pinus taeda isolate 1286 anonymous locus 2_6350_01 genomic sequence
Length = 410

Score = 67.9 bits (34), Expect = 3e-07
Identities = 61/70 (87%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacg 1846
||||| ||| ||||| ||||| ||||| | |||||
Sbjct: 308 tagtgctcatacaattggccaagcacggtgcaccacattcagagcccgcattctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>emb|CU231251.1| Populus EST from mild drought-stressed leaves
Length = 584

Score = 67.9 bits (34), Expect = 3e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| || ||||||||||||||||| ||| ||||| ||||| ||||| |||||||||
Sbjct: 138 cacacaatcgggcaagcaaggtgcacaagctttagagctcgcataatacaatgagaccaac 197

Query: 1855 at 1856
||
Sbjct: 198 at 199

>gb|AY206412.1| Ipomoea batatas anionic peroxidase swpb1 mRNA, complete cds
Length = 1257

Score = 67.9 bits (34), Expect = 3e-07
Identities = 37/38 (97%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaagaattg 2165
||||||||| |||||||||||||||||||||
Sbjct: 1002 cctctcactggtccaatggagaaatcaggaagaattg 1039

Score = 44.1 bits (22), Expect = 4.3
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 1217 aacccaacaggaactctgctcgtgg 1242
||||||||| |||||||||||||
Sbjct: 348 aacccaacagaaactctgctcgtgg 373

>dbj|AK322204.1| Solanum lycopersicum cDNA, clone: LEFL1035AA07, HTC in leaf
Length = 1170

Score = 65.9 bits (33), Expect = 1e-06
Identities = 48/53 (90%)
Strand = Plus / Plus

Query: 2023 ttcaa 2027
|||||
Sbjct: 867 ttcaa 871

>ref|XM_002328955.1| Populus trichocarpa predicted protein, mRNA
Length = 1047

Score = 65.9 bits (33), Expect = 1e-06
Identities = 57/65 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
|||||
Sbjct: 633 cacacaattggacaagcaagatgcacaaactttagggcacgcatatataatgagaccacc 692

Query: 1855 ataga 1859
|||||
Sbjct: 693 ataga 697

Score = 54.0 bits (27), Expect = 0.004
Identities = 66/79 (83%)
Strand = Plus / Plus

Query: 2103 catgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
|||||
Sbjct: 941 catgatcaagatgggagatatcaggcctctcactggatccagaggagagattagaaataa 1000

Query: 2163 ttgtagaaggattaactaa 2181
||| || ||||| |||||
Sbjct: 1001 ttgcaggaggatcaactaa 1019

Score = 44.1 bits (22), Expect = 4.3
Identities = 34/38 (89%)
Strand = Plus / Plus

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactcc 1949
|||||
Sbjct: 750 ggggacaacaacttggcaccacttgattgcaaactcc 787

>ref|XM_002319932.1| Populus trichocarpa predicted protein, mRNA
Length = 1220

Score = 65.9 bits (33), Expect = 1e-06
Identities = 57/65 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| || ||||||||||| |||| ||| ||||| ||||| ||||| |||||||||
Sbjct: 592 cacacaatcgggcaagcaaggtgtacaagctttagagctcgcatatacaatgagaccaac 651

Query: 1855 ataga 1859
|||||
Sbjct: 652 ataga 656

Score = 48.1 bits (24), Expect = 0.27
Identities = 39/44 (88%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgcttcttccacgattgctttgt 779
||||||||||||| ||||||||||| || ||||| |||||
Sbjct: 178 atgggtgcttctcttgttcgcttgcttcttccatgattgctttgt 221

>gb|AC214418.1| Populus trichocarpa clone POP106-D21, complete sequence
Length = 88637

Score = 65.9 bits (33), Expect = 1e-06
Identities = 57/65 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| || ||||||||||| |||| ||| ||||| ||||| ||||| |||||||||
Sbjct: 88236 cacacaatcgggcaagcaaggtgtacaagctttagagctcgcatatacaatgagaccaac 88295

Query: 1855 ataga 1859
|||||
Sbjct: 88296 ataga 88300

Score = 52.0 bits (26), Expect = 0.018
Identities = 41/46 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtca 781
|||||
Sbjct: 86397 atgggtgcttctcttgttcgcttgttcttcatgattgtttgtca 86442

>gb|BT096974.1| Soybean clone JCVI-FLGm-21M8 unknown mRNA
Length = 1201

Score = 63.9 bits (32), Expect = 5e-06
Identities = 44/48 (91%)
Strand = Plus / Plus

Query: 1810 gcaaggtgcacaaacttcagagcccgcactctacaacgagaccaacata 1857
|||||
Sbjct: 639 gcaaggtgcactaccttcagagaccgcactctacaacgacaccaacata 686

>gb|FJ596178.1| Capsicum annuum peroxidase (POD) mRNA, complete cds
Length = 1353

Score = 63.9 bits (32), Expect = 5e-06
Identities = 59/68 (86%)
Strand = Plus / Plus

Query: 1788 agtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcactctacaacga 1847
|||||
Sbjct: 646 agtggtcacacaattggacaagcaaggtgcacatcattcagggcacgtatatacaatga 705

Query: 1848 gaccaaca 1855
|||||
Sbjct: 706 gaccaaca 713

Score = 61.9 bits (31), Expect = 2e-05
Identities = 55/63 (87%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
|||||

Query: 2089 gatttcgccgcccgatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||||||||||||||||| || || | || ||||||| |||||
Sbjct: 888 gatttcgcagccgcccgatgatcaagatgggtgatatcaagcccctcactgggaacaatgga 947

Query: 2149 gaaatcaggaagaa 2162
|| |||||||||
Sbjct: 948 gagatcaggaagaa 961

Score = 44.1 bits (22), Expect = 4.3
Identities = 43/50 (86%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaa 1209
||||||| ||||||| ||||| || ||||| |||||||||||||
Sbjct: 234 tgtgatggatcaattctcttggacgatacatcttccttcaccggagagaa 283

>gb|AC235385.1| Glycine max strain Williams 82 clone GM_WBb0113B18, complete sequence
Length = 137121

Score = 61.9 bits (31), Expect = 2e-05
Identities = 37/39 (94%)
Strand = Plus / Minus

Query: 277 aaattatTTTTCTTTtaatttcttaattaatatacctaa 315
|||| ||||||||||||||| |||||||||||||
Sbjct: 62660 aaataatTTTTCTTTtaatttcttaattaatatacctaa 62622

>gb|GQ258782.1| Brassica rapa peroxidase 52 mRNA, partial cds
Length = 1113

Score = 60.0 bits (30), Expect = 7e-05
Identities = 147/186 (79%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| || ||||| ||||| | ||||||||||||||||| || ||||| | |||||
Sbjct: 172 ggatgcgacggttctattctactagatgacacatcaagctttacgggagaacaaaacgcg 231

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276
||||| || | || ||||||||| || | || | ||||||||| ||||| ||

Sbjct: 232 aacccaaaccgcaattctgctcgtgggtttaatgtgatagacaacattaaaacagcggtt 291

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagac 1336
|| || ||||| || ||||| || || ||||| || ||||| || ||||| || ||||| || |||||

Sbjct: 292 gaagcagcatgtcccgggttgtgtcttgtgctgatatacttagccatcgctagagac 351

Query: 1337 tctggt 1342
|||||

Sbjct: 352 tctggt 357

>gb|FJ099770.1| Pinus taeda isolate 1299 anonymous locus 2_6350_01 genomic sequence
Length = 439

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacg 1846
||||| ||| ||||| ||||| ||||| | ||||| ||||| ||||| |||||

Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcattacaacg 249

Query: 1847 agaccaacat 1856
| |||||

Sbjct: 248 aatccaacat 239

>gb|FJ099768.1| Pinus taeda isolate 1282 anonymous locus 2_6350_01 genomic sequence
Length = 448

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacg 1846
||||| ||| ||||| ||||| ||||| | ||||| ||||| ||||| |||||

Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcattacaacg 249

Query: 1847 agaccaacat 1856
| |||||

Sbjct: 248 aatccaacat 239

>gb|FJ099767.1| Pinus taeda isolate 1292 anonymous locus 2_6350_01 genomic sequence
Length = 439

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | ||||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099766.1| Pinus taeda isolate 1285 anonymous locus 2_6350_01 genomic sequence
Length = 434

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | ||||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099765.1| Pinus taeda isolate 1288 anonymous locus 2_6350_01 genomic sequence
Length = 438

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | ||||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099762.1| Pinus taeda isolate 1298 anonymous locus 2_6350_01 genomic sequence
Length = 357

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||| ||||| ||||| | |||||
Sbjct: 307 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 248

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 247 aatccaacat 238

>gb|FJ099761.1| Pinus taeda isolate 1289 anonymous locus 2_6350_01 genomic sequence
Length = 360

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||| ||||| ||||| | |||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099760.1| Pinus taeda isolate 1297 anonymous locus 2_6350_01 genomic sequence
Length = 357

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||||| ||| ||||||||| ||||||| ||||||||| | |||||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099759.1| Pinus taeda isolate 1283 anonymous locus 2_6350_01 genomic sequence
Length = 357

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||||| ||| ||||||||| ||||||| ||||||||| | |||||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099758.1| Pinus taeda isolate 1287 anonymous locus 2_6350_01 genomic sequence
Length = 449

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||||| ||| ||||||||| ||||||| ||||||||| | |||||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099757.1| Pinus taeda isolate 1291 anonymous locus 2_6350_01 genomic sequence
Length = 358

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 taggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacg 1846
||||||| ||| ||||||||| ||||||| ||||||| | |||||||||||||||||||||
Sbjct: 308 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcattacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|EF433456.1| Ipomoea batatas basic peroxidase swpb5 mRNA, complete cds
Length = 1331

Score = 60.0 bits (30), Expect = 7e-05
Identities = 36/38 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaagaattg 2165
||||||||||| ||| |||||||||||||||||||||
Sbjct: 1038 cctctcactggttcccatggagaaatcaggaagaattg 1075

>gb|AC226196.1| Musa acuminata clone BAC MA4-125A12, complete sequence
Length = 110853

Score = 60.0 bits (30), Expect = 7e-05
Identities = 51/58 (87%)
Strand = Plus / Plus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||| ||||||||| ||| ||||| ||||||||||| || |||||||||||||||||
Sbjct: 32082 cagggctgtgatggatcagttctgctggatgacacgtccagcttcaccggagagaaga 32139

Score = 46.1 bits (23), Expect = 1.1
Identities = 71/87 (81%)
Strand = Plus / Plus

Query: 1960 gacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaa 2019
||||||| ||||||||| ||||| || || ||||||||| || || ||||| || |||||

Sbjct: 32773 gacaacttctacttcaggaacttggtgaagaagaaggcctgctgcactcggaccagcag 32832

Query: 2020 ctgttcaacgggtgggtccaccgactcc 2046

||||||| || || |||||

Sbjct: 32833 ctgttcagtgaggatccaccgactcc 32859

>ref|XM_001754018.1| Physcomitrella patens subsp. patens predicted protein
(PHYPADRAFT_115024) mRNA, complete cds
Length = 1095

Score = 60.0 bits (30), Expect = 7e-05
Identities = 36/38 (94%)
Strand = Plus / Plus

Query: 741 tgcttctctccttcgcttggttcttccacgattgctttg 778

|||| |||| |||||

Sbjct: 273 tgctgctctgcttcgcttggttcttccacgattgctttg 310

>emb|AM449831.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X191828.16,
clone ENTAV 115
Length = 47040

Score = 60.0 bits (30), Expect = 7e-05
Identities = 33/34 (97%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttc 1827

|||||

Sbjct: 34025 tcacacaattggacaagcaaggtgcacaagcttc 33992

>gb|AY206414.1| Ipomoea batatas anionic peroxidase swpb3 mRNA, complete cds
Length = 1290

Score = 60.0 bits (30), Expect = 7e-05
Identities = 63/74 (85%)
Strand = Plus / Plus

Query: 2089 gatttcgcgcccgcgatgatcaagatgggagacattagtcctctcactggetccaatgga 2148

||||||| |||||

Sbjct: 918 gatttcgcagcccgcgatgatcaagatgggtgatatcaagccactcactgggaacaatgga 977

Query: 2149 gaaatcaggaagaa 2162
|| |||||
Sbjct: 978 gagatcaggaagaa 991

Score = 56.0 bits (28), Expect = 0.001
Identities = 46/52 (88%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||| || ||||| | ||||| || |||||
Sbjct: 210 cgc atggggcctctctccttcgcttcttccatgactgctttgtcaatg 261

>gb|AF485265.1| Gossypium hirsutum class III peroxidase (pod3) mRNA, complete cds
Length = 1336

Score = 60.0 bits (30), Expect = 7e-05
Identities = 42/46 (91%)
Strand = Plus / Plus

Query: 737 tgggtgcttctctccttcgcttgttcttccacgattgctttgtcaa 782
||||| ||||| || || |||||
Sbjct: 257 tgggtgcttctctccttcgcttgttcttccatgactgctttgtcaa 302

Score = 52.0 bits (26), Expect = 0.018
Identities = 53/62 (85%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||| ||||| || || ||||| || || ||||| |||||
Sbjct: 979 atgataagatgggagatattaagccactcaccgatcaa atggtgaaatcaggaagaat 1038

Query: 2164 tg 2165
||
Sbjct: 1039 tg 1040

>gb|EZ328614.1| TSA: Artemisia annua strain Madagascar Contig15160, mRNA sequence
Length = 324

Score = 58.0 bits (29), Expect = 3e-04

Identities = 44/49 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||| ||||||||||||||| ||| ||||||| |||||||||||||||
Sbjct: 202 atgggcgcttctctccttcgcttggttgcacttccatgattgctttgtcaatg 250

>gb|EZ256818.1| TSA: Artemisia annua strain Artemis Contig23488, mRNA sequence
Length = 426

Score = 58.0 bits (29), Expect = 3e-04
Identities = 44/49 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||| ||||||||||||||| ||| ||||||| |||||||||||||||
Sbjct: 204 atgggcgcttctctccttcgcttggttgcacttccatgattgctttgtcaatg 252

>gb|EZ397212.1| TSA: Artemisia annua strain Uganda Contig13707, mRNA sequence
Length = 491

Score = 58.0 bits (29), Expect = 3e-04
Identities = 44/49 (89%)
Strand = Plus / Minus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||| ||||||||||||||| ||| ||||||| |||||||||||||||
Sbjct: 167 atgggcgcttctctccttcgcttggttgcacttccatgattgctttgtcaatg 119

>dbj|AK328734.1| Solanum lycopersicum cDNA, clone: LEFL3035G12, HTC in root
Length = 1222

Score = 58.0 bits (29), Expect = 3e-04
Identities = 59/69 (85%)
Strand = Plus / Plus

Query: 1215 caaaccccaacaggaactctgctcgtggattcgaggttattgacaacattaatcagccg 1274
||||||||||||||||| ||||||||||| || || ||||| | ||||||| ||
Sbjct: 354 caaaccccaacaggaactcggtcgtggatttgatgtcattgatgatattaaatctgcac 413

Query: 1275 tggagaaag 1283

|||||
Sbjct: 414 tggagaaag 422

>emb|AJ544515.1| Asparagus officinalis partial mRNA for peroxidase (prx2 gene)
Length = 1041

Score = 58.0 bits (29), Expect = 3e-04
Identities = 53/61 (86%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||
Sbjct: 826 gccatgatcaagatgggagatattagccccctcactgggtctaaaggagagattaggaag 885

Query: 2161 a 2161
|
Sbjct: 886 a 886

>ref|XM_002521820.1| Ricinus communis Lignin-forming anionic peroxidase precursor,
putative, mRNA
Length = 978

Score = 56.0 bits (28), Expect = 0.001
Identities = 49/56 (87%)
Strand = Plus / Plus

Query: 1265 aaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcatatccttgc 1320
|||||
Sbjct: 343 aaatctgcagtgagaaagatatgtcctggagttgtttcctgcgctgatatccttgc 398

>ref|XM_002521805.1| Ricinus communis Lignin-forming anionic peroxidase precursor,
putative, mRNA
Length = 978

Score = 56.0 bits (28), Expect = 0.001
Identities = 49/56 (87%)
Strand = Plus / Plus

Query: 1265 aaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcatatccttgc 1320
|||||
Sbjct: 343 aaatctgcagtgagaaagatatgtcctggagttgtttcctgcgctgatatccttgc 398

>ref|XM_002521804.1| Ricinus communis Peroxidase 30 precursor, putative, mRNA
Length = 891

Score = 56.0 bits (28), Expect = 0.001
Identities = 49/56 (87%)
Strand = Plus / Plus

Query: 1265 aaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcatatccttgc 1320
||||| || |||||||| | ||||| ||||||||||||||||| |||||||||
Sbjct: 343 aaatctgcagtgagagaagatatgtcctggagttgtttcctgcgctgatatccttgc 398

>gb|FJ529216.1| Cucumis sativus 1-aminocyclopropane-1-carboxylate synthase (ACS2) gene,
ACS2-M allele and putative peroxidase gene, complete cds
Length = 52751

Score = 56.0 bits (28), Expect = 0.001
Identities = 34/36 (94%)
Strand = Plus / Minus

Query: 751 cttcgcttgttcttccacgattgctttgtcaatgta 786
||||| ||||||||||||||||||| |||||||
Sbjct: 50350 cttcgcatgttcttccacgattgctttgtaaagta 50315

>ref|XM_002450088.1| Sorghum bicolor hypothetical protein, mRNA
Length = 1265

Score = 56.0 bits (28), Expect = 0.001
Identities = 58/68 (85%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||| ||||| ||||| ||||| | ||||| ||||||||||||| ||| |||||||||
Sbjct: 686 ggtgctcacaccattgggcaagcacggtgcacaaacttcagagcccacatatacaacgac 745

Query: 1849 accaacat 1856
||| |||||
Sbjct: 746 accgacat 753

>gb|FJ050772.1| Pinus taeda isolate 4650 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.001
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||||
Sbjct: 442 cgaatccaacat 431

>gb|FJ050764.1| Pinus taeda isolate 4651 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.001
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||||
Sbjct: 442 cgaatccaacat 431

>gb|FJ050758.1| Pinus taeda isolate 4655 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.001
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtgcgcacacgataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||||
Sbjct: 442 cgaatccaacat 431

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
|||||
Sbjct: 967 atgatcaagatgggagatattcgtccacttactggatcgaatggtgaaattaggaagaa 1025

>dbj|AK320190.1| Solanum lycopersicum cDNA, clone: LEFL1006BD07, HTC in leaf
Length = 1236

Score = 54.0 bits (27), Expect = 0.004
Identities = 48/55 (87%)
Strand = Plus / Plus

Query: 1215 caaaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatc 1269
|||||
Sbjct: 354 caaaccccaacaggaattcagctcgtggattcgaagtccttgacgagattaaatc 408

>gb|AC235342.1| Glycine max strain Williams 82 clone GM_WBb0088H14, complete sequence
Length = 183165

Score = 54.0 bits (27), Expect = 0.004
Identities = 33/35 (94%)
Strand = Plus / Plus

Query: 281 tattttttcttttaatttcttaattaatcctaa 315
|||||
Sbjct: 50421 tattttttcttttaatttctcaattaatgtcctaa 50455

>emb|CT832689.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCRN133B17, full
insert sequence
Length = 1270

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853

||||| ||||| ||||| | ||||| ||||| ||||| | || ||||| |||||
Sbjct: 717 tcacaccattgggcaagcagcatgcacaaacttcagagctcatatatacaacgaaaccaa 776

Query: 1854 cat 1856

|||
Sbjct: 777 cat 779

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 826 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 885

Query: 1963 aactactacttcaagaacctgctcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 886 aacaactactacaagaacctgctcagaagaagggtctcctcattctgatcag 939

>emb|CT832688.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCFA237B02, full
insert sequence
Length = 2326

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||| ||||| | ||||| ||||| ||||| | || ||||| |||||
Sbjct: 1773 tcacaccattgggcaagcagcatgcacaaacttcagagctcatatatacaacgaaaccaa 1832

Query: 1854 cat 1856

|||
Sbjct: 1833 cat 1835

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 1882 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 1941

Query: 1963 aactactacttcaagaacctcgttcagaagaagggctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1942 aacaactactacaagaacctcgtcgtcaagaagggctcctgcattctgatcag 1995

>emb|CT832687.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCFA219E15, full
insert sequence
Length = 1331

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||| ||||| | ||||| ||||| ||||| || ||||| ||||| |||||
Sbjct: 783 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 842

Query: 1854 cat 1856
|||
Sbjct: 843 cat 845

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 892 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 951

Query: 1963 aactactacttcaagaacctcgttcagaagaagggctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 952 aacaactactacaagaacctcgtcgtcaagaagggctcctgcattctgatcag 1005

>ref|NM_001072503.1| Oryza sativa (japonica cultivar-group) Os12g0112000 (Os12g0112000)
mRNA, complete cds
Length = 1318

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||| ||||| ||||| | ||||||||||||||||| | || ||||||| |||||
Sbjct: 719 tcacaccattgggcaagcagcatgcacaaacttcagagctcatatatacaacgaaaccaa 778

Query: 1854 cat 1856
|||
Sbjct: 779 cat 781

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||||||| || ||||||||| || ||||| || ||
Sbjct: 828 tcaggatcaggtgacaataacctggcacctctggatcttcagacccaaccgtgttcgag 887

Query: 1963 aactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||||||| || ||||||| ||||| || |||||||||
Sbjct: 888 aacaactactacaagaacctcgtcgtcaagaagggctcctgcattctgatcag 941

>tpe|BN000664.1| TPA: TPA_inf: Oryza sativa (japonica cultivar-group) prx135 gene for
class III peroxidase 135 precursor, exons 1-4
Length = 2198

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||| ||||| ||||| | ||||||||||||||||| | || ||||||| |||||
Sbjct: 1811 tcacaccattgggcaagcagcatgcacaaacttcagagctcatatatacaacgaaaccaa 1870

Query: 1854 cat 1856
|||
Sbjct: 1871 cat 1873

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 1920 tcaggatcaggtgacaataacctggcacctctggatcttcagacccaaccgtgttcgag 1979

Query: 1963 aactactacttcaagaacctcggtcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1980 acaactactacaagaacctcgctcagaagaagggtctcctcgattctgatcag 2033

>dbj|AK069456.1| Oryza sativa Japonica Group cDNA clone:J023019E08, full insert
sequence
Length = 1319

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||| ||||| | ||||| ||||| ||||| || ||||| |||||
Sbjct: 720 tcacaccattgggcaagcagatgcacaaacttcagagctcatatatacaacgaaaccaa 779

Query: 1854 cat 1856
|||
Sbjct: 780 cat 782

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 829 tcaggatcaggtgacaataacctggcacctctggatcttcagacccaaccgtgttcgag 888

Query: 1963 aactactacttcaagaacctcggtcagaagaagggtctcctccactctgatcag 2016

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Minus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||||||| || ||||||||| || ||||| || ||
Sbjct: 24220 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 24161

Query: 1963 aactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||||||| ||||||||| ||||| || |||||||||
Sbjct: 24160 aacaactactacaagaacctcgtcgtcaagaagggtcctgcattctgatcag 24107

>gb|EZ315890.1| TSA: Artemisia annua strain Madagascar Contig2436, mRNA sequence
Length = 309

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Minus

Query: 2089 gatttcgccgcccgatgatcaagatgggagacattagtcctctcactgg 2138
||||||| || ||||||||| ||||||||| || ||||||||| || |||||
Sbjct: 265 gatttcgcgctgccatgatcaagatgggtgatattagtcacttactgg 216

>gb|EZ359220.1| TSA: Artemisia annua strain Uganda Contig6381, mRNA sequence
Length = 492

Score = 52.0 bits (26), Expect = 0.018
Identities = 41/46 (89%)
Strand = Plus / Plus

Query: 1907 ggtcaggggacaacaatctggcaccacttgatcttcaaactccaac 1952
||||||| ||||||||| ||||||| || ||||| |||||||||
Sbjct: 11 ggtcaggagacaacaatttggcacccgctagatctccaaactccaac 56

>gb|EZ166433.1| TSA: Artemisia annua strain Artemis Contig25839, mRNA sequence
Length = 448

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Identities = 35/38 (92%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactgg 2138
|||||
Sbjct: 874 gccatgatcaaaatgggagacatcagtcctcactgg 911

>ref|NM_001157951.1| Zea mays peroxidase 2 (LOC100285056), mRNA
>gi|195646697|gb|EU970699.1| Zea mays clone 349100
peroxidase 2 precursor, mRNA, complete cds
Length = 1360

Score = 52.0 bits (26), Expect = 0.018
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 2092 ttcgccgcccatgatcaagatggg 2117
|||||
Sbjct: 956 ttcgccgcccatgatcaagatggg 981

>gb|BT044614.1| Arabidopsis thaliana unknown protein (At4g33420) mRNA, complete cds
Length = 978

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 373 tgtccaggagttgtatcatgcgcagatatagttgccatggctgctagaga 422

>gb|FJ099764.1| Pinus taeda isolate 1294 anonymous locus 2_6350_01 genomic sequence
Length = 414

Score = 52.0 bits (26), Expect = 0.018
Identities = 59/70 (84%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
|||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagtcgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099763.1| Pinus taeda isolate 1290 anonymous locus 2_6350_01 genomic sequence
Length = 448

Score = 52.0 bits (26), Expect = 0.018
Identities = 59/70 (84%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | ||||||||| |||||
Sbjct: 307 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 248

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 247 aatccaacat 238

>gb|BT042071.1| Zea mays full-length cDNA clone ZM_BFb0125B03 mRNA, complete cds
Length = 1342

Score = 52.0 bits (26), Expect = 0.018
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 2092 ttcgccgcccgatgatcaagatggg 2117
||||||||||||||||||||
Sbjct: 1003 ttcgccgcccgatgatcaagatggg 1028

>emb|AM450885.2| Vitis vinifera contig VV78X220288.8, whole genome shotgun sequence
Length = 12944

Score = 52.0 bits (26), Expect = 0.018
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 1797 cacaattggacaagcaaggtgcacaa 1822
||||||||||||||||||||
Sbjct: 1055 cacaattggacaagcaaggtgcacaa 1080

>ref|NM_119496.3| Arabidopsis thaliana peroxidase, putative (AT4G33420) mRNA, complete
cds
Length = 1197

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatataccttgccatcgctgccagaga 1335
|||||
Sbjct: 401 tgtccaggagttgtatcatgcgagatatagttgccatggctgctagaga 450

>emb|AM446475.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X020658.13,
clone ENTAV 115
Length = 18355

Score = 52.0 bits (26), Expect = 0.018
Identities = 50/58 (86%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagactctgttc 1343
|||||
Sbjct: 15894 tgtccaggagttgtttcctgcgctgacatactagccatagccgcccagactccgttc 15951

>emb|AM436560.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X083975.17,
clone ENTAV 115
Length = 6769

Score = 52.0 bits (26), Expect = 0.018
Identities = 50/58 (86%)
Strand = Plus / Minus

Query: 1154 cagggatgtagtggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
|||||
Sbjct: 5849 cagggatgtagtgcttctatattattggacgacactgcaagctttaccggagagaaga 5792

Score = 44.1 bits (22), Expect = 4.3
Identities = 49/58 (84%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||||| ||| | ||||| ||| ||| ||| |||||
Sbjct: 1513 cagggatgtgatgcttctatattattggatgacactgcaaactttactggagagaaga 1456

>emb|AM429435.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X154826.4,
clone ENTAV 115
Length = 7609

Score = 52.0 bits (26), Expect = 0.018
Identities = 50/58 (86%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||||| ||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 2278 cagggatgtgatgcttctatattattggacgacactgcaagctttaccggagagaaga 2221

>ref|NM_101322.1| Arabidopsis thaliana anionic peroxidase, putative (AT1G14550) mRNA,
complete cds
Length = 966

Score = 52.0 bits (26), Expect = 0.018
Identities = 32/34 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaaga 2161
||||||| ||||| ||||| ||||| |||||
Sbjct: 913 cctctcactggctctaattggagaaatcaggaaga 946

>gb|AF453791.1| Ipomoea batatas anionic peroxidase (POD) gene, promoter region and
partial cds
Length = 3741

Score = 52.0 bits (26), Expect = 0.018
Identities = 47/54 (87%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgta 786
||||||| ||||| ||| ||||| | ||||| ||||| ||||| |||||
Sbjct: 2101 cgc atggggcttccctcattcgtctcttcttccacgattgctttgtcgatgta 2154

>dbj|AB193816.1| Pisum sativum mRNA for peroxidase, complete cds, clone:PsPOX11
Length = 1217

Score = 52.0 bits (26), Expect = 0.018
Identities = 41/46 (89%)
Strand = Plus / Plus

Query: 739 ggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||||| | ||||||||| || ||||| |||
Sbjct: 197 ggtgcttctatacttcgcttggttcttccatgactgctttgttaatg 242

Score = 44.1 bits (22), Expect = 4.3
Identities = 61/74 (82%)
Strand = Plus / Plus

Query: 1477 gcttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagcca 1536
||||||| || ||||| || | ||||||||| || ||||| || |||||
Sbjct: 433 gcttggaggaccacatggatggttccacttgaagaagagatgcaagaacagcaagcca 492

Query: 1537 atctgctgctaaca 1550
| ||||| |||||
Sbjct: 493 aagtgctgccaaca 506

>dbj|AK176812.1| Arabidopsis thaliana mRNA for peroxidase ATP17a like protein, partial
cds, clone: RAFL25-36-D17
Length = 1203

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatataccttgccatcgctgccagaga 1335
||||||| || ||||||||| ||||| ||||| |||||
Sbjct: 397 tgtccaggagttgtatcatgcgagatatagttgccatggctgctagaga 446

>gb|AY089094.1| Arabidopsis thaliana clone 32346 mRNA, complete sequence
Length = 1179

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatataccttgccatcgctgccagaga 1335
|||||
Sbjct: 395 tgtccaggagttgtatcatgcgagatataccttgccatggctgctagaga 444

>gb|AC108072.3| Homo sapiens BAC clone RP11-704A16 from 2, complete sequence
Length = 36787

Score = 52.0 bits (26), Expect = 0.018
Identities = 29/30 (96%)
Strand = Plus / Minus

Query: 1045 atatatttaagataataaatatttctgct 1074
|||||
Sbjct: 31744 atatatttaagttaataaatatttctgct 31715

>gb|AF451951.1| Arabidopsis thaliana class III peroxidase ATP32 mRNA, complete cds
Length = 1082

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatataccttgccatcgctgccagaga 1335
|||||
Sbjct: 373 tgtccaggagttgtatcatgcgagatataccttgccatggctgctagaga 422

>emb|AL161583.2| Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
Length = 199536

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatataccttgccatcgctgccagaga 1335
|||||
Sbjct: 113403 tgtccaggagttgtatcatgcgagatataccttgccatggctgctagaga 113452

>gb|AC010657.3|AC010657 Genomic sequence for Arabidopsis thaliana BAC T5E21 from chromosome I,
complete sequence
Length = 83351

Score = 52.0 bits (26), Expect = 0.018

Identities = 32/34 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaaga 2161
|||||
Sbjct: 17743 cctctcactggctcctaattggagaaatcagaaaga 17776

>emb|AL035678.1| Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)
Length = 96475

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 48624 tgtccaggagttgtatcatgcgcagatatagttgccatggctgctagaga 48673

>gb|AC012188.2|F14L17 Sequence of BAC F14L17 from Arabidopsis thaliana chromosome 1, complete
sequence
Length = 111686

Score = 52.0 bits (26), Expect = 0.018
Identities = 32/34 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaaga 2161
|||||
Sbjct: 111350 cctctcactggctcctaattggagaaatcagaaaga 111383

>gb|EZ395724.1| TSA: Artemisia annua strain Uganda Contig12219, mRNA sequence
Length = 273

Score = 50.1 bits (25), Expect = 0.069
Identities = 55/65 (84%)
Strand = Plus / Minus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggetccaatggagaaatcaggaag 2160
|||||
Sbjct: 221 gccatgatcaagatgggtgatattagtcacttactggacgtaatggtgagatcaggaag 162

Query: 2161 aattg 2165
 |||||
Sbjct: 161 aattg 157

>gb|EZ362599.1| TSA: Artemisia annua strain Uganda Contig9760, mRNA sequence
 Length = 346

Score = 50.1 bits (25), Expect = 0.069
Identities = 55/65 (84%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
 ||||||| ||||||||||||||| ||||| ||||| | ||| | || ||||| |||||
Sbjct: 216 cttggaggacctacatggaatgtgaaactgggaagacgtgactcaaggactgcgagccaa 275

Query: 1538 tctgc 1542
 |||||
Sbjct: 276 gctgc 280

>gb|BT066765.1| Zea mays full-length cDNA clone ZM_BFb0066D03 mRNA, complete cds
 Length = 1217

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcacatctacaacgagaccaacat 1856
 ||||| ||||||||||||||| ||||||||||||||| ||| |||||
Sbjct: 665 tgcaccaacttcagagcccacacatctacaacgacaccgacat 705

>gb|BT055307.1| Zea mays full-length cDNA clone ZM_BFc0167H14 mRNA, complete cds
 Length = 1194

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcacatctacaacgagaccaacat 1856
 ||||| ||||||||||||||| ||||||||||||||| ||| |||||
Sbjct: 640 tgcaccaacttcagagcccacacatctacaacgacaccgacat 680

>gb|EU962146.1| Zea mays clone 240603 mRNA sequence
Length = 1299

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856
||||| ||||||||||||||| ||||||||||||||| ||| |||||
Sbjct: 737 tgcaccaacttcagagcccacatctacaacgacaccgacat 777

>gb|FJ070719.1| Pinus taeda isolate 7938 anonymous locus 0_3458_02 genomic sequence
Length = 364

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||||| ||||||||| |||||||||||||
Sbjct: 269 ccatgataaagatgggaaacattagccctctcactgg 233

>gb|FJ070718.1| Pinus taeda isolate 7947 anonymous locus 0_3458_02 genomic sequence
Length = 440

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||||| ||||||||| |||||||||||||
Sbjct: 295 ccatgataaagatgggaaacattagccctctcactgg 259

>gb|FJ070717.1| Pinus taeda isolate 7943 anonymous locus 0_3458_02 genomic sequence
Length = 359

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||||| ||||||||| |||||||||||||

Sbjct: 263 ccatgataaagatgggaaacattagccctctcactgg 227

>gb|FJ070716.1| Pinus taeda isolate 7950 anonymous locus 0_3458_02 genomic sequence
Length = 350

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 254 ccatgataaagatgggaaacattagccctctcactgg 218

>gb|FJ070715.1| Pinus taeda isolate 7940 anonymous locus 0_3458_02 genomic sequence
Length = 366

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 270 ccatgataaagatgggaaacattagccctctcactgg 234

>gb|FJ070714.1| Pinus taeda isolate 7948 anonymous locus 0_3458_02 genomic sequence
Length = 440

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 295 ccatgataaagatgggaaacattagccctctcactgg 259

>gb|FJ070713.1| Pinus taeda isolate 7949 anonymous locus 0_3458_02 genomic sequence
Length = 438

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 293 ccatgataaagatgggaaacattagccctctcactgg 257

>gb|FJ070712.1| Pinus taeda isolate 7952 anonymous locus 0_3458_02 genomic sequence
Length = 349

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 253 ccatgataaagatgggaaacattagccctctcactgg 217

>gb|FJ070711.1| Pinus taeda isolate 7941 anonymous locus 0_3458_02 genomic sequence
Length = 350

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 254 ccatgataaagatgggaaacattagccctctcactgg 218

>gb|FJ070710.1| Pinus taeda isolate 7951 anonymous locus 0_3458_02 genomic sequence
Length = 360

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 264 ccatgataaagatgggaaacattagccctctcactgg 228

>gb|FJ070709.1| Pinus taeda isolate 7942 anonymous locus 0_3458_02 genomic sequence
Length = 440

Score = 50.1 bits (25), Expect = 0.069

Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcaactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 295 ccatgataaagatgggaaacattagccctctcaactgg 259

>gb|FJ070708.1| Pinus taeda isolate 7953 anonymous locus 0_3458_02 genomic sequence
Length = 349

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcaactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 254 ccatgataaagatgggaaacattagccctctcaactgg 218

>gb|FJ070707.1| Pinus taeda isolate 7937 anonymous locus 0_3458_02 genomic sequence
Length = 420

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcaactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 275 ccatgataaagatgggaaacattagccctctcaactgg 239

>gb|FJ070706.1| Pinus taeda isolate 7946 anonymous locus 0_3458_02 genomic sequence
Length = 297

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcaactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 191 ccatgataaagatgggaaacattagccctctcaactgg 155

>gb|FJ070705.1| Pinus taeda isolate 7945 anonymous locus 0_3458_02 genomic sequence

Length = 350

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 255 ccatgataaagatgggaaacattagccctctcactgg 219

>gb|FJ070703.1| Pinus taeda isolate 7939 anonymous locus 0_3458_02 genomic sequence
Length = 355

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 259 ccatgataaagatgggaaacattagccctctcactgg 223

>ref|NM_001137528.1| Zea mays hypothetical protein LOC100192105 (LOC100192105), mRNA
>gi|194690673|gb|BT034416.1| Zea mays full-length cDNA
clone ZM_BFc0170D07 mRNA, complete cds
Length = 1217

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcacatctacaacgagaccaacat 1856
||||| ||||||||| ||||||||| ||| |||||
Sbjct: 665 tgcaccaacttcagagcccacacatctacaacgacaccgacat 705

>gb|DQ244260.1| Zea mays clone 3973 mRNA sequence
Length = 1224

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcacatctacaacgagaccaacat 1856

||||| ||||||||||||||| |||||||||||| | ||| |||||
Sbjct: 672 tgcaccaacttcagagcccacatctacaacgacaccgacat 712

>tpe|BN000615.1| TPA: TPA_inf: Oryza sativa (japonica cultivar-group) prx86 gene for
class III peroxidase 86 precursor, exons 1-3
Length = 1188

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 749 tccttcgcttggttcttccacgattgctttgtcaatgtaatt 789
||||||| | ||||||||| ||||||||| ||||||||| |||||
Sbjct: 197 tccttcgcctcttcttccatgattgcttcgtcaatgtaatt 237

>dbj|AP004731.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC
clone:OSJNBa0016D02
Length = 157822

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Minus

Query: 749 tccttcgcttggttcttccacgattgctttgtcaatgtaatt 789
||||||| | ||||||||| ||||||||| ||||||||| |||||
Sbjct: 82216 tccttcgcctcttcttccatgattgcttcgtcaatgtaatt 82176

>dbj|AB007645.1| Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K8K14
Length = 72698

Score = 50.1 bits (25), Expect = 0.069
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 760 ttcttccacgattgctttgtcaatgtaat 788
||||||||||||||||| |||||||||||
Sbjct: 46952 ttcttccacgattgcttcgtcaatgtaat 46980

>emb|Y10465.1| S. oleracea mRNA for peroxidase, clone PC44
Length = 1176

Score = 50.1 bits (25), Expect = 0.069

Identities = 43/49 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||||| | ||||| ||||||||| ||||||| ||||
Sbjct: 209 atgggtgcttccatacttcgtttgttcttccacgactgctttgtaaag 257

Score = 46.1 bits (23), Expect = 1.1
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 1481 ggaggccctacatggaatgttaaacttgaagaagagacgctagaac 1527
||||||| ||||||||| ||||| || ||||||| || |||||
Sbjct: 455 ggaggccccacatggaatgtaaaactaggtagaagagatgcaagaac 501

>gb|CP000102.1| Methanosphaera stadtmanae DSM 3091, complete genome
Length = 1767403

Score = 50.1 bits (25), Expect = 0.069
Identities = 25/25 (100%)
Strand = Plus / Plus

Query: 285 ttttcttttaatttcttaattaata 309
||||||| ||||||||| ||||||||| |||||
Sbjct: 31679 ttttcttttaatttcttaattaata 31703

>emb|FP012230.5| Pig DNA sequence from clone CH242-162F1 on chromosome X, complete
sequence
Length = 116800

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 268 atttctataaaattatTTTTTTTtttaa 295
||||||| ||||||||| ||||||| |||||
Sbjct: 24562 atttctataaaattatTTTTTTTtttaa 24589

>gb|EZ275595.1| TSA: Artemisia annua strain Madagascar Contig1982, mRNA sequence
Length = 688

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||
Sbjct: 69 cacacaattggacaagcaagatgcacaa 96

>gb|EZ286664.1| TSA: Artemisia annua strain Madagascar Contig13051, mRNA sequence
Length = 813

Score = 48.1 bits (24), Expect = 0.27
Identities = 33/36 (91%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggaga 1513
|||||
Sbjct: 789 cttggaggacctacatggaatgtgaaactggaga 754

Score = 46.1 bits (23), Expect = 1.1
Identities = 38/43 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaa 1951
|||||
Sbjct: 501 tcaggggacaacaatttggcaccactagactcaaactccaa 459

>gb|EZ342046.1| TSA: Artemisia annua strain Uganda Contig9262, mRNA sequence
Length = 588

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||
Sbjct: 493 cacacaattggacaagcaagatgcacaa 466

>gb|EZ321242.1| TSA: Artemisia annua strain Madagascar Contig7788, mRNA sequence

Length = 1218

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 |||||
Sbjct: 599 cacacaattggacaagcaagatgcacaa 626

>gb|EZ318330.1| TSA: Artemisia annua strain Madagascar Contig4876, mRNA sequence
Length = 457

Score = 48.1 bits (24), Expect = 0.27
Identities = 33/36 (91%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttgaaga 1513
 |||||
Sbjct: 236 cttggaggacctacatggaatgtgaaactggaaga 201

>gb|EZ247069.1| TSA: Artemisia annua strain Artemis Contig13739, mRNA sequence
Length = 438

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 |||||
Sbjct: 104 cacacaattggacaagcaagatgcacaa 131

>gb|EZ258457.1| TSA: Artemisia annua strain Madagascar Contig1560, mRNA sequence
Length = 246

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 |||||
Sbjct: 68 cacacaattggacaagcaagatgcacaa 95

>gb|EZ396283.1| TSA: Artemisia annua strain Uganda Contig12778, mRNA sequence
Length = 352

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||
Sbjct: 119 cacacaattggacaagcaagatgcacaa 146

>gb|EZ220993.1| TSA: Artemisia annua Contig18004
Length = 707

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||
Sbjct: 649 cacacaattggacaagcaagatgcacaa 622

>gb|EZ366681.1| TSA: Artemisia annua strain Uganda Contig132, mRNA sequence
Length = 790

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||
Sbjct: 723 cacacaattggacaagcaagatgcacaa 696

>gb|EZ196247.1| TSA: Artemisia annua strain Artemis Contig9804, mRNA sequence
Length = 252

Score = 48.1 bits (24), Expect = 0.27
Identities = 33/36 (91%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttgaaga 1513
||||||| ||||||||||||| ||||| |||||
Sbjct: 223 cttggaggacctacatggaatgtgaaactgggaaga 188

>gb|EZ355157.1| TSA: Artemisia annua strain Uganda Contig2318, mRNA sequence
Length = 246

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
||||||||||||||||||| |||||
Sbjct: 67 cacacaattggacaagcaagatgcacaa 94

>gb|EZ173232.1| TSA: Artemisia annua strain Artemis Contig32638, mRNA sequence
Length = 709

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
||||||||||||||||||| |||||
Sbjct: 622 cacacaattggacaagcaagatgcacaa 595

>gb|BT102799.1| Picea glauca clone GQ02016_E21 mRNA sequence
Length = 953

Score = 48.1 bits (24), Expect = 0.27
Identities = 42/48 (87%)
Strand = Plus / Plus

Query: 2110 aagatgggagacattagtctctcactggctccaatggagaaatcagg 2157
||||||| ||||| ||||||||| || ||||||||| |||||||||
Sbjct: 768 aagatggggaacatcagtcctcttacaggctccaaggagaaatcagg 815

>gb|BT101612.1| Picea glauca clone GQ01308_P23 mRNA sequence
Length = 919

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)

Strand = Plus / Plus

Query: 1957 ttgacaactactacttcaagaac 1980
 |||||
Sbjct: 605 ttgacaactactacttcaagaac 628

>gb|AC212861.3| Pongo abelii BAC clone CH276-236D6 from chromosome 1, complete sequence
 Length = 192235

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 268 atttctataaaattatTTTTtctt 291
 |||||
Sbjct: 126165 atttctataaaattatTTTTtctt 126188

>ref|XM_002451803.1| Sorghum bicolor hypothetical protein, mRNA
 Length = 837

Score = 48.1 bits (24), Expect = 0.27
Identities = 53/60 (88%), Gaps = 2/60 (3%)
Strand = Plus / Plus

Query: 2059 tacagcacaacccgggcac-cttctcctctgatttcgcccgcccatgatcaagatggg 2117
 ||||| ||||| ||| |||| ||| || ||||| ||||| ||||| |||||
Sbjct: 709 tacagctcaacccgg-cactcttcgctcagaacttcgcccgcccatgataaagatggg 767

>gb|AC235800.1| Solanum lycopersicum chromosome 3 clone C03HBa0137K15, complete
 sequence
 Length = 110892

Score = 48.1 bits (24), Expect = 0.27
Identities = 45/52 (86%)
Strand = Plus / Minus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaa 787
 ||||| || ||||| ||||| | ||||| ||||| ||||| |||||
Sbjct: 31655 atgggagcgtctctcattcgcctcttcttccacgactgctttgtcgatgtaa 31604

>ref|XM_002285687.1| PREDICTED: Vitis vinifera hypothetical protein LOC100257440

(LOC100257440), mRNA
Length = 1215

Score = 48.1 bits (24), Expect = 0.27
Identities = 48/56 (85%)
Strand = Plus / Plus

Query: 1156 gggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||||| ||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 307 gggatgtgatgcttctatattattggacgacactgcaagctttaccggagagaaga 362

>ref|XM_002269022.1| PREDICTED: Vitis vinifera hypothetical protein LOC100263220
(LOC100263220), mRNA
Length = 960

Score = 48.1 bits (24), Expect = 0.27
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcgttcagaagaagggtct 2000
||||||| ||| ||||| ||||| ||||| |||||
Sbjct: 748 tacttcaagaatctcattcagaagaagggtct 779

>dbj|AK323976.1| Solanum lycopersicum cDNA, clone: LEFL1068DD08, HTC in leaf
Length = 1123

Score = 48.1 bits (24), Expect = 0.27
Identities = 45/52 (86%)
Strand = Plus / Plus

Query: 2087 ctgatttgcgccgcccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| || || ||||| || ||||| ||||| ||||| |||||
Sbjct: 924 ctgattttgctgcagccatgattaaaatgggagatattagtcctetaactgg 975

>ref|XM_002320381.1| Populus trichocarpa predicted protein, mRNA
Length = 951

Score = 48.1 bits (24), Expect = 0.27
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 749 tccttcgcttgttcttccacgattgctttgtcaatg 784

||||| ||||||||||||||||||| ||||||||| |||||
Sbjct: 176 tcctccgcttgcttcttccacgaactgctttgtgaatg 211

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1298 gtttctgctgcagatataccttgc 1320
|||||
Sbjct: 352 gtttctgctgcagatataccttgc 374

>gb|CP001098.1| Halothermothrix orenii H 168, complete genome
Length = 2578146

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 188 aaactaattaagaaattaataaaaaat 215
||||| |||||||||||||||
Sbjct: 1223172 aaactaattaagagattaataaaaaat 1223199

>gb|EF677600.1| Picea sitchensis clone WS02771_I11 unknown mRNA
Length = 1895

Score = 48.1 bits (24), Expect = 0.27
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1999 ctctccactctgatcagcaactgttcaacgg 2030
||||| ||||| |||||||
Sbjct: 1536 ctctccactctgatcaggaactattcaacgg 1567

>gb|FJ050773.1| Pinus taeda isolate 4643 anonymous locus 0_13032_02 genomic sequence
Length = 640

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| ||||||||| |||||
Sbjct: 485 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggccgcattctacaa 426

>gb|FJ050767.1| Pinus taeda isolate 4658 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| ||||||||| |||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggccgcattctacaa 443

>gb|FJ050766.1| Pinus taeda isolate 4644 anonymous locus 0_13032_02 genomic sequence
Length = 640

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| ||||||||| |||||
Sbjct: 503 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggccgcattctacaa 444

>gb|FJ050765.1| Pinus taeda isolate 4645 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| ||||||||| |||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggccgcattctacaa 443

>gb|FJ050763.1| Pinus taeda isolate 4660 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtgctcacaccataggccaagcgcggtgcacaagcttcaggcccgcacatctacaa 443

>gb|FJ050762.1| Pinus taeda isolate 4647 anonymous locus 0_13032_02 genomic sequence
Length = 623

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 486 attaggtgctcacaccataggccaagcgcggtgcacaagcttcaggcccgcacatctacaa 427

>gb|FJ050761.1| Pinus taeda isolate 4654 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtgctcacaccataggccaagcgcggtgcacaagcttcaggcccgcacatctacaa 443

>gb|FJ050760.1| Pinus taeda isolate 4646 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtgctcacaccataggccaagcgcggtgcacaagcttcaggcccgcacatctacaa 443

|||||
Sbjct: 2185 aaaattattttttttataattacttaattaatatc 2220

>emb|BX548174.1| Prochlorococcus marinus MED4 complete genome
Length = 1657990

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 279 attattttttcttttaatttctta 302
|||||
Sbjct: 602985 attattttttcttttaatttctta 602962

>gb|CP000647.1| Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete sequence
Length = 5315120

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 881 gaaacaacacttggttccttttatt 904
|||||
Sbjct: 3390746 gaaacaacacttggttccttttatt 3390723

>emb|AM454579.2| Vitis vinifera contig VV78X062755.15, whole genome shotgun sequence
Length = 6610

Score = 48.1 bits (24), Expect = 0.27
Identities = 30/32 (93%)
Strand = Plus / Minus

Query: 192 taattaagaaattaaataaaaaatatttatca 223
|||||
Sbjct: 2152 taattaagaaattaaataaaaaatatttatca 2121

>emb|AM428729.2| Vitis vinifera contig VV78X273545.5, whole genome shotgun sequence
Length = 39883

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 284 tttttcttttaatttcttaattaa 307
|||||
Sbjct: 39856 tttttcttttaatttcttaattaa 39879

>emb|AM462968.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X116164.8,
clone ENTAV 115
Length = 13500

Score = 48.1 bits (24), Expect = 0.27
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcgttcagaagaagggtct 2000
||||| |||
Sbjct: 6764 tacttcaagaatctcattcagaagaagggtct 6795

>emb|AM453059.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X216487.15,
clone ENTAV 115
Length = 18125

Score = 48.1 bits (24), Expect = 0.27
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcgttcagaagaagggtct 2000
||||| |||
Sbjct: 4424 tacttcaagaatctcattcagaagaagggtct 4455

>emb|AM481723.1| Vitis vinifera contig VV78X090480.3, whole genome shotgun sequence
Length = 13986

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 1747 ttttggtgaggaatattgcatggt 1770
|||||
Sbjct: 3837 ttttggtgaggaatattgcatggt 3860

>dbj|AP006865.1| Lotus japonicus genomic DNA, chromosome 2, clone: LjT37H21, TM1032,

complete sequence
Length = 95067

Score = 48.1 bits (24), Expect = 0.27
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 1154 cagggatgtgatggttcaattctattggatgacaca 1189
|||||
Sbjct: 32185 cagggatgtgatgcatcaataactattggatgacaca 32220

>dbj|AB049589.1| Avicennia marina PER mRNA for secretory peroxidase, complete cds
Length = 1345

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1292 ggagttggttctctgcgagatattccttg 1319
|||||
Sbjct: 412 ggagttggttctctgcgagatattccttg 439

>emb|BX828399.1| Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTPGH84ZE10 of Hormone Treated Callus of strain col-0
of Arabidopsis thaliana (thale cress)
Length = 1002

Score = 48.1 bits (24), Expect = 0.27
Identities = 39/44 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttggttctctgcgagatattccttgccatcgctgc 1329
|||||
Sbjct: 380 tgtccaggagttggtatcatgcatgagatattggtccatggctgc 423

>emb|BX832751.1| Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTPGH95ZG01 of Hormone Treated Callus of strain col-0
of Arabidopsis thaliana (thale cress)
Length = 1192

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1956 ctttgacaactactacttcaagaacctc 1983
|||||
Sbjct: 820 ctttcacaactactacttcaagaacctc 847

>dbj|AB010692.1| Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18I23
Length = 72691

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 760 ttcttccacgattgctttgtcaatgtaa 787
|||||
Sbjct: 31924 ttcttccacgattgctttgtcaacgtaa 31897

>emb|Y10467.1| S.oleracea mRNA for peroxidase, clone PC23
Length = 1091

Score = 48.1 bits (24), Expect = 0.27
Identities = 45/52 (86%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 127 cgc atgggcgttcaataacttcgcttgttcttccatgactgctttgtcaatg 178

>ref|XM_670091.1| Plasmodium berghei strain ANKA hypothetical protein (PB301568.00.0)
partial mRNA
Length = 2721

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 275 taaaattatTTTTCTTTAATTT 298
|||||
Sbjct: 2667 taaaattatTTTTCTTTAATTT 2644

>gb|AF109124.1|AF109124 Ipomoea batatas anionic peroxidase swpa2 (swpa2) mRNA, complete cds
Length = 1291

Score = 48.1 bits (24), Expect = 0.27
Identities = 42/48 (87%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtc 780
 ||||| ||||| ||| ||| | ||||| ||||| ||||| |||||
Sbjct: 322 cgc atggggcttccctcattcgtctcttcttccacgattgctttgtc 369

>gb|EZ295716.1| TSA: Artemisia annua strain Madagascar Contig1601, mRNA sequence
 Length = 540

Score = 46.1 bits (23), Expect = 1.1
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1796 acacaattggacaagcaaggtgcacaa 1822
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 72 acacaattggacaagcaagatgcacaa 98

>gb|EZ256521.1| TSA: Artemisia annua strain Artemis Contig23191, mRNA sequence
 Length = 253

Score = 46.1 bits (23), Expect = 1.1
Identities = 43/50 (86%)
Strand = Plus / Plus

Query: 2089 gatttcgcccgcgatgatcaagatgggagacattagtcctctcactgg 2138
 ||||| || ||||| ||||| ||||| || ||||| || |||||
Sbjct: 165 gatttcgcgctgcatgatcaagatggntgatattagtcgcttactgg 214

>gb|EZ360402.1| TSA: Artemisia annua strain Uganda Contig7563, mRNA sequence
 Length = 276

Score = 46.1 bits (23), Expect = 1.1
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaa 1951
 ||||| ||||| ||||| || || ||||| |||||
Sbjct: 208 tcaggggacaacaattggcaccactagacgtcacaactccaa 250

>gb|EZ150610.1| TSA: Artemisia annua strain Artemis Contig10016, mRNA sequence
Length = 265

Score = 46.1 bits (23), Expect = 1.1
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactcaa 1951
|||||
Sbjct: 176 tcaggggacaacaatttggcaccactagacgtccaaactcaa 218

>gb|AC239433.3| Solanum lycopersicum strain Heinz 1706 chromosome 1 clone hba-208m24
map 1, complete sequence
Length = 154446

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 274 ataaaattatTTTTCTTTAAT 296
|||||
Sbjct: 83633 ataaaattatTTTTCTTTAAT 83655

>ref|NW_003037936.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000150
Length = 760080

Score = 46.1 bits (23), Expect = 1.1
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 172 aatcagtatctttgaaaactaattaagaaattaa 206
|||||
Sbjct: 116245 aatcagtatctttgaaaactaattatgaaattaa 116279

>gb|BT095984.1| Soybean clone JCVI-FLGm-20M19 unknown mRNA
Length = 1268

Score = 46.1 bits (23), Expect = 1.1
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1810 gcaaggtgcacaaacttcagagcccgcatctacaacgagacca 1852
||||||| | ||||| | ||||| ||||| |||||
Sbjct: 643 gcaaggtgcactaccttcaggaccgcatctacaacgacacca 685

>gb|BT093602.1| Soybean clone JCVI-FLGm-17D17 unknown mRNA
Length = 1079

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattct 1176
||||||| ||||| ||||| ||||| |||||
Sbjct: 850 cagggatgtgatggttcaattct 828

>gb|AC237089.1| Oryza granulata clone OG_ABa0096023, complete sequence
Length = 145921

Score = 46.1 bits (23), Expect = 1.1
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 762 cttccacgattgctttgtcaatgtaat 788
||||||| ||||| ||||| ||||| |||||
Sbjct: 78176 cttccacgattgctttgtaaataatgtaat 78150

>ref|XM_002448761.1| Sorghum bicolor hypothetical protein, mRNA
Length = 2469

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483
||||||| ||||| ||||| ||||| |||||
Sbjct: 1616 gttttgcttttgcttctaaatta 1594

>emb|FN357570.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000279
Length = 107846

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)

Strand = Plus / Plus

Query: 2232 attgtgtttaataagttgtaa 2254
|||||
Sbjct: 30598 attgtgtttaataagttgtaa 30620

>emb|FN357441.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000150
Length = 760080

Score = 46.1 bits (23), Expect = 1.1
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 172 aatcagtatctttgaaaactaattaagaaattaa 206
|||||
Sbjct: 116245 aatcagtatctttgaaaactaattaagaaattaa 116279

>gb|BT086529.1| Zea mays full-length cDNA clone ZM_BFc0177005 mRNA, complete cds
Length = 2218

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483
|||||
Sbjct: 1467 gttttgcttttgcttctaaatta 1445

>gb|EZ053600.1| TSA: Zea mays contig54722, mRNA sequence
Length = 1441

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483
|||||
Sbjct: 688 gttttgcttttgcttctaaatta 666

>emb|AL844509.2| Plasmodium falciparum 3D7 chromosome 13
Length = 2895605

Score = 46.1 bits (23), Expect = 1.1
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 193 aattaagaaattaaataaaaaatattt 219
|||||
Sbjct: 2326925 aattaagaaattaaataaaaaatattt 2326951

>gb|AC235371.1| Glycine max strain Williams 82 clone GM_WBb0104B04, complete sequence
Length = 191941

Score = 46.1 bits (23), Expect = 1.1
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 269 tttctataaaattatTTTTCTTTAATTTCTTAATTAATATCCTAA 315
|||||
Sbjct: 155381 tttcaataaaaattatTTTTCTTTAATTTCTTAATTAATATCCTAA 155427

>gb|AC235196.1| Glycine max strain Williams 82 clone GM_WBb0014G10, complete sequence
Length = 114082

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1154 cagggatgtgatggttcaattct 1176
|||||
Sbjct: 65728 cagggatgtgatggttcaattct 65750

>gb|AC235187.1| Glycine max strain Williams 82 clone GM_WBb0010C08, complete sequence
Length = 184070

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 281 tatttttcttttaatttcttaa 303
|||||
Sbjct: 7796 tatttttcttttaatttcttaa 7774

>gb|AC235182.1| Glycine max strain Williams 82 clone GM_WBb0008C11, complete sequence
Length = 100806

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 293 taatttcttaattaatcctaa 315
|||||
Sbjct: 22206 taatttcttaattaatcctaa 22184

>ref|XM_002319931.1| Populus trichocarpa predicted protein, mRNA
Length = 939

Score = 46.1 bits (23), Expect = 1.1
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaa 782
|||||
Sbjct: 148 atgggtgcttctcttgttcgcttgttcttccatgattgctttgtcaa 194

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1993 aagggtctcctccactctgatca 2015
|||||
Sbjct: 751 aagggtctcctccactctgatca 773

>ref|NM_001158468.1| Zea mays peroxidase 52 (LOC100285577), mRNA
>gi|195651250|gb|EU972975.1| Zea mays clone 391021
peroxidase 52 precursor, mRNA, complete cds
Length = 1358

Score = 46.1 bits (23), Expect = 1.1
Identities = 53/63 (84%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaagggtgcacaaacttcagagcccgcactctacaacgagaccaa 1853

||||| || || ||||| | |||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 670 tcacaccatcgccaagcacgctgcaccaacttcagagcccacgtgtacaacgacaccaa 729

Query: 1854 cat 1856

|||
Sbjct: 730 cat 732

>gb|EU954765.1| Zea mays clone 1482328 mRNA sequence
Length = 1445

Score = 46.1 bits (23), Expect = 1.1
Identities = 47/55 (85%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaa 787

||||||| || || ||||| ||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 241 cgcattggggcgctccctcctcgcctcttcttccacgactgcttcgtcaatgtaa 295

>gb|EU951047.1| Zea mays clone 687198 mRNA sequence
Length = 845

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483

||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 231 gttttgcttttgcttctaaatta 209

>gb|FJ088527.1| Pinus taeda isolate 6658 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162

||||| ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088526.1| Pinus taeda isolate 6661 anonymous locus 2_10243_02 genomic sequence

Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088525.1| Pinus taeda isolate 6650 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088524.1| Pinus taeda isolate 6653 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088523.1| Pinus taeda isolate 6663 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088522.1| Pinus taeda isolate 6662 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088521.1| Pinus taeda isolate 6654 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088520.1| Pinus taeda isolate 6655 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088519.1| Pinus taeda isolate 6657 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088518.1| Pinus taeda isolate 6664 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088517.1| Pinus taeda isolate 6651 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088516.1| Pinus taeda isolate 6649 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088515.1| Pinus taeda isolate 6666 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)

Strand = Plus / Minus

```
Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
          ||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318
```

>gb|FJ088514.1| Pinus taeda isolate 6660 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

```
Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
          ||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318
```

>gb|FJ088513.1| Pinus taeda isolate 6665 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

```
Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
          ||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318
```

>gb|FJ088512.1| Pinus taeda isolate 6656 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

```
Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
          ||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318
```

>gb|FJ088511.1| Pinus taeda isolate 4039 anonymous locus 2_10243_01 genomic sequence
Length = 579

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 60 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 2

>gb|FJ088510.1| Pinus taeda isolate 4033 anonymous locus 2_10243_01 genomic sequence
Length = 580

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 60 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 2

>gb|FJ088509.1| Pinus taeda isolate 4024 anonymous locus 2_10243_01 genomic sequence
Length = 580

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 60 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 2

>gb|FJ088508.1| Pinus taeda isolate 4026 anonymous locus 2_10243_01 genomic sequence
Length = 580

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 60 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 2

>gb|FJ088507.1| Pinus taeda isolate 4025 anonymous locus 2_10243_01 genomic sequence
Length = 580

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| ||| | ||||| |||||
Sbjct: 60 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 2

>gb|FJ088506.1| Pinus taeda isolate 4031 anonymous locus 2_10243_01 genomic sequence
Length = 580

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| ||| | ||||| |||||
Sbjct: 60 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 2

Database: /usr/local/blast/db/blastlibs/nt
Posted date: Feb 13, 2010 7:27 AM
Number of letters in database: 30,212,464,392
Number of sequences in database: 10,930,266

Lambda K H
1.37 0.711 1.31

Gapped
Lambda K H
1.37 0.711 1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 10930266
Number of Hits to DB: 956,652,574
Number of extensions: 59923270
Number of successful extensions: 1533110
Number of sequences better than 10.0: 507
Number of HSP's gapped: 1533086
Number of HSP's successfully gapped: 615

Length of query: 2730
Length of database: 30,212,464,392
Length adjustment: 24
Effective length of query: 2706
Effective length of database: 29,950,138,008
Effective search space: 81045073449648
Effective search space used: 81045073449648
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 50 (99.1 bits)
S1: 14 (28.2 bits)
S2: 22 (44.1 bits)

BLASTn Output of the 5' Border Sequence Flanking the Insert in Soybean Event DAS-68416-4 against GenBank No_human and No_mouse ESTs (est_others)

BLASTN 2.2.21 [Jun-14-2009]

+

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Query= 68416_5_border
(2730 letters)

Database: /usr/local/blast/db/blastlibs/est_others
51,680,690 sequences; 29,218,461,503 total letters

Searching..... done

Sequences producing significant alignments:			Score	E
			(bits)	Value
gb CX703225.1	gmrtDrNS01_14-B_M13R_D10_074.s2	Water stressed 5h...	1070	0.0
gb CX709633.1	gmrtDrNS01_10-D_M13R_A04_032.s2	Water stressed 5h...	1063	0.0
gb CF807990.1	psHB031xA07f	USDA-IFAFS:Expression of Phytophthor...	1059	0.0
gb BG509781.1	sad25h05.y1	Gm-c1074 Glycine max cDNA clone GENOM...	924	0.0
gb BM731124.1	sal68a04.y1	Gm-c1061 Glycine max cDNA clone SOYBE...	894	0.0
gb BG882707.1	sae51e08.y2	Gm-c1051 Glycine max cDNA clone GENOM...	880	0.0
gb EV267121.1	GLLBF04TF	JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	731	0.0
gb CF806428.1	psHB011xIO5f	USDA-IFAFS:Expression of Phytophthor...	646	0.0
gb AW349107.1	GM210004A21E9	Gm-r1021 Glycine max cDNA clone Gm-...	626	e-175
gb BG156628.1	sab31a07.y1	Gm-c1026 Glycine max cDNA clone GENOM...	618	e-173
gb FK018609.1	GLND133TF	JCVI-SOY3 Glycine max cDNA 5', mRNA seq...	557	e-154
gb BU577048.1	sar71e12.y1	Gm-c1074 Glycine max cDNA clone SOYBE...	545	e-151
gb BM093025.1	saj04a09.y1	Gm-c1065 Glycine max cDNA clone GENOM...	527	e-145
gb BE210375.1	so42h10.y1	Gm-c1039 Glycine max cDNA clone GENOME...	527	e-145
gb EV263181.1	GLLA357TF	JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	525	e-145
gb CF806168.1	psHB004x020f	USDA-IFAFS:Expression of Phytophthor...	523	e-144
gb BI972311.1	sag89h02.y1	Gm-c1084 Glycine max cDNA clone GENOM...	502	e-138
gb BE209964.1	so37a08.y1	Gm-c1039 Glycine max cDNA clone GENOME...	490	e-134
gb BG725689.1	sae39d12.y1	Gm-c1051 Glycine max cDNA clone GENOM...	464	e-126
gb FG889629.1	UCRVU08_CCNS10828_g1	Cowpea IT97K-461-4 Mixed Tis...	444	e-120
gb BE022389.1	sm85b11.y1	Gm-c1015 Glycine max cDNA clone GENOME...	438	e-119
gb BG359695.1	sac27d09.y1	Gm-c1051 Glycine max cDNA clone GENOM...	436	e-118
gb EV265313.1	GLLAS95TF	JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	412	e-111
gb AW132280.1	se02a03.y1	Gm-c1013 Glycine max cDNA clone GENOME...	381	e-101
gb CF809087.1	psHB042xH14f	USDA-IFAFS:Expression of Phytophthor...	373	3e-99

gb	BU577870.1	sar93g05.y1 Gm-c1074 Glycine max cDNA clone SOYBE...	373	3e-99
gb	AW432575.1	sh76b11.y1 Gm-c1015 Glycine max cDNA clone GENOME...	361	1e-95
gb	FG825601.1	UCRVU04_CCNI8859_g1 Cowpea 524B Mixed Tissue and ...	343	3e-90
gb	FF387035.1	MOOBI56TF MOO Vigna unguiculata cDNA 5', mRNA seq...	335	8e-88
gb	BE807926.1	ss31h12.y1 Gm-c1061 Glycine max cDNA clone GENOME...	331	1e-86
gb	FF386168.1	MOOBI56TRB MOO Vigna unguiculata cDNA, mRNA sequence	321	1e-83
gb	AI441922.1	sa51f09.y1 Gm-c1004 Glycine max cDNA clone GENOME...	291	1e-74
gb	G0029196.1	LJMAW92T0 JCVI-LJ2 Lotus japonicus cDNA 3', mRNA ...	289	4e-74
dbj	BP048143.1	BP048143 Lotus corniculatus var. japonicus pods ...	289	4e-74
dbj	BP048038.1	BP048038 Lotus corniculatus var. japonicus pods ...	289	4e-74
dbj	AV768169.1	AV768169 Lotus japonicus Young plants (two-weeks...	289	4e-74
dbj	BP048158.1	BP048158 Lotus corniculatus var. japonicus pods ...	274	2e-69
gb	G0017605.1	LJGBF85T0 JCVI-LJ1 Lotus japonicus cDNA 3', mRNA ...	266	6e-67
gb	G0023584.1	LJMCD71TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA ...	262	9e-66
gb	FG825600.1	UCRVU04_CCNI8859_b1 Cowpea 524B Mixed Tissue and ...	246	5e-61
gb	FF394030.1	MOODS81TF MOO Vigna unguiculata cDNA 5', mRNA seq...	246	5e-61
gb	FF387818.1	MOOC268TF MOO Vigna unguiculata cDNA 5', mRNA seq...	246	5e-61
gb	FF383796.1	MOOB233TF MOO Vigna unguiculata cDNA 5', mRNA seq...	246	5e-61
dbj	FS240762.1	FS240762 RPSC Glycyrrhiza uralensis cDNA clone K...	244	2e-60
gb	FG889628.1	UCRVU08_CCNS10828_b1 Cowpea IT97K-461-4 Mixed Tis...	238	1e-58
gb	FF403045.1	MOOF734TF MOO Vigna unguiculata cDNA 5', mRNA seq...	238	1e-58
gb	FF392448.1	MOOCV65TF MOO Vigna unguiculata cDNA 5', mRNA seq...	238	1e-58
gb	FF399144.1	MOOEV84TF MOO Vigna unguiculata cDNA 5', mRNA seq...	234	2e-57
gb	G0019707.1	LJMAW92TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA ...	208	1e-49
dbj	AV412875.1	AV412875 Lotus japonicus young plants (two-week ...	208	1e-49
dbj	AV771838.1	AV771838 Lotus japonicus Pods (20-30 mm in lengt...	202	7e-48
dbj	BW620524.1	BW620524 Lotus japonicus protoplasts from suspen...	196	4e-46
dbj	BW630489.1	BW630489 Lotus japonicus salicylic acid and meth...	196	4e-46
dbj	BW629863.1	BW629863 Lotus japonicus salicylic acid and meth...	196	4e-46
dbj	BW628107.1	BW628107 Lotus japonicus salicylic acid and meth...	196	4e-46
dbj	BW627140.1	BW627140 Lotus japonicus salicylic acid and meth...	196	4e-46
dbj	BW624354.1	BW624354 Lotus japonicus salicylic acid and meth...	196	4e-46
dbj	BW595840.1	BW595840 Lotus japonicus suspension-cultured cel...	196	4e-46
gb	EY976963.1	EST 83 Alfalfa aluminum suppression subtractive l...	190	3e-44
gb	EH613355.1	EST 02 Alfalfa aluminum suppression subtractive l...	190	3e-44
dbj	BB913062.1	BB913062 Trifolium pratense three week-old plant...	190	3e-44
gb	BI969832.1	GM830009A23A12 Gm-r1083 Glycine max cDNA clone Gm...	180	3e-41
gb	BI700509.1	sag61f05.y1 Gm-c1082 Glycine max cDNA clone GENOM...	180	3e-41
gb	BU578183.1	sar49a02.y1 Gm-c1074 Glycine max cDNA clone SOYBE...	176	4e-40
gb	G0258927.1	VBL1_16_M09_E001.g1 Normalized cDNA library from ...	174	2e-39
gb	CA852976.1	E14E06_J06_09.ab1 cDNA Peking library 6, 8 day SC...	174	2e-39
gb	CA852554.1	E09B05_C17_03.ab1 cDNA Peking library 6, 8 day SC...	174	2e-39
gb	AW350788.1	GM210009A20D5 Gm-r1021 Glycine max cDNA clone Gm...	174	2e-39
gb	FF401698.1	MOOE192TF MOO Vigna unguiculata cDNA 5', mRNA seq...	168	1e-37
gb	EY476317.1	METAQ01TF JCVI-MT3 Medicago truncatula cDNA 5', m...	167	4e-37
gb	EX530374.1	MTGland_A066_2007-06-28/MTGlandA066_C04_014_1 Med...	167	4e-37
gb	CX528854.1	s13dNF01B01MJ009_243775 Methyl Jasmonate-Elicited...	167	4e-37
gb	CF068375.1	EST669096 MTUS Medicago truncatula cDNA clone MTU...	167	4e-37
gb	AW268020.1	EST306242 DSIR Medicago truncatula cDNA clone pDS...	167	4e-37

gb	BI969294.1	GM830007B20G07 Gm-r1083 Glycine max cDNA clone Gm...	165	2e-36
gb	FG998035.1	GLPA295TF JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	163	6e-36
gb	EY477044.1	METAY48TF JCVI-MT3 Medicago truncatula cDNA 5', m...	163	6e-36
gb	BG448404.1	NF024B09EC1F1074 Elicited cell culture Medicago t...	155	2e-33
gb	BF644619.1	NF017G06EC1F1051 Elicited cell culture Medicago t...	155	2e-33
gb	CA919059.1	EST636777 MTUS Medicago truncatula cDNA clone MTU...	151	2e-32
gb	AW830120.1	sm23a02.y1 Gm-c1028 Glycine max cDNA clone GENOME...	151	2e-32
gb	CO513054.1	s13dSG89B0900073_122034 Glandular trichomes Medic...	149	9e-32
gb	FG998036.1	GLPA295TR JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	147	4e-31
gb	CO516034.1	s13dSG64B1200101_445396 Glandular trichomes Medic...	147	4e-31
gb	CO514259.1	s13dSG76D0500042_157180 Glandular trichomes Medic...	147	4e-31
gb	AW686470.2	NF041G08NR1F1000 Nodulated root Medicago truncatu...	145	1e-30
gb	BF639633.1	NF015A12IN1F1097 Insect herbivory Medicago trunca...	145	1e-30
gb	CX530413.1	s13dNF99F02MJ016_246858 Methyl Jasmonate-Elicited...	141	2e-29
gb	CX529528.1	s13dNF97C05MJ034_245107 Methyl Jasmonate-Elicited...	141	2e-29
gb	BF647501.1	NF068D03EC1F1029 Elicited cell culture Medicago t...	141	2e-29
gb	BF645317.1	NF030B11EC1F1092 Elicited cell culture Medicago t...	141	2e-29
gb	CO515766.1	s13dSG77F0400043_419681 Glandular trichomes Medic...	139	9e-29
gb	AW830346.1	sm33e02.y1 Gm-c1028 Glycine max cDNA clone GENOME...	139	9e-29
gb	AW703873.1	sk25b09.y1 Gm-c1028 Glycine max cDNA clone GENOME...	139	9e-29
gb	AI495213.1	sb02b01.y1 Gm-c1004 Glycine max cDNA clone GENOME...	139	9e-29
gb	AW830098.1	sm22c01.y1 Gm-c1028 Glycine max cDNA clone GENOME...	137	4e-28
gb	AW704238.1	sk18d12.y1 Gm-c1028 Glycine max cDNA clone GENOME...	135	1e-27
emb	CU524253.1	CU524253 STSSHWB2Sb_KZOACB Theobroma cacao cDNA ...	133	6e-27
dbj	AV771209.1	AV771209 Lotus japonicus Pods (20-30 mm in lengt...	133	6e-27
gb	CO516246.1	s13dSG69B0900075_445820 Glandular trichomes Medic...	131	2e-26
gb	BF071209.1	st04h08.y1 Gm-c1065 Glycine max cDNA clone GENOME...	131	2e-26
gb	EX660929.1	JS1BF51JG Salt stressed Fragaria vesca (strain Ha...	129	9e-26
gb	DN950706.1	Ost2T_331 Oak tissue culture growing 2 days in hy...	129	9e-26
gb	CO511866.1	s13dSG02H0700064_103632 Glandular trichomes Medic...	129	9e-26
gb	BF650349.1	NF096E02EC1F1017 Elicited cell culture Medicago t...	129	9e-26
gb	BE022178.1	sm68f01.y1 Gm-c1028 Glycine max cDNA clone GENOME...	129	9e-26
gb	AW666186.1	sk33d05.y1 Gm-c1028 Glycine max cDNA clone GENOME...	125	1e-24
gb	AW685593.1	NF029D05NR1F1000 Nodulated root Medicago truncatu...	117	3e-22
dbj	FS263447.1	FS263447 RPSC Glycyrrhiza uralensis cDNA clone S...	113	5e-21
gb	BF650698.1	NF099E07EC1F1053 Elicited cell culture Medicago t...	113	5e-21
gb	EV262518.1	MTYEW71TF JCVI-MT1 Medicago truncatula cDNA 5', m...	111	2e-20
gb	EV260463.1	MTYE803TF JCVI-MT1 Medicago truncatula cDNA 5', m...	111	2e-20
gb	EV258111.1	MTYDG59TF JCVI-MT1 Medicago truncatula cDNA 5', m...	111	2e-20
gb	DW017370.1	EST1226331 MTY Medicago truncatula cDNA clone MTY...	111	2e-20
gb	DW015340.1	EST1224301 MTY Medicago truncatula cDNA clone MTY...	111	2e-20
gb	CO513179.1	s13dSG23G0900068_129522 Glandular trichomes Medic...	111	2e-20
gb	CO512465.1	s13dSG100C120008_114444 Glandular trichomes Medic...	111	2e-20
gb	BG456493.1	NF082E02PL1F1017 Phosphate starved leaf Medicago ...	111	2e-20
gb	BG456057.1	NF073F02PL1F1025 Phosphate starved leaf Medicago ...	111	2e-20
gb	DW481567.1	GH_RMIRS_031_E08_R Cotton Normalized Library rand...	109	8e-20
gb	DW481566.1	GH_RMIRS_031_E08_056_F Cotton Normalized Library ...	109	8e-20
gb	DV443257.1	CV01009B1D06.f1 CV01-normalized library Manihot e...	107	3e-19
gb	DY633234.1	Medicago--03-I06.g1 Subtracted medicago cDNA libr...	105	1e-18

gb DY633115.1	Medicago--03-I06.b1 Subtracted medicago cDNA libr...	105	1e-18
gb BG359643.1	sac26g07.y1 Gm-c1051 Glycine max cDNA clone GENOM...	105	1e-18
gb GT138697.1	METCC85TF JCVI-MT3 Medicago truncatula cDNA 5', m...	103	5e-18
gb AW235016.1	sf21h05.y1 Gm-c1028 Glycine max cDNA clone GENOME...	103	5e-18
emb CU485516.1	CU485516 CUSHIONC_KZOACAC Theobroma cacao cDNA c...	101	2e-17
gb BG454205.1	NF108A01LF1F1001 Developing leaf Medicago truncat...	101	2e-17
gb BE943474.1	EST423053 MGHG Medicago truncatula cDNA clone pMG...	101	2e-17
gb ES840062.1	UFL_061_05 Cotton fiber 0-10 day post anthesis Go...	100	8e-17
gb BI262826.1	NF091E03EC1F1023 Elicited cell culture Medicago t...	100	8e-17
gb AW666202.1	sk33f05.y1 Gm-c1028 Glycine max cDNA clone GENOME...	100	8e-17
gb G0006531.1	LJGBF85TF JCVI-LJ1 Lotus japonicus cDNA 5', mRNA ...	98	3e-16
gb C0511819.1	s13dSG02D0500046_103538 Glandular trichomes Medic...	98	3e-16
gb BF648119.1	NF027G10EC1F1083 Elicited cell culture Medicago t...	98	3e-16
gb AW309606.1	sf21h05.x1 Gm-c1028 Glycine max cDNA clone GENOME...	98	3e-16
gb C0513848.1	s13dSG73C1100082_156358 Glandular trichomes Medic...	96	1e-15
gb AW691930.2	NF050G04ST1F1000 Developing stem Medicago truncat...	96	1e-15
emb AJ548283.1	AJ548283 MTAPHEU Medicago truncatula cDNA clone ...	88	3e-13
gb BF520761.1	EST458234 DSIL Medicago truncatula cDNA clone pDS...	88	3e-13
emb FN039861.1	FN039861 Petunia axillaris subsp. axillaris pool...	86	1e-12
emb FN039860.1	FN039860 Petunia axillaris subsp. axillaris pool...	86	1e-12
gb EG559283.1	CR03032H04 Root CR03 cDNA library Catharanthus ro...	86	1e-12
gb DW500373.1	GH_TMIRS_045_H05_F Cotton Normalized Library dT p...	86	1e-12
dbj CI189311.1	CI189311 Oryza sativa (japonica cultivar-group) ...	86	1e-12
dbj CI256090.1	CI256090 Oryza sativa (japonica cultivar-group) ...	86	1e-12
gb C0498078.1	G.h.fbr-sw07468 G.h.fbr-sw Gossypium hirsutum cDN...	86	1e-12
gb EY707107.1	CS00-C3-701-064-H11-CT.F Sweet orange fruit, deve...	84	5e-12
gb FD423297.1	RT00024R_T3_024_F11_31MAY2004_085_ab1 CrUniGene r...	84	5e-12
gb FD422675.1	RT00017R_T3_017_E10_31MAY2004_072_ab1 CrUniGene r...	84	5e-12
gb FD422951.1	RT00020R_T3_020_G01_31MAY2004_003_ab1 CrUniGene r...	84	5e-12
gb FD420140.1	1_SM-JB_R10-G12_T3_G12_3100394_14_ab1 CrUniGene ...	84	5e-12
gb DW508346.1	GH_TMIRS_123_D07_F Cotton Normalized Library dT p...	82	2e-11
gb GT143205.1	METCC85TR JCVI-MT3 Medicago truncatula cDNA 3', m...	80	7e-11
gb DR280730.1	157654 CERES-148 Arabidopsis thaliana cDNA clone ...	80	7e-11
gb CN910539.1	030128ABLC005555HT (ABLC) Braeburn cell culture t...	80	7e-11
gb CN908859.1	030122ABLC003031HT (ABLC) Braeburn cell culture t...	80	7e-11
gb CN908310.1	030109ABLC001919HT (ABLC) Braeburn cell culture t...	80	7e-11
dbj AU238571.1	AU238571 RAFL17 Arabidopsis thaliana cDNA clone ...	80	7e-11
emb FN019009.1	FN019009 Petunia axillaris subsp. axillaris pool...	78	3e-10
emb FN019008.1	FN019008 Petunia axillaris subsp. axillaris pool...	78	3e-10
emb FN021689.1	FN021689 Petunia axillaris subsp. axillaris pool...	78	3e-10
emb FN021688.1	FN021688 Petunia axillaris subsp. axillaris pool...	78	3e-10
emb FN034858.1	FN034858 Petunia axillaris subsp. axillaris pool...	78	3e-10
emb FN019751.1	FN019751 Petunia axillaris subsp. axillaris pool...	78	3e-10
gb FC869557.1	C31102G05EF AbioticR1 Citrus reshni cDNA clone C3...	78	3e-10
gb FC870159.1	C31109C09EF AbioticR1 Citrus reshni cDNA clone C3...	78	3e-10
gb FC924498.1	C31806G11EF StrCleopN Citrus reshni cDNA clone C3...	78	3e-10
gb FC875256.1	C31505H10EF CEVdCidro1 Citrus medica cDNA clone C...	78	3e-10
gb FC921479.1	C32105D10EF RVDevelopN Citrus clementina cDNA clo...	78	3e-10
gb FC875071.1	C31503H10EF CEVdCidro1 Citrus medica cDNA clone C...	78	3e-10

gb	EY867689.1	CL06-C4-500-007-B02-CT.F Rangpur lime root, green...	78	3e-10
gb	FC325468.1	P00462_C7-H9_M13-F_A09_079.ab1 Onu-Ua-pathc Ulmus...	78	3e-10
gb	EG985866.1	GLE049_D04_013 Cyamopsis tetragonoloba (L.) Taub ...	78	3e-10
gb	EG356679.1	P00462_C7-H9_M13-F_A09_079 Onu-Ua-pathc Ulmus ame...	78	3e-10
emb	FN034857.1	FN034857 Petunia axillaris subsp. axillaris pool...	76	1e-09
emb	FN045147.1	FN045147 Petunia axillaris subsp. axillaris pool...	76	1e-09
emb	FN019752.1	FN019752 Petunia axillaris subsp. axillaris pool...	76	1e-09
gb	G0517646.1	Mdfbg8014P16.g1 Apple_EST_Mdfbg Malus hybrid root...	76	1e-09
gb	EV227910.1	VV_PeA016c06.b1 Vitis vinifera cv. perlette LibA ...	76	1e-09
gb	EH047301.1	AS2RM4P1E10.ab1 Roots inoculated with Meloidogyne...	76	1e-09
gb	EC991497.1	WIN1142.C21_L14 Muscat Hamburg pre-veraison berry...	76	1e-09
gb	EC987303.1	WIN1130.C21_E15 Muscat Hamburg pre-veraison berry...	76	1e-09
gb	EC985323.1	WIN1124.C21_I01 Muscat Hamburg pre-veraison berry...	76	1e-09
gb	CV861937.1	gonad_EST09518 Embryonic gonad cDNA Library Gallu...	76	1e-09
gb	CX309187.1	C18022D10Rv Drought2 Citrus reshni cDNA clone C18...	76	1e-09
gb	CA105303.1	SCJFHR1C05E10.g HR1 Saccharum officinarum cDNA cl...	76	1e-09
gb	CA102350.1	SCBGHR1058E08.g HR1 Saccharum officinarum cDNA cl...	76	1e-09
gb	CF205258.1	RR890915I0004_IVa_Ra_B09 Vitis sp. RR890915I Viti...	76	1e-09
dbj	FS421608.1	FS421608 normalized full-length tobacco cDNA lib...	74	4e-09
dbj	FS420315.1	FS420315 normalized full-length tobacco cDNA lib...	74	4e-09
gb	ES441310.1	TSH_EST01528 Theobroma cacao-Moniliophthora perni...	74	4e-09
emb	CU488677.1	CU488677 DROUGHTLS_KZOACAF Theobroma cacao cDNA ...	74	4e-09
gb	FG154278.1	AGN_RNC104xj04f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	4e-09
gb	FG173223.1	AGN_RNC126xi04f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	4e-09
gb	FG156951.1	AGN_RNC026xe21f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	4e-09
gb	FG157638.1	AGN_RNC025xk16f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	4e-09
dbj	DB920515.1	DB920515 full-length enriched cassava cDNA libra...	74	4e-09
gb	EB450877.1	KT7C.108P16F.051219T7 KT7 Nicotiana tabacum cDNA ...	74	4e-09
gb	DY356036.1	ZO_Ec0009K09.f ZO_Ec Zingiber officinale cDNA c...	74	4e-09
gb	CV005110.1	atr02-9ms3-h07 Atr02 Amborella trichopoda cDNA cl...	74	4e-09
gb	CN782128.1	EST00224 cqseed Chenopodium quinoa cDNA clone SO2...	74	4e-09
gb	FC869818.1	C31105F02EF AbioticR1 Citrus reshni cDNA clone C3...	72	2e-08
gb	FC874065.1	C31202A05EF BiotPhyR1 Citrus aurantium cDNA clone...	72	2e-08
gb	GD471713.1	454PCS0099417 Scarlet Runner Bean globular-stage ...	72	2e-08
gb	GD391465.1	454PCS0019156 Scarlet Runner Bean globular-stage ...	72	2e-08
gb	FG480776.1	020324KANA001021HT (KANA) Actinidia setosa stem A...	72	2e-08
gb	EY845171.1	CA26-C1-002-040-C02-CT.F Sour orange leaf, field ...	72	2e-08
gb	EY794850.1	CR05-C3-701-027-F03-CT.F Mandarin fruit, developm...	72	2e-08
gb	EY776217.1	CR05-C1-103-015-D05-CT.F Mandarin leaf, infected ...	72	2e-08
gb	EY725128.1	CS00-C3-703-086-B09-CT.F Sweet orange fruit, deve...	72	2e-08
gb	C0500329.1	KH01008A04 KH01 Ipomoea batatas cDNA, mRNA sequence	72	2e-08
gb	DW500299.1	GH_TMIRS_045_B08_F Cotton Normalized Library dT p...	72	2e-08
gb	CX670039.1	UCRCP01_048_E06_T7 Swingle citrumelo nematode-cha...	72	2e-08
gb	CX050341.1	UCRCS09_31H06_b Ruby Orange Developing Seed cDNA ...	72	2e-08
gb	CV717574.1	UCRCS08_0009D08_f Parent Washington Navel Orange ...	72	2e-08
gb	CV093292.1	FAMU_USDA_FP_1315 Vitis shuttleworthii L., grape ...	72	2e-08
gb	C0866271.1	Mdfrt3046b02.y1 Mdfrt Malus x domestica cDNA clon...	72	2e-08
gb	C0417575.1	Mdfrt3031k23.y1 Mdfrt Malus x domestica cDNA clon...	72	2e-08
gb	C0070833.1	GR_Ea28B05.r GR_Ea Gossypium raimondii cDNA clo...	72	2e-08

gb	G0566201.1	Mddb5025B21_e2932.g1 Mddb Malus x domestica cDNA ...	70	7e-08
emb	CU537036.1	CU537036 TISCIVS_KZOAAQ Theobroma cacao cDNA clo...	70	7e-08
emb	CU505430.1	CU505430 PODMEUPA_KZOACAB Theobroma cacao cDNA c...	70	7e-08
emb	CU478688.1	CU478688 COPHAS_KZOAAAL Theobroma cacao cDNA clon...	70	7e-08
emb	CU478933.1	CU478933 COPHAS_KZOAAAL Theobroma cacao cDNA clon...	70	7e-08
emb	CU480774.1	CU480774 CORTEXS_KZOAAT Theobroma cacao cDNA clo...	70	7e-08
dbj	DC895850.1	DC895850 PCC Citrus unshiu cDNA clone PCC0206 5'...	70	7e-08
gb	EX266960.1	1447232_5_A14_063 PY06 Carica papaya cDNA, mRNA s...	70	7e-08
gb	EX289762.1	1577761_5_L07_022 PY06 Carica papaya cDNA, mRNA s...	70	7e-08
gb	EX272151.1	1452845_5_K11_038 PY06 Carica papaya cDNA, mRNA s...	70	7e-08
gb	EB110403.1	000430AFBC008068HT (AFBC) Royal Gala pre-opened f...	70	7e-08
gb	DW157696.1	CLVX9795.b1_E02.ab1 CLV(XYZ) lettuce virosa Lactu...	70	7e-08
gb	DW145800.1	CLVX10900.b1_H13.ab1 CLV(XYZ) lettuce virosa Lactu...	70	7e-08
gb	CO900249.1	Mddb5025b21.y1 Mddb Malus x domestica cDNA clone ...	70	7e-08
gb	CO051719.1	Mdfw2055d05.y1 Mdfw Malus x domestica cDNA clone ...	70	7e-08
gb	CN880015.1	010418AASA009843HT (AASA) Royal Gala 10 DAFB frui...	70	7e-08
gb	GR871114.1	Pq_F_00457 American ginseng Flower cDNA Library P...	68	3e-07
gb	GR875194.1	Pq_R_02677 American ginseng Root cDNA Library Pan...	68	3e-07
gb	GR873483.1	Pq_R_00966 American ginseng Root cDNA Library Pan...	68	3e-07
gb	GR873276.1	Pq_R_00759 American ginseng Root cDNA Library Pan...	68	3e-07
gb	GR871777.1	Pq_F_01120 American ginseng Flower cDNA Library P...	68	3e-07
gb	GR874357.1	Pq_R_01840 American ginseng Root cDNA Library Pan...	68	3e-07
gb	GR874227.1	Pq_R_01710 American ginseng Root cDNA Library Pan...	68	3e-07
emb	CU507988.1	CU507988 PODSSHWB1Sb_KZOACD Theobroma cacao cDNA...	68	3e-07
gb	EY664481.1	CS00-C1-101-067-A09-CT.F Sweet orange leaf, infec...	68	3e-07
gb	EW712042.1	Ginseng-Feq Contig4 Ginseng F. equiseti subtracti...	68	3e-07
gb	EL366609.1	CCES2712.b1_005.ab1 CCE(LMS) endive Cichorium end...	68	3e-07
gb	EH664510.1	11.2E05 Transformed tobacco Lambda Zap II library...	68	3e-07
gb	EC600006.1	PNSSH3G-1469 panax notoginseng subtracted cDNA li...	68	3e-07
dbj	CI205074.1	CI205074 Oryza sativa (japonica cultivar-group) ...	68	3e-07
gb	CO898341.1	Mdfrt3034e04.y3 Mdfrt Malus x domestica cDNA clon...	68	3e-07
gb	CN848323.1	PG07017B01 Ginseng cDNA library from MeJA treated...	68	3e-07
gb	CN847185.1	PG07026G09 Ginseng cDNA library from MeJA treated...	68	3e-07
gb	CN846818.1	PG07018H01 Ginseng cDNA library from MeJA treated...	68	3e-07
gb	CN846698.1	PG07019B09 Ginseng cDNA library from MeJA treated...	68	3e-07
gb	CN846059.1	PG07005D12 Ginseng cDNA library from MeJA treated...	68	3e-07
gb	CN845966.1	PG07006B07 Ginseng cDNA library from MeJA treated...	68	3e-07
gb	CK265901.1	EST711979 potato abiotic stress cDNA library Sola...	68	3e-07
gb	CK259240.1	EST742877 potato callus cDNA library, normalized ...	68	3e-07
gb	CK257963.1	EST741600 potato callus cDNA library, normalized ...	68	3e-07
gb	CK257684.1	EST741321 potato callus cDNA library, normalized ...	68	3e-07
gb	CK256437.1	EST740074 potato callus cDNA library, normalized ...	68	3e-07
gb	CK256141.1	EST739778 potato callus cDNA library, normalized ...	68	3e-07
gb	CK254968.1	EST738605 potato callus cDNA library, normalized ...	68	3e-07
gb	CK254173.1	EST737810 potato callus cDNA library, normalized ...	68	3e-07
gb	CK253943.1	EST737580 potato callus cDNA library, normalized ...	68	3e-07
gb	CK252132.1	EST735769 potato callus cDNA library, normalized ...	68	3e-07
gb	CK250936.1	EST734573 potato callus cDNA library, normalized ...	68	3e-07
gb	CK250929.1	EST734566 potato callus cDNA library, normalized ...	68	3e-07

gb	CK249912.1	EST733549 potato callus cDNA library, normalized ...	68	3e-07
gb	CK249875.1	EST733512 potato callus cDNA library, normalized ...	68	3e-07
gb	CK249724.1	EST733361 potato callus cDNA library, normalized ...	68	3e-07
gb	CK249638.1	EST733275 potato callus cDNA library, normalized ...	68	3e-07
gb	CK248882.1	EST732519 potato callus cDNA library, normalized ...	68	3e-07
gb	CK248392.1	EST732029 potato callus cDNA library, normalized ...	68	3e-07
gb	CK247774.1	EST731411 potato callus cDNA library, normalized ...	68	3e-07
gb	CK247097.1	EST730734 potato callus cDNA library, normalized ...	68	3e-07
gb	CK246328.1	EST729965 potato callus cDNA library, normalized ...	68	3e-07
gb	CK246259.1	EST729896 potato callus cDNA library, normalized ...	68	3e-07
gb	CK246252.1	EST729889 potato callus cDNA library, normalized ...	68	3e-07
gb	CK245537.1	EST729174 potato callus cDNA library, normalized ...	68	3e-07
gb	CK245042.1	EST728679 potato callus cDNA library, normalized ...	68	3e-07
gb	CK243469.1	EST727106 potato callus cDNA library, normalized ...	68	3e-07
gb	CK243468.1	EST727105 potato callus cDNA library, normalized ...	68	3e-07
dbj	AU229763.1	AU229763 RAFL17 Arabidopsis thaliana cDNA clone ...	68	3e-07
gb	BF273768.1	GA_Eb0018024f Gossypium arboreum 7-10 dpa fiber ...	68	3e-07
dbj	FS194878.1	FS194878 Solanum lycopersicum cv Micro-Tom root ...	66	1e-06
dbj	FS205634.1	FS205634 Solanum lycopersicum cv Micro-Tom root ...	66	1e-06
dbj	FS197980.1	FS197980 Solanum lycopersicum cv Micro-Tom root ...	66	1e-06
gb	GE650850.1	EST1177 Tender roots cDNA library of tea plant Ca...	66	1e-06
gb	EY412917.1	pOP-E008268_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	66	1e-06
gb	FG526917.1	030704KAYC002574HT (KAYC) Actinidia chinensis you...	66	1e-06
gb	FG525755.1	030628KAYC001240HT (KAYC) Actinidia chinensis you...	66	1e-06
gb	FE966530.1	PLATE_T3_028_D07_01DEC2004_057 Opium poppy elicite...	66	1e-06
gb	FE968334.1	PLATE_T3_047_H06_03DEC2004_034 Opium poppy elicite...	66	1e-06
gb	FE966485.1	PLATE_T3_027_H10_01DEC2004_066 Opium poppy elicite...	66	1e-06
gb	FE967467.1	PLATE_T3_038_E11_01DEC2004_087 Opium poppy elicite...	66	1e-06
gb	FE966062.1	PLATE_T3_023_D04_02DEC2004_026 Opium poppy elicite...	66	1e-06
gb	EX165442.1	A05_P-14_034 Cotton 1-14 day post anthesis Lambda...	66	1e-06
gb	EH665793.1	26.2D06 Transformed tobacco Lambda Zap II library...	66	1e-06
dbj	DB685271.1	DB685271 Solanum lycopersicum cv. Micro-Tom leaf...	66	1e-06
dbj	DB689063.1	DB689063 Solanum lycopersicum cv. Micro-Tom leaf...	66	1e-06
dbj	DB699350.1	DB699350 Solanum lycopersicum cv. Micro-Tom leaf...	66	1e-06
dbj	DB692736.1	DB692736 Solanum lycopersicum cv. Micro-Tom leaf...	66	1e-06
gb	DW080731.1	CLPX3640.b1_P21.ab1 CLP (XYZ) lettuce perennis Lac...	66	1e-06
gb	DT523193.1	WS02039.B21_A17 PTxN-IB-N-A-11 Populus trichocarp...	66	1e-06
gb	DT517809.1	WS02435.B21_F23 PTxD-ICC-N-A-14 Populus trichocar...	66	1e-06
gb	DT516973.1	WS02432.B21_P02 PTxD-ICC-N-A-14 Populus trichocar...	66	1e-06
gb	DT515726.1	WS02429.B21.1_F18 PTxD-ICC-N-A-14 Populus trichoc...	66	1e-06
gb	DT511026.1	WS02429.BR_F18 PTxD-ICC-N-A-14 Populus trichocarp...	66	1e-06
gb	DT507952.1	WS02419.BR_K15 PTxD-ICC-N-A-14 Populus trichocarp...	66	1e-06
gb	DN586754.1	46565.1 Late Blight-Challenged Tubers Solanum tub...	66	1e-06
gb	DN485372.1	M129C08.3pR Populus female catkins cDNA library P...	66	1e-06
gb	CV475162.1	23658.1 Developing Tubers Solanum tuberosum cDNA ...	66	1e-06
gb	CV269494.1	WS0208.B21_G14 PTxN-IB-N-A-11 Populus trichocarpa...	66	1e-06
gb	CV269008.1	WS0207.B21_B07 PTxN-IB-N-A-11 Populus trichocarpa...	66	1e-06
gb	CV256197.1	WS0243.B21_D05 PTxD-ICC-N-A-14 Populus trichocarp...	66	1e-06
gb	CK298355.1	EST761069 Nicotiana benthamiana mixed tissue cDNA...	66	1e-06

gb CK296485.1	EST759199	Nicotiana benthamiana mixed tissue cDNA...	66	1e-06
gb CK295751.1	EST758465	Nicotiana benthamiana mixed tissue cDNA...	66	1e-06
gb CK293902.1	EST756616	Nicotiana benthamiana mixed tissue cDNA...	66	1e-06
gb CK283472.1	EST746194	Nicotiana benthamiana mixed tissue cDNA...	66	1e-06
gb CK277562.1	EST723640	potato abiotic stress cDNA library Sola...	66	1e-06
gb CK268372.1	EST714450	potato abiotic stress cDNA library Sola...	66	1e-06
gb CK260187.1	EST706265	potato abiotic stress cDNA library Sola...	66	1e-06
gb CK245041.1	EST728678	potato callus cDNA library, normalized ...	66	1e-06
gb CA927256.1	MTU6CR.P6.H02	Aspen root cDNA Library Populus tre...	66	1e-06
gb BG597610.1	EST496288	cSTS Solanum tuberosum cDNA clone cSTS1...	66	1e-06
gb BG594826.1	EST493516	cSTS Solanum tuberosum cDNA clone cSTS8...	66	1e-06
gb AW429264.1	EST306720	tomato flower buds 0-3 mm, Cornell Univ...	66	1e-06
gb AW035301.1	EST280664	tomato callus, TAMU Solanum lycopersicu...	66	1e-06
gb G0345282.1	CS01010G03	Hotpepper under oxidative stress Capsi...	64	4e-06
dbj FS200575.1	FS200575	Solanum lycopersicum cv Micro-Tom root ...	64	4e-06
gb GD103440.1	KS21047N18	KS21 Capsicum annuum cDNA, mRNA sequence	64	4e-06
gb FG173286.1	AGN_RNC126xi04r1.ab1	AGN_RNC Nicotiana tabacum cD...	64	4e-06
gb FG157705.1	AGN_RNC025xk16r1.ab1	AGN_RNC Nicotiana tabacum cD...	64	4e-06
gb FG157012.1	AGN_RNC026xe21r1.ab1	AGN_RNC Nicotiana tabacum cD...	64	4e-06
gb EY868947.1	CL06-C4-500-024-E11-CT.F	Rangpur lime root, green...	64	4e-06
gb FE964503.1	PLATE_T3_006_A01_18NOV2004_015	Opium poppy elicite...	64	4e-06
gb EL689149.1	OPSC00922	Elaeis guineensis Suspension cell cultu...	64	4e-06
gb EL688532.1	OPSC00287	Elaeis guineensis Suspension cell cultu...	64	4e-06
gb EL689060.1	OPSC00829	Elaeis guineensis Suspension cell cultu...	64	4e-06
gb EW741112.1	10	Capsicum annuum with binucleate Rhizoctonia Li...	64	4e-06
emb AM806126.1	AM806126	seedling library, SL Nicotiana tabacum ...	64	4e-06
gb EV281455.1	GLNB506TF	JCVI-SOY3 Glycine max cDNA 5', mRNA seq...	64	4e-06
gb EB125073.1	010417AASA002377HT	(AASA) Royal Gala 10 DAFB frui...	64	4e-06
gb DY357012.1	ZO_Ed0001B05.r	ZO_Ed Zingiber officinale cDNA c...	64	4e-06
gb CN910664.1	030221ABLC006597HT	(ABLC) Braeburn cell culture t...	64	4e-06
gb CN909288.1	030123ABLC003427HT	(ABLC) Braeburn cell culture t...	64	4e-06
gb CN908413.1	030121ABLC002155HT	(ABLC) Braeburn cell culture t...	64	4e-06
gb CN908053.1	030109ABLC001478HT	(ABLC) Braeburn cell culture t...	64	4e-06
gb CF446769.1	EST683114	normalized cDNA library of onion Allium...	64	4e-06
gb CF445486.1	EST681831	normalized cDNA library of onion Allium...	64	4e-06
gb CF437063.1	EST673408	normalized cDNA library of onion Allium...	64	4e-06
gb BM878736.1	P12-A07	Sweetpotato Ipomoea batatas cDNA similar ...	64	4e-06
dbj FS124984.1	FS124984	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS024422.1	FS024422	library MLF Solanum melongena cDNA clon...	62	2e-05
dbj FS121328.1	FS121328	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS117052.1	FS117052	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS105158.1	FS105158	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS107745.1	FS107745	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS109925.1	FS109925	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS110172.1	FS110172	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS119211.1	FS119211	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS049153.1	FS049153	library PST Solanum melongena cDNA clon...	62	2e-05
dbj FS021644.1	FS021644	library LS5 Solanum melongena cDNA clon...	62	2e-05
dbj FS020310.1	FS020310	library LS5 Solanum melongena cDNA clon...	62	2e-05

gb	GR347634.1	CCOX3299.g1 CCOX Avena barbata root, pooled from ...	62	2e-05
gb	GE299450.1	P006002D02 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299223.1	P005007B06 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299125.1	P005005G03 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299103.1	P005005D09 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299068.1	P005004H11 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299038.1	P005004D05 Subtractive cDNA library from laminari...	62	2e-05
gb	EY410241.1	pOP-E007772_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	62	2e-05
gb	EY410393.1	pOP-E004088_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	62	2e-05
gb	EY412233.1	pOP-E002255_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	62	2e-05
gb	DW248736.1	pOP-EON01090_EST_C_1_pSK_SK EON (Oil Palm Embryoi...	62	2e-05
gb	EY032292.1	CAIT669.fwd CAIT Artemisia annua leaf Artemisia a...	62	2e-05
gb	DY980921.1	CLSS2910.b1_K08.ab1 CLS(LMS) lettuce sativa Lactu...	62	2e-05
gb	DY963072.1	CLSM13334.b1_K22.ab1 CLS(LMS) lettuce sativa Lactu...	62	2e-05
gb	DW141853.1	CLSY9921.b1_B10.ab1 CLS(XYZ) lettuce sativa Lactu...	62	2e-05
gb	DW118586.1	CLRY7219.b1_F06.ab1 CLR(XYZ) lettuce serriola Lac...	62	2e-05
gb	DN494839.1	M129C08.5pR Populus female catkins cDNA library P...	62	2e-05
gb	CX658639.1	P001020D11 Poplar SC cDNA library Populus alba x ...	62	2e-05
gb	CX658354.1	P001034B06 Poplar SC cDNA library Populus alba x ...	62	2e-05
gb	CX656775.1	P002024B08 Poplar SC cDNA library Populus alba x ...	62	2e-05
gb	CO754834.1	Mdfrt3051n10.y1 Mdfrt Malus x domestica cDNA clon...	62	2e-05
gb	GR182521.1	CBPG8855.g1 CBPG Mimulus guttatus IM62 roots, see...	60	7e-05
gb	GR182520.1	CBPG8855.b1 CBPG Mimulus guttatus IM62 roots, see...	60	7e-05
gb	GR101494.1	CCIF25878.b1 CCIF Mimulus guttatus IM62 leaves (H...	60	7e-05
gb	GR030153.1	CCIC14356.g1 CCIC Mimulus guttatus IM62 roots (H)...	60	7e-05
gb	GR010964.1	CCIC3934.g1 CCIC Mimulus guttatus IM62 roots (H) ...	60	7e-05
gb	GR010963.1	CCIC3934.b1 CCIC Mimulus guttatus IM62 roots (H) ...	60	7e-05
gb	GE591881.1	CCPW15817.b1_A19.ab1 CCP(UWX) Globe Artichoke Cyn...	60	7e-05
gb	GE347117.1	MEUB360TF JCVI-MT2 Medicago truncatula cDNA 5', m...	60	7e-05
gb	GE299609.1	P006004H07 Subtractive cDNA library from laminari...	60	7e-05
dbj	BY912248.1	BY912248 Cryptomeria japonica male strobilus Cry...	60	7e-05
gb	FG610783.1	stem_S064_F03.SEQ Opium poppy stem cDNA library P...	60	7e-05
gb	FG230888.1	pvreacc010002_J13_M13rev_phred13_vc root hairs of...	60	7e-05
gb	FD792211.1	08VNAA8_T7_003_G04_17FEB2006_020 08VNAA8 Phaseolu...	60	7e-05
gb	FD793984.1	08VNAA8_T7_031_G10_16MAR2006_068 08VNAA8 Phaseolu...	60	7e-05
gb	EX135466.1	BR119296 root cDNA library KHRT Brassica rapa sub...	60	7e-05
gb	EX114527.1	BR100817 whole plant cDNA library KFYP Brassica r...	60	7e-05
gb	EX032022.1	BR016666 callus cDNA library KBCG Brassica rapa s...	60	7e-05
gb	EL424106.1	CHCM3704.b1_014.ab1 CHC(LMS) Texas blueweed Helia...	60	7e-05
gb	EL362738.1	CCEM7256.b1_P14.ab1 CCE(LMS) endive Cichorium end...	60	7e-05
gb	EL022129.1	EBENXNS02I7QWK 8-day Arabidopsis seedlings, aeria...	60	7e-05
gb	EH665640.1	24E09 Transformed tobacco Lambda Zap II library N...	60	7e-05
gb	EC927161.1	WIN0214.TB24_N12 Cab Sauv flower, leaf and root n...	60	7e-05
gb	DW520518.1	GH_TMIRS_241_D04_F Cotton Normalized Library dT p...	60	7e-05
dbj	BW994485.1	BW994485 Cryptomeria japonica male cone Cryptome...	60	7e-05
dbj	BW990328.1	BW990328 Chamaecyparis obtusa cambium and surrou...	60	7e-05
gb	DV857611.1	col4871 Colonial bentgrass EST Agrostis capillari...	60	7e-05
gb	DV127237.1	CV03047B1C06.f1 CV03-normalized library Euphorbia...	60	7e-05
gb	DV126025.1	CV03044A1B02.f1 CV03-normalized library Euphorbia...	60	7e-05

gb	DT512242.1	WS02418.B21_L24 PTxD-ICC-N-A-14 Populus trichocar...	60	7e-05
gb	DT507614.1	WS02418.BR_L24 PTxD-ICC-N-A-14 Populus trichocarp...	60	7e-05
gb	DT492311.1	WS02550.C21_F01 PT-MB-N-A-15 Populus trichocarpa ...	60	7e-05
gb	DT487692.1	WS02534.B21_G10 PT-MB-N-A-15 Populus trichocarpa ...	60	7e-05
gb	DT487423.1	WS02533.B21_K13 PT-MB-N-A-15 Populus trichocarpa ...	60	7e-05
gb	DT483262.1	WS02522.B21_B19 PT-MB-N-A-15 Populus trichocarpa ...	60	7e-05
gb	DT482024.1	WS02533.BR_K13 PT-MB-N-A-15 Populus trichocarpa c...	60	7e-05
gb	DT478196.1	WS02522.BR_B19 PT-MB-N-A-15 Populus trichocarpa c...	60	7e-05
gb	CX169952.1	B06_69-16_04.ab1 leaf inoculated with Marssonnia p...	60	7e-05
gb	CV278268.1	WS0145.B21_021 PTxD-IL-A-5 Populus trichocarpa x ...	60	7e-05
gb	CV277650.1	WS0144.B21_C22 PTxD-IL-A-5 Populus trichocarpa x ...	60	7e-05
gb	CV131018.1	L1P03d05 Populus stem seasonal library Populus de...	60	7e-05
gb	CN848150.1	PG07006D08 Ginseng cDNA library from MeJA treated...	60	7e-05
gb	CK288635.1	EST751357 Nicotiana benthamiana mixed tissue cDNA...	60	7e-05
gb	CK258594.1	EST742231 potato callus cDNA library, normalized ...	60	7e-05
gb	CK255769.1	EST739406 potato callus cDNA library, normalized ...	60	7e-05
gb	CK255201.1	EST738838 potato callus cDNA library, normalized ...	60	7e-05
gb	CK244542.1	EST728179 potato callus cDNA library, normalized ...	60	7e-05
gb	CK244541.1	EST728178 potato callus cDNA library, normalized ...	60	7e-05
gb	CA992234.1	HC0822 GIBCOBRL CAT. NO. 19643-014 Brassica rapa ...	60	7e-05
gb	CA296237.1	SCAGLV1043F09.g LV1 Saccharum officinarum cDNA cl...	60	7e-05
dbj	BP175580.1	BP175580 Cryptomeria japonica inner bark Cryptom...	60	7e-05
gb	AI054926.1	coau0002I16 Cotton Boll Abscission Zone cDNA Libr...	60	7e-05
dbj	FS184353.1	FS184353 Solanum lycopersicum cv Micro-Tom root ...	58	3e-04
dbj	FS185438.1	FS185438 Solanum lycopersicum cv Micro-Tom root ...	58	3e-04
gb	GD111776.1	KS23009A10 KS23 Capsicum annuum cDNA, mRNA sequence	58	3e-04
gb	GE508830.1	CCFT6761.b1_A12.ab1 CCF(STU) sunflower Helianthus...	58	3e-04
gb	GE507030.1	CCFT5541.g1_J17.ab1 CCF(STU) sunflower Helianthus...	58	3e-04
gb	GE507029.1	CCFT5541.b1_J17.ab1 CCF(STU) sunflower Helianthus...	58	3e-04
gb	ES294238.1	_08Y_C12 Bermudagrass Normalized cDNA Library Cyn...	58	3e-04
gb	GD594567.1	454PCS0222258 Scarlet Runner Bean globular-stage ...	58	3e-04
gb	FG509216.1	030312KAPC001477HT (KAPC) Actinidia eriantha peta...	58	3e-04
gb	FG486094.1	021104KAUB001004HT (KAUB) Actinidia chinensis CK5...	58	3e-04
gb	FG486083.1	021015KAUB999084HT (KAUB) Actinidia chinensis CK5...	58	3e-04
gb	ES595125.1	000001603252_M19.ab1 Eucalyptus globulus under lo...	58	3e-04
gb	EY948213.1	RS3DN57TF RS3(RT) Raphanus sativus cDNA 5', mRNA ...	58	3e-04
gb	EY063068.1	CATF7534.fwd CATF Artemisia annua, Tanzanian, fro...	58	3e-04
gb	EY063067.1	CATF7534.rev CATF Artemisia annua, Tanzanian, fro...	58	3e-04
gb	EY091175.1	CAZI19752.rev CAZI Artemisia annua normalized lea...	58	3e-04
gb	EX515663.1	Hops-Column-29R_2007-06-04/Hops-Column-29R_F02_00...	58	3e-04
gb	DN965021.1	218e04 longbai no.2 one month old leaves Brassica...	58	3e-04
gb	EL434417.1	CHTL1481.b2_B12.ab1 CHT (LMS) Jerusalem artichoke ...	58	3e-04
gb	EL425067.1	CHCM4607.b1_N24.ab1 CHC (LMS) Texas blueweed Helia...	58	3e-04
gb	EL424239.1	CHCM3838.b1_L24.ab1 CHC (LMS) Texas blueweed Helia...	58	3e-04
gb	DY012178.1	40JKME7D_UP_003_D09_25MAR2004_073 40JKME7D Brassi...	58	3e-04
gb	DT212598.1	E002_B10 Embryogenic SSH library Cichorium intybu...	58	3e-04
gb	DT014039.1	VVH007H01_739521 CabSau Flower Nectary Stage 25 (...)	58	3e-04
gb	DT010226.1	VVH055D09_748099 CabSau Flower Nectary Stage 25 (...)	58	3e-04
gb	DR929061.1	EST1120600 Aquilegia cDNA library Aquilegia formo...	58	3e-04

gb DR742871.1	RTCU1_7_C01.g2_A029	Roots plus added copper Pinus...	58	3e-04
gb DR742794.1	RTCU1_7_C01.b2_A029	Roots plus added copper Pinus...	58	3e-04
gb DR094964.1	STRR1_17_H08.g1_A033	Stem Response Resistant Pinu...	58	3e-04
gb DR094953.1	STRR1_17_G08.g1_A033	Stem Response Resistant Pinu...	58	3e-04
gb DR094872.1	STRR1_17_G08.b1_A033	Stem Response Resistant Pinu...	58	3e-04
gb DR090538.1	RTAL1_15_F06.g1_A029	Roots plus added aluminum Pi...	58	3e-04
gb DR090469.1	RTAL1_15_F06.b1_A029	Roots plus added aluminum Pi...	58	3e-04
gb DR089595.1	RTAL1_9_E05.g1_A029	Roots plus added aluminum Pin...	58	3e-04
gb DR088958.1	RTAL1_5_E09.g1_A029	Roots plus added aluminum Pin...	58	3e-04
gb DR023270.1	STRS1_56_B11.g1_A034	Shoot tip pitch canker susce...	58	3e-04
gb DR021354.1	STRS1_44_C09.b1_A034	Shoot tip pitch canker susce...	58	3e-04
gb CX658976.1	P001024H07	Poplar SC cDNA library Populus alba x ...	58	3e-04
gb C0499512.1	G.h.fbr-sw08902	G.h.fbr-sw Gossypium hirsutum cDN...	58	3e-04
gb C0498821.1	G.h.fbr-sw08211	G.h.fbr-sw Gossypium hirsutum cDN...	58	3e-04
gb C0498720.1	G.h.fbr-sw08110	G.h.fbr-sw Gossypium hirsutum cDN...	58	3e-04
gb C0496527.1	G.h.fbr-sw05917	G.h.fbr-sw Gossypium hirsutum cDN...	58	3e-04
gb C0494300.1	G.h.fbr-sw03690	G.h.fbr-sw Gossypium hirsutum cDN...	58	3e-04
gb C0491848.1	G.h.fbr-sw01238	G.h.fbr-sw Gossypium hirsutum cDN...	58	3e-04
gb CV094175.1	FAMU_USDA_FP_2198	Vitis shuttleworthii L., grape ...	58	3e-04
emb AJ805072.1	AJ805072	Antirrhinum majus whole plant Antirrhin...	58	3e-04
emb AJ795563.1	AJ795563	Antirrhinum majus whole plant Antirrhin...	58	3e-04
emb AJ795101.1	AJ795101	Antirrhinum majus whole plant Antirrhin...	58	3e-04
emb AJ793569.1	AJ793569	Antirrhinum majus whole plant Antirrhin...	58	3e-04
gb C0200887.1	RTCNT2_2_F01.b1_A029	Root control 2 (late) Pinus ...	58	3e-04
gb CN604982.1	USDA_FP_132082	Vitis shuttleworthii L., grape Vit...	58	3e-04
gb CN604205.1	USDA_FP_131305	Vitis shuttleworthii L., grape Vit...	58	3e-04
gb CF476953.1	RTWW3_4_G10.g1_A022	Well-watered loblolly pine ro...	58	3e-04
gb CF401192.1	RTWW1_10_H07.g1_A015	Well-watered loblolly pine r...	58	3e-04
gb CF401118.1	RTWW1_10_H07.b1_A015	Well-watered loblolly pine r...	58	3e-04
gb CF400173.1	RTWW1_3_F07.g1_A015	Well-watered loblolly pine ro...	58	3e-04
gb CF400086.1	RTWW1_3_F07.b1_A015	Well-watered loblolly pine ro...	58	3e-04
gb CF387460.1	RTDR1_20_H12.b1_A015	Loblolly pine roots recoveri...	58	3e-04
gb CF387171.1	RTDR1_11_H09.b1_A015	Loblolly pine roots recoveri...	58	3e-04
gb CF387078.1	RTDR1_10_H09.g1_A015	Loblolly pine roots recoveri...	58	3e-04

>gb|CX703225.1| gmrtDrNS01_14-B_M13R_D10_074.s2 Water stressed 5h segment 2
gmrtDrNS01 Glycine max cDNA 3', mRNA sequence
Length = 743

Score = 1070 bits (540), Expect = 0.0
Identities = 543/544 (99%)
Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 640 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 581

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 580 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 521

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 520 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 461

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactggttcaac 2028
|||||
Sbjct: 460 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactggttcaac 401

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctct 2088
|||||
Sbjct: 400 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctct 341

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||
Sbjct: 340 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 281

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagcttgaatattaagggt 2208
|||||
Sbjct: 280 gaaatcaggaagaattgtagaaggattaactaatttaattcagcttgaatattaagggt 221

Query: 2209 cctacacatacgaagcaatttaattgtgttaataagttgttaaacatgttttggttg 2268
|||||
Sbjct: 220 cctacacatacgaagcaatttaattgtgttaataagttgttaaacatgttttggttg 161

Query: 2269 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtggttctact 2328
|||||
Sbjct: 160 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtggttctact 101

Query: 2329 tccc 2332
|||
Sbjct: 100 tccc 97

Score = 210 bits (106), Expect = 3e-50
Identities = 106/106 (100%)
Strand = Plus / Minus

Query: 1540 tgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatt 1599
|||||
Sbjct: 743 tgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatt 684

Query: 1600 tagcgctcttggactttccaccaaggacttggtcgccttgtccggt 1645
|||||
Sbjct: 683 tagcgctcttggactttccaccaaggacttggtcgccttgtccggt 638

Score = 79.8 bits (40), Expect = 7e-11
Identities = 40/40 (100%)
Strand = Plus / Minus

Query: 2388 tcctttatcaagcatttatcaagaacggagtttgcttttt 2427
|||||
Sbjct: 40 tcctttatcaagcatttatcaagaacggagtttgcttttt 1

>gb|CX709633.1| gmrtDrNS01_10-D_M13R_A04_032.s2 Water stressed 5h segment 2
gmrtDrNS01 Glycine max cDNA 3', mRNA sequence
Length = 791

Score = 1063 bits (536), Expect = 0.0
Identities = 542/544 (99%)
Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||||
Sbjct: 640 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 581

Query: 1849 accaacaatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 580 accaacaatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 521

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 520 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 461

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 460 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 401

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctct 2088
|||||

Sbjct: 400 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttttctct 341

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||

Sbjct: 340 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 281

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagcttgaatattaagggt 2208
|||||

Sbjct: 280 gaaatcaggaagaattgtagaaggattaactaatttaattcagcttgaatattaagggt 221

Query: 2209 cctacacatacgcaagcaatttaattgtgttaataagttgttaaacatgttttggttg 2268
|||||

Sbjct: 220 cctacacatacgcaagcaatttaattgtgttaataagttgttaaacatgttttggttg 161

Query: 2269 tattttggattcctagtgtagtttcgggatcaatgccgtctactttagtggttctact 2328
|||||

Sbjct: 160 tattttggattcctagtgtagtttcgggatcaatgccgtctactttagtggttctact 101

Query: 2329 tccc 2332
||||

Sbjct: 100 tccc 97

Score = 297 bits (150), Expect = 2e-76
Identities = 153/154 (99%)
Strand = Plus / Minus

Query: 1492 atggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaaca 1551
|||||

Sbjct: 791 atggaatgttaaacttgaagaagagacgctagaattgctagccaatctgctgctaaca 732

Query: 1552 tggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttgg 1611
|||||

Sbjct: 731 tggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttgg 672

Query: 1612 accttccaccaaggacttggtcgccttgtccggt 1645
|||||
Sbjct: 671 accttccaccaaggacttggtcgccttgtccggt 638

Score = 79.8 bits (40), Expect = 7e-11
Identities = 40/40 (100%)
Strand = Plus / Minus

Query: 2388 tcctttatcaagcatttatcaagaacggagtttgcttttt 2427
|||||
Sbjct: 40 tcctttatcaagcatttatcaagaacggagtttgcttttt 1

>gb|CF807990.1| psHB031xA07f USDA-IFAFS:Expression of Phytophthora sojae genes during
infection and propagation Glycine max cDNA clone
sHB031A07 5, mRNA sequence
Length = 708

Score = 1059 bits (534), Expect = 0.0
Identities = 543/545 (99%), Gaps = 1/545 (0%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||||
Sbjct: 149 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 208

Query: 1849 accaacaatagaaacccgatttgaaggactaggcagcaaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 209 accaacaatagaaacccgatttgaaggactaggcagcaaaagctgccctagaacatcaggg 268

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
|||||
Sbjct: 269 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 328

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 329 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 388

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccacccgggcaccttctcctct 2088
|||||
Sbjct: 389 ggtgggtccaccgactccattgtgcgtggctacagcaccacccgggcaccttctcctct 448

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||

Sbjct: 449 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 508

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||

Sbjct: 509 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 568

Query: 2209 cctacacatacgaagcaatttaattgtgtttaataagttgttaaacat-gttttgggt 2267
|||||

Sbjct: 569 cctacacatacgaagcaatttaattgtgtttaataagttgttaaacatggttttgggt 628

Query: 2268 gtattttggattcctagtgtagtttcgggatcaatgccgtctactttagtggttctac 2327
|||||

Sbjct: 629 gtattttggattcctagtgtagnttcgggatcaatgccgtctactttagtggttctac 688

Query: 2328 ttccc 2332
|||||

Sbjct: 689 ttccc 693

Score = 299 bits (151), Expect = 4e-77

Identities = 151/151 (100%)

Strand = Plus / Plus

Query: 1495 gaatgttaacttgaagaagagacgctagaactgctagccaatctgctgctaacaatgg 1554
|||||

Sbjct: 1 gaatgttaacttgaagaagagacgctagaactgctagccaatctgctgctaacaatgg 60

Query: 1555 catccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgact 1614
|||||

Sbjct: 61 catccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgact 120

Query: 1615 ttccaccaaggacttggcgccttgtccgggt 1645
|||||

Sbjct: 121 ttccaccaaggacttggcgccttgtccgggt 151

>gb|BG509781.1| sad25h05.y1 Gm-c1074 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1074-1498 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
; , mRNA sequence
Length = 493

Score = 924 bits (466), Expect = 0.0
Identities = 472/474 (99%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||||
Sbjct: 20 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 79

Query: 1849 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 80 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagatcatcaggg 139

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 140 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 199

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 200 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 259

Query: 2029 ggtgggtccaccgactccattgtgctgggtacagcaccacccgggcacettctcctct 2088
|||||
Sbjct: 260 ggtgggtccaccgactccattgtgctgggtacagcaccacccgggcacettctcctct 319

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||
Sbjct: 320 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 379

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagcttgaatattaagggt 2208
|||||
Sbjct: 380 gaaatcaggaagaattgtagaaggattaactaatttaattcagcttgaatattaagggt 439

Query: 2209 cctacacatacgaagcaatttaattgtgtttaataagttgttaaacaatgttt 2262
|||||
Sbjct: 440 cctacacatacgaagcaatttaattgtgtttaataagttgttaaacaatgttt 493

Score = 44.1 bits (22), Expect = 4.0
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1624 ggacttggtcgccttgtccggt 1645
 |||||
Sbjct: 1 ggacttggtcgccttgtccggt 22

>gb|BM731124.1| sal68a04.y1 Gm-c1061 Glycine max cDNA clone SOYBEAN CLONE ID:
 Gm-c1061-4231 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
 ;, mRNA sequence
 Length = 506

Score = 894 bits (451), Expect = 0.0
Identities = 454/455 (99%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
 |||||
Sbjct: 52 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 111

Query: 1849 accaacatagaaacgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
 |||||
Sbjct: 112 accaacatagaaacgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 171

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
 |||||
Sbjct: 172 tcagaggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 231

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctcactctgatcagcaactgttcaac 2028
 |||||
Sbjct: 232 tacttcaagaacctcgttcagaagaagggtctcctcactctgatcagcaactgttcaac 291

Query: 2029 ggtgggtccaccgactccattgtgctgggtacagcaccaacccgggcacettctcctct 2088
 |||||
Sbjct: 292 ggtgggtccaccgactccattgtgctgggtacagcaccaacccgggcacettctcctct 351

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
 |||||
Sbjct: 352 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 411

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||
Sbjct: 412 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 471

Query: 2209 cctacacatacgcaagcaatttaattgtgtttaat 2243
|||||
Sbjct: 472 cctacacatacgcaagcaatttaattgtgtttaat 506

Score = 107 bits (54), Expect = 3e-19
Identities = 54/54 (100%)
Strand = Plus / Plus

Query: 1592 tcaagatntagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
|||||
Sbjct: 1 tcaagatntagcgctcttggactttccaccaaggacttggcgccttgtccggt 54

>gb|BG882707.1| sae51e08.y2 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1051-8679 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 483

Score = 880 bits (444), Expect = 0.0
Identities = 444/444 (100%)
Strand = Plus / Plus

Query: 1889 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948
|||||
Sbjct: 1 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 60

Query: 1949 caaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccact 2008
|||||
Sbjct: 61 caaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccact 120

Query: 2009 ctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcacca 2068
|||||
Sbjct: 121 ctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcacca 180

Query: 2069 accgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtc 2128

Sbjct: 181 |||
acccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtc 240

Query: 2129 ctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaatttgatt 2188
|||

Sbjct: 241 ctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaatttgatt 300

Query: 2189 cagtcttgaatattaagggtcctacacatacgcaagcaatttaattgtgtttaataagtt 2248
|||

Sbjct: 301 cagtcttgaatattaagggtcctacacatacgcaagcaatttaattgtgtttaataagtt 360

Query: 2249 gttaaaacatgttttggttgattttggattcctagtgtagtttcggtgatcaatgccgt 2308
|||

Sbjct: 361 gttaaaacatgttttggttgattttggattcctagtgtagtttcggtgatcaatgccgt 420

Query: 2309 ctactttagtggttctacttccc 2332
|||

Sbjct: 421 ctactttagtggttctacttccc 444

>gb|EV267121.1| GLLBF04TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 719

Score = 731 bits (369), Expect = 0.0
Identities = 467/498 (93%), Gaps = 5/498 (1%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||

Sbjct: 113 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 172

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaaagctgccctagaacatcaggg 1908
| |||

Sbjct: 173 agcaacatagacaccgcatttgcaaggacaaggcaaaaagctgccaagaacatcaggg 232

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||

Sbjct: 233 tcaggggacaataatcttgcgacgcttgatcttcaaactccaaccgaattcgacaactac 292

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||

Sbjct: 293 tacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgttcaat 352

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagaccaacccggcaccttctcctct 2088
|||||

Sbjct: 353 ggtgggtccaccgactccattgtgcgtggctacagaccaacccgagctccttctcctct 412

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||

Sbjct: 413 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaacgga 472

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt--tgattcagcttgaatattaagg 2206
|||||

Sbjct: 473 gaaatcaggaagaattgtagaaggattaactaattactaattgagctccaatattaagg 532

Query: 2207 gtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaacatgtttt 2263
|||

Sbjct: 533 gtctactacacatacgaagcaatttaattgtgtttaataagttgttaaacatgtttt 592

Query: 2264 gttgtatgttgattcc 2281
|||||

Sbjct: 593 gttgtatgttgattcc 610

Score = 210 bits (106), Expect = 3e-50
Identities = 112/114 (98%)
Strand = Plus / Plus

Query: 1532 agccaatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatc 1591
|||||

Sbjct: 2 agccaatctgctgctaacaatggcatccctccaccacttcaaaccttaaccaactcatc 61

Query: 1592 tcaagatttagcgctcttgactttccaccaaggacttggcgccttgtccgg 1645
|||||

Sbjct: 62 tcaagatttagcgctcttgactttccaccaaggacttggcgccttgtccgg 115

>gb|CF806428.1| psHB011xI05f USDA-IFAFS:Expression of Phytophthora sojae genes during
infection and propagation Glycine max cDNA clone
sHB011I05 5, mRNA sequence
Length = 606

Score = 646 bits (326), Expect = 0.0
Identities = 415/443 (93%), Gaps = 5/443 (1%)
Strand = Plus / Minus

Query: 1844 acgagaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgcccctagaacat 1903
||||| ||||||| ||||||| ||||||| ||||| ||||||| |||||||
Sbjct: 606 acgagagcaacatagacaccgcatttgcaaggacaaggcaacaaagctgcccagaacat 547

Query: 1904 cagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgaca 1963
||||| ||||||| ||||| ||||| ||||||| ||||||| ||||||| |||||
Sbjct: 546 cagggtcaggggacaataatcttgcaccgcttgatcttcaaactccaaccgaattcgaca 487

Query: 1964 actactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgt 2023
||||| ||||||| ||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 486 actactacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgt 427

Query: 2024 tcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttct 2083
||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Sbjct: 426 tcaatgggtgggtccaccgactccattgtgcgtggctacagcaccaaccgagctccttct 367

Query: 2084 cctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctcca 2143
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 366 cctctgacttcgccgcccatgatcaagatgggagacattagtcctctcactggctcca 307

Query: 2144 atggagaaatcaggaagaattgtagaaggattaactaatt--tgattcagcttgaatat 2201
| ||||||| ||||||| ||||||| ||||||| ||||| ||||| |||||||
Sbjct: 306 acggagaaatcaggaagaattgtagaaggattaactaattactaattgagctcgaatat 247

Query: 2202 taagggtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaaacat 2258
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 246 taagggtcctactacacatacgaagcaatttaattgtgtttaataagttgttaaaacat 187

Query: 2259 gttttggttgatatttggattcc 2281
||||| |||||||
Sbjct: 186 gttttggttgatatttggattcc 164

Score = 63.9 bits (32), Expect = 4e-06
Identities = 38/40 (95%)
Strand = Plus / Minus

Query: 2388 tcctttatcaagcatttatcaagaacggagtttgcttttt 2427
|||||
Sbjct: 41 tcctttatcaagaatttatcaagaacagagtttgcttttt 2

>gb|AW349107.1| GM210004A21E9 Gm-r1021 Glycine max cDNA clone Gm-r1021-1362 3', mRNA
sequence
Length = 609

Score = 626 bits (316), Expect = e-175
Identities = 449/498 (90%), Gaps = 5/498 (1%)
Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcactacaacgag 1848
|||||
Sbjct: 604 ggtggtcacacaannnacaagcaaggtgcacnannnnngagcccgcactacaacgag 545

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaagctgccttagaacatcaggg 1908
| |||||
Sbjct: 544 agcaacatagannncgatttgcaaggacaagcaacaaagctgccaagaacatcaggg 485

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
|||||
Sbjct: 484 tcaggggacaataatcttgcaacgcttgatcttcaactccaaccgaattcgacnntac 425

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 424 tacttcaagaatcttgttcaaaagaagggtctcctccactctgatcagcnnctgttcaat 365

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggaccttctcctct 2088
|||||
Sbjct: 364 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccggagctccttctcctct 305

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtctctcactggctccaatgga 2148
|| |||||
Sbjct: 304 gacttcgccgcccatgatcaagatgggagacattagtctctcactggctccaacgga 245

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt--tgattcagcttgaatattaagg 2206
|||||
Sbjct: 244 gaaatcaggaagaattgtagaaggattaactaattactaattgagctccaatattaagg 185

Query: 2207 gtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaacatgtttt 2263
||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 184 gtcctactacacatacgaagcaatttaattgtgtttaataagttgttaaacatgtttt 125

Query: 2264 ggttgatattttggattcc 2281
||||| |||||||||
Sbjct: 124 ggttgatattttggattcc 107

>gb|BG156628.1| sab31a07.y1 Gm-c1026 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1026-3086 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 425

Score = 618 bits (312), Expect = e-173
Identities = 325/328 (99%), Gaps = 1/328 (0%)
Strand = Plus / Plus

Query: 2005 cactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagc 2064
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3 cactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagc 62

Query: 2065 accaaccggggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacatt 2124
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 63 accaaccggggcaccttctcctctgatttcgccgccgc-atgatcaagatgggagacatt 121

Query: 2125 agtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaattt 2184
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 122 agtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaattt 181

Query: 2185 gattcagcttgaatattaagggtcctacacatacgaagcaatttaattgtgtttaata 2244
|||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct: 182 aattcagcttgaatattaagggtcctacacatacgcagcaatttaattgtgtttaata 241

Query: 2245 agttgttaaacatgttttggttgatattttggattcctagtgtagtttcggtgatcaatg 2304
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 242 agttgttaaacatgttttggttgatattttggattcctagtgtagtttcggtgatcaatg 301

Query: 2305 ccgtctacttttagtgtgttctacttccc 2332
||||||||||||||||||||||||||||||

Sbjct: 302 cegtctacttttagtgtgttctacttccc 329

>gb|FK018609.1| GLND133TF JCVI-SOY3 Glycine max cDNA 5', mRNA sequence
Length = 464

Score = 557 bits (281), Expect = e-154
Identities = 291/293 (99%), Gaps = 1/293 (0%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||||
Sbjct: 172 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 231

Query: 1849 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 232 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 291

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
|||||
Sbjct: 292 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 351

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 352 tacttcaaggacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 411

Query: 2029 ggtgggtccaccgactcca-ttgtgcgtggctacagcaccaaccgggcacct 2080
|||||
Sbjct: 412 ggtgggtccaccgactccatttgtgcgtggctacagcaccaaccgggcacct 464

Score = 333 bits (168), Expect = 3e-87
Identities = 168/168 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 7 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 66

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||

Sbjct: 67 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 126

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 1645

|||||

Sbjct: 127 tttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 174

>gb|BU577048.1| sar71e12.y1 Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1074-7896 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
; , mRNA sequence
Length = 432

Score = 545 bits (275), Expect = e-151
Identities = 376/408 (92%), Gaps = 5/408 (1%)
Strand = Plus / Plus

Query: 1879 aggcagcaaagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgat 1938

|||||

Sbjct: 1 aggcacaacaagctgcccaagaacatcagggtcaggggacaataatcttgcaacgcttgat 60

Query: 1939 cttcaactccaaccagctttgacaactactacttcaagaacctcgttcagaagaagggt 1998

|||||

Sbjct: 61 cttcaactccaaccgaattcgacaactactacttcaagaatcttgttcagaagaagggt 120

Query: 1999 ctctccactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggc 2058

|||||

Sbjct: 121 ctctccactctgatcagcaactgttcaatgggtgggtccaccgactccattgtgcgtggc 180

Query: 2059 tacagcaccaaccgggcaccttctcctctgatttcgccgccgcatgatcaagatggga 2118

|||||

Sbjct: 181 tacagcaccaacttttttcttctcctctgacttcgccgccgcatgatcaagatggga 240

Query: 2119 gacattagtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaac 2178

|||||

Sbjct: 241 gacattagtcctctcactggctccaacggagaaatcaggaagaattgtagaaggattaac 300

Query: 2179 taatt--tgattcagcttgaatattaagggtc---ctacacatacgcaagcaatttaac 2233

|||||

Sbjct: 301 taattactaattgagctctccaatattaagggtcctactacacatacgcaagcaatttaac 360

Query: 2234 tgtgtttaataagttgttaaacaatgttttggttgattttggattcc 2281

|||||
Sbjct: 361 tgtgtttaataagttgttaaacaatgttttggtgtgttttgattcc 408

>gb|BM093025.1| saj04a09.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1065-9257 5' similar to TR:Q9XIV9 Q9XIV9
PEROXIDASE ;, mRNA sequence
Length = 568

Score = 527 bits (266), Expect = e-145
Identities = 266/266 (100%)
Strand = Plus / Plus

Query: 519 atcaaacacaaacacttgaagtactaagttagtggtttgagcaaattaactatggcttc 578
|||||
Sbjct: 1 atcaaacacaaacacttgaagtactaagttagtggtttgagcaaattaactatggcttc 60

Query: 579 gttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaa 638
|||||
Sbjct: 61 gttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaa 120

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaaccttctcctctgtgaa 698
|||||
Sbjct: 121 tgcacaactttctacaaacttttactaccattcatgtccaaaccttctcctctgtgaa 180

Query: 699 atccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctccttcgctt 758
|||||
Sbjct: 181 atccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctccttcgctt 240

Query: 759 gttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 241 gttcttccacgattgctttgtcaatg 266

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 266 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 325

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 326 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 385

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 1336
|||||
Sbjct: 386 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 445

Query: 1337 tctgttcagatt 1348
|||||
Sbjct: 446 tctgttcagatt 457

Score = 218 bits (110), Expect = 1e-52
Identities = 110/110 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 458 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 517

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaact 1587
|||||
Sbjct: 518 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaact 567

>gb|BE210375.1| so42h10.y1 Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1039-668 5' similar to TR:024336 024336
KOREAN-RADISH ISOPEROXIDASE ;, mRNA sequence
Length = 520

Score = 527 bits (266), Expect = e-145
Identities = 266/266 (100%)
Strand = Plus / Plus

Query: 519 atcaaacacaacacttgaagtactaagttagtggtttgagcaaattaactatggcttc 578
|||||
Sbjct: 7 atcaaacacaacacttgaagtactaagttagtggtttgagcaaattaactatggcttc 66

Query: 579 gttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaa 638
|||||

Sbjct: 67 gttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaa 126

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaacaccttctcctctgtgaa 698
|||||

Sbjct: 127 tgcacaactttctacaaacttttactaccattcatgtccaacaccttctcctctgtgaa 186

Query: 699 atccacagtgaatctgccatatctaaggagaccgcatgggtgcttctccttcgctt 758
|||||

Sbjct: 187 atccacagtgaatctgccatatctaaggagaccgcatgggtgcttctccttcgctt 246

Query: 759 gttcttccacgattgctttgtcaatg 784
|||||

Sbjct: 247 gttcttccacgattgctttgtcaatg 272

Score = 373 bits (188), Expect = 3e-99
Identities = 191/192 (99%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||

Sbjct: 272 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 331

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||

Sbjct: 332 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 391

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagac 1336
|||||

Sbjct: 392 gagaaagtgtgtccaggagttgtttcctgcgagatatccttgccatcactgccagagac 451

Query: 1337 tctgttcagatt 1348
|||||

Sbjct: 452 tctgttcagatt 463

Score = 97.6 bits (49), Expect = 3e-16
Identities = 55/57 (96%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagc 1534
||||| ||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct: 464 cttggaagccctacatggaatgttaaacttgaagaagagacgctagaactgctagc 520

>gb|EV263181.1| GLLA357TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 813

Score = 525 bits (265), Expect = e-145
Identities = 274/277 (98%)
Strand = Plus / Plus

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtggtttgagcaaatta 567
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 3 acaccctttcaatcaaacacaaacactcgaagtactaagttagtggttcgagcaaatta 62

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 63 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 122

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 123 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 182

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttct 747
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 183 tcctctgtgaaatccgcagtgcaatctgccatatctaaggagaccgcgatgggtgcttct 242

Query: 748 ctcttcgcttgttcttccacgattgctttgtcaatg 784
||||| ||||||||||||||||||||||| |||||||
Sbjct: 243 ctcttcgcttgttcttccacgattgctttgtcaatg 279

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 279 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 338

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 339 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 398

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 1336
|||||
Sbjct: 399 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 458

Query: 1337 tctgttcagatt 1348
|||||
Sbjct: 459 tctgttcagatt 470

Score = 333 bits (168), Expect = 3e-87
Identities = 168/168 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 471 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 530

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 531 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 590

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtccggt 1645
|||||
Sbjct: 591 tttagcgctcttggactttccaccaaggacttggctgccttgtccggt 638

Score = 270 bits (136), Expect = 4e-68
Identities = 178/184 (96%), Gaps = 6/184 (3%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacgag 1848
|||||
Sbjct: 636 ggtggtcacacaattggacaagcaag-tgcacaaacttcagagcccgcattacaacgag 694

Query: 1849 accaacaatagaaccgatttgaaggacttaggcagcaaagctgccctagaacatcaggg 1908

Score = 250 bits (126), Expect = 3e-62
Identities = 126/126 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 272 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 331

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 332 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 391

Query: 1277 gagaaa 1282
|||||
Sbjct: 392 gagaaa 397

>gb|BI972311.1| sag89h02.y1 Gm-c1084 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1084-1515 5' similar to TR:Q9XIV9 Q9XIV9
PEROXIDASE ;, mRNA sequence
Length = 573

Score = 502 bits (253), Expect = e-138
Identities = 253/253 (100%)
Strand = Plus / Plus

Query: 532 acttgaagtactaagttagtggtttgagcaaattaactatggcttcgttttgttctaga 591
|||||
Sbjct: 1 acttgaagtactaagttagtggtttgagcaaattaactatggcttcgttttgttctaga 60

Query: 592 ttgacaatttgtttggctctgtttgtcctcatatgggggagtgccaatgcacaactttct 651
|||||
Sbjct: 61 ttgacaatttgtttggctctgtttgtcctcatatgggggagtgccaatgcacaactttct 120

Query: 652 acaaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaa 711
|||||
Sbjct: 121 acaaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaa 180

Query: 712 tctgcatatctaaggagaccgcatgggtgcttctctccttcgcttgttctccacgat 771
|||||
Sbjct: 181 tctgcatatctaaggagaccgcatgggtgcttctctccttcgcttgttctccacgat 240

Query: 772 tgctttgtcaatg 784
 |||||||
Sbjct: 241 tgctttgtcaatg 253

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 |||||||
Sbjct: 253 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 312

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 |||||||
Sbjct: 313 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 372

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcatatccttgccatcgctgccagagac 1336
 |||||||
Sbjct: 373 gagaaagtgtgtccaggagttgtttcctgcgcatatccttgccatcgctgccagagac 432

Query: 1337 tctgttcagatt 1348
 |||||||
Sbjct: 433 tctgttcagatt 444

Score = 240 bits (121), Expect = 3e-59
Identities = 127/129 (98%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
 |||||||
Sbjct: 445 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 504

Query: 1538 tctgctgctaacaatggcatcctgcaccacttcaaacttaaccaactcatctcaaga 1597
 |||||||
Sbjct: 505 tctgctgctaacaatggcatcctgcaccacttcaaacttaaccaactcatctcaaga 564

Query: 1598 tttagcgct 1606
|||||||
Sbjct: 565 tttagcgct 573

>gb|BE209964.1| so37a08.y1 Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1039-111 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 391

Score = 490 bits (247), Expect = e-134
Identities = 247/247 (100%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 114 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 173

Query: 1849 accaacatagaaacgcatttgaaggactaggcagcaaagctgcacctagaacatcaggg 1908
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 174 accaacatagaaacgcatttgaaggactaggcagcaaagctgcacctagaacatcaggg 233

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 234 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 293

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 294 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 353

Query: 2029 ggtgggt 2035
|||||||
Sbjct: 354 ggtgggt 360

Score = 230 bits (116), Expect = 3e-56
Identities = 116/116 (100%)
Strand = Plus / Plus

Query: 1530 ctagccaatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactca 1589
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1 ctagccaatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactca 60

Query: 1590 tctcaagatttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 1645
|||||
Sbjct: 61 tctcaagatttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 116

>gb|BG725689.1| sae39d12.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1051-7487 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 499

Score = 464 bits (234), Expect = e-126
Identities = 285/302 (94%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacgag 1848
|||||
Sbjct: 197 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacgag 256

Query: 1849 accaacatagaaacgcatttgaaggacttaggcagcaaaagctgccctagaacatcaggg 1908
| |||||
Sbjct: 257 agcaacatagacaccgcatttgaaggacaaggcaacaaagctgccaagaacatcaggg 316

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 317 tcaggggacaataatctggcaccgcttgatcttcaaactccaaccgaattcgacaactac 376

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 377 tacttcaagaatcttgggttcagaagaagggtctcctccactctgatcagcaactgttcaat 436

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggacettctctct 2088
|||||
Sbjct: 437 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccggagctccttctctct 496

Query: 2089 ga 2090
||
Sbjct: 497 ga 498

Score = 293 bits (148), Expect = 3e-75

Identities = 163/168 (97%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 32 cttggaggccctagttggaatgttaaagtgaagaagagacgctagaactgctagccaa 91

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 92 tctgctgctaacaatggcatccctccaccacttcaaaccttaaccaactcatctcaaga 151

Query: 1598 tttagcgccttggactttccaccaaggacttggcgccttgtccggt 1645
||
Sbjct: 152 ttcagcgccttggactttccaccaaggacttggcgccttgtccggt 199

Score = 50.1 bits (25), Expect = 0.065
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 1319 gccatcgctgccagagactctgttcagat 1347
|||||
Sbjct: 2 gccatagctgccagagactctgttcagat 30

>gb|FG889629.1| UCRVU08_CCNS10828_g1 Cowpea IT97K-461-4 Mixed Tissue and Conditions
cDNA Library UCRVU08-1-2 Vigna unguiculata cDNA clone
CCNS10828.g1, mRNA sequence
Length = 670

Score = 444 bits (224), Expect = e-120
Identities = 341/380 (89%)
Strand = Plus / Minus

Query: 1800 aattggacaagcaaggtgcacaaacttcagagcccgcctctacaacgagaccaacataga 1859
|||||
Sbjct: 670 aattggacaagcaaggtgcacaaatttcagagcccgcctctacaacgagaccaacattga 611

Query: 1860 aaccgcatttgcaaggacttaggcagcaaagctgccctagaacatcagggtcaggggacaa 1919
|||
Sbjct: 610 tacctcatttgccaggacaagacaatcaagctgccccagaacatcagggtcaggggacaa 551

Query: 1920 caatctggcaccacttgatcttcaaactccaaccagctttgacaactactacttcaagaa 1979
|||||
Sbjct: 550 caatctggcaccgcttgatcttcagactccgaccacattcgacaactactacttcaagaa 491

Query: 1980 cctcgttcagaagaagggtctctccactctgatcagcaactggtcaacgggtgggtccac 2039
|||
Sbjct: 490 cctggttcagaagaagggtctctccactctgaccagcaactcttcaatgggtgggtccac 431

Query: 2040 cgactccattgtgcgtggctacagcaccaaccgggcaccttctcctctgatttcgccgc 2099
|||
Sbjct: 430 tgactccatagtgctggctacagcaccaaccggagctccttttctctgattttgtctc 371

Query: 2100 cgccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaa 2159
|||
Sbjct: 370 cgccattatcaagatgggagacattagtcctctcactggctccaaggagaaatcagaaa 311

Query: 2160 gaattgtagaaggattaact 2179
|||
Sbjct: 310 gaactgcagaaggattaact 291

>gb|BE022389.1| sm85b11.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1015-6838 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 571

Score = 438 bits (221), Expect = e-119
Identities = 278/297 (93%)
Strand = Plus / Plus

Query: 1834 cgcactctacaacgagaccaacatagaaaccgcatcttgcaaggactaggcagcaaagctgc 1893
|||
Sbjct: 6 cgcactctacaacgagagcaacatagacaccgcatcttgcaaggacaaggcaacaaagctgc 65

Query: 1894 cctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaacc 1953
|||
Sbjct: 66 ccaagaacatcagggtcaggggacaataatcttgcaacgcttgatcttcaaactccaacc 125

Query: 1954 agctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgat 2013
|||
Sbjct: 126 gaattcgacaactactacttcaagaatcttggttcagaagaagggtctcctccactctgat 185

Query: 2014 cagcaactgttcaacgggtgggtccaccgactccattgtgctggctacagcaccaaccg 2073
|||||
Sbjct: 186 cagcaactgttcaatgggtgggtccaccgactccattgtgctggctacagcaccaaccg 245

Query: 2074 ggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtcct 2130
||
Sbjct: 246 agtccttctcctctgacttcgccgcccatgatcaagatgggagacattagtcct 302

>gb|BG359695.1| sac27d09.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1051-3617 5' similar to TR:Q9XIV9 Q9XIV9
PEROXIDASE :, mRNA sequence
Length = 233

Score = 436 bits (220), Expect = e-118
Identities = 230/232 (99%), Gaps = 1/232 (0%)
Strand = Plus / Plus

Query: 533 cttgaagtactaagttagtggtttgagcaaattaactatggcttcgttttgttctagat 592
|||||
Sbjct: 2 cttgaagtactaagttagtggtttgagcaaattaactatggcttc-ttttgttctagat 60

Query: 593 tgacaattttgtttggctctgtttgcctcatatgggggagtccaatgcacaactttcta 652
|||||
Sbjct: 61 tgacaattttttggctctgtttgcctcatatgggggagtccaatgcacaactttcta 120

Query: 653 caaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaat 712
|||||
Sbjct: 121 caaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaat 180

Query: 713 ctgccatatctaaggagaccgcatgggtgcttctccttcgcttgttctt 764
|||||
Sbjct: 181 ctgccatatctaaggagaccgcatgggtgcttctccttcgcttgttctt 232

>gb|EV265313.1| GLLAS95TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 652

Score = 412 bits (208), Expect = e-111
Identities = 260/277 (93%), Gaps = 4/277 (1%)
Strand = Plus / Plus

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaatta 567
||||||| ||||| ||||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 2 acaccctctcaagcaaacacaaacacttgaagtactaagttagtgtttttgagcaaa--- 58

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||| |
Sbjct: 59 -ctatggcttcgttttgttctagattgaccatttgtttggctctgtttgtcctcatattg 117

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||||||||||||| ||||||||||||||||| ||||||||||||| |||||||||||||
Sbjct: 118 gggagtgccaatgccaaactttctacaaacttttactaccattcgtgtccaaacctcttc 177

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttct 747
||| ||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct: 178 tccactgtgaaatccacagtgcaatctgccatatcaaaggagaccgcatgggtgcttct 237

Query: 748 ctctctcgcttgttcttccacgattgctttgtcaatg 784
||||| ||| |||||||||||||||||||||||||
Sbjct: 238 ctctccgccgcttcttccacgattgctttgtcaatg 274

Score = 331 bits (167), Expect = 1e-86
Identities = 185/191 (96%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct: 274 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 333

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||||||||||||||||||||||||| ||||| |||||||||||||||||||||
Sbjct: 334 aacccaacaggaactctgctcgtggatacagagtcattgacaacattaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgttctctgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||||||||||||| ||||||||||||||||||||| |||||||||
Sbjct: 394 gagaaagcatgtccaggagttgtctctctgcgcagatatccttgccatagctgccagagac 453

Query: 1337 tctgttcagat 1347
|||||||

Sbjct: 454 tctgttcagat 464

Score = 293 bits (148), Expect = 3e-75
Identities = 163/168 (97%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 466 cttggaggccctagtgtgaatgttaaagttggagaagagacgctagaactgctagccaa 525

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 526 tctgctgctaacaatggcatccctccaccacttcaaacttaaccaactcatctcaaga 585

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtccggt 1645
||
Sbjct: 586 ttcagcgctcttggactttccaccaaggacttggctgccttgtccggt 633

Score = 44.1 bits (22), Expect = 4.0
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaag 1810
|||||
Sbjct: 631 ggtggtcacacaattggacaag 652

>gb|AW132280.1| se02a03.y1 Gm-c1013 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1013-2309 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 552

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 151 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 210

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 211 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 270

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 1336
|||||
Sbjct: 271 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 330

Query: 1337 tctgttcagatt 1348
|||||
Sbjct: 331 tctgttcagatt 342

Score = 325 bits (164), Expect = 7e-85
Identities = 167/168 (99%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 343 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 402

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 403 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 462

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtccggt 1645
| |||||
Sbjct: 463 ttagcgctcttggactttccaccaaggacttggctgccttgtccggt 510

Score = 299 bits (151), Expect = 4e-77
Identities = 151/151 (100%)
Strand = Plus / Plus

Query: 634 gccaatgcacaactttctacaaacttttactaccattcatgtccaaaccttctctctct 693
|||||
Sbjct: 1 gccaatgcacaactttctacaaacttttactaccattcatgtccaaaccttctctctct 60

Query: 694 gtgaaatccacagtgaatctgccatataagagaccgcatgggtgcttctctctct 753

|||||
Sbjct: 61 gtgaaatccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctcctt 120

Query: 754 cgcttggttcttccacgattgctttgtcaatg 784

|||||
Sbjct: 121 cgcttggttcttccacgattgctttgtcaatg 151

Score = 83.8 bits (42), Expect = 5e-12
Identities = 44/45 (97%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcc 1833

|||||
Sbjct: 508 ggtggtcacacaattggacaagcaaggtgcacanaacttcagagcc 552

>gb|CF809087.1| psHB042xH14f USDA-IFAFS:Expression of Phytophthora sojae genes during
infection and propagation Glycine max cDNA clone
SHB042H14 5, mRNA sequence
Length = 364

Score = 373 bits (188), Expect = 3e-99
Identities = 188/188 (100%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848

|||||
Sbjct: 177 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 236

Query: 1849 accaacatagaaaccgatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908

|||||
Sbjct: 237 accaacatagaaaccgatttgaaggactaggcagcaaagctgccctagaacatcaggg 296

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

|||||
Sbjct: 297 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 356

Query: 1969 tacttcaa 1976

|||||
Sbjct: 357 tacttcaa 364

Score = 333 bits (168), Expect = 3e-87
Identities = 168/168 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 12 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 71

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 72 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 131

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
|||||
Sbjct: 132 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 179

>gb|BU577870.1| sar93g05.y1 Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1074-9922 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 426

Score = 373 bits (188), Expect = 3e-99
Identities = 231/245 (94%), Gaps = 4/245 (1%)
Strand = Plus / Plus

Query: 540 tactaagttagtgtgtttgagcaaatctatggcttcgttttgttctagattgacaat 599
|||||
Sbjct: 1 tactaagttagtgttttggagcaaa----ctatggcttcgttttgttctagattgacat 56

Query: 600 ttgtttggctctgtttgtcctcatatggggagtgccaatgcacaactttctacaaactt 659
|||||
Sbjct: 57 ttgtttggctctgtttgtcctcatattggggagtgccaatgcacaactttctacaaactt 116

Query: 660 ttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaatctgcat 719
|||||
Sbjct: 117 ctactaccattcgtgtccaaacctcttctcctctgtgaaatccacagtgcaatctgcat 176

Query: 720 atctaaggagaccgcatgggtgcttctctccttcgcttgttcttccacagattgctttgt 779
|||

Sbjct: 177 atcaaaggagaccgcatgggtgcttctctcctccgctgttcttccacgattgctttgt 236

Query: 780 caatg 784

|||||

Sbjct: 237 caatg 241

Score = 321 bits (162), Expect = 1e-83

Identities = 180/186 (96%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

|||||

Sbjct: 241 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 300

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|||||

Sbjct: 301 aacccaacaggaactctgctcgtggatacgaggtcattgacaacattaaatcagccgtg 360

Query: 1277 gagaaagtgtgtccaggagttgttctcctgcgcagatatccttgccatcgtgccagagac 1336

|||||

Sbjct: 361 gagaaagcatgtccaggagttgtcctcctgcgcagatatccttgccatagctgccagagac 420

Query: 1337 tctgtt 1342

|||||

Sbjct: 421 tctgtt 426

>gb|AW432575.1| sh76b11.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1015-5686 5' similar to SW:PERX_BRARA P00434

PEROXIDASE P7 ;, mRNA sequence

Length = 313

Score = 361 bits (182), Expect = 1e-95

Identities = 263/290 (90%)

Strand = Plus / Plus

Query: 1791 tggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagac 1850

|||||

Sbjct: 1 tggtcgcacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagac 60

Query: 1851 caacatagaaacgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtc 1910
||||| ||||| ||||||||| ||| ||||||||| ||||| ||||||||| ||||||||| |||||||||
Sbjct: 61 caacgtagagaccgcattggcatggactaggcgcaaaactgccctagaacatcagggtc 120

Query: 1911 aggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactacta 1970
||||||| ||||||||| ||||||||| ||| ||||||| || | ||||||| ||
Sbjct: 121 aggggacagcaatctggcaccacttgataacttaactccgacatagtagacaactagta 180

Query: 1971 ctcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacgg 2030
||| ||||||||| ||||||||| ||||| ||||||||| ||||||||| |||||||||
Sbjct: 181 cttgtagaacctcgttcataagaagggtctcctcactgtgatcagcaactgttcaacgg 240

Query: 2031 tgggtccaccgactccattgtgcgtggctacagcaccaaccgggacact 2080
||||||| ||||||||| ||||||||| ||||| ||||||||| |||||||||
Sbjct: 241 tgggtccaccgactccgttgcgtggctacagcagcagcccgggacact 290

>gb|FG825601.1| UCRVU04_CCNI8859_g1 Cowpea 524B Mixed Tissue and Conditions cDNA
Library UCRVU04-1-2 Vigna unguiculata cDNA clone
CCNI8859.g1, mRNA sequence
Length = 604

Score = 343 bits (173), Expect = 3e-90
Identities = 263/293 (89%)
Strand = Plus / Minus

Query: 1887 aagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaac 1946
||||||| ||||||||| ||||||||| ||||||||| ||||||||| || || ||||||||| ||
Sbjct: 589 aagctgcccagaacatcagggtcaggggacaacaatctggccccgcttgatcttcagac 530

Query: 1947 tccaaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctcca 2006
||| |||| | ||||||||| ||||||||| ||||||| ||||||||| ||||||||| |||||
Sbjct: 529 tccgaccacattcgacaactactacttcaggaacctggttcagaagaagggtcttctcca 470

Query: 2007 ctctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcac 2066
||||||| ||||||||| ||||| ||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 469 ctctgaccagcaactcttcaatggtggctccactgactccatagtgctggctacagcac 410

Query: 2067 caaccgggacacttctcctctgatttcgccgcccgatgatcaagatgggagacattag 2126
||||||| || ||||| ||||||||| | | ||||||| ||||||||| ||||||||| |||||||||
Sbjct: 409 caaccgaagctcctttcctctgattttgtctccgattatcaagatgggagacattag 350

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 122 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 181

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 182 aaccccaacaggaactctgctcgtggatacgaggtcattgacaacattaaatcagccgtg 241

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 242 gagaaagcatgtccaggagttgtctcctgcgcatatccttgccatagctgccagagac 301

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 302 tctgttcagat 312

Score = 281 bits (142), Expect = 1e-71
Identities = 159/165 (96%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 314 cttggaggccctagttggaatgttaaagttggaagaagagacgctagaactgctagccaa 373

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 374 tctgctgctaacaatggcatccctccaccacttcaaaccttaaccaactcatctcaaga 433

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgtcc 1642
||
Sbjct: 434 ttcagcgtcttggactntccaccaaggacttggctgccttgtcc 478

Score = 202 bits (102), Expect = 7e-48
Identities = 117/122 (95%)
Strand = Plus / Plus

Query: 663 ctaccattcatgtccaaaccttctcctctgtgaaatccacagtgaatctgcatatc 722
|||||

Sbjct: 91 tccgaccacattcgacaactactacttccaggaacctgggttcagaagaagggtcttctcca 150

Query: 2007 ctctgatcagcaactgttcaa-cggtgggtccaccgactccattgtgcgtggctacagca 2065
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 151 ctctgaccagcaactcttcaataggtgggtccactgactccatagtgcgtggctacagca 210

Query: 2066 ccaacccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacatta 2125
||||| || |||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||

Sbjct: 211 ccaaccaagctccttttctcctgattttgtctccgcatatcaagatgggagacatta 270

Query: 2126 gtcctctcaactggctccaatggagaaatcaggaagaattgtagaaggattaact 2179
|||| ||||| ||||| ||||| ||||| ||||| || ||||| ||||| |||||

Sbjct: 271 gtcccctcaccggctccaagagaaatcagaagaactgcagaaggattaact 324

>gb|AI441922.1| sa51f09.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1004-2850 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 480

Score = 291 bits (147), Expect = 1e-74
Identities = 165/171 (96%)
Strand = Plus / Plus

Query: 1177 attgatgacacatcaagcttcaccggagagaagaacgcaaaccaccaaggaactctgc 1236
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 6 attgatgacacatcaagcttcaccggagagaagaacgcaaaccaccaaggaactctgc 65

Query: 1237 tcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtccaggagt 1296
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 66 tcgtgatacagagtcattgacaacattaaatcagccgtggagaaagcatgtccaggagt 125

Query: 1297 tgtttcctgcgcagatataccttgccatcgctgccagagactctgttcagat 1347
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 126 tgtctcctgcgcagatataccttgccatagctgccagagactctgttcagat 176

Score = 287 bits (145), Expect = 2e-73
Identities = 160/165 (96%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 178 cttggaggccctagttggaatgttaaagttggagaagagacgctagaactgctagccaa 237

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 238 tctgctgctaacaatggcatccctccacccacttcaaacttaaccaactcatctcaaga 297

Query: 1598 tttagcgccttggactttccaccaaggacttggcgccttgtcc 1642
||
Sbjct: 298 ttcagcgccttggactttccaccaaggacttggcgccttgtcc 342

Score = 206 bits (104), Expect = 5e-49
Identities = 129/136 (94%), Gaps = 1/136 (0%)
Strand = Plus / Plus

Query: 1790 gtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacgaga 1849
|||||
Sbjct: 344 gtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacgaga 403

Query: 1850 ccaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcagggt 1909
|||||
Sbjct: 404 gcaacatagacaccgcatttgaaggacaaggcaacaaagctgccaagaacatca-ggt 462

Query: 1910 caggggacaacaatct 1925
|||||
Sbjct: 463 caggggacaataatct 478

>gb|G0029196.1| LJMAW92TO JCVI-LJ2 Lotus japonicus cDNA 3', mRNA sequence
Length = 887

Score = 289 bits (146), Expect = 4e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 388 tcaggggacaacaatttggcaccacttgacctcagactccaacctcctttgacaacaac 329

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactggttcaac 2028
|||||
Sbjct: 328 tacttcaagaacctcggttcagaacaaggcctctactccgaccagcaactcttcaac 269

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggaccttctcctct 2088
|||||
Sbjct: 268 ggtggctccaccgactccaccgtgcgtggctacagcaccaaccggagctcatttctcctct 209

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||
Sbjct: 208 gatttcgcccagcgcctatggtcaagatgggagatatcagtcctctcactggatccaacggt 149

Query: 2149 gaaatcaggaagaattgtagaa 2170
|||||
Sbjct: 148 gaaatcaggaagaattgcagaa 127

Score = 180 bits (91), Expect = 3e-41
Identities = 160/183 (87%)
Strand = Plus / Minus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 865 tgtgatggttcagttctacttgatgacacatcaagcttcaccgggagaagaatgcaaac 806

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 805 cccaacagaaactctgctcgcggatttgatgattattgacaacatcaagtcagcagtagag 746

Query: 1280 aaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgtgccagagactct 1339
||
Sbjct: 745 gcagcatgccaggagttgtatcctgcgctgatatcctcgccatctctgctagagactct 686

Query: 1340 gtt 1342
|||
Sbjct: 685 gtt 683

Score = 123 bits (62), Expect = 5e-24
Identities = 134/158 (84%)

Strand = Plus / Minus

Query: 1484 ggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaatctgct 1543
||||| ||||||| ||| | ||||||| ||||||| ||||||| ||||||| ||| ||

Sbjct: 670 ggccccacatggaatgtgaaagtaggaagaagagacgctaaaactgctagccagtcgcc 611

Query: 1544 gctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| |||| | ||||||| ||||||| | | | ||||||| ||||||| || ||

Sbjct: 610 gccaacacagggcatccctgcaccacttctagcttgagccaactcacctcaagttcagt 551

Query: 1604 gctcttggactttccaccaaggacttggcgccttgct 1641
||||| ||||||| ||| ||||||| || |||||

Sbjct: 550 gctcttggactttccagcaaagacttggttgcattgct 513

>dbj|BP048143.1| BP048143 Lotus corniculatus var. japonicus pods (less than 20 mm in length) Lotus japonicus cDNA clone SPD052d03_f 3', mRNA sequence
Length = 472

Score = 289 bits (146), Expect = 4e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

Sbjct: 418 tcaggggacaacaatttggcaccacttgacctcagactccaacctccttgacaacaac 359

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||| ||||||| ||||||| ||||| ||||| ||||| || ||||||| |||||||

Sbjct: 358 tacttcaagaacctgggttcagaacaaggcctctacactccgaccagcaactcttcaac 299

Query: 2029 ggtgggtccaccgactccattgtgctggctacagaccaacccgggaccttctcctct 2088
||||| ||||||| ||||||| ||||||| ||||||| || || || |||||

Sbjct: 298 ggtgggtccaccgactccaccgtgctggctacagaccaacccgagctcattttcctct 239

Query: 2089 gatttcgccgcccgatgatcaagatgggagacattagtctctcactggctccaatgga 2148
||||| ||||||| ||||||| ||||||| || ||||||| ||||||| ||||| ||

Sbjct: 238 gatttcgccagcggcatgggtcaagatgggagatatcagctctcactggatccaacggt 179

Query: 2149 gaaatcaggaagaattgtagaa 2170

|||||
Sbjct: 178 gaaatcaggaagaattgcagaa 157

>dbj|BP048038.1| BP048038 Lotus corniculatus var. japonicus pods (less than 20 mm in length) Lotus japonicus cDNA clone SPD051a08_f 3', mRNA sequence
Length = 513

Score = 289 bits (146), Expect = 4e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 453 tcaggggacaacaattggcaccacttgaccttcagactccaacctcctttgacaacaac 394

Query: 1969 tacttcaagaacctcggttcagaagaagggtctctcctcactctgatcagcaactgttcaac 2028
|||||
Sbjct: 393 tacttcaagaacctgggttcagaacaaggcctctacactccgaccagcaactcttcaac 334

Query: 2029 ggtgggtccaccgactccattgtgctggctacagcaccaacccgggcaccttctctct 2088
|||||
Sbjct: 333 ggtgggtccaccgactccaccgtgctggctacagcaccaacccgagctcattttctct 274

Query: 2089 gatttcgccgcgccatgatcaagatgggagacattagtctctcactggctccaatgga 2148
|||||
Sbjct: 273 gatttcgccagcgccatggtcaagatgggagatatcagtctctcactggatccaacggt 214

Query: 2149 gaaatcaggaagaattgtagaa 2170
|||||
Sbjct: 213 gaaatcaggaagaattgcagaa 192

>dbj|AV768169.1| AV768169 Lotus japonicus Young plants (two-weeks old) Lotus japonicus cDNA clone MWM225a08_f 3', mRNA sequence
Length = 587

Score = 289 bits (146), Expect = 4e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

Query: 2089 gatttcgccgcccgcattgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||| ||||||||| || ||||||||| ||||| ||
Sbjct: 262 gatttcgccagcgcattggtaagatgggagatatcagtcctctcactggatccaacggt 203

Query: 2149 gaaatcaggaagaattgtagaa 2170
||||||| |||||
Sbjct: 202 gaaatcaggaagaattgcagaa 181

>gb|G0017605.1| LJGBF85T0 JCVI-LJ1 Lotus japonicus cDNA 3', mRNA sequence
Length = 420

Score = 266 bits (134), Expect = 6e-67
Identities = 230/262 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||||| ||||| ||||| || ||||| || ||||| || ||||| ||
Sbjct: 265 tcaggggacaacaatttggcaccacttgaccttcagacaccaacctccttcgacaacaac 206

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctcactctgatcagcaactgttcaac 2028
||||| ||||| ||||| || ||||| ||||| ||||||||| |||||
Sbjct: 205 tacttcaagaacctggttcaaaacaaggcctctacactctgatcagcaacttttcaac 146

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccacccggcactttctcctct 2088
||||| || ||||| || ||||| ||||| ||||| || || |||||
Sbjct: 145 ggtggctccgccgactccaccgtgcgtggctacagcaccacccgagctcattttctct 86

Query: 2089 gatttcgccgcccgcattgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||| ||||||||| || ||||||||| ||||| ||
Sbjct: 85 gatttcgccagcgcattggtaagatgggagatatcagtcctctcactggatccaacggt 26

Query: 2149 gaaatcaggaagaattgtagaa 2170
||||||| |||||
Sbjct: 25 gaaatcaggaagaattgcagaa 4

>gb|G0023584.1| LJMCD71TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA sequence
Length = 630

Score = 262 bits (132), Expect = 9e-66
Identities = 210/236 (88%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 387 tcaggggacaacaatttggcaccacttgaccttcagactccaacctcctttgacaacaac 446

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 447 tacttcaagaacctggttcagaacaaggcctctacactccgaccagcaactcttcaac 506

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
|||||
Sbjct: 507 ggtggctccaccgactccaccgtgcgtggctacagcaccaacccgagctcattttctcct 566

Query: 2089 gatttcgccgcccgatgatcaagatgggagacattagtctctcactggctcaa 2144
|||||
Sbjct: 567 gatttcgccagcggcatggtcaagatgggagatatcagtcctctcactggatcaa 622

Score = 123 bits (62), Expect = 5e-24
Identities = 134/158 (84%)
Strand = Plus / Plus

Query: 1484 ggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaatctgct 1543
|||||
Sbjct: 105 ggccccacatggaatgtgaaagtaggaagaagagacgctaaaactgctagccagtcgcc 164

Query: 1544 gctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| ||||
Sbjct: 165 gccaacacaggcatccctgcaccacttctagcttgagccaactcacctcaagttcagt 224

Query: 1604 gctcttggactttccaccaaggacttggctgccttgtc 1641
|||||
Sbjct: 225 gctcttggactttccagcaaagacttggttgcattgtc 262

Score = 69.9 bits (35), Expect = 7e-08
Identities = 77/91 (84%)
Strand = Plus / Plus

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||||||| ||||||| ||||||||| ||||||||| ||||
Sbjct: 510 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 569

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgct 1641
|| || ||||| ||||||||| ||||||||| ||||||||| |||||
Sbjct: 570 ttcagtgccttaggactttccaccaaggacttggctgccttgct 613

Score = 234 bits (118), Expect = 2e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatggggg 630
||||||| ||||||||| || || ||||| ||||||||| || ||||
Sbjct: 45 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 104

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
||| ||||||||| ||||| ||||| ||| || ||||| ||| |||||
Sbjct: 105 tgtgtcaatgcacaactttctactgacttctactacagttcttgcceaaaactcctctcc 164

Query: 691 tctgtgaaatccacagtgcfaatctgccatatctaaggagaccgcatgggtgcttctctc 750
||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||
Sbjct: 165 actgtgagatccacagtgcfaatctgccatatcaaaggagaccgcatgggtgcttctctc 224

Query: 751 cttcgcttgttcttccacgattgctttgtcaatg 784
|| ||||||||| ||||||||| ||||||||| |||||
Sbjct: 225 ctccgcttgttcttccacgattgctttgtcaatg 258

Score = 83.8 bits (42), Expect = 5e-12
Identities = 48/50 (96%)
Strand = Plus / Plus

Query: 1789 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcat 1838
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||
Sbjct: 615 ggtgggcacacaattggacaagcaaggtgcacaaatttcagagcccgcat 664

>gb|FF394030.1| MOODS81TF MOO Vigna unguiculata cDNA 5', mRNA sequence
Length = 786

Score = 246 bits (124), Expect = 5e-61
Identities = 172/188 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 274 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccgggagaagaacgca 333

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||||| ||||||||| || || || ||||| ||| |||||||||
Sbjct: 334 aacccaacagaaactctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgtttcctgctgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||||| || || ||||||||| || |||||||||
Sbjct: 394 gagaaagtgtgtccaggagttgtttcctgctgcgatatccttgctattgctgccagagac 453

Query: 1337 tctgttca 1344
|||||||
Sbjct: 454 tctgttca 461

Score = 238 bits (120), Expect = 1e-58
Identities = 153/164 (93%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 466 cttggaggccctagtgtgaatgttaaacttggagaagagatgctagaactgctagccaa 525

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||||||| ||||| ||||||||| ||||||||| |||||
Sbjct: 526 tctgctgccaacaatggcattcctgcaccttctcaaaccttaaccaactcatctctaga 585

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtc 1641
|| || ||||| ||||||||| ||||||||| |||||||||
Sbjct: 586 ttcagtgccttaggactttccaccaaggacttggctgccttgtc 629

Score = 234 bits (118), Expect = 2e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttgtttggtctctgtttgtcctcatatggggg 630
|||||
Sbjct: 61 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 120

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctttctcc 690
|||
Sbjct: 121 tgtgtcaatgcacaactttctactgacttctactacagttcttgccaaaaactcctctcc 180

Query: 691 tctgtgaaatccacagtgcgaatctgccatatctaaggagaccgcatgggtgcttctctc 750
|||||
Sbjct: 181 actgtgagatccacagtgcgaatctgccatatcaaaggagaccgcatgggtgcttctctc 240

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784
||
Sbjct: 241 ctccgcttggttcttccacgattgctttgtcaatg 274

Score = 180 bits (91), Expect = 3e-41
Identities = 140/155 (90%), Gaps = 1/155 (0%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||||
Sbjct: 631 ggtggccacacaattggacaagcaaggtgcacaaatttcagagcccgcacatctacaacgag 690

Query: 1849 accaacatagaaaccgcatTTTgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
|
Sbjct: 691 agcaacatagatacctcattagccaggacaagacaatcaagctgccccagaacatcaggg 750

Query: 1909 tcaggggacaacaatctggcaccacttgatcttca 1943
|||
Sbjct: 751 tca-gggacaacaatctggcaccgcttgatcttca 784

>gb|FF387818.1| M00C268TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 625

Score = 246 bits (124), Expect = 5e-61
Identities = 172/188 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 226 ggatgtgacggttcgattcctttggatgacacgtcaagcttcaccgggagaagaacgca 285

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276
||||||| || ||||||||| || || ||||||| ||| |||||||||
Sbjct: 286 aacccaacagaaattctgctcgtggatgatgaagtcattgacagcataaaatcagccgtg 345

Query: 1277 gagaaagtgtgtccaggagttgtttcctgctgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||||| ||||||||| || ||||||||| ||||||||| |||||||||
Sbjct: 346 gagaaagtgtgtccaggagttgtttcctgctgcggatatccttgccattgctgccagagac 405

Query: 1337 tctgttca 1344
|||||||
Sbjct: 406 tctgttca 413

Score = 226 bits (114), Expect = 5e-55
Identities = 189/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttgtttggctctgtttgcctcatatggggg 630
||||||| || || ||||| ||||||||| || |||
Sbjct: 13 atggcttcgttttgttctagattaactatcagtttgggtgctgtttgcctcgtactgggt 72

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
||| ||||||||| ||||| ||||| ||| || ||||| ||| |||||
Sbjct: 73 tgtgtcaatgcacaactttctactgacttctactacagttcttgccaaaactcctctcc 132

Query: 691 tctgtgaaatccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctc 750
||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 133 actgtgagatccacagtgaatctgccatatcaaaggagaccgcgatgggtgcttctctc 192

Query: 751 cttcgttgttcttccacgattgctttgtcaatg 784
|| ||||||||| ||||||||| |||||||||

|||||
Sbjct: 206 aacccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 265

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagac 1336

|||||
Sbjct: 266 gagaaagtgtgtccaggagttgtttcctggtgagatatccttgccattgctgccagagac 325

Query: 1337 tctgttca 1344

|||||
Sbjct: 326 tctgttca 333

Score = 216 bits (109), Expect = 5e-52
Identities = 148/161 (91%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537

|||||
Sbjct: 338 cttggaggccctagtgtgaatgttaaacttggagaagagatgctagaactgctagccga 397

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 1597

|||||
Sbjct: 398 tctgctgccaacaatggcattcctgcaccttctcaaacttaaccaactcatctctaga 457

Query: 1598 tttagcgctcttggactttccaccaaggacttgggtgcctt 1638

|| || |||||
Sbjct: 458 ttcagtgtcttaggactttccaccaaaggacttgggtgcctt 498

Score = 178 bits (90), Expect = 1e-40
Identities = 132/146 (90%)
Strand = Plus / Plus

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaaccttctcctctgtgaa 698

|||||
Sbjct: 1 tgcacaactttctactgacttctactacagttcttgccaaaactcctctccactgtgag 60

Query: 699 atccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctctcctcgctt 758

|||||
Sbjct: 61 atccacagtgaatctgccatatcaaaggagaccgcatgggtgcttctctccccgctt 120

Query: 759 gttcttccacgattgctttgtcaatg 784
 |||||
Sbjct: 121 gttcttccacgattgctttgtcaatg 146

>dbj|FS240762.1| FS240762 RPSC Glycyrrhiza uralensis cDNA clone KAN050-D13.F 5', mRNA
 sequence
 Length = 554

Score = 244 bits (123), Expect = 2e-60
Identities = 174/191 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 |||||
Sbjct: 246 ggatgtgatggttcaattctactggatgacacatcaagctttacaggggagaagaacgca 305

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 |||||
Sbjct: 306 aaccgaaacaggaactcagctcgtgggttcgaagtcacgacaacatcaagtcagccgta 365

Query: 1277 gagaaagtgtgtccaggagttgttctcctgcgcagatatccttgccatcgctgccagagac 1336
 |||||
Sbjct: 366 gagaaagtgtgccctggagttgttctcctgcgcctgatataccttgccatcgctgccagagac 425

Query: 1337 tctgttcagat 1347
 ||
Sbjct: 426 tccgttcagat 436

Score = 178 bits (90), Expect = 1e-40
Identities = 159/182 (87%)
Strand = Plus / Plus

Query: 603 tttggctctgtttgtcctcatatgggggagtgccaatgcacaactttctacaaactttta 662
 |||||
Sbjct: 65 tttggctctctgtttctcataatgggggagtgccaatgcacaactctctacaaactteta 124

Query: 663 ctaccattcatgtccaacctcttctcctctgtgaaatccacagtgcaatctgccatatac 722
 |||

Sbjct: 125 ctccagttcttgtccaaaactggtttccactgtaaaatccacagtacaatccgcatatc 184

Query: 723 taaggagaccgcatgggtgcttctctctccttcgcttgttcttccacgattgctttgtcaa 782

|||||

Sbjct: 185 aaaggagaccgcatgggtgcttccctcctccgcttgttcttccatgattgctttgtcaa 244

Query: 783 tg 784

||

Sbjct: 245 tg 246

Score = 137 bits (69), Expect = 4e-28

Identities = 105/117 (89%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537

|||||

Sbjct: 438 cttggaggacctacttgaatgttaaacttggagaagagacgctaagacggctagccag 497

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctca 1594

|||||

Sbjct: 498 tctgctgccaacaacggcatccctcctcccacttctaacctcaaccaactcatctca 554

>gb|FG889628.1| UCRVU08_CCNS10828_b1 Cowpea IT97K-461-4 Mixed Tissue and Conditions
cDNA Library UCRVU08-1-2 Vigna unguiculata cDNA clone
CCNS10828.b1, mRNA sequence
Length = 692

Score = 238 bits (120), Expect = 1e-58

Identities = 171/188 (90%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

|||||

Sbjct: 257 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccggggagaagaacgca 316

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|||||

Sbjct: 317 aacccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 376

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 1336
|||||
Sbjct: 377 gagaaagtgtgtccaggagttgtttcctgtgcgagatataccttgctattgctgccagagac 436

Query: 1337 tctgttca 1344
|||||
Sbjct: 437 tctgttca 444

Score = 238 bits (120), Expect = 1e-58
Identities = 153/164 (93%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 449 cttggaggccctagttggaatgttaaacttgaagaagagatgctagaactgctagccaa 508

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 509 tctgctgccaacaatggcattcctgcaccttctcaaacttaaccaactcatctctaga 568

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgtc 1641
|||
Sbjct: 569 ttcagtgtcttagactttccaccaaggacttggctgccttgtc 612

Score = 226 bits (114), Expect = 5e-55
Identities = 189/214 (88%)
Strand = Plus / Plus

Query: 571 atggettctgtttgttctagattgacaatttgtttggctctgtttgtcctcatatggggg 630
|||||
Sbjct: 44 atggettctgtttgttctagattaactttcagtttggttctgtttgtcctctactgggt 103

Query: 631 agtgccaatgcacaactttctacaaactttactaccattcatgtccaaacctttctcc 690
|||
Sbjct: 104 tgtgtcaatgcacaactttctactgacttctactacagttcttgcceaaaactcctctcc 163

Query: 691 tctgtgaaatccacagtgcaatctgccatataagagaccgcatgggtgcttctctc 750
|||||

Sbjct: 164 actgtgagatccacagtgcaatctgccatatcaaaggagaccgcatgggtgcttctctc 223

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784

|| ||||||||||||||||||||||||||||||||||||

Sbjct: 224 ctccgcttggttcttccacgattgctttgtcaatg 257

Score = 111 bits (56), Expect = 2e-20

Identities = 65/68 (95%)

Strand = Plus / Plus

Query: 1789 ggtggcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848

||||| ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||

Sbjct: 614 ggtggccacacaattggacaagcaaggtgcacaaatttcagagcccgcatctacaacgag 673

Query: 1849 accaacat 1856

| |||||

Sbjct: 674 agcaacat 681

>gb|FF403045.1| M00F734TF M00 Vigna unguiculata cDNA 5', mRNA sequence

Length = 745

Score = 238 bits (120), Expect = 1e-58

Identities = 153/164 (93%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537

||||||||||| ||||||||||||||||||||||||| ||||||||||||||||||||

Sbjct: 465 cttggaggccctagttggaatgttaaacttggagaagagatgctagaactgctagccaa 524

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597

||||||| ||||||||| ||||||| ||||||||||||||||||||||||| |||

Sbjct: 525 tctgctgccaacaatggcattcctgcaccttctcaaaccttaaccaactcatctctaga 584

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgtc 1641

|| || ||||| |||||||||||||||||||||||||

Sbjct: 585 ttcagtgtctaggaactttccaccaaggacttggctgccttgtc 628

Score = 234 bits (118), Expect = 2e-57

Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggettcgttttgttctagattgacaatttgtttggtctctgtttgcctcatatggggg 630
|||||
Sbjct: 61 atggettcgttttgttctagattaactatcagtttggttctgtttgcctcgtactgggt 120

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 121 tgtgtcaatgcacaactttctactgacttctactacagtcttgcccaaaactcctctcc 180

Query: 691 tctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttctctc 750
|||
Sbjct: 181 actgtgagatccacagtgcaatctgccatatcaaaggagaccgcatgggtgcttctctc 240

Query: 751 cttegcttggttcttccacgattgctttgtcaatg 784
||
Sbjct: 241 ctccgcttggttcttccacgattgctttgtcaatg 274

Score = 222 bits (112), Expect = 8e-54
Identities = 170/188 (90%), Gaps = 1/188 (0%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||
Sbjct: 274 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccggggagaagaacgca 333

Query: 1217 aaccccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276
|||
Sbjct: 334 aaccccaacagaaattctgctcgtggatgatgaagtcattgacagcataaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgttctcgtcgcagatatccttgccatcgctgccagagac 1336
|||
Sbjct: 394 gagaaagtgtgt-caggggtgttctcgtcgcgatataccttgccattgctgccagagac 452

Query: 1337 tctgttca 1344
|||
Sbjct: 453 tctgttca 460

Query: 571 atggcttcgttttgttctagattgacaatttgttggctctgtttgtcctcatatggggg 630
|||||
Sbjct: 59 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 118

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 119 tgtgtcaatgcacaactttctactgacttctactacagttcttgccaaaactcctctcc 178

Query: 691 tctgtgaaatccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctc 750
|||||
Sbjct: 179 actgtgagatccacagtgaatctgccatatcaaaggagaccgcatgggtgcttctctc 238

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784
||
Sbjct: 239 ctccgcttggttcttccacgattgctttgtcaatg 272

Score = 198 bits (100), Expect = 1e-46
Identities = 133/144 (92%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 464 cttggaggccctagtgtgaatgttaaacttgaagaagagatgctagaactgctagccaa 523

Query: 1538 tctgctgtaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 524 tctgctgcaacaatggcattcctgcaccttctcaaaccttaaccaactcatctctaga 583

Query: 1598 tttagcgctcttggaactttccacc 1621
||
Sbjct: 584 ttcagtgctctaggactttccacc 607

>gb|FF399144.1| M00EV84TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 345

Score = 234 bits (118), Expect = 2e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttgtttgctctgtttgtcctcatatggggg 630
|||||
Sbjct: 64 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 123

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 124 tgtgtcaatgcacaactttctactgacttctactacagttcttgcccaaaactcctctcc 183

Query: 691 tctgtgaaatccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctc 750
|||||
Sbjct: 184 actgtgagatccacagtgaatctgccatatcaaaggagaccgcgatgggtgcttctctc 243

Query: 751 cttcgcttggttcttccacagattgctttgtcaatg 784
||
Sbjct: 244 ctccgcttggttcttccacagattgctttgtcaatg 277

Score = 89.7 bits (45), Expect = 8e-14
Identities = 63/69 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 277 ggatgtgacggttcgattctttggatgacacgtcaagcttccccgggagaagaacgca 336

Query: 1217 aacccaac 1225
|||||
Sbjct: 337 aacccaac 345

>gb|G0019707.1| LJMAW92TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA sequence
Length = 663

Score = 208 bits (105), Expect = 1e-49
Identities = 180/205 (87%)
Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttgctctgtttgtcctcatatgggggagtgccaat 639
|||||
Sbjct: 71 ttttgttctagattaactatctgttttgctctctttgtcctcatattgggggagtgccaat 130

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaacacttctctcctctgtgaaa 699
|| ||||| ||||| || | ||| ||||| ||||| || |||||
Sbjct: 131 gctcaactttctacaaacttctattctagttcttgtccaacacttcttccactgtgaaa 190

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcgcatgggtgcttctctccttcgcttg 759
||| ||||| ||||| ||||| | ||||| ||||| ||||| |||||
Sbjct: 191 tcctcagtgcaatccgccatatcaaaggaggctcgcgcatgggtgcttctctcctccgcttg 250

Query: 760 ttcttccacgattgctttgtcaatg 784
||| ||||| |||||
Sbjct: 251 ttcttccatgattgcttcgtcaatg 275

Score = 180 bits (91), Expect = 3e-41
Identities = 160/183 (87%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
||| ||||| ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 278 tgtgatggttcagttctacttgatgacacatcaagcttcaccgggagaagaatgcaaac 337

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 338 cccaacagaaactctgctcgggatttgatgttattgacaacatcaagtcagcagtagag 397

Query: 1280 aaagtgtgtccaggagttgtttctgctgcagatataccttgccatcgtgccagagactct 1339
|| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 398 gcagcatgccaggagttgtatcctgctgatataccttgccatctctgctagagactct 457

Query: 1340 gtt 1342
|||
Sbjct: 458 gtt 460

Score = 123 bits (62), Expect = 5e-24
Identities = 134/158 (84%)
Strand = Plus / Plus

Query: 1484 ggccctacatggaatgttaaacttggagaagagacgctagaactgtagccaatctgct 1543
||||| |||||||||||| | | |||||||||||||||| |||||||||||| | | ||
Sbjct: 473 ggccccacatggaatgtgaaagtaggaagaagagacgctaaaactgtagccagtccgcc 532

Query: 1544 gctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| |||| | |||||||||||||||||| | | | |||||||| | ||||| | | ||
Sbjct: 533 gccaacacaggcatccctgcaccacttctagcttgagccaactcacctcaagttcagt 592

Query: 1604 gctcttggactttccaccaaggacttggcgccttgtc 1641
|||||||||||||||| | || |||||||| | | |||||
Sbjct: 593 gctcttggactttccagcaaagacttggttgcatgtc 630

>dbj|AV412875.1| AV412875 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM225a08_r 5', mRNA sequence
Length = 282

Score = 208 bits (105), Expect = 1e-49
Identities = 180/205 (87%)
Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttggetctgtttgtcctcatatgggggagtgccaat 639
|||||||||||||| | | |||| | |||| | |||||||||||| | ||||||||||||
Sbjct: 53 ttttgttctagattaactatctgtttgtcctctttgtcctcatattgggggagtgccaat 112

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaaccttctctcctctgtgaaa 699
|| | |||||||||||||||| | | | || | |||||||| | |||| | | |||||
Sbjct: 113 gctcaactttctacaaacttctattctagttcttgcctcaaaactcttttcaactgtgaaa 172

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttg 759
|| | |||||||||| | |||||| | |||| | | |||||||||||||||||| | |||||
Sbjct: 173 tctcagtgcaatccgccatatcaaaggagctcgcctgggtgcttctctcctccgcttg 232

Query: 760 ttcttcacgattgctttgtcaatg 784
||||||| |||||||| | |||||
Sbjct: 233 ttcttccatgattgcttcgtcaatg 257

>dbj|AV771838.1| AV771838 Lotus japonicus Pods (20-30 mm in length) Lotus japonicus cDNA clone MPD027c11_f 3', mRNA sequence
Length = 430

Score = 202 bits (102), Expect = 7e-48

Identities = 208/242 (85%), Gaps = 1/242 (0%)
Strand = Plus / Minus

Query: 1925 tggcaccacttgatcttcaaactccaaccagctttgacaactactacttcaagaacctcg 1984
|||||
Sbjct: 428 tggcaccacttgaccttcagactccaacctctttgactaccactacttcaagtacctgg 369

Query: 1985 ttcagaagaagggtctcctccactctgatcagcaactgttcaacgggtgggtccaccgact 2044
|||||
Sbjct: 368 ttcagaaccagggcctccgacactccgaccagcaactcttcaacgggtgggtccaccgact 309

Query: 2045 ccattgtgctgggtacagcaccaaccgggcaccttctcctctgatttcgccgccgcca 2104
|||
Sbjct: 308 ccaccgtgctgggtacagcaccaaccggagctcatttctcctctgatttcgccagcgcca 249

Query: 2105 -tgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||
Sbjct: 248 ctggtccagatgggagatatcagtcctctcactggatccaacgggtgaaatcaggaagaat 189

Query: 2164 tg 2165
||
Sbjct: 188 tg 187

>dbj|BW620524.1| BW620524 Lotus japonicus protoplasts from suspension-cultured cells
Lotus japonicus cDNA clone LjFL1-sab-002-BB11 5', mRNA
sequence
Length = 480

Score = 196 bits (99), Expect = 4e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 211 tgtgatggttcaattctacttgatgacacatcaagcttcaccggggagaagaatgcaaac 270

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 271 cccaacagaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 330

sequence
Length = 482

Score = 196 bits (99), Expect = 4e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 145 tgtgatggttcaattctacttggatgacacatcaagcttcaccgggagaagaatgcaaac 204

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 205 cccaacagaaactctgctcggattcgatgttattgacaacatcaagtcagcagtagag 264

Query: 1280 aaagtgtgtccaggagttgtttctgctgcagatataccttgccatcgtgccagagactct 1339
||
Sbjct: 265 gcagcatgccaggagttgtatcctgctgatataccttgccatcctctgctagagactct 324

Query: 1340 gtt 1342
|||
Sbjct: 325 gtt 327

Score = 127 bits (64), Expect = 3e-25
Identities = 100/112 (89%)
Strand = Plus / Plus

Query: 673 tgtccaaacctcttctcctctgtgaaatccacagtgcaatctgccatatctaaggagacc 732
|||||
Sbjct: 31 tgtccaaaccttttccactgtgaaatcctccgtgcaatccgccatatcaaaggagct 90

Query: 733 cgcgatgggtgcttctctcctccgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 91 cgcgatgggtgcttctctcctccgcttgttcttccatgattgcttcgtcaatg 142

Score = 119 bits (60), Expect = 8e-23
Identities = 117/136 (86%)
Strand = Plus / Plus

Query: 1484 ggcctacatggaatgttaaacttgaagaagagacgctagaactgctagccaatctgct 1543
||||| ||||||||||||| || ||||||||||||||||||| ||||||||||||| || ||
Sbjct: 340 gccccacatggaatgtgaaagttgaagaagagacgctaaaactgctagccagtccgcc 399

Query: 1544 gctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| ||||| ||||||||||||||||||| | | | ||||||||| ||||||| || ||
Sbjct: 400 gccaacacagggcatccctgcaccacttctagcttgagccaactcacctcaagttcagt 459

Query: 1604 gctcttggactttcca 1619
|||||||||||||||
Sbjct: 460 gctcttggactttcca 475

>dbj|BW629863.1| BW629863 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-024-BE11 5', mRNA
sequence
Length = 471

Score = 196 bits (99), Expect = 4e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
||||||||||||||||| | ||||||||||||||||||| ||||||||| |||||
Sbjct: 276 tgtgatggttcaattctacttgatgacacatcaagcttcaccggggagaagaatgcaaac 335

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
||||||| ||||||||||| ||||||| ||||||||||||||| || ||||| || |||
Sbjct: 336 cccaacagaaactctgctcgcggattcgatgattattgacaacatcaagtcagcagtagag 395

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatataccttgccatcgtgccagagactct 1339
|| || ||||||||||| ||||||| ||||||| ||||| ||||| |||||
Sbjct: 396 gcagcatgccaggagttgtatcctgcgctgatatacctcgccatctctgctagagactct 455

Query: 1340 gtt 1342
|||
Sbjct: 456 gtt 458

Score = 192 bits (97), Expect = 7e-45
Identities = 178/205 (86%)

Strand = Plus / Plus

Query: 580 tttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaat 639
|||||

Sbjct: 69 tttgttctagattaactatctgttttgcctctttgtcctcatatgggggagtgcta 128

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaaccttctcctctgtgaaa 699
|||

Sbjct: 129 gctcaactttctacaaacttctattctagttcttgcctcaaaactctttccactgtgaaa 188

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttg 759
|||

Sbjct: 189 tcctccgtgcaatccgccatatcaaaggaggctcgcgatgggtgcttctctcctccgcttg 248

Query: 760 ttcttccacgattgctttgtcaatg 784
|||

Sbjct: 249 ttcttccatgattgcttctgcaatg 273

>dbj|BW628107.1| BW628107 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-019-CE07 5', mRNA
sequence
Length = 471

Score = 196 bits (99), Expect = 4e-46

Identities = 162/183 (88%)

Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||

Sbjct: 278 tgtgatggttcaattctacttgatgacacatcaagcttcaccggggagaagaatgcaaac 337

Query: 1220 cccaacaggaactctgctcgtggattcagggttattgacaacattaaatcagccgtggag 1279
|||||

Sbjct: 338 cccaacagaaactctgctcggattcaggttattgacaacatcaagtcagcagtagag 397

Query: 1280 aaagtgtgtccaggagtgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
|||

Sbjct: 398 gcagcatgccaggagtgtatcctgcgctgatatccttgccatcctctgctagagactct 457

Query: 1340 gtt 1342

|||
Sbjct: 458 gtt 460

Score = 192 bits (97), Expect = 7e-45
Identities = 178/205 (86%)
Strand = Plus / Plus

Query: 580 tttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaat 639
|||||
Sbjct: 71 tttgttctagattaactatctgttttgcctctttgtcctcatattgggggagtgctaat 130

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaacctcttctcctctgtgaaa 699
||
Sbjct: 131 gctcaactttctacaaacttctattctagttcttgcctcaaaactcttttccactgtgaaa 190

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttg 759
|||
Sbjct: 191 tctcctgcaatccgcatatcaaaggaggctcgcctgggtgcttctctcctccgcttg 250

Query: 760 ttcttccacgattgctttgtcaatg 784
|||
Sbjct: 251 ttcttccatgattgcttctgcaatg 275

>dbj|BW627140.1| BW627140 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-017-AA04 5', mRNA
sequence
Length = 480

Score = 196 bits (99), Expect = 4e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 286 tgtgatggttcaattctacttggatgacacatcaagcttcaccggggagaagaatgcaaac 345

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 346 cccaacagaaactctgctcgggattcgatgttattgacaacatcaagtcagcagtagag 405

Sbjct: 290 tgtgatggttcaattctacttctgatgacacaccaagcttcaccggggagaagaatgcaaac 349

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||

Sbjct: 350 cccaacaggaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 409

Query: 1280 aaagtgtgtccaggagttgtttctctgcgcagatatccttgccatcgtgccagagactct 1339
|||

Sbjct: 410 gcagcatgccaggagttgtatcctgcgctgatatcctcgccatctctgctagagactct 469

Query: 1340 gtt 1342

|||

Sbjct: 470 gtt 472

Score = 184 bits (93), Expect = 2e-42

Identities = 177/205 (86%)

Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttggetctgtttgtcctcatatgggggagtgccaat 639
|||||

Sbjct: 83 ttttgttctagattaactatctgttttgcctctttgtcctcatattggggagtgctaata 142

Query: 640 gcacaactttctacaaaacttttactaccattcatgtccaaaccttctcctctgtgaaa 699
|||

Sbjct: 143 gctcaactttctacaaaacttctattctagttcttgcctcaaaactcttttccactgtgaag 202

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttg 759
|||

Sbjct: 203 tctcctgcaatccgccatatcaaaggagctcgcgatgggtgcttctctcctccgcttg 262

Query: 760 ttcttccacgattgctttgtcaatg 784

|||||

Sbjct: 263 ttcttccatgattgcttctgtcaatg 287

>dbj|BW595840.1| BW595840 Lotus japonicus suspension-cultured cells Lotus japonicus
cDNA clone LjCa-005-DD12 5', mRNA sequence
Length = 485

Score = 196 bits (99), Expect = 4e-46

Identities = 177/203 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 283 tcaggggacaacaatttggcaccacttgaccttcagacaccaacctccttcgacaacaac 342

Query: 1969 tacttcaagaacctcgttcagaagaagggtctctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 343 tactttaagaacctggttcaaacaaggcctcctacactctgatcagcaacttttcaac 402

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggaccttctctct 2088
|||||
Sbjct: 403 ggtggctccgccgactccaccgtgcgtggctacagcaccaacccgagctcattttctct 462

Query: 2089 gatttcgccgcccgatgatcaa 2111
|||||
Sbjct: 463 gatttcgccagcggcatggtcaa 485

Score = 127 bits (64), Expect = 3e-25
Identities = 130/152 (85%)
Strand = Plus / Plus

Query: 1490 acatggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaac 1549
|||||
Sbjct: 7 acatggaatgtgaaagtgaagaagagacgctaaaactgctagccagtcgccgccaac 66

Query: 1550 aatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgtctt 1609
|
Sbjct: 67 acaggcatccctgcaccacttctagcttgagccaactcacctcaaggttcagtgtctt 126

Query: 1610 ggactttccaccaaggacttggctgccttgtc 1641
|||||
Sbjct: 127 ggactttccagcaaagacttgggttcattgtc 158

>gb|EY976963.1| EST 83 Alfalfa aluminum suppression subtractive library Medicago
sativa cDNA clone E2B11, mRNA sequence
Length = 971

Score = 190 bits (96), Expect = 3e-44
Identities = 147/164 (89%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 437 cttggaggcccaacatgggatgtgaaacttgaagaagagatgctagaacagctagtaaa 496

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||
Sbjct: 497 tcagctgcaacaatggcatcccagcaccacttcaagcctcaaccaactcatctcaagg 556

Query: 1598 tttagcgtcttggactttccaccaaggacttggcgccttgtc 1641
||||
Sbjct: 557 tttaatgctcttggactttccaccaaggatttggcgcattgtc 600

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 245 ggatgtgatggttcaattcttctcggatgacacatcaagcttcaccggagagaaaactgcc 304

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 305 aatccaacagaaattcggcccgatgattcgaagtgatcgacaaaatcaaatcagcagtg 364

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 365 gagaaagtatgtccaggatgagtttcatgtgctgatatcctcgccatcactgctagagac 424

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 425 tctgttgagat 435

Score = 111 bits (56), Expect = 2e-20
Identities = 71/76 (93%)

Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 170 caatctgccatatcaaaggagaccgcatgggtgcttctcttctacgtttgttcttccac 229

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 230 gattgctttgttaatg 245

Score = 63.9 bits (32), Expect = 4e-06
Identities = 32/32 (100%)
Strand = Plus / Plus

Query: 1789 gttggtcacacaattggacaagcaaggtgcac 1820
|||||
Sbjct: 602 gttggtcacacaattggacaagcaaggtgcac 633

>gb|EH613355.1| EST 02 Alfalfa aluminum suppression subtractive library Medicago
sativa cDNA clone A4 5', mRNA sequence
Length = 748

Score = 190 bits (96), Expect = 3e-44
Identities = 147/164 (89%)
Strand = Plus / Minus

Query: 1478 cttgaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 545 cttgaggcccaacatgggatgtgaaacttgaagaagagatgctagaacagctagtaaa 486

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|| |||||
Sbjct: 485 tcagctgcaacaatggcatccagcaccacttcaagcctcaaccaactcatctcaagg 426

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgtc 1641
|||||
Sbjct: 425 tttaatgctcttggactttccaccaaggatttggctgcattgtc 382

Score = 149 bits (75), Expect = 9e-32
Identities = 162/191 (84%)
Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 737 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 678

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276
||
Sbjct: 677 aatccaacagaaattcggcccgtggattcgaagtgatcgacaaaatcaaatcagcagtg 618

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 617 gagaaagtatgtccagggtgcagtttcatgtgctgatatcctcgccatcactgctagagac 558

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 557 tctgttgagat 547

Score = 99.6 bits (50), Expect = 8e-17
Identities = 212/266 (79%)
Strand = Plus / Minus

Query: 1900 acatcagggtcaggggacaacaatctggcaccacttgatcttcaactccaaccagcttt 1959
|||||
Sbjct: 269 acatcagggtccggggacaataatttggcacctcttgatcttgcaacaccaacatccttt 210

Query: 1960 gacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaa 2019
|||||
Sbjct: 209 gacaatcactatttcaagaacctagttgacagtaagggactactccactccgaccaacaa 150

Query: 2020 ctgttcaacgggtgggtccaccgactccattgtgcgtggctacagaccaaccgggcacc 2079
||
Sbjct: 149 ctcttcaatgggtggatccactgattccatagtgcatgaatatggttgtatccaagctct 90

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
||
Sbjct: 89 ttttctctgatttcgtcaccgcccatgatcaagatgggagacattagtcctcaccggt 30

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
||||| ||||||||||||||||||||||||| ||| ||||||| ||||| |||||
Sbjct: 585 ggtcatacaattggacaagcaaggtgcacaacctttagagcccgaatctacnngagagc 526

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
||||||| | | | ||||| | | | || | | | | ||| ||||| |||
Sbjct: 525 aacatagatagctcttttgcccgcatgagacaatctaggtgtccccgaacctcaggatca 466

Query: 1912 ggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactactac 1971
||||||| || | ||||| ||||| || | ||||| || | ||||||||| |||||
Sbjct: 465 ggggacaacaaccttgacccattgactttgccactcccacttttctttgacaacctactac 406

Query: 1972 ttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacggt 2031
||||||| ||||| ||||||||||||||||||| ||| ||| ||| ||||| |||
Sbjct: 405 ttcaagaacctcattcagaagaagggtctcatccattccgaccaagaactcttcaatggt 346

Query: 2032 ggttccaccgactccattgtgctgtgctacagcaccaaccgggcaccttctcctctgat 2091
|| ||||| ||||| | ||||| ||||||||||||||||||| | ||||| | | |||
Sbjct: 345 ggttccactgactccttgggtgctacactacagcaccaaccggcctcctttttcgccgat 286

Query: 2092 ttgccgccccatgatcaagatgggagacattagtcctctcactggctccaatggagaa 2151
||| ||||||||||||||||| ||||||||||||||||||| ||||||||||||| |||||
Sbjct: 285 ttgccgccccatgatcaggatgggagacattagtcctctcactggctcccgcggagaa 226

Query: 2152 atcaggaagaattgtagaaggattaactaatt 2183
|| ||| |||| | | || | | |||||
Sbjct: 225 ataagggagaactgcaggagggtcaactaatt 194

Score = 50.1 bits (25), Expect = 0.065
Identities = 25/25 (100%)
Strand = Plus / Minus

Query: 1611 gactttccaccaaggacttggtcgc 1635
|||||||||||||||||||||||
Sbjct: 620 gactttccaccaaggacttggtcgc 596

>gb|BI700509.1| sag61f05.y1 Gm-c1082 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1082-1041 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE

;, mRNA sequence
Length = 472

Score = 180 bits (91), Expect = 3e-41
Identities = 282/343 (82%), Gaps = 2/343 (0%)
Strand = Plus / Plus

Query: 1801 attggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaacatagaa 1860
|||||
Sbjct: 1 attggacaagcaaggtgcacaaacttcagagcccgaatctacaacgagaccaacatagat 60

Query: 1861 accgcatttgcaaggactagcagcaaaagctgccctagaacatcagggtcaggggacaac 1920
|||
Sbjct: 61 agctcttttctcgcacatgagacaatctaggtgtccccgaacctcagggtcaggggacaac 120

Query: 1921 aatctggcaccacttgatcttcaa-actccaaccagctttgacaactactacttcaagaa 1979
|||
Sbjct: 121aacctagcaccattga-cttcgccactcccaggttctttgacaaccactacttcaagaa 179

Query: 1980 cctcgttcagaagaagggtctcctcactctgatcagcaactgttcaacgggtgggtccac 2039
|||||
Sbjct: 180cctcattcagaagaagggectcatcattccgaccaacaactcttcaatgggtgggtccac 239

Query: 2040 cgactccattgtgcgtggctacagcaccaaccgggcaccttctcctctgatttcgccgc 2099
|||||
Sbjct: 240tgactccatagtgctacactacagcaccaaccgggcctcctttttcgccgatttctccgc 299

Query: 2100 cgccatgatcaagatgggagacattagtcctctcactggctcc 2142
|||||
Sbjct: 300cgccatgatccgatgggagacattagtcctcctcaccgctcc 342

>gb|BU578183.1| sar49a02.y1 Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1074-5404 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 271

Score = 176 bits (89), Expect = 4e-40
Identities = 134/149 (89%)
Strand = Plus / Plus

Query: 630 gaggccaatgcacaactttctacaaacttttactaccattcatgtccaacctcttctc 689

Sbjct: 1 gagtgccaatgcccaactttctacaaacttctactaccattcatggccaaacctcttctc 60

Query: 690 ctctgtgaaatccacagtgcaatctgccatatctaaggagacccgcatgggtgcttctct 749

Sbjct: 61 cactgtgaaatccaccagcaatctgccatatcagaagagacccgcatgggtgcttctct 120

Query: 750 ccttcgcttgttcttccacgattgctttg 778

Sbjct: 121 cctccacctgttcttccaccattgctttg 149

Score = 107 bits (54), Expect = 3e-19
Identities = 99/114 (86%)
Strand = Plus / Plus

Query: 1159 atgtgatgggtcaattctattggatgacacatcaagcttcaccggagagaagaacgcaa 1218

Sbjct: 157 atgtgatgggtcaattctattggatgacacctcgagcttcgccgagagaaaacgcgaa 216

Query: 1219 ccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagc 1272

Sbjct: 217 ccccaacaagaactctgctcctggataccaggtccttgaccacctaaatcagc 270

>gb|G0258927.1| VBL1_16_M09_E001.g1 Normalized cDNA library from cotyledon and young
leaves of peanut Arachis hypogaea cDNA, mRNA sequence
Length = 616

Score = 174 bits (88), Expect = 2e-39
Identities = 226/272 (83%)
Strand = Plus / Plus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969

Sbjct: 3 caggggacaacaaccttgccgcttgatctcacaacaccacggccttcgacaacaact 62

Query: 1970 acttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacg 2029

Sbjct: 63 acttcaggaaccttgttcagaacaagggctgtcctccactccgaccagcaactcttcaacg 122

Query: 2030 gtgggtccaccgactccattgtgcgtggctacagcaccacccgggcaccttctctctg 2089
||||| ||||||||| || || | |||||| | ||||||| | |||||||||
Sbjct: 123 gtggctccaccgactctatagtcagaggctacgcctccaaccgacctattctctctg 182

Query: 2090 atttcgccgcccatgatcaagatgggagacattagtcctctcaactggctccaatggag 2149
| ||| | ||||||||| ||||||||| ||||||||| ||||||| ||| ||
Sbjct: 183 acttcatcagcgccatgatcaagatgggagacattagtcctctcaactggatccaacggtg 242

Query: 2150 aatcaggaagaattgtagaaggattaactaa 2181
||||||| || || ||||| |||||
Sbjct: 243 aatcaggaagaactgcaggaggatcaactaa 274

>gb|CA852976.1| E14E06_J06_09.ab1 cDNA Peking library 6, 8 day SCN3 Glycine max cDNA
clone E14E06 5', mRNA sequence
Length = 556

Score = 174 bits (88), Expect = 2e-39
Identities = 193/228 (84%)
Strand = Plus / Plus

Query: 1956 ctttgacaactactacttcaagaacctcgttcagaagaagggtctctcactctgatca 2015
||||||| ||||||||| ||||||||| ||||||||| ||| || || ||
Sbjct: 89 ctttgacaaccactacttcaagaacctcattcagaagaagggtctcatccattccgacca 148

Query: 2016 gcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccacccggg 2075
||||| ||||| ||||| ||||| ||||| | ||||| ||||||||| |||||
Sbjct: 149 agaactcttcaatggtggttccactgactccttgggtgcgtacctacagcaccacccggc 208

Query: 2076 caccttctctctgatcttcgccgcccatgatcaagatgggagacattagtcctctcac 2135
| |||| | | | ||||| ||||||||| ||||||||| ||||||||| |||||
Sbjct: 209 ctctttttcgccatcttctccgcccatgatcaggatgggagacattagtcctctcac 268

Query: 2136 tggctccaatggagaaatcaggaagaattgtagaaggattaactaatt 2183
||||||| ||||||||| ||| |||| || || ||| | |||||||
Sbjct: 269 tggctcccgcggagaataaggagaactgcaggagggtcaactaatt 316

>gb|CA852554.1| E09B05_C17_03.ab1 cDNA Peking library 6, 8 day SCN3 Glycine max cDNA
clone E09B05 5', mRNA sequence
Length = 539

Score = 174 bits (88), Expect = 2e-39

||||| ||||||| ||| |||| || || ||| | |||||||
Sbjct: 264 tggtccccgcggagaaataagggagaactgcaggagggtcaactaatt 217

>gb|FF401698.1| MOOE192TF MOO Vigna unguiculata cDNA 5', mRNA sequence
Length = 826

Score = 168 bits (85), Expect = 1e-37
Identities = 307/381 (80%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
||||| ||||||| ||||||| ||| ||||| ||||||| ||||| |||
Sbjct: 233 ggtcatacaattggactagcaaggtgcacaacctttagagctcgcatctacaacgaaacc 292

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
||||||| | | ||||| | ||| | | ||||| ||| ||||| |||
Sbjct: 293 aacatagatagctcctttgcccacatgagacaatctacatgcacctcgaaactcaggatca 352

Query: 1912 ggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactactac 1971
||||||| | ||||| ||||| || ||||| || ||||| ||||| |||||
Sbjct: 353 ggggacaacagcttagcacccttgattttgcccactcctacttttctttgacaactactac 412

Query: 1972 ttcaagaacctcgttcagaagaagggtctcctcactctgatcagcaactgttcaacggt 2031
||||||| ||||||| ||||||| ||||| || ||||| ||||| || |||||
Sbjct: 413 ttcaagaacctcattcagaagaagggtcttctcattccgatcaacaactctttaatggt 472

Query: 2032 ggttccaccgactccattgtgcgtggctacagcaccaaccgggaccttctcctctgat 2091
|| ||||| ||||||| ||||| ||||||| ||||| | ||||| | |||||
Sbjct: 473 ggttccactgactccactgtgcaaacctacagcaccaaccagcctccttttccactgat 532

Query: 2092 ttgccgcgccatgatcaagatgggagacattagtcctctcactggctccaatggagaa 2151
||| ||||| || ||||||| ||||||| ||||| ||||| ||||| |||||
Sbjct: 533 ttctccgtgctatgatcaagatgggagacatcagtcctcaccggctccaccggagaa 592

Query: 2152 atcaggaagaattgtagaagg 2172
|| ||||||| || |||||
Sbjct: 593 ataaggaagaactgcagaagg 613

Score = 163 bits (82), Expect = 6e-36

||||| ||||||| ||||||||||||| ||||||| |||||
Sbjct: 612 ttaaagctcttggctctttccaccaaggatttggctgcattgtc 655

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||||| ||||||| ||||||| ||||||| |||||
Sbjct: 300 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 359

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276
|| ||||||| || || || || ||||||| || || ||||| || ||||||| |||
Sbjct: 360 aatcccaacaaaaattcgcccggtgattcgaagtgatcgacaaaatcaaatcagcagtg 419

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||| | ||||| ||||| || ||||||| ||||| ||||| |||||
Sbjct: 420 gagaaagtatgtccagggtgcagtttcatgctgacatccttaccatcactgctagagac 479

Query: 1337 tctgttcagat 1347
||||| |||||
Sbjct: 480 tctgttgagat 490

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctctcttcgcttgttcttccac 768
||||| ||||||| || ||||| ||||||| ||||||| || || || ||||||| |||||
Sbjct: 225 caatctgccatatcaaaagagactcgcatgggtgcttctctctctgcgttgttcttccac 284

Query: 769 gattgctttgtcaatg 784
||||| |||||
Sbjct: 285 gattgctttgttaatg 300

Score = 63.9 bits (32), Expect = 4e-06
Identities = 50/56 (89%)

Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacga 1847
|||||
Sbjct: 660 ggtcacacaattggacaagcaaggtgcactacatttagagcccacattacaacga 715

>gb|EX530374.1| MTGland_A066_2007-06-28/MTGlandA066_C04_014_1 Medicago truncatula A17
glandular trichome Medicago truncatula cDNA, mRNA
sequence
Length = 1023

Score = 167 bits (84), Expect = 4e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 487 cttggaggcccaacatgggatgtgaaacttggagaagagatgcaagaacagctagtaaa 546

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
||
Sbjct: 547 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 606

Query: 1598 tttagcgtcttggactttccaccaaggacttggcgccttgtc 1641
|||||
Sbjct: 607 tttaatgctcttggctttccaccaaggatttggcgcattgtc 650

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 295 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 354

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 355 aatccaacaaaaattcggcccgtggattcgaagtgatcgacaaaatcaaatcagcagtg 414

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 1336
||||||| ||||||| | ||||| ||||| || ||||||| ||||| ||||| |||||
Sbjct: 367 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 426

Query: 1337 tctgttcagat 1347
||||||| |||||
Sbjct: 427 tctgttgagat 437

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttccac 768
||||||| ||||||| || ||||||| ||||||| || || ||||||| |||||||
Sbjct: 172 caatctgccatatcaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 231

Query: 769 gattgctttgtcaatg 784
||||||| |||||
Sbjct: 232 gattgctttgttaatg 247

>gb|CF068375.1| EST669096 MTUS Medicago truncatula cDNA clone MTUS-7C2, mRNA sequence
Length = 776

Score = 167 bits (84), Expect = 4e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||||| ||||||| ||||| ||||||| ||||||| || || ||||||| ||||| ||
Sbjct: 461 cttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagtaaa 520

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|| ||||||| ||||||| ||||||| ||||||| ||||| ||||||| |||||||
Sbjct: 521 tcagctgcaacaatgacatccagcaccacttcaagcctcaaccaactcatctcaagg 580

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgtc 1641
|||| | ||||||| ||||||| ||||||| |||||
Sbjct: 581 tttaatgctcttggctttccaccaaggatttggctgcattgtc 624

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 269 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 328

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276
||
Sbjct: 329 aatccaacaaaaattcggcccggtggattcgaagtgatcgacaaaatcaaatcagcagtg 388

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 389 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcaactgctagagac 448

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 449 tctgttgagat 459

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctccac 768
|||||
Sbjct: 194 caatctgccatatcaaaagagactcgcatgggtgcttctctccttcgcttgttctccac 253

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 254 gattgctttgttaatg 269

Score = 71.9 bits (36), Expect = 2e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851

Sbjct: 629 ggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacgactcc 688

Query: 1852 aacataga 1859

Sbjct: 689 aacataga 696

>gb|AW268020.1| EST306242 DSIR Medicago truncatula cDNA clone pDSIR-8B8, mRNA
sequence
Length = 702

Score = 167 bits (84), Expect = 4e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

Sbjct: 447 cttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagtaaa 506

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597

Sbjct: 507 tcagctgcaacaatgacatccagcaccacttcaagcctcaaccaactcatctcaagg 566

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgtc 1641

Sbjct: 567 tttaatgctcttggctttccaccaaggatttggctgcattgtc 610

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

Sbjct: 255 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 314

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

Sbjct: 315 aatccaacaaaaattcggcccgtggattcgaagtgatcgacaaaatcaaatcagcagtg 374

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatccttgccatcgctgccagagac 1336
||||||| ||||||| | ||||| ||||| || ||||||| ||||| ||||| |||||
Sbjct: 375 gagaaagtgtgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 434

Query: 1337 tctgttcagat 1347
||||||| |||||
Sbjct: 435 tctgttgagat 445

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
||||||| ||||||| || ||||||| ||||||| || || ||||||| |||||||
Sbjct: 180 caatctgccatatcaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 239

Query: 769 gattgctttgtcaatg 784
||||||| |||||
Sbjct: 240 gattgctttgttaatg 255

Score = 71.9 bits (36), Expect = 2e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
||||||| ||||||| || ||||||| ||||| ||||||| ||
Sbjct: 615 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacgactcc 674

Query: 1852 aacataga 1859
|||||||
Sbjct: 675 aacataga 682

>gb|BI969294.1| GM830007B20G07 Gm-r1083 Glycine max cDNA clone Gm-r1083-2630 3', mRNA
sequence
Length = 779

Score = 165 bits (83), Expect = 2e-36
Identities = 161/187 (86%)
Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 302 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 361

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 362 aatccaacaaaaattcgcccggtggattcgaagtgatcgacaaaatcaaatcagcagtg 421

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatccttgccatcgctgccagagac 1336
|||||
Sbjct: 422 gagaaagtatgtccagggtgcagtttctgctgacatccttaccatcactgctagagac 481

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 482 tctgttgagat 492

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttctccac 768
|||||
Sbjct: 227 caatctgccatatcaaaagagactcgcatgggtgcttctctctgcttgttctccac 286

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 287 gattgctttgttaatg 302

Score = 63.9 bits (32), Expect = 4e-06
Identities = 50/56 (89%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
|||||
Sbjct: 662 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacga 717

>gb|BG448404.1| NF024B09EC1F1074 Elicited cell culture Medicago truncatula cDNA clone

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 214 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 273

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 274 gattgctttgttaatg 289

Score = 48.1 bits (24), Expect = 0.26
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaagg 1815
|||||
Sbjct: 649 ggtcacacaattggacaagcaagg 672

>gb|BF644619.1| NF017G06EC1F1051 Elicited cell culture Medicago truncatula cDNA clone
NF017G06EC 5', mRNA sequence
Length = 684

Score = 155 bits (78), Expect = 2e-33
Identities = 142/164 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 479 cttggaggcccaacatgggatgtgaaacttggagaagagatgcaagaacagctagtaaa 538

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
|||
Sbjct: 539 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaang 598

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgcgcttgtc 1641
|||
Sbjct: 599 tttaatgctcttggcttttccaccaangatttggctgcgcttgtc 642

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 287 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 346

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 347 aatccaacaaaaattcgcccgtggattcgaagtgatcgacaaaatcaaatcagcagtg 406

Query: 1277 gagaaagtgtgtccaggagttgttctcctgcgagatccttgccatcgctgccagagac 1336
|||||
Sbjct: 407 gagaaagtgtgtccagggtgcagtttcatgctgacatccttaccatcactgctagagac 466

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 467 tctgttgagat 477

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 212 caatctgccatatcaaagagactcgcatgggtgcttctctccttcgcttgttcttccac 271

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 272 gattgctttgttaatg 287

Score = 58.0 bits (29), Expect = 3e-04
Identities = 29/29 (100%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcac 1820
|||||
Sbjct: 647 ggtcacacaattggacaagcaaggtgcac 675

>gb|CA919059.1| EST636777 MTUS Medicago truncatula cDNA clone MTUS-7C2, mRNA sequence
Length = 802

Score = 151 bits (76), Expect = 2e-32
Identities = 143/164 (87%), Gaps = 1/164 (0%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 754 cttggaggcccaacatgggatgtgaaact-ggaagaagagatgcaagaacagctagtaa 696

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||
Sbjct: 695 tcagctgcaacaatgacatccagcaccacttcaagcctcaaccaactcatctcaagg 636

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgtc 1641
|||||
Sbjct: 635 tttaatgctcttggctttccaccaaggatttggctgcattgtc 592

Score = 117 bits (59), Expect = 3e-22
Identities = 284/359 (79%)
Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
|||||
Sbjct: 587 ggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacgactcc 528

Query: 1852 aacatagaacccgcatcttgaaggactaggcagcaaagctgccctagaacatcagggtca 1911
|||||
Sbjct: 527 aacatagataacttcttggctgcacaaggcaatcagggtgccccagacatcgggttcc 468

Query: 1912 ggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactactac 1971
|||||
Sbjct: 467 ggggacaataatttggcacccttgatcttgaacaccaacatcctttgacaaccattac 408

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||| ||||||| ||||||| || || || ||||| || ||||
Sbjct: 141 gggagtaccaatgcacaactttctacaagttttactccaaaacttgccccaaactctct 200

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttct 747
|| | ||||||| || || || ||||||| |||||| | || | ||||||| |||||
Sbjct: 201 accacagtgaaatccacactacaaactgccatatcaaaggaggcccgaatgggtgcttct 260

Query: 748 ctctctgcttgttcttccacgattgcttgtcaatg 784
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 261 atccttcgcttgttcttccacgattgcttgtcaatg 297

Score = 58.0 bits (29), Expect = 3e-04
Identities = 53/61 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| || || || ||||||| ||||||| ||||||| ||||||| || || || ||||| ||||
Sbjct: 489 cttggaggtccaacctggaatgtaaaacttggagaagagatgctaaaacggctagtcaa 548

Query: 1538 t 1538
|
Sbjct: 549 t 549

>gb|AW686470.2| NF041G08NR1F1000 Nodulated root Medicago truncatula cDNA clone
NF041G08NR 5', mRNA sequence
Length = 481

Score = 145 bits (73), Expect = 1e-30
Identities = 136/157 (86%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||| ||||||| ||||||| || || || ||||| || ||||
Sbjct: 118 gggagtgccaatgcacaactttctacaaacttttactcaaaaacttgccccaaactctct 177

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttct 747
|| | ||||||| || || || ||||||| |||||| | || | ||||||| |||||

Sbjct: 178 accacagtgaatccacactgcaaactgccatatcaaaggaggccccgaatgggtgctct 237

Query: 748 ctcttcgcttgttcttccacgattgctttgtcaatg 784

||||| |||||||||||||||||||||||||||||||||||

Sbjct: 238 atctccgcttgttcttccacgattgctttgtcaatg 274

Score = 123 bits (62), Expect = 5e-24
Identities = 155/186 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||||||| ||||||||| || ||||||||||||||||||| ||||| ||||||||| |||

Sbjct: 274 ggatgtgatggatcaattctcttagatgacacatcaagctttaccggtgagaagaatgca 333

Query: 1217 aacccaacaggaactctgctcgtggattcgaggtattgacaacattaaatcagccgtg 1276

|| || || || ||||| ||||||||||||| || || || ||||||||| || |||||||||

Sbjct: 334 aatccaaatagaaactccgctcgtggatttgatgtcatcgacaacataaagacagccgta 393

Query: 1277 gagaaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336

||||||| || || || || ||||||||| || || || || ||||||||| ||||| ||||||| |||||

Sbjct: 394 gagaacgtatgccccggagttgtatcatgtgctgatatcctagccattgctgccgagac 453

Query: 1337 tctgtt 1342

|||||||

Sbjct: 454 tctgtt 459

>gb|BF639633.1| NF015A12IN1F1097 Insect herbivory Medicago truncatula cDNA clone
NF015A12IN 5', mRNA sequence
Length = 516

Score = 145 bits (73), Expect = 1e-30
Identities = 136/157 (86%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687

||||||||||||||||||||||||||||||||||||| | ||||||| || |||||

Sbjct: 61 gggagtgccaatgcacaactttctacaaacttttactcaaaaacttgtccaaacctctct 120

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttct 747

>gb|CX530413.1| s13dNF99F02MJ016_246858 Methyl Jasmonate-Elicited Root Cell
Suspension Culture Medicago truncatula cDNA, mRNA
sequence
Length = 585

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 281 ggatgtgatggttcaattcttctc gatgacacatcaagcttcaccggagagaaaactgcc 340

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 341 aatcccaacaaaaattcggcccgtggattcgaagtgatcgacaaaatcaaatcagcagtg 400

Query: 1277 gagaaagtgtgtccaggagtgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 401 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcaactgctagagac 460

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 461 tctgttgagat 471

Score = 113 bits (57), Expect = 5e-21
Identities = 99/113 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 473 cttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagtaaa 532

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcat 1590
||
Sbjct: 533 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcat 585

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 206 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 265

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 266 gattgctttgttaatg 281

>gb|CX529528.1| s13dNF97C05MJ034_245107 Methyl Jasmonate-Elicited Root Cell
Suspension Culture Medicago truncatula cDNA, mRNA
sequence
Length = 545

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 290 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 349

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 350 aatccaacaaaaattcgcccggtggattcgaagtgatcgacaaaatcaaatcagcagtg 409

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 410 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 469

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 470 tctgttgagat 480

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 215 caatctgccatatcaaaagagactcgcatgggtgcttctctctgcgcttgttcttccac 274

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 275 gattgctttgttaatg 290

Score = 63.9 bits (32), Expect = 4e-06
Identities = 50/56 (89%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctag 1533
|||||
Sbjct: 482 cttggaggcccaacatgggatgtgaaacttggagaagagatgcaagaacagctag 537

>gb|BF647501.1| NF068D03EC1F1029 Elicited cell culture Medicago truncatula cDNA clone
NF068D03EC 5', mRNA sequence
Length = 658

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 288 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 347

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 348 aatccaacaaaaattcgcccggtgattcgaagtgatcgacaaaatcaaatcagcagtg 407

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 408 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 467

Query: 1337 tctgttcagat 1347
|||||

Sbjct: 468 tctgttgagat 478

Score = 141 bits (71), Expect = 2e-29
Identities = 142/165 (86%), Gaps = 1/165 (0%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 480 cttggaggcccaacatgggatgtgaaacttggagaagagatgcaagaacagctagtaaa 539

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||
Sbjct: 540 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctnaagg 599

Query: 1598 tttagcgct-cttggactttccaccaaggacttggtegccttgtc 1641
||||
Sbjct: 600 tttaatgctccttggctctttncaccaaggatttggtegcattgtc 644

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 213 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgcttgttcttccac 272

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 273 gattgctttgttaatg 288

>gb|BF645317.1| NF030B11EC1F1092 Elicited cell culture Medicago truncatula cDNA clone
NF030B11EC 5', mRNA sequence
Length = 603

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 281 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 340

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 341 aatccaacaaaaattcggcccggtggattcgaagtgatcgacaaaatcaaatcagcagtg 400

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagac 1336
||
Sbjct: 401 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 460

Query: 1337 tctgttcagat 1347
||
Sbjct: 461 tctgttgagat 471

Score = 107 bits (54), Expect = 3e-19
Identities = 108/125 (86%), Gaps = 1/125 (0%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||
Sbjct: 473 cttggaggcccaacatgggatgtgaaactnggaagaagagatgcaagaacagctagtaa 532

Query: 1538 tctgctgctaacaatggcat-ccctgcacccaacttcaaaccttaaccaactcatctcaag 1596
||
Sbjct: 533 tcagctgcaacaatgacatccccagcaccacttcaagcctcaaccaactcatctcaag 592

Query: 1597 attta 1601
||
Sbjct: 593 gttta 597

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttctccac 768
||

Sbjct: 206 caatctgccatatcaaaagagaactcgcgatgggtgcttctcttctgcgtttgttctccac 265

Query: 769 gattgctttgtcaatg 784

|||||||

Sbjct: 266 gattgctttgttaatg 281

>gb|C0515766.1| s13dSG77F0400043_419681 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 572

Score = 139 bits (70), Expect = 9e-29

Identities = 157/186 (84%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

|||||||

Sbjct: 299 ggatgtgatgatcaattctcttggatgacacatcaagctttaccggtgagaagaatgca 358

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276

|||||

Sbjct: 359 aacccaatagaaactctgctcgtggatttgggtgtcatcgacaacataaagacagccgta 418

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336

|||||

Sbjct: 419 gagaacgtatgccccggagttgtctcatgtgccgatatccttgctattgctgccgagac 478

Query: 1337 tctgtt 1342

|||||

Sbjct: 479 tctgtt 484

Score = 137 bits (69), Expect = 4e-28

Identities = 135/157 (85%)

Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687

|||||

Sbjct: 143 gggagtaccaatgcacaactttctacaagtttttactccaaaacttgcctccaaactctct 202

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttct 747

|| | ||||||||| | ||| ||||||||| ||||| |||| | |||||||||
Sbjct: 203 accacagtgaatccacactacaaactgccatatcaaaggaggccccgaatgggtgcttct 262

Query: 748 ctccttcgcttggttcttccacgattgctttgtcaatg 784

||||||||||||||||||||||||||||||||||||||
Sbjct: 263 atccttcgcttggttcttccacgattgctttgtcaatg 299

Score = 75.8 bits (38), Expect = 1e-09
Identities = 71/82 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

||||||| || | ||||||||| ||||||||||||||||||||| |||| | ||| ||||| |||
Sbjct: 491 cttggaggtccaacctggaatgtaaaacttgaagaagagatgctaaaacggctagtcaa 550

Query: 1538 tctgctgctaacaatggcatcc 1559

|| ||||||||| || |||||
Sbjct: 551 tccgctgctaacaactgccatcc 572

>gb|AW830346.1| sm33e02.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-5715 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 459

Score = 139 bits (70), Expect = 9e-29
Identities = 136/158 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

||||||||||| || ||| ||||| ||||||||||||||||||||| | || | || | |||||
Sbjct: 160 cttggaggcccaacttgggatgtgaaacttgaagaagagactccaggacggcaagccaa 219

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597

||||||| ||||||||| ||||||||| ||||||||||||||||||||| || || | |||
Sbjct: 220 tctgctgccaacaatgacatccaagaccacttcaaacttaaccaacttatttccaga 279

Query: 1598 tttagcgtcttggactttccaccaaggacttggtcgc 1635

|||| | |||| | |||||||||||||||| | |||||||||
Sbjct: 280 tttaatgctctcggactttccaccaaagacttggtcgc 317

Sbjct: 136 cttggaggcccaacttgggatgtgaaacttggagaagagactccaggacggcaagccaa 195
|||||

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||

Sbjct: 196 tctgctgccaacaatgacatcccaagaccacttcaaacctcaaccaacttatttccaga 255
|||||

Query: 1598 tttagcgtcttggactttccaccaaggacttggtcgc 1635
|||||

Sbjct: 256 tttaatgctctcggactttccaccaaagacttggtcgc 293
|||||

Score = 111 bits (56), Expect = 2e-20
Identities = 65/68 (95%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
|||||

Sbjct: 304 ggtcacacaattggacaagcaaggtgcacaaacttttagagcccgaatctacaacgagacc 363
|||||

Query: 1852 aacataga 1859
|||||

Sbjct: 364 aacataga 371
|||||

Score = 73.8 bits (37), Expect = 4e-09
Identities = 103/125 (82%)
Strand = Plus / Plus

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|||||

Sbjct: 10 aacaggaactctgcccgtggttttgaagtgatcgatcaaattaagtcagctgtggaaaaa 69
|||||

Query: 1283 gtgtgtccaggagtgtttctctgcgcagatatccttgccatcgctgccagagactctgtt 1342
|||||

Sbjct: 70 gtgtgtccgggtgtgtctctctgcgctgacatccttgccatcgctgcaagagactccgtt 129
|||||

Query: 1343 cagat 1347
|||||

Sbjct: 130 gagat 134
|||||

Sbjct: 318 cctaacaggaattctgcccgatgtgaagtgatcgaccaaatacaatcagctgtggag 377

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||

Sbjct: 378 aaagtgtgtccgggtgtggtttcttgcgctgacattcttgccatcgctgccagagac 434

Score = 121 bits (61), Expect = 2e-23
Identities = 85/93 (91%)
Strand = Plus / Plus

Query: 692 ctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttctctcc 751
|||||

Sbjct: 163 ctgtgaaacgcacagtggaatcgccatatcaaaggagaccgcatgggtgcttctctcc 222

Query: 752 ttcgcttggttcttccacgattgctttgtcaatg 784
|||

Sbjct: 223 tacgtttgttcttccacgattgctttgttaatg 255

>gb|AW704238.1| sk18d12.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-2544 5' similar to TR:024336 024336
KOREAN-RADISH ISOPEROXIDASE ;, mRNA sequence
Length = 566

Score = 135 bits (68), Expect = 1e-27
Identities = 158/188 (84%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||

Sbjct: 243 tgtgatgggtcaattctacttggatgacacatcaagcttcaccggagagaaaaacgcagga 302

Query: 1220 cccaacaggaactctgctcgatggattcgaggttattgacaacattaaatcagccgtggag 1279
|||

Sbjct: 303 cctaacaggaactctgcccggttttgaagtgatcgatcaaattaagtcagctgtggaa 362

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactct 1339
|||||

Sbjct: 363 aaagtgtgtccgggtgtggtctcttgcgctgacatccttgccatcgctgcaagagactcc 422

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| || ||| |||| | ||||| ||||| | || |||||

Sbjct: 243 ctgccaaggacaacaggctcaggggacaacaacttggcacccttgatatccagactcc 302

Query: 1950 aaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccactc 2009
||| ||||| ||||| ||||| | | | ||| ||||| |||||

Sbjct: 303 aacatTTTTgacaacaactacttcaagaacctcatcaacaggaggggactcctccactc 362

Query: 2010 tgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaa 2069
|| || | ||||| || || ||||| || ||||| ||||| || ||||| |||

Sbjct: 363 cgaccaacagctgttcaatgggggctccacggattccatcgtgcggggttacagcaaca 422

Query: 2070 cccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtc 2129
|||| | ||||| ||||| || | | ||| ||||| ||||| ||||| |||||

Sbjct: 423 cccgagctcctcagttctgactttgtcaccggcatgatcaagatgggagacatcagtc 482

Query: 2130 tctcactggctccaatggagaaatcaggaagaattgtagaagg 2172
||||||| || | ||||| ||||| ||||| || |||||

Sbjct: 483 cctcactggatcaaggggagagatcaggaagaactgcagaagg 525

Score = 58.0 bits (29), Expect = 3e-04
Identities = 101/125 (80%)
Strand = Plus / Plus

Query: 1508 ggaagaagagacgctagaactgctagccaatctgctgctaacaatggcatccctgcaccc 1567
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 7 ggaaggagagatgctaggactgctagccaggctgctgccaacaacagcattcctcctcca 66

Query: 1568 acttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccaccaaggac 1627
||||| ||| | ||| ||||| || ||||| | ||||| ||||| ||||| |||||

Sbjct: 67 acttctaactgaacagactcatttctagattcaatgctcttggactttccaccaggac 126

Query: 1628 ttggt 1632
||||

Sbjct: 127 atggt 131

>dbj|AV771209.1| AV771209 Lotus japonicus Pods (20-30 mm in length) Lotus japonicus

Sbjct: 342 tctggt 347

Score = 121 bits (61), Expect = 2e-23
Identities = 133/157 (84%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||||||||||||||||| ||||||| | | | ||||| || ||||
Sbjct: 6 gggagtaccaatgcacaactttctacaagtttttactccaaaacttgccccaaactctct 65

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttct 747
|| | ||||||||||||| | ||| || ||||||| ||||| |||| | |||||||||
Sbjct: 66 accacagtgaaatccacactacaaactaccatatcaaaggaggcccgaatgggtgcttct 125

Query: 748 ctctctgcttgttcttccacgattgctttgtcaatg 784
|||| | |||||||||||||||||||||||||||||
Sbjct: 126 atcctccgcttgttcttccacgattgctttgtcaatg 162

Score = 103 bits (52), Expect = 5e-18
Identities = 130/156 (83%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| || || | ||||||| ||||||||||||||||| |||| | || | ||||| |||
Sbjct: 354 cttggaggctccaaactggaatgtaaaacttggagaagagatgctaaaacggctagtcaa 413

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
|| | ||||||||| || | ||||| ||||| ||||| ||||| || | ||||| |||||
Sbjct: 414 tccgctgctaacaactgccatcccagcaccacttcaaactcaatacactcacctcaatg 473

Query: 1598 tttagcgctcttggactttccaccaaggacttggtc 1633
||||||| |||| | ||||||| ||||||| |||||||
Sbjct: 474 tttagcgcggttggtctttccagcaaggatttggtc 509

>gb|BF071209.1| st04h08.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1065-376 5' similar to TR:Q9XFL7 Q9XFL7 PEROXIDASE 6
; mRNA sequence
Length = 319

Score = 131 bits (66), Expect = 2e-26
Identities = 114/130 (87%)
Strand = Plus / Plus

Query: 1218 accccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtgg 1277
||||||| ||||| ||||||||||||||| ||||||| ||||||| ||||||| ||||| |||||
Sbjct: 81 accccaataggatctctgctcgtggatacagaggtcattgactacattagatcatccgtgt 140

Query: 1278 agaaagtgtgtccaggagttgtttcctgcgagatatccttgccatgctgccagagact 1337
||||| | ||||||||| | ||||| ||||||||||||||| ||||||||| ||||||||| |||||
Sbjct: 141 agaatgcgtgtccagtatttgtctctgcgagatatgcttgccatagctgccagatact 200

Query: 1338 ctgttcagat 1347
|||||||||||
Sbjct: 201 ctgttcagat 210

Score = 58.0 bits (29), Expect = 3e-04
Identities = 66/77 (85%), Gaps = 1/77 (1%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||||||||||| | | ||||||||| ||||||||| ||||||||| ||||||| |||||
Sbjct: 212 cttggaggccctagtgttgtatgttaaagttggaagatgagacgctagatctgcttgcccta 271

Query: 1538 tctgctgctaacaatgg 1554
||||| || |||||||||
Sbjct: 272 tctggtg-taacaatgg 287

>gb|EX660929.1| JS1BF51JG Salt stressed *Fragaria vesca* (strain Hawaii-4) cDNA library
Fragaria vesca cDNA clone JS1BF51, mRNA sequence
Length = 758

Score = 129 bits (65), Expect = 9e-26
Identities = 214/263 (81%), Gaps = 3/263 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
||||||||||||||| ||||| ||||||||||||||| ||||||||| ||||| ||||||| |||||
Sbjct: 238 tcaggggacaacaacttggctccacttgatcttcaatctccaacagccttcgacaacaac 297

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttc--- 2025
||||| ||| || || | ||||| | ||||| ||||| ||||| |||||
Sbjct: 298 tactacaataatcttatcaagaacagagggtctcctccactccgatcagcagttgttcttg 357

Query: 2026 aacggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcc 2085
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 358 aatggtgggtccaccgattccatagtgctggctacagcagcagccagagcacattcaca 417

Query: 2086 tctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaat 2145
||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 418 tctgactttgctgcccaatgatcaagatgggaaacatcaaccgctcactggatccaat 477

Query: 2146 ggagaaatcaggaagaattgtag 2168
||||| || ||||| ||||| |||||
Sbjct: 478 ggagagattaggaagaactgtag 500

Score = 61.9 bits (31), Expect = 2e-05
Identities = 52/59 (88%)
Strand = Plus / Plus

Query: 1574 aacctaaccaactcatctcaagattagcgtcttggactttccaccaaggacttggt 1632
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 46 aacctaaccagctcatctccagattcaacgctcttggcctttccaccaaggacatggt 104

>gb|DN950706.1| Ost2T_331 Oak tissue culture growing 2 days in hypertonic medium
Quercus robur cDNA 5', mRNA sequence
Length = 852

Score = 129 bits (65), Expect = 9e-26
Identities = 98/109 (89%)
Strand = Plus / Plus

Query: 676 ccaaacctcttctcctctgtgaaatccacagtgcaatctgcatatctaaggagaccgc 735
||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 151 ccaaaactctttccactgtgaaatccaccgtgcaatctgcatatcaaaggaagccga 210

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgcttgtcaatg 784
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 211 atgggtgectctctcctgcgcttgttcttccatgattgctttgtcaatg 259

Score = 101 bits (51), Expect = 2e-17
Identities = 120/143 (83%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
|||||
Sbjct: 466 tggaatgttaaacttgaagaagagatgctaggactgagccaggctgctgctaataat 525

Query: 1553 ggcattccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttggga 1612
||||
Sbjct: 526 agcattcctcctccaacttctaacctaaaccaactcatttctagatttaacaatttggga 585

Query: 1613 ctttccaccaaggacttgggtcgc 1635
|||||
Sbjct: 586 ctttccactaggacatgggtcgc 608

Score = 81.8 bits (41), Expect = 2e-11
Identities = 59/65 (90%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcactctacaacgagaccaac 1854
|||||
Sbjct: 622 cacacaattgggcaagcaaggtgtacatccttcagagctcgcatatataacgagaccaac 681

Query: 1855 ataga 1859
||||
Sbjct: 682 ataga 686

>gb|C0511866.1| s13dSG02H0700064_103632 Glandular trichomes *Medicago sativa* cDNA,
mRNA sequence
Length = 483

Score = 129 bits (65), Expect = 9e-26
Identities = 149/177 (84%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| ||| | ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 307 gatgggtcaatcctactagatgacacatcaaattttaccggagagaagaacgactcccc 366

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| ||||| ||||| || ||||| || ||||| || ||||| ||||| |||||
Sbjct: 367 aataggaactctgttcgaggattcgatgtcattgacaacataaagacagccgtagagaac 426

Query: 1283 gtgtgtccaggagttgtttcctgcgagatatccttgccatcgtgccagagactct 1339
| ||||| ||||| || || || ||||| ||||| ||||| ||||| |||||
Sbjct: 427 atatgtccaggagttgtatcatgtgtgatatcctagccattgctgccacagactct 483

Score = 87.7 bits (44), Expect = 3e-13
Identities = 166/206 (80%), Gaps = 3/206 (1%)
Strand = Plus / Plus

Query: 582 ttgttctagattgacaattt---gtttggctctgtttgtcctcatatgggggagtgcca 638
||||| ||||| ||||| | ||||| ||| ||| ||||| ||||| ||||| |||||
Sbjct: 96 ttgttctagattaacaatgttcagtttggttctattttctcataataggagtgcca 155

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaaccttctctctgtgaa 698
||||| ||||| ||||| ||||| | | ||||| || ||||| ||| ||| |
Sbjct: 156 tgcacaactctctacaaacttttactcaaaaactgtccaaactctctccattgtcca 215

Query: 699 atccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctctcctt 758
| | ||||| || ||||| ||||| | || ||||| ||||| || || |||
Sbjct: 216 acgccaagtgaatccgctatatcaaaggaggcagaatgggtgcttctattctccgatt 275

Query: 759 gttcttccacgattgctttgtcaatg 784
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 276 gttcttccacgattgctttgtcaatg 301

>gb|BF650349.1| NF096E02EC1F1017 Elicited cell culture Medicago truncatula cDNA clone
NF096E02EC 5', mRNA sequence
Length = 474

Score = 129 bits (65), Expect = 9e-26
Identities = 154/184 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 291 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 350

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 351 aatccaacaaaaattcggcccgaggattcgaagtgatcnacaaatcaaatcagcagtg 410

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 1336
|||||
Sbjct: 411 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 470

Query: 1337 tctg 1340
|||
Sbjct: 471 tctg 474

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 216 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcttgttcttccac 275

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 276 gattgctttgttaatg 291

>gb|BE022178.1| sm68f01.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-9074 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 352

Score = 129 bits (65), Expect = 9e-26
Identities = 86/93 (92%)
Strand = Plus / Plus

Query: 692 ctgtgaaatccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctcc 751
|||||

Score = 111 bits (56), Expect = 2e-20
Identities = 65/68 (95%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
|||||
Sbjct: 157 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 216

Query: 1852 aacataga 1859
|||||
Sbjct: 217 aacataga 224

>gb|AW685593.1| NF029D05NR1F1000 Nodulated root Medicago truncatula cDNA clone
NF029D05NR 5', mRNA sequence
Length = 677

Score = 117 bits (59), Expect = 3e-22
Identities = 284/359 (79%)
Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
|||||
Sbjct: 592 ggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacgactcc 533

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
|||||
Sbjct: 532 aacatagataacttcctttgctcgcacaaggcaatcagggtgcccgaagacatcgggttcc 473

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaaactccaaccagctttgacaactactac 1971
|||||
Sbjct: 472 ggggacaataatttggcacccttgatcttgaacaccaacatcctttgacaaccattac 413

Query: 1972 ttcaagaacctcgttcagaagaagggtctcctcactctgatcagcaactgttcaacggt 2031
|||||
Sbjct: 412 ttcaagaacctagttgacagtaagggtactcactccgaccaacaactctttaatggt 353

Query: 2032 ggtccaccgactccattgtgctggctacagcaccaaccgggaccttctcctctgat 2091
|||||
Sbjct: 352 ggatccaccgattccatagtgacgaatatagcttgtatccaagctcttttctcctctgat 293

Query: 2092 ttgcccgcgcatgatcaagatgggagacattagtcctctcactggctccaatggaga 2150
|||| | |||||||||||||||||||||||||||||||||| |||| | | ||||||||
Sbjct: 292 ttcgtcaccgcatgatcaagatgggagacattagtcctcaccggttcaaatggaga 234

Score = 81.8 bits (41), Expect = 2e-11
Identities = 72/81 (88%), Gaps = 1/81 (1%)
Strand = Plus / Minus

Query: 1562 gcaccacttcaaaccttaaccaactcatctcaagatttagcgctc-ttggactttccac 1620
||||||| ||| |||||||||||||||||| |||| |||| |||| ||||||||
Sbjct: 677 gcaccacttcaagcctcaaccaactcatctcaaggttaatgctctttggtctttccac 618

Query: 1621 caaggacttggtcgccttgtc 1641
|||||| | |||||| | ||||
Sbjct: 617 caaggatttggtcgcatgtc 597

>dbj|FS263447.1| FS263447 RPSC Glycyrrhiza uralensis cDNA clone S02198-34-013 5', mRNA
sequence
Length = 146

Score = 113 bits (57), Expect = 5e-21
Identities = 72/77 (93%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||||||||||| |||||||||||||| || | | |||||||||
Sbjct: 70 ggatgtgatggttcaattctactggatgacacatcaagctttacaggggagaagaacgca 129

Query: 1217 aacccaacaggaactc 1233
|||| | |||||||||
Sbjct: 130 aaccgaacaggaactc 146

Score = 107 bits (54), Expect = 3e-19
Identities = 66/70 (94%)
Strand = Plus / Plus

Query: 715 gccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccacgattgc 774
||||||| |||||||||||||||||| |||| | ||||||||| |||||

Sbjct: 1 gccatatcaaaggagaccgcgatgggtgcttccctcctccgcttgttcttccatgattgc 60

Query: 775 tttgtcaatg 784

|||||||||

Sbjct: 61 tttgtcaatg 70

>gb|BF650698.1| NF099E07EC1F1053 Elicited cell culture Medicago truncatula cDNA clone
NF099E07EC 5', mRNA sequence
Length = 501

Score = 113 bits (57), Expect = 5e-21

Identities = 157/191 (82%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||||||||||||||||| | ||||||||||||||||||||||||||||||| | ||

Sbjct: 283 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 342

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276

|| ||||||| || || || || ||||||||| | || || || || || || || || || ||

Sbjct: 343 aatccaacaaaaattcggcccgtggattccaagtgatcgacaaaatcaaatcancagng 402

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336

||||||||| ||||||||| | |||||| ||| | || ||||||| |||||| |||||| |||||||

Sbjct: 403 gagaaagtatgtccagggtgcagtttcatgcctgacatccttaccatcactgctagagac 462

Query: 1337 tctgttcagat 1347

||||||| |||||

Sbjct: 463 tctgttgagat 473

Score = 95.6 bits (48), Expect = 1e-15

Identities = 69/76 (90%)

Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttccac 768

||||||||||||||||| || ||||| ||||||||||||||||||| || || |||||||||||||||

Sbjct: 208 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 267

Query: 769 gattgctttgtcaatg 784

|||||
Sbjct: 268 gattgctttgttaatg 283

>gb|EV262518.1| MTYEW71TF JCVI-MT1 Medicago truncatula cDNA 5', mRNA sequence
Length = 742

Score = 111 bits (56), Expect = 2e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacc 1222
|||||
Sbjct: 287 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactccc 346

Query: 1223 aacaggaactctgctcgtggattcagagttattgacaacattaaatcagccgtggagaaa 1282
|||
Sbjct: 347 aataagaactctgttcgaggattcgatgctcattgacaacataaagacggcggtagagaac 406

Query: 1283 gtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagactc 1338
|||
Sbjct: 407 gtatgccccggagttgtatcatgtgctgatataccttgccattgctgccacagactc 462

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
|||||
Sbjct: 202 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttgttctt 261

Query: 765 ccacgattgctttgtcaatg 784
|||||
Sbjct: 262 ccacgattgctttgtcaatg 281

Score = 71.9 bits (36), Expect = 2e-08
Identities = 132/164 (80%)
Strand = Plus / Plus

Sbjct: 660 ||||| ||||||||||||||||||| ||||||| || || | || ||||||| ||
agtgctcacacaattggacaagcaaagtgcacaacatttaggtacgaatctacaatga 719

Query: 1848 gaccaacataga 1859

|||||||||||
Sbjct: 720 gaccaacataga 731

>gb|EV258111.1| MTYDG59TF JCVI-MT1 Medicago truncatula cDNA 5', mRNA sequence
Length = 677

Score = 111 bits (56), Expect = 2e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||||||| | ||||||||||||| ||| ||||||||||||||||| |||
Sbjct: 305 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactccc 364

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||||||| ||| ||||||||| || ||||||||||||| || | || || |||||
Sbjct: 365 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 424

Query: 1283 gtgtgtccaggagttgtttctgcgagatatccttgccatcgctgccagagactc 1338
|| || || ||||||||| || || || ||||||||||||| ||||||| |||||
Sbjct: 425 gtatgccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 480

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
||||||||| ||||||||| ||||| | || || ||||||||| |||| | |||||||||
Sbjct: 220 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatctccgcttgttctt 279

Query: 765 ccacgattgctttgtcaatg 784
|||||||||||
Sbjct: 280 ccacgattgctttgtcaatg 299

Score = 79.8 bits (40), Expect = 7e-11
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| ||||||||||||||||| || | ||||||| |||
Sbjct: 491 cttggtggcccaacctggaatgtaaaacttggagaagagatgccacaactgctagtcaa 550

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||| ||| |||| || ||||||| ||| ||||| ||||||| ||||| |||||
Sbjct: 551 tctgatgcgaacaactgccatcccaagaccgacttccaaccttaataactcacctcaatg 610

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtc 1641
|||| | |||| ||||||||||||||||| ||||| |||||
Sbjct: 611 ttaagaatgttggctttccaccaaggacttagtgcattgtc 654

>gb|DW017370.1| EST1226331 MTY Medicago truncatula cDNA clone MTYAS77, mRNA sequence
Length = 793

Score = 111 bits (56), Expect = 2e-20
Identities = 203/252 (80%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacga 1847
||||| ||||||||||||||||||||||||| || || | ||||||| |||
Sbjct: 307 aggtgctcacacaattggacaagcaaggtgcacaacatttagggtacgaatctacaatga 366

Query: 1848 gaccaacatagaaaccgcatttgcaaggacttaggcagcaaagctgccctagaacatcagg 1907
||||||||||| || | ||||| || || ||||| | ||||| | |||||||
Sbjct: 367 gaccaacatagatacttcttttgctagcacaaggcaatctaattgcccaagacatcagg 426

Query: 1908 gtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaacta 1967
||||||||||||||| ||||||| ||||||| || ||||| || |||||||||
Sbjct: 427 atcaggggacaacaatttggcacctcttgatctccatactcccacttctttgacaactg 486

Query: 1968 ctacttcaagaacctcgttcagaagaaggtctctcactctgatcagcaactgttcaa 2027
||||| || ||||||| ||||| || ||||||| || || || || || ||||| |||||
Sbjct: 487 ctactacaggaacctgttcaaaacaaggtctcttcttattcagaccaacaacttttcaa 546

Query: 2028 cgggtgggtccac 2039

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||||| | ||||||||||||| ||| ||||||||||||||||| |||
Sbjct: 311 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgactcccg 370

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||||| ||| ||||||| | ||||||||||||| || | || || |||||
Sbjct: 371 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 430

Query: 1283 gtgtgtccaggagttgtttcctgcgagatatccttgccatcgtgccagagactc 1338
|| || | ||||||| || || || ||||||||||||| ||||||| |||||
Sbjct: 431 gtatgccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 486

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttctt 764
||||||| ||||||| ||||| | || || ||||||||| |||| | |||||||||
Sbjct: 226 agtgcaatccgccatatcaaaggaggcacgaattgggtgcttctatcctccgcttgttctt 285

Query: 765 ccacgattgctttgtcaatg 784
|||||||||||||||||||
Sbjct: 286 ccacgattgctttgtcaatg 305

Score = 79.8 bits (40), Expect = 7e-11
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| ||||||||||||||||| || | ||||||||| |||
Sbjct: 497 cttggtggcccaacctggaatgttaaacttggagaagagatgccacaactgctagtcaa 556

Query: 1538 tctgctgtaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
|||| ||| |||| || ||||| ||| ||||| ||||||| ||||| |||||
Sbjct: 557 tctgatgcaaacactgccatcccaagaccaacttcaaacttaataactcacctcaatg 616

Query: 1598 tttagcgtccttggactttccaccaaggacttggctgccttgtc 1641
|||| | |||| | ||||||||||||||||| |||| | |||||

Sbjct: 617 ttttaagaatgttggtctttccaccaaggacttagtgcattgtc 660

Score = 71.9 bits (36), Expect = 2e-08
Identities = 63/72 (87%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaagggtgcacaaacttcagagcccgcacatctacaacga 1847
||||| |||||||||||||||||||||||||||| || || | || |||||||| ||
Sbjct: 661 agtgctcacacaattggacaagcaagggtgcacaacatttaggtacgaatctacaatga 720

Query: 1848 gaccaacataga 1859
|||||||||||
Sbjct: 721 gaccaacataga 732

>gb|C0513179.1| s13dSG23G0900068_129522 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 561

Score = 111 bits (56), Expect = 2e-20
Identities = 169/206 (82%), Gaps = 3/206 (1%)
Strand = Plus / Plus

Query: 582 ttgttctagattgacaat---gtttggtctgtttgtcctcatatgggggagtgcca 638
||||||||||| ||||| | |||||| || || || ||||||||| |||||||||
Sbjct: 102 ttgttctagattaacaatgttcagtttggttctatttctcctcataatagggagtgcca 161

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaaccttctcctctgtgaa 698
||||||||| ||||| ||||||||| | | | ||||| || |||| | || |||| |
Sbjct: 162 tgcacaactctctacgaacttttactccaaaacttgcccaactctcttccactgtcca 221

Query: 699 atccacagtgcaatctgccatatctaaggagaccgcacatgggtgcttctctccttcgctt 758
| | ||||||||| || ||||| |||||| | || ||||||||||||| ||||| |||||
Sbjct: 222 acgccaagtgcaatccgctatatcgaaggaggcagaatgggtgcttctctcctccgctt 281

Query: 759 gttcttccacgattgctttgtcaatg 784
|||||||||||||||||||||||
Sbjct: 282 gttcttccacgattgctttgtcaatg 307

Score = 111 bits (56), Expect = 2e-20
Identities = 149/180 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| ||| | ||||| ||||| || || ||||| ||||| ||||| |||
Sbjct: 313 gatgggtcaatcctactagatgacacatcaaattttaccggagagaagaacgcactcccg 372

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| ||||| ||||| ||| ||||| || || ||||| ||||| || ||||| |||||
Sbjct: 373 aataggaactctgttcgaggatttgatgtcattgacaacataaagacagccgtagagaac 432

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactctgtt 1342
| ||||| ||||| || || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 433 atatgtccaggagttgtatcatgtgtgatatcctagccattgctgccacatactctgtt 492

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| | ||||| ||||| ||||| ||||| || || ||||| ||||| |||
Sbjct: 499 cttggaggcccaaactggaatgttaaacttggagaagagatgccacgactgctagtcaa 558

Query: 1538 tct 1540
|||
Sbjct: 559 tct 561

>gb|C0512465.1| s13dSG100C120008_114444 Glandular trichomes *Medicago sativa* cDNA,
mRNA sequence
Length = 614

Score = 111 bits (56), Expect = 2e-20
Identities = 149/180 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| ||| | ||||| ||||| || || ||||| ||||| ||||| |||
Sbjct: 77 gatgggtcaatcctactagatgacacatcaaattttactggagagaagaacgcactcccg 136

Score = 69.9 bits (35), Expect = 7e-08
Identities = 59/67 (88%)
Strand = Plus / Plus

Query: 718 atatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccacgattgcttt 777
||||| ||||| | || ||||| ||||| | || || ||||| ||||| |||||
Sbjct: 5 atatcaaaggaggcacgaatgggtgcttctattctccgattgttcttccacgattgcttt 64

Query: 778 gtcaatg 784
|||||
Sbjct: 65 gtcaatg 71

>gb|BG456493.1| NF082E02PL1F1017 Phosphate starved leaf Medicago truncatula cDNA
clone NF082E02PL 5', mRNA sequence
Length = 675

Score = 111 bits (56), Expect = 2e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacc 1222
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 280 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcaactccc 339

Query: 1223 aacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 340 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggttagagaac 399

Query: 1283 gtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagactc 1338
|| || | ||||| || || || ||||| ||||| ||||| ||||| |||||
Sbjct: 400 gtatgccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 455

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttctt 764
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 195 agtgcaatccgccatatcaaaggaggcacgaattgggtgcttctatcctccgcttgttctt 254

Score = 109 bits (55), Expect = 8e-20
Identities = 112/131 (85%)
Strand = Plus / Minus

Query: 1502 aaacttggagaagagacgctagaactgctagccaatctgctgctaacaatggcatccct 1561
|||||
Sbjct: 230 aaacttggagaagagatgcaagaagtgctagccagctgctgcgtaataatggcattcct 171

Query: 1562 gcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccacc 1621
|||||
Sbjct: 170 gcaccaacttcgaacttgaaccaactcattccagttcaatgctcttggactttccacc 111

Query: 1622 aaggacttggt 1632
|
Sbjct: 110 agggacttggt 100

Score = 75.8 bits (38), Expect = 1e-09
Identities = 50/54 (92%)
Strand = Plus / Minus

Query: 731 cccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 499 cccgaatgggtgcttctctccttcgattgttcttccacgactgctttgtcaatg 446

Score = 56.0 bits (28), Expect = 0.001
Identities = 118/148 (79%)
Strand = Plus / Minus

Query: 1195 cttcaccggagagaagaacgcaaaccacaggaactctgctcgtggattcgaggttat 1254
|||||
Sbjct: 408 cttcaccggagagaaaaatgctatcccgaatcggaaactcagctcgcgattcgatgtgt 349

Query: 1255 tgacaacattaaatcagccgtggagaaagtgtgtccaggagttgttctcgcgagatat 1314
|||
Sbjct: 348 tgataacatcaagttagctgttgagaatgtttgccctggtgtagtttcttctgtctgatat 289

Query: 1315 ccttgccatcgctgccagagactctgtt 1342
|

Sbjct: 288 cttggccattactgctagagaactctgtt 261

>gb|DW481566.1| GH_RMIRS_031_E08_056_F Cotton Normalized Library random primed
Gossypium hirsutum cDNA, mRNA sequence
Length = 716

Score = 109 bits (55), Expect = 8e-20
Identities = 112/131 (85%)
Strand = Plus / Plus

Query: 1502 aaacttggagaagagacgctagaactgctagccaatctgctgctaacaatggcatccct 1561
|||||
Sbjct: 486 aaacttggagaagagatgcaagaagtgctagccagtctgctgctaataatggcattcct 545

Query: 1562 gcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccacc 1621
|||||
Sbjct: 546 gcaccaacttcgaacttgaaccaactcattccagttcaatgctcttggactttccacc 605

Query: 1622 aaggacttgg 1632
|
Sbjct: 606 aaggacttgg 616

Score = 75.8 bits (38), Expect = 1e-09
Identities = 50/54 (92%)
Strand = Plus / Plus

Query: 731 cccgcatgggtgcttctctctctcgcttgttcttccacgattgcttgtcaatg 784
|||||
Sbjct: 217 cccgaatgggtgcttctctctctcgattgttcttccacgactgcttgtcaatg 270

Score = 56.0 bits (28), Expect = 0.001
Identities = 118/148 (79%)
Strand = Plus / Plus

Query: 1195 cttcaccggagagaagaacgcaaaccacaacaggaactctgctcgtggattcgaggttat 1254
|||||
Sbjct: 308 cttcaccggagagaaaatgctatcccgaatcgggaactcagctcgggattcgatgtgt 367

Query: 1256 gacaacattaaatcagccgtggagaaagtgtgtccaggagttgttctctgcgcagatatic 1315
||||| || ||||| || || ||||| ||||| ||||| || || || || |||||
Sbjct: 310 gacaatataaaatccgcagttgagaaagcttgcctggagtagtctcatgtgctgatatic 369

Query: 1316 cttgccatcgctgccagagactct 1339
||||||| |||||
Sbjct: 370 cttgccatcgctgctagagactct 393

Score = 54.0 bits (27), Expect = 0.004
Identities = 27/27 (100%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcaca 1821
||||||| |||||
Sbjct: 574 cacacaattggacaagcaaggtgcaca 600

>gb|DY633234.1| Medicago--03-I06.g1 Subtracted medicago cDNA library specific for
UV-B irradiation Medicago truncatula cDNA clone
Medicago--03-I06, mRNA sequence
Length = 290

Score = 105 bits (53), Expect = 1e-18
Identities = 122/145 (84%)
Strand = Plus / Plus

Query: 1901 catcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttg 1960
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 104 catcaggatcaggtgacaacaatttggcacctcttgatcttcagactcctagttcttttg 163

Query: 1961 acaactactacttcaagaacctgttcagaagaagggtctcctccactctgatcagcaac 2020
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 164 acaacaactacttcaagaacctgttcagaacaagggtcttctccattcagaccaacaac 223

Query: 2021 tgttcaacgggtgggtccaccgactc 2045
|| || ||||| ||||| |||||
Sbjct: 224 tttttaacggcgggtccaccaactc 248

>gb|DY633115.1| Medicago--03-I06.b1 Subtracted medicago cDNA library specific for

UV-B irradiation Medicago truncatula cDNA clone
Medicago--03-I06, mRNA sequence
Length = 290

Score = 105 bits (53), Expect = 1e-18
Identities = 122/145 (84%)
Strand = Plus / Minus

Query: 1901 catcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttg 1960
||||||| ||||| ||||||||| ||||||| ||||||||| ||||| | |||||
Sbjct: 187 catcaggatcaggtgacaacaatttggcacctcttgatcttcagactcctagttctttg 128

Query: 1961 acaactactacttcaagaacctggtcagaagaagggtctcctccactctgatcagcaac 2020
||||| ||||||||| ||||||| ||||||| ||||| || || || |||||
Sbjct: 127 acaacaactacttcaagaacctgttcagaacaagggtcttctccattcagaccaacaac 68

Query: 2021 tgttcaacgggtgggtccaccgactc 2045
| || ||||| ||||||||| |||||
Sbjct: 67 tttttaacggcgggtccaccaactc 43

>gb|BG359643.1| sac26g07.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1051-3398 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 633

Score = 105 bits (53), Expect = 1e-18
Identities = 120/133 (90%), Gaps = 7/133 (5%)
Strand = Plus / Plus

Query: 1508 ggaagaagagacgc-tagaa-ctgctagcc-aatctgct-gctaacaatggca-tccctg 1562
||||||||||| ||||| ||||| || ||||||||| ||||||||| |||||
Sbjct: 334 ggaagaagagacgcctagaaactgctaaccaatctgcttggtaacaatggcaattcctc 393

Query: 1563 caccacttcaaaa-ccttaaccaactcatctcaagatttagcgctcttggactttcca-c 1620
||||||||||| ||||||||||| ||||||||| || ||||||||| ||||||||| |||||
Sbjct: 394 caccacttcaaaaaccttaaccaactcatctcaagattcaccgctcttggactttccacc 453

Query: 1621 caaggacttggtc 1633
||| |||||||||
Sbjct: 454 caaagacttggtc 466

Score = 91.7 bits (46), Expect = 2e-14
Identities = 109/124 (87%), Gaps = 12/124 (9%)
Strand = Plus / Plus

Query: 1162 tgatggttcaattcta-ttggatgacacatcaag--cttcaccggagagaagaa--cgca 1216
|||||
Sbjct: 87 tgatggttcaattctatttggatgacacatcaagnncttcaccggagagaagaanncgca 146

Query: 1217 aaccccaacagg---aactctgctcgtggat--tcgaggttattgaca--acattaaatc 1269
|||||
Sbjct: 147 aaccccaacaggggaaacctctgctcgtggatacccgaggtcattgacannacattaaatc 206

Query: 1270 agcc 1273
|||
Sbjct: 207 agcc 210

>gb|GT138697.1| METCC85TF JCVI-MT3 Medicago truncatula cDNA 5', mRNA sequence
Length = 726

Score = 103 bits (52), Expect = 5e-18
Identities = 70/76 (92%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 227 caatctgccatatcaaaagagaccgcgatgggtgcttctcttctgcgttgttcttccac 286

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 287 gattgctttgttaatg 302

Score = 91.7 bits (46), Expect = 2e-14
Identities = 208/262 (79%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||
Sbjct: 410 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacgactcc 469

Gm-c1028-658 5' similar to TR:P93548 P93548 PEROXIDASE
PRECURSOR ;, mRNA sequence
Length = 286

Score = 103 bits (52), Expect = 5e-18
Identities = 103/120 (85%)
Strand = Plus / Plus

Query: 2023 ttcaacggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttc 2082
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 16 ttcaatggtggttccactgactccatagtgctacactacagcaccaacccggcctccttt 75

Query: 2083 tcctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctcc 2142
| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 76 ttgccgatttctccgccgcatgatccgatgggagacattagtcctcaccggctcc 135

>emb|CU485516.1| CU485516 CUSHIONC_KZOACAC Theobroma cacao cDNA clone KZOACAC4Y017FM1,
mRNA sequence
Length = 540

Score = 101 bits (51), Expect = 2e-17
Identities = 225/283 (79%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaactctggcaccacttgatcttcaaactcc 1949
||||| | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 516 ctgccaaggaacaacaggttcaggggacaacaacttggcacccttgatatccagactcc 457

Query: 1950 aaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccactc 2009
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 456 aacatTTTTGACAACGATTACTTCAAGAACCTCATCAACAGGAGAGGACTCCTCCACTC 397

Query: 2010 tgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaa 2069
|| || | ||||| || || ||||| || ||| | ||||| || ||||| |||||
Sbjct: 396 cgaccaacagctgttcaatgggggtccacggattccttctgtcggggttacagcaacaa 337

Query: 2070 cccgggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacattagtc 2129
|||| | ||||| | ||| || | | ||| ||||| ||||| ||||| ||||| |||||
Sbjct: 336 cccgagctcctttagttttagctttgtcaccggcatgatcaagatgggagacatcagtc 277

Query: 2130 tctcactggctccaatggagaatcaggaagaattgtagaagg 2172

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaac 1854
|||||
Sbjct: 556 cacacaattggacaagcaaggtgtacaaatcttagggcacgaatctacaacgagaccaac 615

Query: 1855 ata 1857
|||
Sbjct: 616 ata 618

>gb|BE943474.1| EST423053 MGHG Medicago truncatula cDNA clone pMGHG-15J14, mRNA
sequence
Length = 480

Score = 101 bits (51), Expect = 2e-17
Identities = 138/167 (82%)
Strand = Plus / Plus

Query: 1172 attctattggatgacacatcaagcttcaccggagagaagaacgcaaacccaacaggaac 1231
|||||
Sbjct: 1 attctactagatgacacatcaaaactttaccggagagaagaacgcactcccgaataagaac 60

Query: 1232 tctgctcgtggattcagggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291
|||||
Sbjct: 61 tctgttcgaggattcagtgctgattgacaacataaagacggcggtagagaacgtatgcccc 120

Query: 1292 ggagttgtttctcgcgagatataccttgccatcgtgccagagactc 1338
|||||
Sbjct: 121 ggagttgtatcatgtgctgattccttgccattgctgccacagactc 167

Score = 79.8 bits (40), Expect = 7e-11
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 178 cttggtggcccaacctggaatgtaaaacttggagaagagatgccacaactgctagtcaa 237

Query: 1538 tctgctgtaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 238 tctgatgcgaacctgccatcccaagaccaacttccaaccttaataactcactcaatg 297

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgct 1641
|||| | |||| |||||||||||||||||| |||| ||||
Sbjct: 298 tttagaatgttggctttccaccaaggacttagtcgattgct 341

Score = 71.9 bits (36), Expect = 2e-08
Identities = 63/72 (87%)
Strand = Plus / Plus

Query: 1788 agtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacga 1847
|||| |||||||||||||||||||||||||| || || | || |||||| ||
Sbjct: 342 agtgctcacacaattggacaagcaaggtgcacaacatttaggtacgaatctacaatga 401

Query: 1848 gaccaacataga 1859
||||||||||
Sbjct: 402 gaccaacataga 413

>gb|ES840062.1| UFL_061_05 Cotton fiber 0-10 day post anthesis Gossypium hirsutum
cDNA, mRNA sequence
Length = 1368

Score = 99.6 bits (50), Expect = 8e-17
Identities = 221/278 (79%)
Strand = Plus / Plus

Query: 1906 gggtcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaac 1965
|||||||||||||||| || |||| |||| | || |||||| || ||||||
Sbjct: 204 gggtcaggggacaacaatttgtcaccgcttgacatccagactccaacatattttgacaac 263

Query: 1966 tactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttc 2025
| |||||| |||||| | |||| || | |||||| |||| | ||||
Sbjct: 264 aagtacttcaacaacctcatcggcaagaggggctgctccactcggatcaagagttgttc 323

Query: 2026 aacgggtgggtccaccgactccattgtgctggctacagaccaaccgggaccttctcc 2085
|| || | |||||||||||||| || | |||| | |||||| || |||| |
Sbjct: 324 aatgggggatccaccgactccattgtaagggttacagtaaaaaccgagctccttcagc 383

Query: 2086 tctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaat 2145
|||||| | | |||||| |||||||||||||| |||||| || ||

Sbjct: 384 tctgattttgttacagccatgattaagatgggagacattagtcactcactggatcaaag 443

Query: 2146 ggagaaatcaggaagaattgtagaaggattaactaatt 2183

||||| ||||||||||||| || |||||| |||| |||||

Sbjct: 444 ggagagatcaggaagaactgcagaagggttaattaatt 481

>gb|BI262826.1| NF091E03EC1F1023 Elicited cell culture Medicago truncatula cDNA clone
NF091E03EC 5', mRNA sequence
Length = 409

Score = 99.6 bits (50), Expect = 8e-17

Identities = 108/128 (84%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||||||||||||||| | ||||||||||||||||||||||||||||| | ||

Sbjct: 281 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 340

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276

|| ||||||| || || || || ||||||||| | || || ||||| || ||||||||| |||

Sbjct: 341 aatccaacaaaaattcngcccgtggattcnaagtgatcgacaaaatcaaatcagcagtg 400

Query: 1277 gagaaagt 1284

|||||||

Sbjct: 401 gagaaagt 408

Score = 83.8 bits (42), Expect = 5e-12

Identities = 67/76 (88%)

Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttcac 768

||||||||||||||| || ||||| ||||||||||||||||||| | || ||||||||| |||

Sbjct: 206 caatctgccatatcaaaagagactcgcatgggtgcttctcttntgcgttgttcttncac 265

Query: 769 gattgctttgtcaatg 784

||||||||||| ||||

Sbjct: 266 gattgctttgttaatg 281

>gb|AW666202.1| sk33f05.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1028-3994 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 329

Score = 99.6 bits (50), Expect = 8e-17
Identities = 112/133 (84%)
Strand = Plus / Plus

Query: 1497 atgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaatggca 1556
||||| |||||||||||||||||||| | || || || |||||||||||||||| |||||||| ||
Sbjct: 8 atgtgaaacttggagaagagactccaggacggcaagccaatctgctgccaacaatgaca 67

Query: 1557 tcctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgacttt 1616
||||| |||||||||||||||||| |||||||| || || |||||||| |||||| ||||||
Sbjct: 68 tccaagaccacttcaaacctcaaccaacttatttcagatttaatgctctncaacttt 127

Query: 1617 ccaccaaggactt 1629
||||||| ||||||
Sbjct: 128 ccaccaagactt 140

Score = 71.9 bits (36), Expect = 2e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
|||||||||||||| |||||||| |||||||| ||| ||| ||| ||||||||| ||||||
Sbjct: 157 ggtcacacaattgaacaagcaaggtgcacaacctttagaacccaaatctacaacaagacc 216

Query: 1852 aacataga 1859
|||||||
Sbjct: 217 aacataga 224

>gb|G0006531.1| LJGBF85TF JCVI-LJ1 Lotus japonicus cDNA 5', mRNA sequence
Length = 292

Score = 97.6 bits (49), Expect = 3e-16
Identities = 139/165 (84%), Gaps = 3/165 (1%)
Strand = Plus / Plus

Query: 586 tctagattgacaatttgtttgctctgtttgtcctcatatgggggagtgccaatgcacaa 645

>gb|C0513848.1| s13dSG73C1100082_156358 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 629

Score = 95.6 bits (48), Expect = 1e-15
Identities = 135/164 (82%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| ||||||||||||||||||| || | ||||||| |||
Sbjct: 162 cttggtggcccaacctggaatgtaaaacttggagaagagatgccacgactgctagtcaa 221

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||||| |||| | |||||| | |||| | |||| | ||||| | |||| | |||||
Sbjct: 222 tctgctggaacactgccatcccagcaccaactccaaccttaatgtactcacctcaatg 281

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgct 1641
||| | ||| ||||||||||||||||||| |||| | |||||
Sbjct: 282 ttaagaatgttggctttccaccaaggacttagtgcattgct 325

Score = 89.7 bits (45), Expect = 8e-14
Identities = 132/161 (81%)
Strand = Plus / Plus

Query: 1900 acatcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt 1959
||||||| ||||||||||| || ||||||| ||||||| || ||||| || |||
Sbjct: 438 acatcaggatcaggggacaataatttggcacctcttgatctccatactcccacttcttt 497

Query: 1960 gacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaa 2019
||||||| |||| | |||||| | |||| | ||||||| || || | || | |||
Sbjct: 498 gacaactgtactacaggaaccttgttcaaaacaagggtcttcttcttattcagaccaaca 557

Query: 2020 ctgttcaacgggtgggtccaccgactccattgtgctgggcta 2060
|| ||||||| ||||||||||| |||| | ||| |||||||
Sbjct: 558 cttttcaacggcgggtccaccaactcaatagtgagtggtgcta 598

Score = 81.8 bits (41), Expect = 2e-11
Identities = 116/141 (82%)
Strand = Plus / Plus

Query: 1202 ggagagaagaacgcaaaccccaacaggaactctgctcgtggattcgaggttattgacaac 1261
|||||
Sbjct: 15 ggagagaagaacgcactcccgaataggaactctgttcgaggattcgatgcatgacaac 74

Query: 1262 attaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagatatccttgcc 1321
|||
Sbjct: 75 ataaagacagatgtagagaacatatgtccaggggttgatcatgtgctgatatcctagcc 134

Query: 1322 atcgtgccagagactctggt 1342
||
Sbjct: 135 attgctgccacagactctggt 155

>gb|AW691930.2| NF050G04ST1F1000 Developing stem Medicago truncatula cDNA clone
NF050G04ST 5', mRNA sequence
Length = 372

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttggttctt 764
|||||
Sbjct: 215 agtgcaatccgccatatcaaaggaggcacgaattgggtgcttctatcctccgcttggttctt 274

Query: 765 ccacgattgctttgtcaatg 784
|||||
Sbjct: 275 ccacgattgctttgtcaatg 294

Score = 67.9 bits (34), Expect = 3e-07
Identities = 49/54 (90%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 300 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgca 353

>emb|AJ548283.1| AJ548283 MTAPHEU Medicago truncatula cDNA clone mtaehac110006d12,
mRNA sequence

Sbjct: 204 cttggtggcccaacctggaatgtaaaaacttggagaagagatgccacaactgctagtcaa 263

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
||||| ||| ||||| || ||||| ||| ||||| ||||| ||||| |||||

Sbjct: 264 tctgatgcgaacctgccatcccaagaccaactccaaccttaataactcacctcaatg 323

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttggc 1641
||||| | ||||| ||||| ||||| ||||| |||||

Sbjct: 324 tttagaatgttggctttccaccaaggacttagtcgattggc 367

Score = 75.8 bits (38), Expect = 1e-09
Identities = 131/162 (80%)
Strand = Plus / Plus

Query: 1788 agtggtcacacaattggacaagcaaggcgcacaaacttcagagcccgcatctacaacga 1847
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 368 agtgctcacacaattggacaagcaaggcgcacaacatttaggtacgaatctacaatga 427

Query: 1848 gaccaacatagaaaccgcatttgaaggacttaggcagcaaagctgcctagaacatcagg 1907
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 428 gaccaacatagatacttcttttggctagcacaaggcaatctaattgcccaaagacatcatg 487

Query: 1908 gtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 488 atcaggggacaacaatttggcacctcttgatctcactactcc 529

>emb|FN039861.1| FN039861 *Petunia axillaris* subsp. *axillaris* pool of root and petal
tissue *Petunia axillaris* subsp. *axillaris* cDNA clone
drs21P0001M16_R.ab1 2007-08-10, mRNA sequence
Length = 485

Score = 85.7 bits (43), Expect = 1e-12
Identities = 118/143 (82%)
Strand = Plus / Minus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 400 tcaggttcaggggacaacaacttagcaccacttgatcttcaaactcctacaactttgac 341

Query: 1963 aactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactg 2022
||| || ||||| ||| | | ||||| || | | ||||| |||||
Sbjct: 340 aacagttatttcaagaaccttgtaacagaaagggtctgcttcattctgatcaacaactc 281

Query: 2023 ttcaacggtgggtccaccgactc 2045
|| || ||||| ||||| |||||
Sbjct: 280 tttaatggtggatccactgactc 258

>emb|FN039860.1| FN039860 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs21P0001M16_F.ab1 2007-08-10, mRNA sequence
Length = 485

Score = 85.7 bits (43), Expect = 1e-12
Identities = 118/143 (82%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaactctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| | ||||| ||||| ||||| || | |||||
Sbjct: 85 tcaggttcaggggacaacaacttagcaccacttgatcttcaaactcctacaactttgac 144

Query: 1963 aactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactg 2022
||| || ||||| ||||| ||| | | ||||| || | | ||||| |||||
Sbjct: 145 aacagttatttcaagaaccttgtaacagaaagggtctgcttcattctgatcaacaactc 204

Query: 2023 ttcaacggtgggtccaccgactc 2045
|| || ||||| ||||| |||||
Sbjct: 205 tttaatggtggatccactgactc 227

>gb|EG559283.1| CR03032H04 Root CR03 cDNA library Catharanthus roseus cDNA clone
CR03032H04 5', mRNA sequence
Length = 560

Score = 85.7 bits (43), Expect = 1e-12
Identities = 109/131 (83%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||||| ||||| || | ||||| ||||| ||||| |||||
Sbjct: 376 tggaatgtgaaacttgaagaagagatgcaacaactgcaagccaagctgctgctaacaat 435

roseus cDNA similar to peroxidase, mRNA sequence
Length = 708

Score = 83.8 bits (42), Expect = 5e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
||||| ||||||||| || ||||||||||||||||||||||||| ||||||||| | |||||
Sbjct: 376 ttctactctgattttgctgccgcccatgatcaagatgggagatattagtcctttgactggt 435

Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
|| ||||||||| | ||||| ||||||||| || |||||
Sbjct: 436 tcaaatggagaggttaggaaaaattgtaggagggttaa 473

Score = 46.1 bits (23), Expect = 1.0
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcaca 1821
||||||||||| |||||||||||||
Sbjct: 91 cacacaattggtcaagcaaggtgcaca 117

>gb|FD420140.1| 1_SM-JB_R10-G12_T3_G12_3100394_14_ab1 CrUniGene root Catharanthus
roseus cDNA similar to peroxidase, mRNA sequence
Length = 494

Score = 83.8 bits (42), Expect = 5e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
||||| ||||||||| || ||||||||||||||||||||||||| ||||||||| | |||||
Sbjct: 266 ttctactctgattttgctgccgcccatgatcaagatgggagatattagtcctttgactggt 325

Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
|| ||||||||| | ||||| ||||||||| || |||||
Sbjct: 326 tcaaatggagaggttaggaaaaattgtaggagggttaa 363

>gb|DW508346.1| GH_TMIRS_123_D07_F Cotton Normalized Library dT primed Gossypium

hirsutum cDNA, mRNA sequence
Length = 325

Score = 81.8 bits (41), Expect = 2e-11
Identities = 74/85 (87%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||
Sbjct: 160 gccatgatcaagatgggagacattagtcctcctcactggatcacgtgggagatcaggaag 219

Query: 2161 aattgtagaaggattaactaatttg 2185
|||
Sbjct: 220 aactgcagaagggtgaactaatttg 244

>gb|GT143205.1| METCC85TR JCVI-MT3 Medicago truncatula cDNA 3', mRNA sequence
Length = 534

Score = 79.8 bits (40), Expect = 7e-11
Identities = 61/68 (89%)
Strand = Plus / Minus

Query: 2083 tcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctcc 2142
|||||
Sbjct: 326 tcctctggttcgtcaccgccatgatcaagatgggagacattagtcctcaccggtca 267

Query: 2143 aatggaga 2150
|||||
Sbjct: 266 aatggaga 259

>gb|DR280730.1| 157654 CERES-148 Arabidopsis thaliana cDNA clone 124846 5', mRNA
sequence
Length = 461

Score = 79.8 bits (40), Expect = 7e-11
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 229 cgc atgggtgcttctctccttcgcttgttcttccatgattgctttgtcaatg 280

>gb|CN910539.1| 030128ABLC005555HT (ABLC) Braeburn cell culture three days after subculture Malus x domestica cDNA clone ABLC005555, mRNA sequence
Length = 643

Score = 79.8 bits (40), Expect = 7e-11
Identities = 205/260 (78%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| || ||||| ||| ||||| ||||| ||||| || || || ||||| ||
Sbjct: 15 tcaggagataacaattggctccacttgaccttcaaaccctacttctttcgacaacaac 74

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||||| ||||| | ||||| || ||||| ||||| ||||| ||||| || |||||
Sbjct: 75 tacttcaaaaacctaatccagaataaagggtctcctccactctgaccagcagcttccaat 134

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
||||| ||||| || || || || || ||||| || | ||||| |||
Sbjct: 135 ggtggttccaccgattcgatagtgagagcctacagcaacagctacaacgccttcagtct 194

Query: 2089 gatttcgcccgccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|| || || ||||| ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 195 gactttgcgagtgccatgatcaagatgggagacatcaaacctctcactggatccagtggg 254

Query: 2149 gaaatcaggaagaattgtag 2168
|| || ||||| |||||
Sbjct: 255 gagattaggaagaattgtag 274

>gb|CN908859.1| 030122ABLC003031HT (ABLC) Braeburn cell culture three days after subculture Malus x domestica cDNA clone ABLC003031, mRNA sequence
Length = 563

Score = 79.8 bits (40), Expect = 7e-11
Identities = 205/260 (78%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| || ||||| ||| ||||| ||||| ||||| || || || ||||| ||
Sbjct: 15 tcaggagataacaattggctccacttgaccttcaaaccctacttctttcgacaacaac 74

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||||| |||| | ||||| || ||||||||||||||||||| |||| | |||||
Sbjct: 75 tacttcaaaaacctaataccagaataaagggtctcctccactctgaccagcagctcttcaat 134

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
||||| ||||||| || || ||| | | ||||||| || | ||||| |||
Sbjct: 135 ggtggttccaccgattcgatagtgagagcctacagcaacagctacaacgccttcagtct 194

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|| || | ||||||||||||||||||| | ||||||||| ||| |||
Sbjct: 195 gactttgcgagtgccatgatcaagatgggagacatcaaacctctcactggatccagtggg 254

Query: 2149 gaaatcaggaagaattgtag 2168
|| || |||||||||||||
Sbjct: 255 gagattaggaagaattgtag 274

>gb|CN908310.1| 030109ABLC001919HT (ABLC) Braeburn cell culture three days after
subculture Malus x domestica cDNA clone ABLC001919, mRNA
sequence
Length = 627

Score = 79.8 bits (40), Expect = 7e-11
Identities = 205/260 (78%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
||||| || ||||||| |||| ||||||| ||||||| || || || ||||| |||
Sbjct: 15 tcaggagataacaattggctccacttgaccttcaaacctacttctttcgacaacaac 74

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||||| ||||| | ||||| || ||||||||||||||||||| |||| | |||||
Sbjct: 75 tacttcaaaaacctaataccagaataaagggtctcctccactctgaccagcagctcttcaat 134

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
||||| ||||||| || || ||| | | ||||||| || | ||||| |||
Sbjct: 135 ggtggttccaccgattcgatagtgagagcctacagcaacagctacaacgccttcagtct 194

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|| || | ||||||||||||||||||| | ||||||||| ||| |||

Sbjct: 195 gactttgcgagtgccatgatcaagatgggagacatcaaacctctcactggatccagtggg 254

Query: 2149 gaaatcaggaagaattgtag 2168

|| || |||||

Sbjct: 255 gagattaggaagaattgtag 274

>dbj|AU238571.1| AU238571 RAFL17 Arabidopsis thaliana cDNA clone RAFL17-40-J20 5',
mRNA sequence
Length = 647

Score = 79.8 bits (40), Expect = 7e-11
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784

|||||

Sbjct: 226 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 277

>emb|FN019009.1| FN019009 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0005I02_R.ab1 2007-08-10, mRNA sequence
Length = 553

Score = 77.8 bits (39), Expect = 3e-10
Identities = 69/79 (87%)
Strand = Plus / Minus

Query: 706 gtgcaatctgcatatctaaggagaccgcattgggtgcttctctccttcgcttgttcttc 765

|||||

Sbjct: 427 gtgcaatctgcatatcaataaggaaactcgaatgggtgcttctctccttcgcctattcttc 368

Query: 766 cacgattgctttgtcaatg 784

|||||

Sbjct: 367 cacgattgctttgtcaatg 349

Score = 75.8 bits (38), Expect = 1e-09
Identities = 110/134 (82%)
Strand = Plus / Minus

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552

Score = 54.0 bits (27), Expect = 0.004
Identities = 60/71 (84%)
Strand = Plus / Plus

Query: 1232 tctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291
||||| | ||||| || || ||||| ||||| || || ||||| ||||| ||
Sbjct: 355 tctgctagaggatttgaagtcattgacaacattaaatctgctgtagagaaagtgtgcct 414

Query: 1292 ggagttgtttc 1302
|| |||||
Sbjct: 415 ggtgtgtttc 425

Score = 52.0 bits (26), Expect = 0.016
Identities = 82/101 (81%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||| | ||||| || ||||| || ||||| ||||| ||||| ||
Sbjct: 487 tggaatgtaaaattgggaagaagagatgcaagaacagcaagccaagctgctgcaaacagt 546

Query: 1553 ggcattcctgcaccacttcaaaccttaaccaactcatctc 1593
|||| | ||| || || || ||||| | |||||
Sbjct: 547 agcattcctccactacgtctaaccttantcgactcatctc 587

>emb|FN021689.1| FN021689 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0009N11_R.ab1 2007-08-10, mRNA sequence
Length = 556

Score = 77.8 bits (39), Expect = 3e-10
Identities = 117/143 (81%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaactctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| | ||||| ||||| || || |||||
Sbjct: 84 tcaggttcaggggacaacaacttagcaccacctgatcttcaaactcctacaaactttgac 143

Query: 1963 aactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactg 2022

|||| | ||||| ||| | | ||||| || | ||||| |||||
Sbjct: 144 aacagttatttcaagaaccttgtaacagaaaggtctgcttcattctgatcaacaactc 203

Query: 2023 ttcaacggtgggtccaccgactc 2045

|| || ||||| ||||| |||||
Sbjct: 204 tttaatggtggatccactgactc 226

>emb|FN021688.1| FN021688 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0009N11_F.ab1 2007-08-10, mRNA sequence
Length = 526

Score = 77.8 bits (39), Expect = 3e-10
Identities = 117/143 (81%)
Strand = Plus / Minus

Query: 1903 tcagggtcaggggacaacaactctggcaccacttgatcttcaaactccaaccagctttgac 1962

||||| ||||| ||||| | ||||| ||||| ||||| || | |||||
Sbjct: 502 tcagggtcaggggacaacaacttagcaccacctgatcttcaaactcctacaactttgac 443

Query: 1963 aactactacttcaagaacctcgttcagaagaaggtctcctccactctgatcagcaactg 2022

||| || ||||| ||||| ||| | | ||||| || | ||||| |||||
Sbjct: 442 aacagttatttcaagaaccttgtaacagaaaggtctgcttcattctgatcaacaactc 383

Query: 2023 ttcaacggtgggtccaccgactc 2045

|| || ||||| ||||| |||||
Sbjct: 382 tttaatggtggatccactgactc 360

>emb|FN034858.1| FN034858 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs13P0012A19_R.ab1 2007-08-10, mRNA sequence
Length = 697

Score = 77.8 bits (39), Expect = 3e-10
Identities = 51/55 (92%)
Strand = Plus / Plus

Query: 730 acccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784

||||| ||||| ||||| ||||| | ||||| ||||| |||||
Sbjct: 214 accggaatgggtgcttctctccttcgcttcttcttccacgattgcttcgtcaatg 268

Score = 71.9 bits (36), Expect = 2e-08
Identities = 54/60 (90%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||||||||||||||||||| ||||| || ||||| |||||||||||||||||
Sbjct: 630 tcacactattggacaagcaaggtgcacaaagtttcagggcacgcatttacaacgagaccaa 689

>emb|FN019751.1| FN019751 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0006L16_F.ab1 2007-08-10, mRNA sequence
Length = 604

Score = 77.8 bits (39), Expect = 3e-10
Identities = 51/55 (92%)
Strand = Plus / Plus

Query: 730 acccgcattgggtgcttctctctcttcgcttgttcttccacgattgctttgtcaatg 784
||||| ||||||||||||||||||||| | ||||||||||||||||||| |||||||
Sbjct: 211 acccgaatgggtgcttctctctcttcgcttttcttccacgattgcttctgtcaatg 265

>gb|FC869557.1| C31102G05EF AbioticR1 Citrus reshni cDNA clone C31102G05, mRNA
sequence
Length = 706

Score = 77.8 bits (39), Expect = 3e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagaccgcattgggtgcttctctctcttcgcttgttcttc 765
||||||||||| || || || ||| | ||||||||| || |||||||||||||||||||||
Sbjct: 200 gtgcaatctgctatttcaaaagagctcgcatggggcctctctctcttcgcttgttcttc 259

Query: 766 cacgattgctt 776
|||||||||||
Sbjct: 260 cacgattgctt 270

Score = 56.0 bits (28), Expect = 0.001
Identities = 122/151 (80%), Gaps = 2/151 (1%)
Strand = Plus / Plus

Sbjct: 206 gtgcaatctgctatttcaaaagaggctcgcgatgggcgctctctccttcgcttggttcttc 265

Query: 766 cacgattgctt 776

|||||||||

Sbjct: 266 cacgattgctt 276

Score = 50.1 bits (25), Expect = 0.065

Identities = 91/113 (80%)

Strand = Plus / Plus

Query: 1154 cagggatgigatggttcaattctattggatgacacatcaagcttcaccggagagaagaac 1213

||||||| ||||| ||| ||||| ||||| ||||||||| ||||| ||||||||| ||

Sbjct: 561 cagggatgicgatggatcagttctactggacgacacatcatctttcactggagagaaaaat 620

Query: 1214 gcaaaccceaacaggaactctgctcgttgattcgaggttattgacaacattaa 1266

|| || |||| | ||||| || || ||||||||| || |||||||||

Sbjct: 621 gcgaatgccaatcgttaactccgcccgattcgaggatcatcgacaacattaa 673

>gb|FC924498.1| C31806G11EF StrCleopN Citrus reshni cDNA clone C31806G11, mRNA
sequence

Length = 699

Score = 77.8 bits (39), Expect = 3e-10

Identities = 63/71 (88%)

Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttcttc 765

||||||||||| || || || |||| | ||||||||| || |||||||||||||||||||||

Sbjct: 211 gtgcaatctgctatttcaaaagaggctcgcgatgggcgctctctccttcgcttggttcttc 270

Query: 766 cacgattgctt 776

|||||||||

Sbjct: 271 cacgattgctt 281

Score = 52.0 bits (26), Expect = 0.016

Identities = 104/130 (80%)

Strand = Plus / Plus

Query: 1598 tttagcgctcttggactttccac 1620
 || | ||||| |||||
Sbjct: 593 ttcaacgctctcggactttccac 615

Score = 54.0 bits (27), Expect = 0.004
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 ||||| ||||| ||| ||||| | || ||||| ||| ||||| ||||| || |||
Sbjct: 281 ggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 340

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 ||||| | ||||| || || ||||| ||||| || ||||| || || |||
Sbjct: 341 gtccccaatcgtaactccgccgaggattcgaggtcatcgacaacattaaagtcgcagtt 400

Query: 1277 gagaaag 1283
 |||||
Sbjct: 401 gagaaag 407

>gb|FC921479.1| C32105D10EF RVDdevelopN Citrus clementina cDNA clone C32105D10, mRNA
 sequence
 Length = 690

Score = 77.8 bits (39), Expect = 3e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

Query: 706 gtgcaatctgcatatctaaggagaccgcatgggtgcttctctctcttcgcttgttcttc 765
 ||||| || || || ||| | ||||| || ||||| ||||| |||||
Sbjct: 206 gtgcaatctgctatttcaaaaggctcgcacatgggcgctctctctcttcgcttgttcttc 265

Query: 766 cacgattgctt 776
 |||||
Sbjct: 266 cacgattgctt 276

Score = 67.9 bits (34), Expect = 3e-07
Identities = 115/142 (80%)

||||| ||| |||||
Sbjct: 199 tgatcagcagctcttcaa 182

Score = 71.9 bits (36), Expect = 2e-08
Identities = 54/60 (90%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||||||| ||||||||| ||||| || ||||| ||||||||| |||||
Sbjct: 418 tcacactattggacaagcaaggtgcacaagtttcagggcacgcatttacaacgagaccaa 359

Score = 50.1 bits (25), Expect = 0.065
Identities = 67/81 (82%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||| ||||||||| ||| || ||||| || ||||| || ||||| || |||||||||
Sbjct: 105 atgattaagatgggagactttcgtccccttactggatctaattggcgagatcaggaagaac 46

Query: 2164 tgtagaaggattaactaattt 2184
|| || ||||| |||||||||
Sbjct: 45 tgcaggaggatcaactaattt 25

>emb|FN045147.1| FN045147 *Petunia axillaris* subsp. *axillaris* pool of root and petal
tissue *Petunia axillaris* subsp. *axillaris* cDNA clone
drs21P0009020_F.ab1 2007-08-10, mRNA sequence
Length = 489

Score = 75.8 bits (38), Expect = 1e-09
Identities = 113/138 (81%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaactctggcaccacttgatcttcaactcc 1949
||||| ||||| ||||| ||||||||| ||||||||| ||||||||| || |||||
Sbjct: 318 ctgccaagaacctcaggttcaggggacaacaacttggcaccctcttgatctccagactcc 259

Query: 1950 aaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctctccactc 2009
|| ||||||||| || ||||| || ||||| || ||||| ||||||||| |||||||||
Sbjct: 258 tacatactttgacaaccattatctcataaatcttgtaacaaaaagggtctgctccactc 199

Query: 2010 tgatcagcaactgttcaa 2027
 ||||| ||| |||||
Sbjct: 198 tgatcagcagctcttcaa 181

Score = 71.9 bits (36), Expect = 2e-08
Identities = 54/60 (90%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 417 tcacactattggacaagcaaggtgcacaagtttcagggcacgcatttacaacgagaccaa 358

Score = 50.1 bits (25), Expect = 0.065
Identities = 67/81 (82%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
 ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 104 atgattaagatgggagcactttcgtccccttactggatctaattggcgagatcaggaagaac 45

Query: 2164 tgtagaaggattaactaattt 2184
 || || ||||| ||||| |||||
Sbjct: 44 tgcaggaggatcaactaattt 24

>emb|FN019752.1| FN019752 *Petunia axillaris* subsp. *axillaris* pool of root and petal
tissue *Petunia axillaris* subsp. *axillaris* cDNA clone
drs31P0006L16_R.ab1 2007-08-10, mRNA sequence
Length = 590

Score = 75.8 bits (38), Expect = 1e-09
Identities = 113/138 (81%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaacttggcaccacttgatcttcaaactcc 1949
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 301 ctgccaagaacctcaggttcaggggacaacaacttggcacctcttgatctccagactcc 242

Sbjct: 441 tcaggagataacaatttggctccacttgaccttcaaaccctacttcttttcgacaacaac 500

Query: 1969 tacttcaagaacctcgttcagaagaaggtctctccactctgatcagcaactgttcaac 2028

||||||| ||||| | ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 501 tacttcaaaaacctaatccagaataaaggtctctccactctgaccagcagctcttcaat 560

Query: 2029 ggtgggtccaccga 2042

||||| |||||

Sbjct: 561 ggtggtccaccga 574

Score = 63.9 bits (32), Expect = 4e-06

Identities = 50/56 (89%)

Strand = Plus / Plus

Query: 1798 acaattggacaagcaaggtgcacaaacttcagagcccgcactctacaacgagaccaa 1853

||||||| ||||||||| ||||| ||||| |||||||||

Sbjct: 330 acaattgggcaagcaaggtgcacatcattcagaccccgcataatacaacgagaccaa 385

Score = 50.1 bits (25), Expect = 0.065

Identities = 100/125 (80%)

Strand = Plus / Plus

Query: 1508 ggaagaagagacgctagaactgctagccaatctgctgctaacaatggcatccctgcacc 1567

||||||||| || ||||| ||||| | ||||||||| ||||| | ||

Sbjct: 186 ggaagaagagacgcaaggactgcaagccaagccgctgctaacaacaacatccccctcca 245

Query: 1568 acttcaaaccttaaccaactcatctcaagatttagcgctcttgactttcaccaaggac 1627

|| ||||| ||||| ||||||| | ||| || ||| ||||| ||||||||| |||

Sbjct: 246 acccgaaacctaaaccagctcatctctacattcagtgctgttggtctttccaccagagac 305

Query: 1628 ttggt 1632

|||||

Sbjct: 306 ttggt 310

>gb|EV227910.1| VV_PeA016c06.b1 Vitis vinifera cv. perlette LibA Vitis vinifera cDNA,
mRNA sequence
Length = 1149

Score = 75.8 bits (38), Expect = 1e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 284 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 343

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 344 tactacaagaacct 357

>gb|EH047301.1| AS2RM4P1E10.ab1 Roots inoculated with Meloidogyne arenaria (RM)
Arachis stenosperma cDNA 5', mRNA sequence
Length = 725

Score = 75.8 bits (38), Expect = 1e-09
Identities = 164/206 (79%)
Strand = Plus / Plus

Query: 1960 gacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaa 2019
||||| ||||||| ||||||| | ||| || | ||||||| || || |||||||
Sbjct: 80 gacaaccactacttcaacaacctcgtcgaccggaaaggccccctccattccgaccagcaa 139

Query: 2020 ctgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcacc 2079
|| ||||||| || || || ||||||| || ||||||| | ||||||| || |
Sbjct: 140 ctettcaacggaggatctactgactccattgttcgcggtacagctcaaaccctagctct 199

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
|| | | ||||| ||| ||||||| ||||||| || ||| |||||||
Sbjct: 200 tttttgccgattttgccagtccatgatcaagatgggagacataaatcccctcactgga 259

Query: 2140 tccaatggagaaatcaggaagaattg 2165
||||| ||||| || || |||||||
Sbjct: 260 tccaaggagagattagaaagaattg 285

>gb|EC991497.1| WIN1142.C21_L14 Muscat Hamburg pre-veraison berry normalized (WIN11)
Vitis vinifera cDNA clone WIN1142_L14 3', mRNA sequence
Length = 465

Score = 75.8 bits (38), Expect = 1e-09

Identities = 65/74 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 449 tcagagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 390

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 389 tactacaagaacct 376

>gb|EC987303.1| WIN1130.C21_E15 Muscat Hamburg pre-veraison berry normalized (WIN11)
Vitis vinifera cDNA clone WIN1130_E15 3', mRNA sequence
Length = 851

Score = 75.8 bits (38), Expect = 1e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 694 tcagagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 753

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 754 tactacaagaacct 767

>gb|EC985323.1| WIN1124.C21_I01 Muscat Hamburg pre-veraison berry normalized (WIN11)
Vitis vinifera cDNA clone WIN1124_I01 3', mRNA sequence
Length = 906

Score = 75.8 bits (38), Expect = 1e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 478 tcagagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 537

Query: 1969 tacttcaagaacct 1982
|||| |||||||

Sbjct: 538 tactacaagaacct 551

>gb|CV861937.1| gonad_EST09518 Embryonic gonad cDNA Library Gallus gallus cDNA 5',
mRNA sequence
Length = 1288

Score = 75.8 bits (38), Expect = 1e-09
Identities = 59/66 (89%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313
||||| ||||| ||||| || ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 348 ttgacaccattaaagaagccgtggagagagagtgccaggagttgtttcctgtgcagata 407

Query: 1314 tccttg 1319
|||||
Sbjct: 408 tccttg 413

>gb|CX309187.1| C18022D10Rv Drought2 Citrus reshni cDNA clone C18022D10, mRNA
sequence
Length = 712

Score = 75.8 bits (38), Expect = 1e-09
Identities = 122/150 (81%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 516 cttggaggcccaagctggcaagtaaaactcgggaaggagagatgctagaactgcaagccta 457

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 1597
||||| ||||| || ||| || || ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 456 tctgctgctaataagcggcattcctgctcctacctcaaacttgaatcaaccatctctag 397

Query: 1598 tttagcgtcttggactttccaccaaggac 1627
|| | ||||| ||||| ||||| |||||
Sbjct: 396 ttcaacgtctcggactttccaacaaggac 367

Score = 60.0 bits (30), Expect = 7e-05
Identities = 105/130 (80%)

Strand = Plus / Minus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
||||| ||||||| ||||||| ||||||| ||||||| || || ||||||| ||

Sbjct: 230 cagggcacaacaacttggcaccgcttgatctgcaaactcctacttgttttgacaacaatt 171

Query: 1970 acttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacg 2029
||||| ||||||| || || || ||||||| || ||||||| || ||||||| ||

Sbjct: 170 acttcaggaacctggtcaacagaaagggttctcctccactctgatcaacagctgttcaatg 111

Query: 2030 gtgggtccac 2039
|||||||||

Sbjct: 110 gtgggtccac 101

Score = 46.1 bits (23), Expect = 1.0

Identities = 101/127 (79%)

Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||||| ||| ||||||| ||||| ||||||| || || ||||||| || ||

Sbjct: 708 ggatgcatggttcaattctattggatgacacatcaagcttcaccggagagaaaaatgca 649

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| ||||| | ||||||| || || ||||||| || || ||||||| || || ||

Sbjct: 648 aatgccaatcgtaactccgcccggttctgaggtcatcgacaacattaaatcagccagtt 589

Query: 1277 gagaaag 1283
|||||||

Sbjct: 588 gagaaag 582

>gb|CA105303.1| SCJFHR1C05E10.g HR1 Saccharum officinarum cDNA clone SCJFHR1C05E10
5', mRNA sequence
Length = 857

Score = 75.8 bits (38), Expect = 1e-09

Identities = 80/94 (85%)

Strand = Plus / Plus

Query: 1889 gctgcctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948

|||||
Sbjct: 402 gctgccctagaacctcaggttcaggtgacaacaatttggcgcctctggaccttcaaacc 461

Query: 1949 caaccagctttgacaactactacttcaagaacct 1982

|||||
Sbjct: 462 caaccgtctttgagaacaactactacaagaacct 495

Score = 44.1 bits (22), Expect = 4.0
Identities = 40/46 (86%)
Strand = Plus / Plus

Query: 2137 ggctccaatggagaaatcaggaagaattgtagaaggattaactaat 2182

|||||
Sbjct: 650 ggctccaatgggcagatcaggaagaactgcagaagggttaactaat 695

>gb|CA102350.1| SCBGHR1058E08.g HR1 Saccharum officinarum cDNA clone SCBGHR1058E08
5', mRNA sequence
Length = 664

Score = 75.8 bits (38), Expect = 1e-09
Identities = 80/94 (85%)
Strand = Plus / Plus

Query: 1889 gctgccctagaacctcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948

|||||
Sbjct: 402 gctgccctagaacctcaggttcaggtgacaacaatttggcgcctctggaccttcaaacc 461

Query: 1949 caaccagctttgacaactactacttcaagaacct 1982

|||||
Sbjct: 462 caaccgtctttgagaacaactactacaagaacct 495

>gb|CF205258.1| RR890915I0004_IVa_Ra_B09 Vitis sp. RR890915I Vitis hybrid cultivar
cDNA clone RR890915I0004_IVa_Ra_B09 3', mRNA sequence
Length = 746

Score = 75.8 bits (38), Expect = 1e-09
Identities = 65/74 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

5' similar to class III peroxidase [Gossypium hirsutum]
Length = 320, mRNA sequence
Length = 337

Score = 73.8 bits (37), Expect = 4e-09
Identities = 49/53 (92%)
Strand = Plus / Plus

Query: 732 ccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 117 ccgcatgggtgcttctctcgttcgcttgttcttccatgactgtttgtcaatg 169

>emb|CU488677.1| CU488677 DROUGHTLS_KZOACAF Theobroma cacao cDNA clone
KZOACAF8YE10FM1, mRNA sequence
Length = 501

Score = 73.8 bits (37), Expect = 4e-09
Identities = 49/53 (92%)
Strand = Plus / Plus

Query: 732 ccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 269 ccgcatgggtgcttctctcgttcgcttgttcttccatgactgtttgtcaatg 321

>gb|FG154278.1| AGN_RNC104xj04f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 798

Score = 73.8 bits (37), Expect = 4e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaat 783
|||||
Sbjct: 174 aaggaaaccgcatgggtgcttccctccttcgcctattcttccacgattgcttcgtcaat 233

Query: 784 g 784
|
Sbjct: 234 g 234

Score = 73.8 bits (37), Expect = 4e-09

Score = 73.8 bits (37), Expect = 4e-09
Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| |||| | ||| |||| ||||| ||||| ||||| || ||||| || |||||
Sbjct: 434 cttggaggccctaattgggatgtaaaactcggagaagagatgccagaacagcaagccaa 493

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||| | |||| | |||| || | || ||||| ||||| ||||| || ||||| ||
Sbjct: 494 gctgccgcaaacagtagcattcctcctccaacttctaaccttaaccggetcatctctagc 553

Query: 1598 tttagcgctcttggactttccaccaagga 1626
|| || ||| |||| ||||| ||||| |||||
Sbjct: 554 ttcagtgtgttggcctttccaccaagga 582

Score = 63.9 bits (32), Expect = 4e-06
Identities = 53/60 (88%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||| ||||| ||||| ||||| | ||||| || ||||| ||||| ||||| |||||
Sbjct: 604 tcacaccattggacaagcaaggtgcactagtttcagggcagcatatacaacgagaccaa 663

>gb|FG156951.1| AGN_RNC026xe21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 921

Score = 73.8 bits (37), Expect = 4e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcgatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaat 783
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 374 aaggaaaccgcatgggtgcttccctccttcgctattcttccacgattgcttctgtcaat 433

Query: 784 g 784
|
Sbjct: 434 g 434

Score = 58.0 bits (29), Expect = 3e-04
Identities = 120/149 (80%), Gaps = 1/149 (0%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||||| |||| ||| |||| ||||| ||||| ||||| ||| ||| | || |||||
Sbjct: 625 cttggaggcctaattgggatgtaaaactcggaagaagagatgccaga-cagcaagccaa 683

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||| | |||| | |||| ||| | || ||||| ||||| ||||| ||||| ||
Sbjct: 684 gctgccgcaaacagtagcattcctcctccaacttctaaccttaaccggctcatctctagc 743

Query: 1598 tttagcgctcttggactttccaccaagga 1626
|| || ||| |||| ||||| ||||| |||||
Sbjct: 744 ttcagtgctgttggcctttccaccaagga 772

>gb|FG157638.1| AGN_RNC025xk16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 907

Score = 73.8 bits (37), Expect = 4e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcatgggtgcttctctctctccttgccttgttcttccacgattgctttgcaat 783
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 201 aaggaaaccgcatgggtgcttccctcctcctcgcctattcttccacgattgcttctgcaat 260

Query: 784 g 784
|
Sbjct: 261 g 261

Score = 73.8 bits (37), Expect = 4e-09
Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 221 atgggtgcttcctcctcgttcgcttggttcttccatgattgctttgttaatg 269

Score = 56.0 bits (28), Expect = 0.001
Identities = 70/84 (83%)
Strand = Plus / Plus

Query: 1256 gacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttctgcgagatatac 1315
||||| || ||||| || || ||||| || ||||| ||||| || || || || |||||
Sbjct: 368 gacaatataaaatccgcagttgagaaagcttgctcctggagtagtctcatgtgctgatatac 427

Query: 1316 cttgccatcgctgccagagactct 1339
||||| ||||| ||||| ||||| |||||
Sbjct: 428 cttgccatcgctgctagagactct 451

>gb|EB450877.1| KT7C.108P16F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108P16,
mRNA sequence
Length = 785

Score = 73.8 bits (37), Expect = 4e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaat 783
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 194 aaggaaaccgcatgggtgcttccctccttcgcttattcttccacgattgcttctgtcaat 253

Query: 784 g 784
|
Sbjct: 254 g 254

Score = 73.8 bits (37), Expect = 4e-09
Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||
Sbjct: 263 gccatgatcaagatgggtgacatcaaacctctcaccggctctaattggagaaattcgcaag 322

Query: 2161 aattgtagaaggattaactaa 2181
|||||
Sbjct: 323 aattgtagaaagatcaactaa 343

Score = 71.9 bits (36), Expect = 2e-08
Identities = 87/104 (83%)
Strand = Plus / Plus

Query: 1939 cttcaaactccaaccagctttgacaactactacttcaagaacctcgttcagaagaagggt 1998
|||||
Sbjct: 101 cttcaaaccccaacggcctttgacaacaagtatttcaagaacctgattaacaagaagggc 160

Query: 1999 ctctccactctgatcagcaactgttcaacgggtgggtccaccga 2042
||
Sbjct: 161 ctctccactctgatcagcagctcttcaatgggtgggtccgccga 204

>gb|CN782128.1| EST00224 cqseed Chenopodium quinoa cDNA clone S02D05 5' similar to
peroxidase, putative At5g05340, mRNA sequence
Length = 803

Score = 73.8 bits (37), Expect = 4e-09
Identities = 46/49 (93%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgcttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 238 atgggtgcttctctcctacgcttgcttcttccacgattgcttcgctcaatg 286

Score = 46.1 bits (23), Expect = 1.0
Identities = 68/83 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| || || ||||| || || || || ||||| ||||| || |||||
Sbjct: 478 cttggaggaccaacttggaacgtaaagctaggtagaagagatgctaggacagctagccaa 537

Query: 1538 tctgctgctaacaatggcatccc 1560
|| |||| ||||| |||||
Sbjct: 538 tccactgcaacaatgacatccc 560

>gb|FC869818.1| C31105F02EF AbioticR1 Citrus reshni cDNA clone C31105F02, mRNA
sequence
Length = 630

Score = 71.9 bits (36), Expect = 2e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcgatgggtgcttctctccttcgcttgttcttccacgattgctt 776
||||||| || ||||||||||||||||||||||||||||||||||
Sbjct: 51 cgcgatgggcctctctccttcgcttgttcttccacgattgctt 94

Score = 54.0 bits (27), Expect = 0.004
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||||||| ||||||||||||| || |||
Sbjct: 102 ggatgcatggttcaattctattggatgacacatcatcttcaccggagaaaaatgca 161

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaatcagccgtg 1276
|||||| | ||||| || || ||||||||||||| || ||||||||||||| || || ||
Sbjct: 162 gtcccaatcgtaactccgcccggttcgaggtcatcgacaacattaagtcgcagtt 221

Query: 1277 gagaaag 1283
|||||||
Sbjct: 222 gagaaag 228

Score = 54.0 bits (27), Expect = 0.004
Identities = 87/107 (81%)
Strand = Plus / Plus

Query: 1521 ctagaactgctagccaatctgctgctaacaatggcatccctgcaccacttcaaactta 1580
||||||| ||||||| ||| | ||| | || | ||||| | |
Sbjct: 337 ctagaactgcaagccaatctgctgctaataagcggcttctcctctacctcaaactga 396

Query: 1581 accaactcatctcaagatttagcgctcttggactttccaaccaaggac 1627
| ||||| ||| || | ||||| ||||||| |||||
Sbjct: 397 atcaactcacctctaggttcaacgctctcggactttccaacaaggac 443

>gb|FC874065.1| C31202A05EF BiotPhyR1 Citrus aurantium cDNA clone C31202A05, mRNA
sequence
Length = 689

Score = 71.9 bits (36), Expect = 2e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcattgggtcttctctcttcgcttgttcttccacgattgctt 776
||||||| || ||||||| ||||||| ||||||| |||||||
Sbjct: 228 cgcattgggcctctctcttcgcttgttcttccacgattgctt 271

Score = 56.0 bits (28), Expect = 0.001
Identities = 82/100 (82%)
Strand = Plus / Plus

Query: 1521 ctagaactgctagccaatctgctgctaacaatggcatccctgcaccacttcaaactta 1580
||||||| ||||||| ||| | ||||| ||| | || | ||||| | |
Sbjct: 514 ctagaactgcaagccaatctgctgctaataagcggcattctcctctacctcaaactga 573

Query: 1581 accaactcatctcaagatttagcgctcttggactttccac 1620
| ||||| ||| || | ||||| |||||||
Sbjct: 574 atcaactcacctctaggttcaacgctctcggactttccac 613

Score = 54.0 bits (27), Expect = 0.004
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

Query: 2085 ctctgatttcgccgcccgatgatcaagatgggagacattagtcctctcactggctccaa 2144
||||||| || ||||| ||||||||||||||| || ||||||| || ||||| |||||
Sbjct: 33 ctctgattttgctgccgcatgatcaagatgggtgatattagtccttactgggtccaa 92

Query: 2145 tggagaaatcaggaag 2160
||| ||||| |||||
Sbjct: 93 tggcgaataaggaag 108

>gb|EY845171.1| CA26-C1-002-040-C02-CT.F Sour orange leaf, field plant Citrus
aurantium cDNA, mRNA sequence
Length = 812

Score = 71.9 bits (36), Expect = 2e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcattgggtcttctctctcttcgcttgttcttccacgattgctt 776
||||||| || |||||||||||||||||||||||||||||||
Sbjct: 267 cgcattgggcctctctctcttcgcttgttcttccacgattgctt 310

Score = 60.0 bits (30), Expect = 7e-05
Identities = 120/150 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgggaagaagagacgctagaactgctagccaa 1537
||||||| || ||| || || ||||| || || ||||| ||||||||| |||||
Sbjct: 510 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 569

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||||| || ||||| ||| || || || ||||| || || ||||| ||| ||
Sbjct: 570 tctgctgctaataagcggcattcctcctctacctcaaacttgaatcaactcacctctagg 629

Query: 1598 tttagcgtcttggactttccaccaaggac 1627
| | ||||| ||||||||| |||||
Sbjct: 630 tccaacgctctcggactttccaacaaggac 659

Score = 54.0 bits (27), Expect = 0.004

Score = 54.0 bits (27), Expect = 0.004
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 286 ggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 345

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| | ||||| || || ||||| ||||| || ||||| ||||| || || ||
Sbjct: 346 gtcccaatcgtaactccgccgaggattcgaggtcatcgacaacattaaagtcgcagtt 405

Query: 1277 gagaaag 1283
|||||||
Sbjct: 406 gagaaag 412

>gb|EY776217.1| CR05-C1-103-015-D05-CT.F Mandarin leaf, infected with Xylella
fastidiosa (stage 2 of 2) Citrus reticulata cDNA, mRNA
sequence
Length = 968

Score = 71.9 bits (36), Expect = 2e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctctcttcgcttgttcttccacgattgctt 776
||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 225 cgcattgggcctctctctcttcgcttgttcttccacgattgctt 268

Score = 54.0 bits (27), Expect = 0.004
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 276 ggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 335

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| | ||||| || || ||||| ||||| || ||||| ||||| || || ||

Sbjct: 336 gtccccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaagtccgcagtt 395

Query: 1277 gagaaag 1283

|||||||

Sbjct: 396 gagaaag 402

>gb|EY725128.1| CS00-C3-703-086-B09-CT.F Sweet orange fruit, development stadium (4 of 6) Citrus sinensis cDNA, mRNA sequence
Length = 840

Score = 71.9 bits (36), Expect = 2e-08

Identities = 42/44 (95%)

Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctt 776

||||||| || ||||||||||||||||||||||||||||||||||||

Sbjct: 210 cgc atgggcctctctccttcgcttgttcttccacgattgctt 253

Score = 67.9 bits (34), Expect = 3e-07

Identities = 121/150 (80%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

||||||||||| | ||| | || ||||| | | ||||| ||||||||| |||||||

Sbjct: 453 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 512

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597

||||||||||| | ||||| ||| | || || ||||| | || ||||||| ||| ||

Sbjct: 513 tctgctgctaataagcgcattcctcctctacactcaaacttgaatcaactcacctctagg 572

Query: 1598 tttagcgtcttggactttccaccaaggac 1627

|| | ||||| ||||||||| |||||||

Sbjct: 573 ttcaacgctctcggactttccaacaaggac 602

Score = 54.0 bits (27), Expect = 0.004

Identities = 102/127 (80%)

Strand = Plus / Plus

Score = 46.1 bits (23), Expect = 1.0
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 2005 cactctgatcagcaactgttcaacgggtgggtccac 2039
|||||
Sbjct: 626 cactctgatcaacagctgttcaatgggtgggtccac 660

>gb|CV093292.1| FAMU_USDA_FP_1315 Vitis shuttleworthii L., grape Vitis shuttleworthii
cDNA clone JLVs077_F09 5', mRNA sequence
Length = 666

Score = 71.9 bits (36), Expect = 2e-08
Identities = 101/120 (84%), Gaps = 2/120 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt-gacaacta 1967
|||||
Sbjct: 230 tcaggggacaacaacttgcccctctggatcttcaaactcctac-agcttttgagaaca 288

Query: 1968 ctacttcaagaacctcgttcagaagaagggtctcctcactctgatcagcaactgttcaa 2027
|||||
Sbjct: 289 ctactacaagaacctgatcaagaagaaggacttctcactctgatcagcagctgttcaa 348

Score = 60.0 bits (30), Expect = 7e-05
Identities = 54/62 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattgggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
|||||
Sbjct: 116 cacacaattgggacaagcaaggtgcacatccttcagggtcgcataataatgagaccaac 175

Query: 1855 at 1856
||
Sbjct: 176 at 177

Score = 50.1 bits (25), Expect = 0.065
Identities = 58/69 (84%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
|||||
Sbjct: 426 atgatcaagatgggagatatcagccactcactggatcaaacggagagattaggaagaac 485

Query: 2164 tgtagaagg 2172
||
Sbjct: 486 tgcagaagg 494

Score = 48.1 bits (24), Expect = 0.26
Identities = 81/100 (81%)
Strand = Plus / Plus

Query: 1539 ctgctgctaacaatggcatcctgcaccacttcaaaccttaaccaactcatctcaagat 1598
|||||
Sbjct: 6 ctgctgcaaacacagcatcctcctccaacttcaaacctgaaccaactaatctctagtt 65

Query: 1599 ttagcgctcttggactttccaccaaggacttggctgcctt 1638
|
Sbjct: 66 tccaagctcttggcctctcaaccaggacttggctgcctt 105

>gb|C0866271.1| Mdfrt3046b02.y1 Mdfrt Malus x domestica cDNA clone Mdfrt3046b02 5'
similar to TR:Q41326 Q41326 PEROXIDASE ;, mRNA sequence
Length = 509

Score = 71.9 bits (36), Expect = 2e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||
Sbjct: 277 gccatgatcaagatgggagacatcaaacctctcactggatccagtggggagattaggaag 336

Query: 2161 aattgtag 2168
|||||
Sbjct: 337 aattgtag 344

>gb|G0566201.1| Mddb5025B21_e2932.g1 Mddb Malus x domestica cDNA 5' similar to
dbj|BAA82306.1| peroxidase [Nicotiana tabacum], mRNA
sequence
Length = 687

Score = 69.9 bits (35), Expect = 7e-08
Identities = 56/63 (88%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
|||||
Sbjct: 560 tcacacaattgggcaagcaaggtgtacaactttcagagctcgcatatataacgagaccaa 501

Query: 1854 cat 1856
|||
Sbjct: 500 cat 498

>emb|CU537036.1| CU537036 TISCIVS_KZ0AAQ Theobroma cacao cDNA clone KZ0AAQ5YH15FM1,
mRNA sequence
Length = 744

Score = 69.9 bits (35), Expect = 7e-08
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 463 cttggaggccccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 522

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 523 gctgctgccaacaacagcattcctctccaacttctaactgaacagactcatttctaga 582

Query: 1598 tttagcgcctcttgactttccaccaaggacttggt 1632
|||
Sbjct: 583 ttcaatgctcttgactttccaccaggacatggt 617

Score = 48.1 bits (24), Expect = 0.26
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcaca 1821
 |||||
Sbjct: 633 tcacacaattggactagcaaggtgcaca 660

>emb|CU505430.1| CU505430 PODMEUPA_KZOACAB Theobroma cacao cDNA clone KZOACAB5YF04FM1,
 mRNA sequence
 Length = 769

Score = 69.9 bits (35), Expect = 7e-08
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
 |||||
Sbjct: 455 cttggaggccccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 514

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
 |||||
Sbjct: 515 gctgctgccaacaacagcattcctcctccaacttctaacttgaacagactcatttctaga 574

Query: 1598 tttagcgctcttggactttccaccaaggacttgggt 1632
 |||
Sbjct: 575 ttcaatgctcttggactttccaccaggacatggt 609

Score = 48.1 bits (24), Expect = 0.26
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcaca 1821
 |||||
Sbjct: 625 tcacacaattggactagcaaggtgcaca 652

>emb|CU478688.1| CU478688 COPHAS_KZOAAAL Theobroma cacao cDNA clone KZOAAAL11YB20FM1,
 mRNA sequence
 Length = 642

Score = 69.9 bits (35), Expect = 7e-08
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||||||||||||||| || ||||| || |||||| |||||||||||||||||
Sbjct: 686 cacacgattggacaagcaaggtgcacgaatttcagggtcgcataatacaacgagaccaa 744

>gb|EB110403.1| 000430AFBC008068HT (AFBC) Royal Gala pre-opened floral bud Malus x
domestica cDNA clone AFBC008068, mRNA sequence
Length = 481

Score = 69.9 bits (35), Expect = 7e-08
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||||||||||||||| ||||| ||||||| ||||| || |||||||||||||
Sbjct: 217 tcacacaattgggcaagcaaggtgtacaactttcagagctcgcataatacaacgagaccaa 276

Query: 1854 cat 1856
|||
Sbjct: 277 cat 279

>gb|DW157696.1| CLVX9795.b1_E02.ab1 CLV(XYZ) lettuce virosa Lactuca virosa cDNA clone
CLVX9795, mRNA sequence
Length = 440

Score = 69.9 bits (35), Expect = 7e-08
Identities = 65/75 (86%)
Strand = Plus / Plus

Query: 2088 tgatttcgcccgcccatgatcaagatgggagacattagtcctctcactggtccaatgg 2147
||||| || ||||||||||||||||||||| ||||| ||| ||||| ||||||||||||||||| ||
Sbjct: 198 tgattttgcgcccgcccatgatcaacatgggtgatattcgtcccctcactggtccaacgg 257

Query: 2148 agaatcaggaagaa 2162
|| |||||||||||||
Sbjct: 258 cgagatcaggaagaa 272

>gb|DW145800.1| CLVX10900.b1_H13.ab1 CLV(XYZ) lettuce virosa Lactuca virosa cDNA
clone CLVX10900, mRNA sequence
Length = 453

Score = 69.9 bits (35), Expect = 7e-08
Identities = 65/75 (86%)
Strand = Plus / Plus

Query: 2088 tgatttcgccgcccgcacatgatcaagatgggagacattagtcctctcactggctccaatgg 2147
||||||| || ||||||||||||||| ||||| || ||| ||||| ||||||||||||||| ||
Sbjct: 211 tgattttgcggcccgcacatgatcaacatgggtgatattcgtcccctcactggctccaacgg 270

Query: 2148 agaatcaggaagaa 2162
|| |||||||||||
Sbjct: 271 cgagatcaggaagaa 285

>gb|C0900249.1| Mddb5025b21.y1 Mddb Malus x domestica cDNA clone Mddb5025b21 5'
similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE ;, mRNA sequence
Length = 671

Score = 69.9 bits (35), Expect = 7e-08
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||||||||||| ||||||||||| ||||| ||||||||| ||||| || |||||||||||
Sbjct: 344 tcacacaattgggcaagcaaggtgtacaactttcagagctcgcatatataacgagaccaa 403

Query: 1854 cat 1856
|||
Sbjct: 404 cat 406

>gb|C0051719.1| Mdfw2055d05.y1 Mdfw Malus x domestica cDNA clone Mdfw2055d05 5'
similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE ;, mRNA sequence
Length = 537

Score = 69.9 bits (35), Expect = 7e-08
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||||||||||| ||||||||||| ||||| ||||||||| ||||| || |||||||||||
Sbjct: 93 tcacacaattgggcaagcaaggtgtacaactttcagagctcgcatatataacgagaccaa 152

Query: 1854 cat 1856

|||
Sbjct: 153 cat 155

>gb|CN880015.1| 010418AASA009843HT (AASA) Royal Gala 10 DAFB fruit Malus x
domestica cDNA clone AASA009843, mRNA sequence
Length = 687

Score = 69.9 bits (35), Expect = 7e-08
Identities = 65/75 (86%)
Strand = Plus / Plus

Query: 710 aatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttcttccacg 769
||||||| |||| ||||| | ||||||||||||||||||||||||| | |||||
Sbjct: 168 aatctgccgatcaaggaaaagcgcatgggtgcttctctccttcgctccatttccacg 227

Query: 770 attgctttgtcaatg 784
|||||||||||||||
Sbjct: 228 attgctttgtcaatg 242

Score = 67.9 bits (34), Expect = 3e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| ||||||||||||||||| ||| || ||||||||||||| |||||||||
Sbjct: 608 cacacaataggacaagcaaggtgcaccgtcttccgaaccgcatctacaccgagaccaac 667

Query: 1855 at 1856
||
Sbjct: 668 at 669

>gb|GR871114.1| Pq_F_00457 American ginseng Flower cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 519

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgttctctgcgagata 1313

||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 354 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 413

Query: 1314 tccttg 1319

|||||
Sbjct: 414 tccttg 419

>gb|GR875194.1| Pq_R_02677 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 453

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313

||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 354 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 413

Query: 1314 tccttg 1319

|||||
Sbjct: 414 tccttg 419

>gb|GR873483.1| Pq_R_00966 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 494

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313

||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 292 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 351

Query: 1314 tccttg 1319

|||||
Sbjct: 352 tccttg 357

>gb|GR873276.1| Pq_R_00759 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence

Length = 557

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313
||||| ||||||| || ||||||| || ||| ||||||||||||||||||| |||||||
Sbjct: 341 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 400

Query: 1314 tccttg 1319
|||||
Sbjct: 401 tccttg 406

>gb|GR871777.1| Pq_F_01120 American ginseng Flower cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 435

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313
||||| ||||||| || ||||||| || ||| ||||||||||||||||||| |||||||
Sbjct: 293 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 352

Query: 1314 tccttg 1319
|||||
Sbjct: 353 tccttg 358

>gb|GR874357.1| Pq_R_01840 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 397

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313
||||| ||||||| || ||||||| || ||| ||||||||||||||||||| |||||||
Sbjct: 315 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 374

Query: 1314 tccttg 1319
 |||||
Sbjct: 375 tccttg 380

>gb|GR874227.1| Pq_R_01710 American ginseng Root cDNA Library Panax quinquefolius
 cDNA 5', mRNA sequence
 Length = 415

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313
 ||||| ||||||| || ||||||| || || ||||||| ||||||| |||||||
Sbjct: 67 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 126

Query: 1314 tccttg 1319
 |||||
Sbjct: 127 tccttg 132

>emb|CU507988.1| CU507988 PODSSHWB1Sb_KZOACD Theobroma cacao cDNA clone
 KZOACD3YE10FM1, mRNA sequence
 Length = 336

Score = 67.9 bits (34), Expect = 3e-07
Identities = 61/70 (87%)
Strand = Plus / Minus

Query: 2103 catgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
 ||||| ||||||| ||||||| || || ||||||| ||||||| |||||||
Sbjct: 328 catgatcaagatgggagacatcagtcctcactggatcaagggagagatcaggaagaa 269

Query: 2163 ttgtagaagg 2172
 || |||||||
Sbjct: 268 ctgcagaagg 259

>gb|EY664481.1| CS00-C1-101-067-A09-CT.F Sweet orange leaf, infected with Xylella
 fastidiosa (stage 1 of 2) Citrus sinensis cDNA, mRNA
 sequence
 Length = 677

>gb|EL366609.1| CCES2712.b1_005.ab1 CCE(LMS) endive Cichorium endivia cDNA clone
CCES2712, mRNA sequence
Length = 465

Score = 67.9 bits (34), Expect = 3e-07
Identities = 64/74 (86%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcccgatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||||||||||||| ||||| || ||| ||||| ||||| ||||||||| ||
Sbjct: 267 gatttcgccgcccgatgatcaatatgggtgatattcgtcccctcaccggctccaacggc 326

Query: 2149 gaaatcaggaagaa 2162
|| |||||||||||
Sbjct: 327 gagatcaggaagaa 340

>gb|EH664510.1| 11.2E05 Transformed tobacco Lambda Zap II library Nicotiana tabacum
cDNA 5', mRNA sequence
Length = 1034

Score = 67.9 bits (34), Expect = 3e-07
Identities = 54/61 (88%)
Strand = Plus / Plus

Query: 724 aaggagaccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaat 783
||||| ||||| ||||||||||| ||||||||| | ||||| ||||||||||| |||||||
Sbjct: 206 aaggaaaccgcatgggtgcttccctccttcgctattcttccnagattgcttctgtcaat 265

Query: 784 g 784
|
Sbjct: 266 g 266

>gb|EC600006.1| PNSSH3G-1469 panax notoginseng subtracted cDNA libraries Panax
notoginseng cDNA 5' similar to secretory peroxidase, mRNA
sequence
Length = 454

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaatcagccgtggagaaagtgtgtccaggagttgttctcgcgagata 1313

||||| ||||| || ||||| || ||| ||||||||||||||| |||||
Sbjct: 30 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 89

Query: 1314 tccttg 1319

|||||
Sbjct: 90 tccttg 95

Database: /usr/local/blast/db/blastlibs/est_others
Posted date: Feb 13, 2010 7:48 AM
Number of letters in database: 29,218,461,503
Number of sequences in database: 51,680,690

Lambda K H
1.37 0.711 1.31

Gapped

Lambda K H
1.37 0.711 1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 51680690
Number of Hits to DB: 860,649,786
Number of extensions: 51423138
Number of successful extensions: 14543517
Number of sequences better than 10.0: 2195
Number of HSP's gapped: 14543355
Number of HSP's successfully gapped: 2740
Length of query: 2730
Length of database: 29,218,461,503
Length adjustment: 24
Effective length of query: 2706
Effective length of database: 27,978,124,943
Effective search space: 75708806095758
Effective search space used: 75708806095758
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 50 (99.1 bits)
S1: 12 (24.3 bits)
S2: 22 (44.1 bits)

BLASTx Output of the 5' Border Sequence Flanking the Insert in Soybean Event DAS-68416-4 against GenBank Non-redundant Protein Sequences (nr)

BLASTX 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Query= 68416_5_border
(2730 letters)

Database: /usr/local/blast/db/blastlibs/nr
10,432,217 sequences; 3,559,509,877 total letters

Searching..... done

Sequences producing significant alignments:	Score	E
	(bits)	Value
gb ACU17608.1 unknown [Glycine max]	249	2e-63
gb ACU17865.1 unknown [Glycine max]	242	2e-61
gb AAP76387.1 class III peroxidase [Gossypium hirsutum]	218	2e-54
gb AB077632.1 peroxidase [Medicago truncatula]	217	7e-54
dbj BAA82306.1 peroxidase [Nicotiana tabacum]	212	2e-52
ref XP_002278996.1 PREDICTED: hypothetical protein [Vitis vinif...	211	5e-52
gb AAX44001.2 putative secretory peroxidase [Catharanthus roseus]	209	1e-51
gb AAP42508.1 anionic peroxidase swpb3 [Ipomoea batatas]	209	1e-51
gb ABR23054.1 basic peroxidase swpb4 [Ipomoea batatas]	209	1e-51
gb ACU23245.1 unknown [Glycine max]	208	2e-51
gb ACM47317.1 peroxidase [Capsicum annuum]	205	3e-50
ref XP_002328991.1 predicted protein [Populus trichocarpa] >gi ...	204	4e-50
ref XP_002269918.1 PREDICTED: hypothetical protein [Vitis vinif...	204	4e-50
emb CAD67479.1 peroxidase [Asparagus officinalis]	203	1e-49
ref NP_196153.1 peroxidase, putative [Arabidopsis thaliana] >gi ...	202	2e-49
dbj BAF27413.2 Os11g0112400 [Oryza sativa Japonica Group]	201	5e-49
ref NP_001065568.1 Os11g0112400 [Oryza sativa (japonica cultiva...	201	5e-49
gb EAY79693.1 hypothetical protein OsI_34840 [Oryza sativa Indi...	199	1e-48
ref NP_001065971.1 Os12g0112000 [Oryza sativa (japonica cultiva...	199	1e-48
ref XP_002450132.1 hypothetical protein SORBIDRAFT_05g001000 [S...	199	2e-48
gb ACT35473.1 peroxidase 52 [Brassica rapa]	197	7e-48
ref XP_002441703.1 hypothetical protein SORBIDRAFT_08g000990 [S...	196	1e-47
ref XP_002450133.1 hypothetical protein SORBIDRAFT_05g001010 [S...	196	1e-47
gb ABV24960.2 putative secretory peroxidase [Catharanthus roseus]	196	1e-47
sp P00434.3 PERP7_BRARA RecName: Full=Peroxidase P7; AltName: Fu...	196	1e-47

gb AAD37423.1 AF149281_1 peroxidase 6 [Phaseolus vulgaris]	195	3e-47
ref XP_002520835.1 Peroxidase 52 precursor, putative [Ricinus c...	194	4e-47
ref XP_002319968.1 predicted protein [Populus trichocarpa] >gi ...	193	8e-47
ref NP_001151940.1 peroxidase 52 [Zea mays] >gi 195651251 gb AC...	191	3e-46
ref XP_002489046.1 hypothetical protein SORBIDRAFT_0246s002010 ...	190	7e-46
ref XP_002441702.1 hypothetical protein SORBIDRAFT_08g000980 [S...	190	7e-46
gb AAA96137.1 peroxidase [Stylosanthes humilis]	190	7e-46
gb AAL93151.1 AF485265_1 class III peroxidase [Gossypium hirsutum]	189	2e-45
emb CAD67478.1 peroxidase [Asparagus officinalis]	188	3e-45
gb AAR31108.1 peroxidase precursor [Quercus suber]	188	3e-45
gb AAR31106.1 peroxidase precursor [Quercus suber]	187	8e-45
ref NP_001131000.1 hypothetical protein LOC100192105 [Zea mays]...	186	1e-44
gb AAD43561.1 AF155124_1 bacterial-induced peroxidase precursor ...	185	2e-44
gb ACN33662.1 unknown [Zea mays]	184	4e-44
emb CBI25393.1 unnamed protein product [Vitis vinifera]	184	7e-44
gb ACU23223.1 unknown [Glycine max]	182	2e-43
emb CAA71491.1 peroxidase [Spinacia oleracea]	182	2e-43
gb ABK21858.1 unknown [Picea sitchensis]	180	7e-43
emb CAD67477.1 peroxidase [Asparagus officinalis]	179	1e-42
emb CAA62597.1 korean-radish isoperoxidase [Raphanus sativus]	179	1e-42
gb AC090366.1 peroxidase precursor [Triticum aestivum]	179	2e-42
gb ACN34270.1 unknown [Zea mays]	179	2e-42
gb ACU24215.1 unknown [Glycine max]	178	4e-42
gb AAB48184.1 peroxidase precursor [Linum usitatissimum]	178	4e-42
emb CBI27506.1 unnamed protein product [Vitis vinifera]	177	5e-42
ref XP_002274550.1 PREDICTED: hypothetical protein [Vitis vinif...	177	5e-42
gb ACN42168.1 peroxidase 1 [Sesuvium portulacastrum]	177	6e-42
ref XP_002269058.1 PREDICTED: hypothetical protein [Vitis vinif...	177	8e-42
emb CBI27505.1 unnamed protein product [Vitis vinifera]	177	8e-42
emb CAL25300.1 properoxidase [Picea abies]	176	1e-41
ref XP_002269145.1 PREDICTED: hypothetical protein [Vitis vinif...	175	2e-41
gb ACJ85500.1 unknown [Medicago truncatula]	174	5e-41
emb CAN80097.1 hypothetical protein [Vitis vinifera]	173	1e-40
emb CBI27503.1 unnamed protein product [Vitis vinifera]	172	2e-40
emb CBI27502.1 unnamed protein product [Vitis vinifera]	172	2e-40
ref XP_002269169.1 PREDICTED: hypothetical protein [Vitis vinif...	172	2e-40
gb AA013838.1 AF405326_1 peroxidase 2 [Lupinus albus]	172	2e-40
gb ABA96220.1 Cationic peroxidase 1 precursor, putative, expres...	172	2e-40
tpe CAH69378.1 TPA: class III peroxidase 136 precursor [Oryza s...	172	2e-40
ref XP_002269216.1 PREDICTED: hypothetical protein [Vitis vinif...	172	2e-40
emb CAH10839.1 peroxidase [Picea abies]	172	2e-40
ref XP_002266365.1 PREDICTED: hypothetical protein [Vitis vinif...	172	3e-40
ref NP_001106040.1 plasma membrane-bound peroxidase 2b precurs...	172	3e-40
gb EAY82023.1 hypothetical protein OsI_37207 [Oryza sativa Indi...	171	3e-40
gb ABA91154.1 Cationic peroxidase 1 precursor, putative, expres...	171	3e-40
ref NP_001065566.1 Os11g0112200 [Oryza sativa (japonica cultiva...	171	3e-40
gb EEE67815.1 hypothetical protein OsJ_25569 [Oryza sativa Japo...	171	4e-40
ref NP_001060628.1 Os07g0677200 [Oryza sativa (japonica cultiva...	171	4e-40
tpe CAH69353.1 TPA: class III peroxidase 111 precursor [Oryza s...	171	4e-40

emb	CBI27501.1	unnamed protein product [Vitis vinifera]	170	7e-40
ref	XP_002269266.1	PREDICTED: hypothetical protein [Vitis vinif...	170	7e-40
ref	XP_002509730.1	Lignin-forming anionic peroxidase precursor,...	170	7e-40
emb	CBI18066.1	unnamed protein product [Vitis vinifera]	170	1e-39
ref	XP_002268259.1	PREDICTED: hypothetical protein [Vitis vinif...	170	1e-39
ref	XP_002299006.1	predicted protein [Populus trichocarpa] >gi ...	170	1e-39
ref	XP_002333334.1	predicted protein [Populus trichocarpa] >gi ...	170	1e-39
ref	XP_002285723.1	PREDICTED: hypothetical protein [Vitis vinif...	170	1e-39
emb	CAA46916.1	peroxidase [Oryza sativa (japonica cultivar-grou...	170	1e-39
ref	XP_002319967.1	predicted protein [Populus trichocarpa] >gi ...	169	1e-39
gb	ABK24123.1	unknown [Picea sitchensis]	169	2e-39
gb	AAA20473.1	peroxidase [Cenchrus ciliaris]	169	2e-39
gb	ABK23423.1	unknown [Picea sitchensis]	168	3e-39
ref	NP_001060629.1	Os07g0677300 [Oryza sativa (japonica cultiva...	168	3e-39
gb	ACJ11762.1	class III peroxidase [Gossypium hirsutum]	168	4e-39
gb	ABK25962.1	unknown [Picea sitchensis]	168	4e-39
gb	EAZ05133.1	hypothetical protein OsI_27326 [Oryza sativa Indi...	168	4e-39
ref	NP_001046400.1	Os02g0240100 [Oryza sativa (japonica cultiva...	168	4e-39
gb	AAC49818.1	peroxidase [Oryza sativa Indica Group]	168	4e-39
dbj	BAD28869.1	putative bacterial-induced peroxidase precursor ...	168	4e-39
ref	XP_002274693.1	PREDICTED: hypothetical protein [Vitis vinif...	167	5e-39
gb	EEC82680.1	hypothetical protein OsI_27324 [Oryza sativa Indi...	167	5e-39
ref	NP_001060626.1	Os07g0676900 [Oryza sativa (japonica cultiva...	167	5e-39
emb	CAH10840.1	peroxidase [Picea abies]	167	5e-39
dbj	BAC83101.1	putative peroxidase precursor [Oryza sativa Japo...	167	5e-39
tpe	CAH69351.1	TPA: class III peroxidase 109 precursor [Oryza s...	167	5e-39
ref	XP_002451848.1	hypothetical protein SORBIDRAFT_04g008620 [S...	167	6e-39
gb	ACN33811.1	unknown [Zea mays]	167	6e-39
gb	ABR18139.1	unknown [Picea sitchensis]	167	6e-39
sp	A2YPX3.2	PER2_ORYSI RecName: Full=Peroxidase 2; Flags: Precu...	167	8e-39
ref	XP_002461208.1	hypothetical protein SORBIDRAFT_02g042850 [S...	166	1e-38
ref	XP_002320417.1	predicted protein [Populus trichocarpa] >gi ...	166	1e-38
ref	NP_001130666.1	hypothetical protein LOC100191769 [Zea mays]...	166	1e-38
ref	NP_200648.1	peroxidase, putative [Arabidopsis thaliana] >gi...	166	1e-38
ref	XP_002338628.1	predicted protein [Populus trichocarpa] >gi ...	166	1e-38
ref	XP_002336344.1	predicted protein [Populus trichocarpa] >gi ...	166	1e-38
emb	CAA71493.1	peroxidase [Spinacia oleracea]	166	1e-38
gb	AAX53172.1	peroxidase [Populus alba x Populus tremula var. g...	166	1e-38
ref	XP_002509738.1	Lignin-forming anionic peroxidase precursor,...	166	2e-38
ref	XP_002453592.1	hypothetical protein SORBIDRAFT_04g008630 [S...	165	2e-38
gb	ACN60163.1	class III peroxidase [Tamarix hispida]	164	5e-38
ref	XP_002450134.1	hypothetical protein SORBIDRAFT_05g001030 [S...	163	9e-38
gb	AAC05277.1	peroxidase FLXPER4 [Linum usitatissimum]	163	9e-38
ref	XP_002269343.1	PREDICTED: hypothetical protein [Vitis vinif...	163	1e-37
gb	EAY85148.1	hypothetical protein OsI_06503 [Oryza sativa Indi...	163	1e-37
ref	XP_002269301.1	PREDICTED: hypothetical protein [Vitis vinif...	162	2e-37
gb	AAD37428.1	AF149278_1 peroxidase 3 precursor [Phaseolus vulga...	162	2e-37
ref	XP_002334243.1	predicted protein [Populus trichocarpa] >gi ...	162	2e-37
ref	XP_002438530.1	hypothetical protein SORBIDRAFT_10g021630 [S...	162	3e-37

ref XP_002281755.1	PREDICTED: hypothetical protein [Vitis vinif...	162	3e-37
ref XP_002437128.1	hypothetical protein SORBIDRAFT_10g021610 [S...	161	3e-37
ref XP_002517727.1	Cationic peroxidase 1 precursor, putative [R...	160	6e-37
ref NP_001057822.1	Os06g0547400 [Oryza sativa (japonica cultiva...	160	6e-37
ref XP_002285724.1	PREDICTED: hypothetical protein [Vitis vinif...	160	8e-37
ref XP_002521867.1	Lignin-forming anionic peroxidase precursor,...	160	8e-37
emb CAH10841.1	peroxidase [Picea abies]	160	8e-37
gb EEE67814.1	hypothetical protein OsJ_25568 [Oryza sativa Japo...	160	1e-36
tpe CAH69352.1	TPA: class III peroxidase 110 precursor [Oryza s...	160	1e-36
ref NP_001060627.1	Os07g0677100 [Oryza sativa (japonica cultiva...	160	1e-36
gb ABD66594.1	peroxidase [Litchi chinensis]	159	1e-36
emb CBI19219.1	unnamed protein product [Vitis vinifera]	159	1e-36
ref XP_002334317.1	predicted protein [Populus trichocarpa] >gi ...	159	1e-36
emb CAN73051.1	hypothetical protein [Vitis vinifera]	159	1e-36
gb EEE67818.1	hypothetical protein OsJ_25573 [Oryza sativa Japo...	159	2e-36
gb EEE56633.1	hypothetical protein OsJ_06032 [Oryza sativa Japo...	159	2e-36
ref XP_002281731.1	PREDICTED: hypothetical protein [Vitis vinif...	159	2e-36
gb EAO5136.1	hypothetical protein OsI_27329 [Oryza sativa Indi...	159	2e-36
ref NP_001046402.1	Os02g0240500 [Oryza sativa (japonica cultiva...	159	2e-36
ref NP_001060630.1	Os07g0677400 [Oryza sativa (japonica cultiva...	159	2e-36
emb CAA59487.1	peroxidase [Triticum aestivum] >gi 193074375 gb ...	159	2e-36
gb AAB02554.1	cationic peroxidase [Stylosanthes humilis]	159	2e-36
sp P16147.2	PERX_LUPPO RecName: Full=Peroxidase >gi 1345541 emb ...	159	2e-36
dbj BAA77389.1	peroxidase 3 [Scutellaria baicalensis]	159	2e-36
ref XP_002461207.1	hypothetical protein SORBIDRAFT_02g042840 [S...	158	3e-36
gb EEC82684.1	hypothetical protein OsI_27330 [Oryza sativa Indi...	158	3e-36
gb AAW52720.1	peroxidase 6 [Triticum monococcum]	158	3e-36
gb AAQ55292.1	class III peroxidase GvPx2b [Vitis vinifera]	158	3e-36
gb AAF65464.2	AF247700_1 peroxidase POC1 [Oryza sativa Indica Gr...	158	3e-36
ref XP_002311022.1	predicted protein [Populus trichocarpa] >gi ...	158	4e-36
gb EEE67819.1	hypothetical protein OsJ_25574 [Oryza sativa Japo...	158	4e-36
ref NP_001147216.1	LOC100280824 [Zea mays] >gi 195608630 gb ACG...	158	4e-36
ref NP_001060631.1	Os07g0677500 [Oryza sativa (japonica cultiva...	158	4e-36
pdb 1SCH A Chain A, Peanut Peroxidase >gi 1633131 pdb 1SCH B Cha...		158	4e-36
sp P22195.2	PER1_ARAHY RecName: Full=Cationic peroxidase 1; AltN...	158	4e-36
gb ACU22965.1	unknown [Glycine max]	157	5e-36
ref XP_002311955.1	predicted protein [Populus trichocarpa] >gi ...	157	5e-36
gb AAM61588.1	peroxidase [Arabidopsis thaliana]	157	5e-36
ref NP_200647.1	peroxidase, putative [Arabidopsis thaliana] >gi...	157	5e-36
ref XP_002460939.1	hypothetical protein SORBIDRAFT_02g037840 [S...	157	7e-36
ref XP_002334018.1	predicted protein [Populus trichocarpa] >gi ...	157	7e-36
gb EAY85151.1	hypothetical protein OsI_06506 [Oryza sativa Indi...	157	7e-36
emb CAH10842.1	peroxidase [Picea abies]	157	7e-36
emb CBI22007.1	unnamed protein product [Vitis vinifera]	157	9e-36
ref XP_002283995.1	PREDICTED: hypothetical protein [Vitis vinif...	157	9e-36
emb CAN81400.1	hypothetical protein [Vitis vinifera]	157	9e-36
emb CAN63655.1	hypothetical protein [Vitis vinifera]	157	9e-36
gb AAA20472.1	peroxidase [Cenchrus ciliaris]	156	1e-35
gb ACF08096.1	class III peroxidase [Triticum aestivum]	156	1e-35

ref XP_002461211.1	hypothetical protein SORBIDRAFT_02g042870 [S...	156	1e-35
sp Q02200.1 PERX_NICSY	RecName: Full=Lignin-forming anionic pero...	156	1e-35
ref XP_002437129.1	hypothetical protein SORBIDRAFT_10g021620 [S...	155	2e-35
gb AAW52718.1	peroxidase 4 [Triticum monococcum]	155	2e-35
gb ACI03401.1	peroxidase 1 [Litchi chinensis]	155	2e-35
ref XP_002284007.1	PREDICTED: hypothetical protein [Vitis vinif...	155	2e-35
ref XP_002323054.1	predicted protein [Populus trichocarpa] >gi ...	155	2e-35
gb EEC82681.1	hypothetical protein OsI_27325 [Oryza sativa Indi...	155	2e-35
gb EAZ01280.1	hypothetical protein OsI_23303 [Oryza sativa Indi...	155	2e-35
gb AAY89058.1	class III peroxidase [Phelipanche ramosa]	155	2e-35
gb AAW52719.1	peroxidase 5 [Triticum monococcum]	155	2e-35
gb AAC49819.1	peroxidase [Oryza sativa Indica Group]	155	2e-35
dbj BAD97435.1	peroxidase [Pisum sativum]	155	2e-35
ref NP_001057821.1	Os06g0547100 [Oryza sativa (japonica cultiva...	155	2e-35
emb CBI19220.1	unnamed protein product [Vitis vinifera]	155	3e-35
gb ACN30737.1	unknown [Zea mays]	155	3e-35
gb ACG40622.1	peroxidase 2 precursor [Zea mays]	155	3e-35
emb CAN83972.1	hypothetical protein [Vitis vinifera]	154	4e-35
ref XP_002509737.1	Lignin-forming anionic peroxidase precursor,...	154	6e-35
ref XP_002268412.1	PREDICTED: hypothetical protein [Vitis vinif...	154	6e-35
dbj BAD36900.1	peroxidase [Lotus japonicus]	154	6e-35
gb ACN26131.1	unknown [Zea mays]	154	7e-35
gb ACF08094.1	class III peroxidase [Triticum aestivum]	153	9e-35
ref XP_002509733.1	Lignin-forming anionic peroxidase precursor,...	153	9e-35
ref XP_002319407.1	predicted protein [Populus trichocarpa] >gi ...	153	9e-35
dbj BAA77388.1	peroxidase 2 [Scutellaria baicalensis]	153	9e-35
gb ACF08095.1	class III peroxidase [Triticum aestivum]	153	1e-34
gb EAZ01279.1	hypothetical protein OsI_23302 [Oryza sativa Indi...	153	1e-34
ref NP_001046392.1	Os02g0236600 [Oryza sativa (japonica cultiva...	152	2e-34
gb EAZ37287.1	hypothetical protein OsJ_21626 [Oryza sativa Japo...	152	2e-34
gb ABD47726.1	peroxidase [Eucalyptus globulus subsp. globulus]	152	2e-34
ref NP_001057820.1	Os06g0546500 [Oryza sativa (japonica cultiva...	152	2e-34
ref XP_002438534.1	hypothetical protein SORBIDRAFT_10g021650 [S...	152	2e-34
ref NP_001140437.1	hypothetical protein LOC100272496 [Zea mays]...	152	2e-34
gb ACF82414.1	unknown [Zea mays]	152	2e-34
dbj BAF19735.2	Os06g0547100 [Oryza sativa Japonica Group]	152	3e-34
ref XP_002438533.1	hypothetical protein SORBIDRAFT_10g021640 [S...	151	4e-34
gb ACE00594.1	lignin biosynthetic peroxidase [Leucaena leucocep...	151	4e-34
emb CBI19221.1	unnamed protein product [Vitis vinifera]	151	5e-34
ref XP_002451846.1	hypothetical protein SORBIDRAFT_04g008590 [S...	151	5e-34
emb CAL25299.1	properoxidase [Picea abies]	151	5e-34
emb CBI15847.1	unnamed protein product [Vitis vinifera]	150	6e-34
ref XP_002451850.1	hypothetical protein SORBIDRAFT_04g008650 [S...	150	6e-34
ref XP_002276796.1	PREDICTED: hypothetical protein [Vitis vinif...	150	6e-34
gb EAZ22364.1	hypothetical protein OsJ_06022 [Oryza sativa Japo...	150	6e-34
gb EAY85141.1	hypothetical protein OsI_06496 [Oryza sativa Indi...	150	6e-34
tpe CAH69268.1	TPA: class III peroxidase 26 precursor [Oryza sa...	150	6e-34
ref NP_001046393.1	Os02g0236800 [Oryza sativa (japonica cultiva...	150	6e-34
gb ABK22680.1	unknown [Picea sitchensis]	150	8e-34

emb CAN61440.1	hypothetical protein [Vitis vinifera]	150	8e-34
gb AAC31550.1	peroxidase PXC2 precursor [Avena sativa]	150	8e-34
gb AAC31551.1	peroxidase PXC6 precursor [Avena sativa]	150	8e-34
emb CAA71492.1	peroxidase [Spinacia oleracea]	149	2e-33
ref NP_001054096.1	Os04g0651000 [Oryza sativa (japonica cultiva...]	149	2e-33
ref XP_002308244.1	predicted protein [Populus trichocarpa] >gi ...	149	2e-33
emb CBI19222.1	unnamed protein product [Vitis vinifera]	148	3e-33
ref XP_002467656.1	hypothetical protein SORBIDRAFT_01g031740 [S...]	148	3e-33
gb EEE61812.1	hypothetical protein OsJ_16433 [Oryza sativa Japo...]	148	3e-33
gb EEC78144.1	hypothetical protein OsI_17703 [Oryza sativa Indi...]	148	3e-33
emb CAJ86184.1	H0212B02.16 [Oryza sativa (indica cultivar-group...]	148	3e-33
gb EAZ22372.1	hypothetical protein OsJ_06030 [Oryza sativa Japo...]	148	3e-33
ref NP_001046401.1	Os02g0240300 [Oryza sativa (japonica cultiva...]	148	3e-33
gb ABK21983.1	unknown [Picea sitchensis]	148	4e-33
ref XP_002461210.1	hypothetical protein SORBIDRAFT_02g042860 [S...]	148	4e-33
emb CBI18065.1	unnamed protein product [Vitis vinifera]	147	5e-33
gb ACF08091.1	class III peroxidase [Triticum aestivum]	147	5e-33
gb EAY85149.1	hypothetical protein OsI_06504 [Oryza sativa Indi...]	147	5e-33
gb AAW52716.1	peroxidase 2 [Triticum monococcum]	147	5e-33
gb AAA32972.1	peroxidase [Hordeum vulgare]	147	5e-33
emb CBI22008.1	unnamed protein product [Vitis vinifera]	147	7e-33
gb ACD70388.1	class III peroxidase [Triticum aestivum]	147	7e-33
gb ABF48527.1	cell wall peroxidase [Capsicum annuum] >gi 110348...]	147	9e-33
gb ACF08092.1	class III peroxidase [Triticum aestivum]	146	1e-32
gb ACN37032.1	unknown [Zea mays]	146	1e-32
sp P27337.1	PER1_HORVU RecName: Full=Peroxidase 1; Flags: Precur...]	146	1e-32
gb ABV24961.1	peroxidase [Catharanthus roseus]	146	2e-32
emb CAL25298.1	properoxidase [Picea abies]	146	2e-32
gb ACF08089.1	class III peroxidase [Triticum aestivum]	146	2e-32
ref XP_002467893.1	hypothetical protein SORBIDRAFT_01g036000 [S...]	145	2e-32
gb EEC75221.1	hypothetical protein OsI_11488 [Oryza sativa Indi...]	145	2e-32
gb ABF95843.1	Peroxidase 52 precursor, putative, expressed [Ory...]	145	2e-32
tpe CAH69282.1	TPA: class III peroxidase 40 precursor [Oryza sa...]	145	2e-32
ref XP_002531319.1	Peroxidase 2 precursor, putative [Ricinus co...]	145	2e-32
ref NP_001147254.1	peroxidase 52 [Zea mays] >gi 195609124 gb AC...]	145	2e-32
ref XP_002465306.1	hypothetical protein SORBIDRAFT_01g035990 [S...]	145	3e-32
emb CAA39486.1	peroxidase [Triticum aestivum]	145	3e-32
gb ACR36744.1	unknown [Zea mays]	145	3e-32
ref XP_002323056.1	predicted protein [Populus trichocarpa] >gi ...	145	3e-32
gb ACF88317.1	unknown [Zea mays]	145	3e-32
gb AAZ42168.1	lignin peroxidase-like [Cucumis sativus]	145	3e-32
gb AAB48986.1	peroxidase precursor [Medicago truncatula]	144	4e-32
ref XP_002521852.1	Lignin-forming anionic peroxidase precursor,...	144	4e-32
ref NP_001106020.1	plasma membrane-bound peroxidase 3-2 precurs...]	144	4e-32
ref XP_002521866.1	Lignin-forming anionic peroxidase precursor,...	144	6e-32
ref XP_002521851.1	Lignin-forming anionic peroxidase precursor,...	144	6e-32
gb EEC75545.1	hypothetical protein OsI_12177 [Oryza sativa Indi...]	144	6e-32
ref NP_001050435.1	Os03g0434800 [Oryza sativa (japonica cultiva...]	144	6e-32
gb AAU89207.1	peroxidase, putative [Oryza sativa Japonica Group...]	144	6e-32

gb ACU21160.1	unknown [Glycine max]	144	6e-32
gb ACF08090.1	class III peroxidase [Triticum aestivum]	144	7e-32
emb CAA59484.1	pox1 [Triticum aestivum]	144	7e-32
gb AAW52715.1	peroxidase 1 [Triticum monococcum]	143	1e-31
ref NP_001042342.1	Os01g0205900 [Oryza sativa (japonica cultiva...]	143	1e-31
tpe CAH69245.1	TPA: class III peroxidase 2 precursor [Oryza sat...]	143	1e-31
gb ACU20213.1	unknown [Glycine max]	143	1e-31
gb EEC75220.1	hypothetical protein OsI_11487 [Oryza sativa Indi...]	143	1e-31
emb CAB99487.1	peroxidase [Hordeum vulgare subsp. vulgare]	143	1e-31
ref NP_001050059.1	Os03g0339300 [Oryza sativa (japonica cultiva...]	143	1e-31
emb CAD92857.1	peroxidase [Picea abies]	142	2e-31
gb ACF08086.1	class III peroxidase [Triticum aestivum]	142	2e-31
emb CAN80096.1	hypothetical protein [Vitis vinifera]	142	2e-31
gb AAB97854.1	ferriprotein porphyrin-containing peroxidase [Str...]	142	2e-31
emb CAC81821.1	peroxidase [Beta vulgaris]	142	2e-31
gb ACF08083.1	class III peroxidase [Triticum aestivum]	142	2e-31
ref NP_001106019.1	LOC100101533 precursor [Zea mays] >gi 221272...]	142	2e-31
ref NP_172906.1	anionic peroxidase, putative [Arabidopsis thali...]	142	2e-31
gb ACF70708.1	root peroxidase [Triticum aestivum]	142	3e-31
gb ACF70706.1	root peroxidase [Triticum aestivum]	142	3e-31
ref NP_001050434.1	Os03g0434500 [Oryza sativa (japonica cultiva...]	142	3e-31
gb AAU89205.1	peroxidase, putative [Oryza sativa Japonica Group...]	142	3e-31
gb EEC70139.1	hypothetical protein OsI_00829 [Oryza sativa Indi...]	141	4e-31
ref XP_002319422.1	predicted protein [Populus trichocarpa] >gi ...]	141	5e-31
gb ACF70710.1	root peroxidase [Triticum aestivum]	140	6e-31
gb ACF70709.1	root peroxidase [Triticum aestivum]	140	6e-31
gb ACF70705.1	root peroxidase [Triticum aestivum] >gi 194425605...]	140	6e-31
gb ACF70701.1	root peroxidase [Triticum aestivum]	140	6e-31
gb AAM76682.1	AF387866_1 peroxidase [Triticum aestivum]	140	6e-31
ref XP_002448660.1	hypothetical protein SORBIDRAFT_06g030940 [S...]	140	8e-31
gb AAM65211.1	peroxidase [Arabidopsis thaliana] >gi 42494611 gb...]	140	8e-31
gb ACF08087.1	class III peroxidase [Triticum aestivum]	140	8e-31
ref XP_002270068.1	PREDICTED: hypothetical protein [Vitis vinif...]	140	8e-31
ref XP_002323055.1	predicted protein [Populus trichocarpa] >gi ...]	140	8e-31
gb AAF43956.1	AC012188_33 Strong similarity to an Anionic Peroxi...]	140	8e-31
gb AAF63165.1	AC010657_1 T5E21.5 [Arabidopsis thaliana]	140	8e-31
ref NP_172907.1	anionic peroxidase, putative [Arabidopsis thali...]	140	8e-31
ref NP_001147443.1	peroxidase 52 [Zea mays] >gi 195611432 gb AC...]	140	1e-30
gb ACF08085.1	class III peroxidase [Aegilops ventricosa]	140	1e-30
gb ACF70703.1	root peroxidase [Triticum aestivum]	140	1e-30
gb ACT78791.1	putative peroxidase [Cucumis sativus]	139	1e-30
gb ACD87898.1	class III peroxidase [Aegilops ventricosa]	139	1e-30
gb ACF70707.1	root peroxidase [Triticum aestivum]	139	1e-30
emb CAN61439.1	hypothetical protein [Vitis vinifera]	139	1e-30
gb AAW52717.1	peroxidase 3 [Triticum monococcum] >gi 193074352 ...]	139	1e-30
sp Q05855.1	PER1_WHEAT RecName: Full=Peroxidase; AltName: Full=W...]	139	1e-30
gb ACF08084.1	class III peroxidase [Triticum aestivum]	139	2e-30
ref XP_002521868.1	Lignin-forming anionic peroxidase precursor,...]	139	2e-30
gb ACF70702.1	root peroxidase [Triticum aestivum]	139	2e-30

ref XP_002327780.1 predicted protein [Populus trichocarpa] >gi ...	139	2e-30
gb EEE54081.1 hypothetical protein OsJ_00811 [Oryza sativa Japo...	139	2e-30
gb AAQ55233.1 peroxidase [Orobanche cernua var. cumana]	138	3e-30
emb CAN80051.1 hypothetical protein [Vitis vinifera]	138	4e-30
ref XP_002521850.1 Peroxidase 30 precursor, putative [Ricinus c...	138	4e-30
gb ABR13314.1 putative peroxidase class III [Prunus dulcis]	138	4e-30
ref XP_002530724.1 Peroxidase 53 precursor, putative [Ricinus c...	137	5e-30
emb CAA59485.1 peroxidase [Triticum aestivum]	137	5e-30
gb ABK59095.1 peroxidase 1 [Sesbania rostrata]	137	9e-30
gb AAP42504.1 anionic peroxidase swpa5 [Ipomoea batatas]	137	9e-30
emb CBI27504.1 unnamed protein product [Vitis vinifera]	136	1e-29
emb CBI17443.1 unnamed protein product [Vitis vinifera]	136	1e-29
gb ACU23405.1 unknown [Glycine max]	136	1e-29
ref XP_002521512.1 Peroxidase 72 precursor, putative [Ricinus c...	136	1e-29
ref XP_002275309.1 PREDICTED: hypothetical protein [Vitis vinif...	136	1e-29
ref XP_002531320.1 Cationic peroxidase 1 precursor, putative [R...	136	1e-29
gb ABG49114.1 peroxidase [Dimocarpus longan]	136	2e-29
gb AAP42506.1 anionic peroxidase swpb1 [Ipomoea batatas]	136	2e-29
gb ACU24350.1 unknown [Glycine max]	135	2e-29
gb ACU21179.1 unknown [Glycine max]	135	2e-29
ref XP_002310274.1 predicted protein [Populus trichocarpa] >gi ...	135	2e-29
gb ABR17414.1 unknown [Picea sitchensis]	135	2e-29
gb AAB97853.1 ferriprotein porphyrin-containing peroxidase [Str...	135	2e-29
ref XP_002322726.1 predicted protein [Populus trichocarpa] >gi ...	135	3e-29
gb ACI22425.1 pericarp peroxidase 3 [Litchi chinensis]	134	5e-29
ref XP_002304885.1 predicted protein [Populus trichocarpa] >gi ...	134	6e-29
gb ABR17480.1 unknown [Picea sitchensis]	134	6e-29
gb ABZ80408.1 class III peroxidase [Casuarina glauca]	134	6e-29
gb AAK52085.1 peroxidase [Nicotiana tabacum]	134	6e-29
ref XP_002455406.1 hypothetical protein SORBIDRAFT_03g010250 [S...	134	8e-29
ref XP_002455405.1 hypothetical protein SORBIDRAFT_03g010240 [S...	134	8e-29
gb ACG44598.1 peroxidase 72 precursor [Zea mays]	134	8e-29
ref NP_001136736.1 hypothetical protein LOC100216875 [Zea mays]...	134	8e-29
ref NP_195361.1 peroxidase, putative [Arabidopsis thaliana] >gi ...	134	8e-29
gb ABR23055.1 basic peroxidase swpb5 [Ipomoea batatas]	133	1e-28
gb EAY85142.1 hypothetical protein OsI_06497 [Oryza sativa Indi...	133	1e-28
gb AAC49822.1 peroxidase [Oryza sativa Indica Group]	133	1e-28
gb ACU21377.1 unknown [Glycine max]	133	1e-28
ref NP_001148509.1 peroxidase 72 [Zea mays] >gi 195619908 gb AC...	132	2e-28
gb ABK26974.1 unknown [Picea sitchensis]	132	2e-28
gb AAF63025.1 AF244922_1 peroxidase prx13 precursor [Spinacia ol...	132	2e-28
gb AAM61616.1 putative peroxidase [Arabidopsis thaliana]	132	2e-28
ref NP_179407.1 peroxidase, putative [Arabidopsis thaliana] >gi ...	132	2e-28
emb CBI27500.1 unnamed protein product [Vitis vinifera]	132	2e-28
gb AAP42507.1 anionic peroxidase swpb2 [Ipomoea batatas]	132	2e-28
gb ABV26013.1 peroxidase [Musa acuminata]	132	3e-28
sp Q9LEH3.1 PER15_IPOBA RecName: Full=Peroxidase 15; Short=Prx15...	132	3e-28
ref XP_002300745.1 predicted protein [Populus trichocarpa] >gi ...	131	4e-28
gb ABC60345.1 putative peroxidase [Musa acuminata AAA Group]	131	4e-28

emb CAA66964.1	peroxidase [Arabidopsis thaliana] >gi 1429215 em...	131	4e-28
gb AAR15704.3	peroxidase [Brassica napus]	131	5e-28
gb AAM63684.1	peroxidase, putative [Arabidopsis thaliana]	131	5e-28
ref NP_175117.1	peroxidase, putative [Arabidopsis thaliana] >gi...	131	5e-28
ref NP_001050060.1	Os03g0339400 [Oryza sativa (japonica cultiva...	131	5e-28
sp Q4W1I8.1	PER1_ZINEL RecName: Full=Basic peroxidase; AltName: ...	131	5e-28
sp Q4W1I9.1	PER2_ZINEL RecName: Full=Basic peroxidase; AltName: ...	131	5e-28
gb AAF63026.1	AF244923_1 peroxidase prx14 precursor [Spinacia ol...	130	7e-28
ref NP_001046394.1	Os02g0237000 [Oryza sativa (japonica cultiva...	130	9e-28
dbj BAD27600.1	putative bacterial-induced peroxidase precursor ...	130	9e-28
ref NP_201440.1	peroxidase 72 (PER72) (P72) (PRXR8) [Arabidopsi...	130	9e-28
gb ABB45838.1	hypothetical protein [Thellungiella halophila]	130	1e-27
gb AAS00456.1	acid isoperoxidase [Brassica napus]	129	1e-27
emb CBI25854.1	unnamed protein product [Vitis vinifera]	129	2e-27
ref XP_002281048.1	PREDICTED: hypothetical protein [Vitis vinif...	129	2e-27
ref XP_002263033.1	PREDICTED: hypothetical protein [Vitis vinif...	129	2e-27
ref XP_002510443.1	Peroxidase 9 precursor, putative [Ricinus co...	129	2e-27
emb CBI15846.1	unnamed protein product [Vitis vinifera]	128	3e-27
ref XP_002457158.1	hypothetical protein SORBIDRAFT_03g002370 [S...	128	3e-27
ref XP_002455760.1	hypothetical protein SORBIDRAFT_03g024460 [S...	128	3e-27
ref XP_002438468.1	hypothetical protein SORBIDRAFT_10g020100 [S...	128	3e-27
gb ABI37011.1	peroxidase [Oryza sativa]	128	4e-27
emb CBI16459.1	unnamed protein product [Vitis vinifera]	127	6e-27
ref XP_002285642.1	PREDICTED: hypothetical protein [Vitis vinif...	127	6e-27
gb EAY73397.1	hypothetical protein OsI_01277 [Oryza sativa Indi...	127	6e-27
ref NP_001042657.1	Os01g0263300 [Oryza sativa (japonica cultiva...	127	6e-27
emb CBI16466.1	unnamed protein product [Vitis vinifera]	127	7e-27
ref XP_002463385.1	hypothetical protein SORBIDRAFT_02g042880 [S...	127	7e-27
ref XP_002285649.1	PREDICTED: hypothetical protein [Vitis vinif...	127	7e-27
gb ABI97032.1	peroxidase [Solanum tuberosum]	127	7e-27
gb AAU04440.2	secreted peroxidase [Phelipanche ramosa]	127	7e-27
dbj BAG55221.1	peroxidase 2 [Sesbania rostrata]	127	7e-27
ref NP_001151639.1	peroxidase 68 [Zea mays] >gi 195648284 gb AC...	127	9e-27
gb EAY74439.1	hypothetical protein OsI_02330 [Oryza sativa Indi...	127	9e-27
ref XP_002269425.1	PREDICTED: hypothetical protein [Vitis vinif...	126	2e-26
ref NP_001043276.1	Os01g0543100 [Oryza sativa (japonica cultiva...	126	2e-26
dbj BAB89258.1	putative peroxidase ATP6a [Oryza sativa Japonica...	126	2e-26
dbj BAA94962.1	peroxidase [Asparagus officinalis]	125	2e-26
ref NP_179406.1	peroxidase, putative [Arabidopsis thaliana] >gi...	125	4e-26
emb CBI27497.1	unnamed protein product [Vitis vinifera]	124	5e-26
gb AAM28296.1	peroxidase [Ananas comosus]	124	5e-26
gb ABD47725.1	peroxidase [Eucalyptus globulus subsp. globulus]	124	5e-26
gb ACF88307.1	unknown [Zea mays]	124	6e-26
gb EAZ22365.1	hypothetical protein OsJ_06023 [Oryza sativa Japo...	123	1e-25
ref NP_564948.1	peroxidase, putative [Arabidopsis thaliana] >gi...	122	2e-25
emb CAH69540.1	putative peroxidase [Zinnia elegans]	122	3e-25
ref XP_002312356.1	predicted protein [Populus trichocarpa] >gi ...	121	4e-25
dbj BAD43011.1	peroxidase ATP23a [Arabidopsis thaliana]	121	4e-25
emb CAH69535.1	putative peroxidase [Zinnia elegans]	121	5e-25

gb AA013837.1 AF403735_1	extensin peroxidase [Lupinus albus]	121	5e-25
ref XP_002457609.1	hypothetical protein SORBIDRAFT_03g010230 [S...	120	7e-25
emb CAB65334.1	SPI2 protein [Picea abies]	120	9e-25
gb ACF22712.1	peroxidase precursor [Brachypodium distachyon]	120	1e-24
ref XP_002315983.1	predicted protein [Populus trichocarpa] >gi ...	120	1e-24
emb CAM31942.1	hypothetical protein [Lolium perenne]	120	1e-24
ref XP_002438233.1	hypothetical protein SORBIDRAFT_10g010040 [S...	119	2e-24
ref XP_002451847.1	hypothetical protein SORBIDRAFT_04g008600 [S...	119	2e-24
ref NP_190668.2	electron carrier/ heme binding / peroxidase [Ar...	119	2e-24
emb CAB62621.1	peroxidase-like protein [Arabidopsis thaliana] >...	119	2e-24
gb EAZ05138.1	hypothetical protein OsI_27331 [Oryza sativa Indi...	119	2e-24
ref NP_001060632.1	Os07g0677600 [Oryza sativa (japonica cultiva...	119	2e-24
emb CBI27438.1	unnamed protein product [Vitis vinifera]	119	3e-24
ref XP_002270660.1	PREDICTED: hypothetical protein [Vitis vinif...	119	3e-24
emb CAN65777.1	hypothetical protein [Vitis vinifera]	119	3e-24
gb EAY89162.1	hypothetical protein OsI_10658 [Oryza sativa Indi...	118	3e-24
ref NP_001042655.1	Os01g0263000 [Oryza sativa (japonica cultiva...	118	3e-24
ref NP_001049480.1	Os03g0234500 [Oryza sativa (japonica cultiva...	118	3e-24
ref XP_002509732.1	Lignin-forming anionic peroxidase precursor,...	118	3e-24
ref XP_002509731.1	Lignin-forming anionic peroxidase precursor,...	118	3e-24
gb EEC70836.1	hypothetical protein OsI_02331 [Oryza sativa Indi...	118	4e-24
emb CAH55694.1	putative peroxidase [Lolium perenne]	117	6e-24
emb CAH55692.1	putative peroxidase [Festuca pratensis]	117	6e-24
ref NP_001057377.1	Os06g0274800 [Oryza sativa (japonica cultiva...	117	7e-24
ref XP_002509735.1	Lignin-forming anionic peroxidase precursor,...	117	1e-23
gb ACF08088.1	class III peroxidase [Aegilops ventricosa]	116	1e-23
gb ACG43658.1	hypothetical protein [Zea mays]	116	1e-23
gb ACF80021.1	unknown [Zea mays]	116	1e-23
ref NP_001130123.1	hypothetical protein LOC100191217 [Zea mays]...	116	1e-23
ref XP_002304020.1	predicted protein [Populus trichocarpa] >gi ...	115	2e-23
ref XP_002306459.1	predicted protein [Populus trichocarpa] >gi ...	115	3e-23
gb ABF95842.1	Peroxidase 2 precursor, putative, expressed [Oryz...	115	3e-23
emb CAA59486.1	peroxidase [Triticum aestivum]	115	4e-23
dbj BAA01992.1	peroxidase [Nicotiana tabacum]	114	6e-23
ref XP_002529736.1	Peroxidase 27 precursor, putative [Ricinus c...	114	8e-23
gb ACJ84393.1	unknown [Medicago truncatula]	114	8e-23
gb ACU23010.1	unknown [Glycine max]	113	1e-22
ref XP_001751508.1	predicted protein [Physcomitrella patens sub...	112	2e-22
gb AA013839.1 AF405327_1	peroxidase 1 [Lupinus albus]	112	3e-22
gb AAL58444.1 AF455807_1	anionic peroxidase [Nicotiana tomentososi...	112	3e-22
ref XP_002464560.1	hypothetical protein SORBIDRAFT_01g020830 [S...	111	4e-22
gb ACF70704.1	root peroxidase [Triticum aestivum]	111	4e-22
dbj BAD97439.1	peroxidase [Pisum sativum]	111	4e-22
gb AAQ67366.1	POD9 precursor [Gossypium hirsutum]	111	4e-22
ref XP_002309830.1	predicted protein [Populus trichocarpa] >gi ...	111	5e-22
gb EEE59027.1	hypothetical protein OsJ_10774 [Oryza sativa Japo...	111	5e-22
gb AAA34101.1	peroxidase [Nicotiana tabacum]	110	7e-22
sp P11965.1 PERX_TOBAC	RecName: Full=Lignin-forming anionic pero...	110	7e-22
emb CBI28955.1	unnamed protein product [Vitis vinifera]	110	9e-22

ref XP_002274157.1 PREDICTED: hypothetical protein [Vitis vinif...	110	9e-22
sp P15003.1 PER1_SOLLC RecName: Full=Suberization-associated ani...	110	9e-22
gb EAZ22371.1 hypothetical protein OsJ_06029 [Oryza sativa Japo...	110	1e-21
gb ABK22032.1 unknown [Picea sitchensis]	109	2e-21
ref XP_001783974.1 predicted protein [Physcomitrella patens sub...	108	3e-21
gb EAZ37178.1 hypothetical protein OsJ_21519 [Oryza sativa Japo...	108	3e-21
emb CBI28956.1 unnamed protein product [Vitis vinifera]	108	3e-21
gb ACJ11761.1 class III peroxidase [Gossypium hirsutum]	108	3e-21
dbj BAF08306.2 Os02g0236600 [Oryza sativa Japonica Group]	108	3e-21
gb EAZ01154.1 hypothetical protein OsI_23183 [Oryza sativa Indi...	108	3e-21
tpe CAH69331.1 TPA: class III peroxidase 89 precursor [Oryza sa...	108	3e-21
ref NP_001058379.1 Os06g0681600 [Oryza sativa (japonica cultiva...	108	3e-21
dbj BAD45811.1 putative bacterial-induced peroxidase precursor ...	108	3e-21
ref NP_001057744.1 Os06g0521200 [Oryza sativa (japonica cultiva...	108	3e-21
gb EAZ01158.1 hypothetical protein OsI_23186 [Oryza sativa Indi...	108	5e-21
gb ACJ11766.1 class III peroxidase [Gossypium hirsutum]	108	5e-21
ref XP_002443277.1 hypothetical protein SORBIDRAFT_08g016840 [S...	107	8e-21
emb CAA50597.1 peroxidase [Solanum lycopersicum]	107	8e-21
emb CAB67121.1 peroxidase [Solanum lycopersicum]	107	8e-21
ref XP_002465968.1 hypothetical protein SORBIDRAFT_01g049140 [S...	107	8e-21
gb ACU20287.1 unknown [Glycine max]	107	1e-20
gb EEE65802.1 hypothetical protein OsJ_21515 [Oryza sativa Japo...	107	1e-20
sp P12437.2 PERX_SOLTU RecName: Full=Suberization-associated ani...	107	1e-20
dbj BAD98313.2 peroxidase [Nicotiana tabacum]	107	1e-20
dbj BAD98314.1 peroxidase [Nicotiana tabacum]	107	1e-20
ref NP_001057745.1 Os06g0521400 [Oryza sativa (japonica cultiva...	107	1e-20
sp P15004.1 PER2_SOLLC RecName: Full=Suberization-associated ani...	107	1e-20
gb AAA33837.1 anionic peroxidase [Solanum tuberosum] >gi 228610...	107	1e-20
ref XP_002336172.1 predicted protein [Populus trichocarpa] >gi ...	107	1e-20
ref NP_001136722.1 hypothetical protein LOC100216859 [Zea mays]...	107	1e-20
ref XP_002516846.1 Peroxidase 24 precursor, putative [Ricinus c...	106	1e-20
ref NP_001140982.1 hypothetical protein LOC100273061 [Zea mays]...	106	1e-20
gb ABU63712.1 lignin peroxidase [Garcinia mangostana]	106	1e-20
emb CBI25927.1 unnamed protein product [Vitis vinifera]	106	2e-20

>gb|ACU17608.1| unknown [Glycine max]

Length = 320

Score = 249 bits (635), Expect = 2e-63

Identities = 120/124 (96%), Positives = 121/124 (97%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986

QARCTNFRARIYNETNI TAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV

Sbjct: 197 QARCTNFRARIYNETNIGTAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

QKKG LHSDQQLFNGGSTDSIVRGYSTNPGTF SDFAAAMIKMGDISPLTGSNGE+RKNC

Sbjct: 257 QKKGFLHSDQQLFNGGSTDSIVRGYSTNPGTFPSDFAAAMIKMGDISPLTGSNGEVRKNC 316

Query: 2167 RRIN 2178
RRIN
Sbjct: 317 RRIN 320

Score = 213 bits (543), Expect = 8e-53
Identities = 118/165 (71%), Positives = 120/165 (72%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI
Sbjct: 70 VNGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSVQI+ G PTWNVKLG
Sbjct: 130 RDSVQILGG-----PTWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG
Sbjct: 147 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 191

Score = 145 bits (365), Expect = 3e-32
Identities = 70/71 (98%), Positives = 70/71 (98%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASL 750
MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKS VQSAISKETRMGASL
Sbjct: 1 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKS VQSAISKETRMGASL 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>gb|ACU17865.1| unknown [Glycine max]
Length = 320

Score = 242 bits (618), Expect = 2e-61
Identities = 117/124 (94%), Positives = 120/124 (96%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCTNFRARIYNE+NI+TAFAR RQQSCPRTSGSGDNNLA LDLQTPT FDNYYFKNLV
Sbjct: 197 QARCTNFRARIYNESNIDTAFARARQQSCPRTSGSGDNNLATLDLQTPTFEFDNYYFKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
QKKGLLHSDQQLFNGGSTDSIVRGYSTNP +FSSDFAAAMIKMGDISPLTGSNGEIRKNC
Sbjct: 257 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPSSFSSDFAAAMIKMGDISPLTGSNGEIRKNC 316

Query: 2167 RRIN 2178
RRIN
Sbjct: 317 RRIN 320

Score = 208 bits (530), Expect = 2e-51
Identities = 114/165 (69%), Positives = 119/165 (72%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTSSFTGEKNANPNRNSARG+EVIDNIKSAVEK CPGVVSCADILAI AA
Sbjct: 70 VNGCDGSILLDDTSSFTGEKNANPNRNSARGYEVIDNIKSAVEKACPGVVSCADILAI AA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI* LGGPTWNVKLG 1510
RDSVQI+ GGP+WNVK+G
Sbjct: 130 RDSVQIL-----GGPSWNVKVG 146

Query: 1511 RR DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RR DARTASQSAANNGIP PTSNLNQLISRFSALGLSTKDLVALSG
Sbjct: 147 RR DARTASQSAANNGIPPPTSNLNQLISRFSALGLSTKDLVALSG 191

Score = 138 bits (347), Expect = 4e-30
Identities = 68/71 (95%), Positives = 69/71 (97%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MASFC SRLTICLALFVLI GSANAQLSTNFYHSCPNLFS+VKSTVQSAISKETRMGASL
Sbjct: 1 MASFC SRLTICLALFVLILGSANAQLSTNFYHSCPNLFSTVKSTVQSAISKETRMGASL 60

Query: 751 LRLFFHDCFVN 783
LR FFHDCFVN
Sbjct: 61 LRPFFHDCFVN 71

>gb|AAP76387.1| class III peroxidase [Gossypium hirsutum]
Length = 330

Score = 218 bits (556), Expect = 2e-54
Identities = 100/124 (80%), Positives = 116/124 (93%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT+FRARIYNE+NI+ +FA+TRQ++CPRT+GSGDNNLAPLD+QTPTSFDN YFKNL+
Sbjct: 207 QARCTSFARIYNESNIDASFAQTRQRNCPRRTGSGDNNLAPLDIQTPPTSFDNNYFKNLI 266

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQQLFNGGSTDSIVRGY +P +F+SDF AAMIKMGDISPLTGS GEIRKNC

Sbjct: 267 SQRGLLHSDQQLFNGGSTDSIVRGYGNPSSFNDFVAAMIKMGDISPLTGSRGEIRKNC 326

Query: 2167 RRIN 2178

RR+N

Sbjct: 327 RRVN 330

Score = 196 bits (499), Expect = 1e-47
Identities = 107/169 (63%), Positives = 117/169 (69%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEKNANPNRNS+RGF+V+DNIKSAVE VCPGVVSCADILAIAA

Sbjct: 80 VNGCDGSVLLDDTSSFTGEKNANPNRNSRGFVDVVDNIKSAVENVCPGVVSCADILAIAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I LGGP W VKLG

Sbjct: 140 RDSVEI-----LGGPKWAVKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDAR+ASQSAANNGIP PTSNLN+L SRF+ALGLST+DLVALSG I

Sbjct: 157 RRDARSASQSAANNGIPPTSNLNRLTSRFNALGLSTRDLVALSGAHTI 205

Score = 100 bits (248), Expect = 1e-18
Identities = 51/75 (68%), Positives = 58/75 (77%)
Frame = +1

Query: 559 SKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRM 738
+K+ AS S+ + L L V + GS NAQLSTNFY SCPNL S+VKSTV SAI+KE RM

Sbjct: 7 TKMGSASSFSKFCLTLLLLVDVLGSTNAQLSTNFYSKCPNLLSTVKSTVTSAINKEARM 66

Query: 739 GASLLRRLFHDCFVN 783

GASLLRRLFHDCFVN

Sbjct: 67 GASLLRRLFHDCFVN 81

>gb|AB077632.1| peroxidase [Medicago truncatula]

Length = 322

Score = 217 bits (552), Expect = 7e-54
Identities = 104/124 (83%), Positives = 112/124 (90%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRARIYNETNI A A TRQ +CP+ SGSGDNNLAPLDLQTP+SFDN YFKNLV

Sbjct: 199 QARCTNFRARIYNETNINAAXASTRQSNCPKASGSGDNNLAPLDLQTPSSFDNYYFKNLV 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLLHSDQQLFNGGST+SIV GYST+P +FSSDFAAAMIKMG+I PLTGSNGEIRKNC

Sbjct: 259 QNKGLLHSDQQLFNGGSTNSIVSGYSTSPSSFSSDFAAAMIKMGNIKPLTGSNGEIRKNC 318

Query: 2167 RRIN 2178

R+ N

Sbjct: 319 RKTN 322

Score = 188 bits (478), Expect = 3e-45
Identities = 105/169 (62%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGEKNANPNRNSARGF+VIDNIK+AVE VCPGVVSCADILAI

Sbjct: 72 VNGCDGSILLDDTSSFTGEKNANPNRNSARGFDVIDNIKTAVENVCPGVVSCADILAI 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
DSV I+ G PTWNVKLG

Sbjct: 132 ADSVAILGG-----PTWNVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDA+TASQSAAN IPAPTSNLN L S FSA+GLS+KDLV LSG I

Sbjct: 149 RRDAKTASQSAANTAIPAPTSNLNLTSMFSAVGLSSKDLVTLGSAHTI 197

Score = 100 bits (249), Expect = 9e-19
Identities = 52/68 (76%), Positives = 58/68 (85%), Gaps = 1/68 (1%)
Frame = +1

Query: 583 CSRLT-ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRL 759
CSRLT I L L VLI GSANAQLSTNFY +CP L ++VKST+Q+AISKE RMGAS+LRL

Sbjct: 6 CSRLTMISLVLSVLIIGSANAQLSTNFYSKTCPKLSTTVKSTLQTAISKEARMGASILRL 65

Query: 760 FFHDCFVN 783

FFHDCFVN

Sbjct: 66 FFHDCFVN 73

>dbj|BAA82306.1| peroxidase [Nicotiana tabacum]

Length = 321

Score = 212 bits (540), Expect = 2e-52
Identities = 102/125 (81%), Positives = 110/125 (88%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETN-IETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT+FRARIYNETN ++ +FARTRQ +CPR+SGSGDNNLAPLDLQTP FDN YFKNL
Sbjct: 197 QARCTSFARIYNETNLDASFARTRQSNCPRSSGSGDNNLAPLDLQTPNKFDNYYFKNL 256

Query: 1984 VQKKGLLHSDQQFLNFGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
V KKGLLHSDQQFLNFGGS DSIV YS NP +FSSDF AMIKMGDI PLTGSNGEIRKN
Sbjct: 257 VDKKGLLHSDQQFLNFGGSADSIIVTSYNNPSSFSDFVTAMIKMGDIRPLTGSNGEIRKN 316

Query: 2164 CRRIN 2178
CRR+N
Sbjct: 317 CRRLN 321

Score = 187 bits (476), Expect = 5e-45
Identities = 105/169 (62%), Positives = 113/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEK A PN NSARGFEVIDNIKSAVEKVCPGVVSCADILA+ A
Sbjct: 70 VNGCDGSLLDDTSSFTGEKRAAPNVNSARGFEVIDNIKSAVEKVCPGVVSCADILAVTA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP WNVKLG
Sbjct: 130 RDSVVI-----LGGPNWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTASQSAAN+GIP TSNLN+LIS FSA+GLSTKD+VALSG I
Sbjct: 147 RRDSRTASQSAANSIPPATSNLRLISSFSAVGLSTKDMVALSGAHTI 195

Score = 91.3 bits (225), Expect = 6e-16
Identities = 46/71 (64%), Positives = 53/71 (74%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS + L L+ GS++AQLST FY SCP L+ +VKS VQSAI+KETRMGASL
Sbjct: 1 MASLKINAI VLFILVSLIGSSAQLSTGFYSKSCP KLYQTVKSAVQSAINKETRMGASL 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>ref|XP_002278996.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 321

Score = 211 bits (536), Expect = 5e-52
Identities = 98/124 (79%), Positives = 112/124 (90%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNETNI+ +FA+TRQ +CPR SGSGDNNLAPLDLQTPT+F+N Y+KNL+
Sbjct: 198 QARCTSFARIYNETNIDNSFAKTRQSNCPRASGSGDNNLAPLDLQTPTAFENYYKNLI 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQLFNGGSTDSIVR YS + F++ F A MIKMGDISPLTGSNGEIRKNC
Sbjct: 258 KKKGLLHSDQQLFNGGSTDSIVRKYSNSRSNFNAHFVAGMIKMGDISPLTGSNGEIRKNC 317

Query: 2167 RRIN 2178
RR+N
Sbjct: 318 RRVN 321

Score = 184 bits (466), Expect = 7e-44
Identities = 100/169 (59%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSF GEKNA PN NS RGF+V+D+IKS VE CPGVVSCAD+LAIAA
Sbjct: 71 VNGCDGSVLLDDTSSFIGEKNAAPNANSVRGFVDDIKSKVETACPGVVSCADVLAIAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDSV I+ GGP+WNVKLG
Sbjct: 131 RDSVVIL-----GGPSWNVKLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IP PTSNLNQLISRF ALGLST+DLVAL+G+ I
Sbjct: 148 RRDARTASQAANNSIPPPTSNLNQLISRFAQALGLSTRDLVALAGSHTI 196

Score = 90.1 bits (222), Expect = 1e-15
Identities = 46/72 (63%), Positives = 56/72 (77%), Gaps = 1/72 (1%)
Frame = +1

Query: 571 MASFCSRLTIC-LALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGAS 747
MAS S + I +AL +L GS+ AQLST++Y SCP LF +VKS V+SA++KE RMGAS
Sbjct: 1 MASPSSYMAIVTMALLILFLGSSTAQLSTDYYSQSCPFLFPTVKS AVKSAVAKEARMGAS 60

Query: 748 LLRLFFHDCFVN 783

LLRFFHDCFVN
Sbjct: 61 LLRFFHDCFVN 72

>gb|AAx44001.2| putative secretory peroxidase [Catharanthus roseus]
Length = 318

Score = 209 bits (533), Expect = 1e-51
Identities = 101/125 (80%), Positives = 113/125 (90%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETN-IETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCTNFRARIYNETN ++ A A+TR+ +CPR SGS DNNLAPLDLQTP +FDN Y+KNL
Sbjct: 194 QARCTNFRARIYNETNLDAAALQTRRSNCPSPSGSRDNNLAPLDLQTPRAFDNYYKLN 253

Query: 1984 VQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
V ++GLLHSDQQLFNGGSTDSIVR YS NP +F+SDFAAAMIKMGDISPLTGSNG+IRKN
Sbjct: 254 VNRRLHSDQQLFNGGSTDSIVRSYSGNPASFASDFAAAMIKMGDISPLTGSNGQIRKN 313

Query: 2164 CRRIN 2178
CRRIN
Sbjct: 314 CRRIN 318

Score = 191 bits (484), Expect = 5e-46
Identities = 106/169 (62%), Positives = 114/169 (67%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGEK A PN NSARGFEV+DNIKSAVE VCPGVVSCADILAIAA
Sbjct: 67 VNGCDGSILLDDTSSFTGEKRAAPNFSARGFEVVDNIKSAVENVCPGVVSCADILAIAA 126

Query: 1331 RDSVQIVSGQTTNKNLNLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSVQI+ GGP+WNVKLG
Sbjct: 127 RDSVQIL-----GGPSWNVKLG 143

Query: 1511 RRDARTASQAANNGIPAPTSNLNLQISRFSALGLSTKDLVALSGTKHI 1657
RRDA TASQ+AANN IP PTSNLN L+SRF+ALGLST DLVALSG+ I
Sbjct: 144 RRDATTASQAANNSIPPPTSNLNLVSRFNALGLSTNDLVALSGSHTI 192

Score = 85.1 bits (209), Expect = 4e-14
Identities = 42/61 (68%), Positives = 52/61 (85%), Gaps = 1/61 (1%)
Frame = +1

Query: 604 LALFVL-IWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
L +F+L + GS++AQLST++Y SCPN+F++VKS V SAI KE RMGASLLRFFHDCFV

Sbjct: 8 LGIFLLFLIGSSSAQLSTDYYSKSCPNTVKSQVHSAILKEARMGASLLRRLFHDCFV 67

Query: 781 N 783
N

Sbjct: 68 N 68

>gb|AAP42508.1| anionic peroxidase swpb3 [Ipomoea batatas]
Length = 320

Score = 209 bits (533), Expect = 1e-51
Identities = 100/124 (80%), Positives = 110/124 (88%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRARIYNE+NI+++FA+++R+ +CPR SGSGDNNLAPLDLQTP FDN Y+ NLV
Sbjct: 197 QARCTNFRARIYNESNIDSSFAQSRKGNCPRASGSGDNNLAPLDLQTPIKFDNYYVNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS VRGYSTNP F SFAAAMIKMGDI PLTG+NGEIRKNC
Sbjct: 257 NKKGLLHSDQQLFNGVSTDSTVRGYSTNPSKFKSDFAAAMIKMGDIKPLTGNGEIRKNC 316

Query: 2167 RRIN 2178
RR N

Sbjct: 317 RRRN 320

Score = 184 bits (467), Expect = 5e-44
Identities = 103/169 (60%), Positives = 113/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTSSFTGEK A PN SARGFEVID I KSAVEKVC PGVVSCADILAI A+
Sbjct: 70 VNGCDGSILLDDTSSFTGEKRAAPNFQSARGFEVIDQIKSAVEKVC PGVVSCADILAI AS 129

Query: 1331 RDSVQIVSGQT TNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS ++ LGGP+WNVKLG
Sbjct: 130 RDS-----TVTLGGPSWNVKLG 146

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IPAPTSNLN+LIS FSA+GLST D+V LSG+ I
Sbjct: 147 RRDARTASQAAANNSIPAPTSNLNRLISSFSAVGLSTNDMVVLSGSHTI 195

Score = 82.8 bits (203), Expect = 2e-13
Identities = 42/71 (59%), Positives = 48/71 (67%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA LT L +++ G +AQLS FY SCP LF +V S V+SAI KE RMGASL
Sbjct: 1 MAVSVKALTAVLLCVLVLVGGCSAQLSPGFYKSCPKLFQTVNSVVRSAIQKEARMGASL 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>gb|ABR23054.1| basic peroxidase swpb4 [Ipomoea batatas]
Length = 320

Score = 209 bits (532), Expect = 1e-51
Identities = 100/124 (80%), Positives = 110/124 (88%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRARIYNE+NI+++FA+++R+ +CPR SGSGDNNLAPLDLQTP FDN Y+ NLV
Sbjct: 197 QARCTNFRARIYNESNIDSSFAQSRKGNCPRASGSGDNNLAPLDLQTPIKFDNYYVNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS VRGYSTNP F SDFAAAMIKMGDI PLTG+NGEIRKNC
Sbjct: 257 NKKGLLHSDQQLFNGVSTDSTVRGYSTNPSKFRSDFAAAMIKMGIKPLTGNGEIRKNC 316

Query: 2167 RRIN 2178
RR N
Sbjct: 317 RRRN 320

Score = 182 bits (462), Expect = 2e-43
Identities = 102/169 (60%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGEK A PN SARGFEVID IKSAREKVCPGVVSCADILAIA+
Sbjct: 70 VNGCDGSILLDDTSSFTGEKRAAPNFQSARGFEVIDQIKSAVEKVCPGVVSCADILAIAS 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS ++ LGGP+WNVKLG
Sbjct: 130 RDS-----TVTLGGPSWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDAR ASQ+AANN IPAPTSNLN+LIS FSA+GLST D+V LSG+ I
Sbjct: 147 RRDARAASQAAANNSIPAPTSNLNRLISSFSAVGLSTNDMVVLSGSHTI 195

Score = 80.5 bits (197), Expect = 1e-12
Identities = 40/62 (64%), Positives = 46/62 (74%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPNIFFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777
+ L + VL+ G +AQLS FY SCP LF +V S V+SAI KE RMGASLLRLLFFHDCF
Sbjct: 11 VLLCVLVLV-GGCSAQLSPGFYSKSCPFLFQTVNSVVRSAIQKEARMGASLLRLLFFHDCF 69

Query: 778 VN 783
VN
Sbjct: 70 VN 71

>gb|ACU23245.1| unknown [Glycine max]
Length = 326

Score = 208 bits (530), Expect = 2e-51
Identities = 95/124 (76%), Positives = 111/124 (89%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FRARIYNE+NI+++FAR RQ CPRTSGSGDNNLAP+D TPT FDN+YFKNL+
Sbjct: 203 QARCTTFRARIYNESNIDSSFARMRQSRCPRTSGSGDNNLAPIDFATPTFFDNHYFKNLI 262

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
QKKG +HSDQ+LFNGGSTDS+V YSTNP +F +DF+AAMI+MGDISPLTGS GEIR+NC
Sbjct: 263 QKKGFIHSDQELFNGGSTDSLVTYSTNPASFFADFSAAAMIRMGDISPLTGSRGEIRENC 322

Query: 2167 RRIN 2178
RR+N
Sbjct: 323 RRVN 326

Score = 200 bits (509), Expect = 7e-49
Identities = 111/165 (67%), Positives = 116/165 (70%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGEKNA PNRNSARGFEVID I KSAVEKVC PGVVSCADILAIAA
Sbjct: 76 VNGCDGSILLDDTSSFTGEKNAGPNRNSARGFEVIDQIKSAVEKVC PGVVSCADILAIAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I L GPTW+VKLG
Sbjct: 136 RDSVEI-----LRGPTWDVKLG 152

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+RTASQSAANNGIP PTSNLNQLISRF+ LGLSTKDLVALSG
Sbjct: 153 RRDSRTASQSAANNGIPRPTSNLNQLISRFTLGLSTKDLVALSG 197

Score = 100 bits (248), Expect = 1e-18
Identities = 53/77 (68%), Positives = 57/77 (74%), Gaps = 6/77 (7%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGS-----ANAQLSTNFYHSCPNLFSSVKSTVQSAISKET 732
MAS CS I LAL VL+ G+ AN L TNFY SCF LF +VK TV+SAISKET
Sbjct: 1 MASSCSSMITLALLVLVLGTNTSSANANPTLHTNFYSSCPKLFDTVKRTVESAIKSKET 60

Query: 733 RMGASLLRLLFFHDCFVN 783
RMGASLLRLLFFHDCFVN
Sbjct: 61 RMGASLLRLLFFHDCFVN 77

>gb|ACM47317.1| peroxidase [Capsicum annuum]
Length = 324

Score = 205 bits (521), Expect = 3e-50
Identities = 100/125 (80%), Positives = 108/125 (86%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETN-IETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNL 1983
QARCT+FRARIYNETN I+++FA TRQ++CPR SGSGDNNLAPLDLQTPT FDN YFKNL
Sbjct: 200 QARCTSFARIYNETNIDSSFATTRQRNCPRNSGSGDNNLAPLDLQTPTKFDNNYFKNL 259

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKN 2163
V K+GLLHSDQQLFNGGS DSIV YS NP +FSSDF AMIKMGD PLTGSNGEIRKN
Sbjct: 260 VSKRGLLHSDQQLFNGGSADSIVTSYSNNPSSFSDFVTAMIKMGDNRPLTGSNGEIRKN 319

Query: 2164 CRRIN 2178
CR N
Sbjct: 320 CRTRN 324

Score = 184 bits (468), Expect = 4e-44
Identities = 104/169 (61%), Positives = 109/169 (64%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGS+LLDDTSSFTGEK A PN NS RGFEVIDNIKSAVEK CPGVVSCADILAI A
Sbjct: 73 VNGCDGSLLDDTSSFTGEKRAAPVNSVRGFEVIDNIKSAVEKACPGVVSCADILAITA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP WNVKLG
Sbjct: 133 RDSVVI-----LGGPNWNVKLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ AAN+ IP PTSNLNQLIS FSA+GLST D+VALSG I
Sbjct: 150 RRDARTASQGAANSSIPPPTSNLNQLISSFSAVGLSTTDMVALSGAHTI 198

Score = 89.4 bits (220), Expect = 2e-15
Identities = 44/60 (73%), Positives = 51/60 (85%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCPFLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
L + L+ S++AQLSTNFY SCP LF +VKSTVQSAI++ETRMGASLLRLLFFHDCFVN
Sbjct: 15 LVVNLLIVSSSAQLSTNFYSKSCPFLFQTVKSTVQSAINRETRMGASLLRLLFFHDCFVN 74

>ref|XP_002328991.1| predicted protein [Populus trichocarpa]
gb|EEE77576.1| predicted protein [Populus trichocarpa]
Length = 322

Score = 204 bits (520), Expect = 4e-50
Identities = 96/124 (77%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCTNFRARIYNET I+++ A+TR+ +CPRTSGSGDNNLAPLDLQTPT F+N Y+KNL+
Sbjct: 199 QARCTNFRARIYNETTIDSSLAQTRRSNCPRTSGSGDNNLAPLDLQTPTRFENNYKLI 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQQLFNGGSTDSIV YS+N TF SDF A MIKMGDI PLTGS GEIR NC
Sbjct: 259 NRRGLLHSDQQLFNGGSTDSIVSTYSSNENTFRSDFVAGMIKMGDIRPLTGSRGEIRNNC 318

Query: 2167 RRIN 2178
RRIN
Sbjct: 319 RRIN 322

Score = 194 bits (493), Expect = 5e-47
Identities = 107/169 (63%), Positives = 116/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEKNA PN+NSARGFEVIDNIKSAVEK CPGVVSCADILAIAA
Sbjct: 72 VNGCDGSLLDDTSSFTGEKNAAPKNNSARGFEVIDNIKSAVEKACPGVVSCADILAIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I LGGP W+VKLG
Sbjct: 132 RDSTVI-----LGGPEWDVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IP PTSNLNQLISRF+ALGLST+D+VALSG+ I
Sbjct: 149 RRDARTASQAAANNSIPRPTSNLNQLISRFNALGLSTRDMVALSGSHTI 197

Score = 87.8 bits (216), Expect = 6e-15
Identities = 43/70 (61%), Positives = 52/70 (74%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANAQLSTNFYHSCP NFLSSVKSTVQSAISKETRMGASLL 753
+SF + L +L GS+NAQLS +FY SCP+L S+VK VQSAI+KE RMGAS+L
Sbjct: 4 SSFSKAIIVTLAILVMLSMGSSNAQLSIDFYKSCP HLLSTVKPVVQSAINKEARMGASIL 63

Query: 754 RLFHDCFVN 783
RLFHDCFVN
Sbjct: 64 RLFHDCFVN 73

>ref|XP_002269918.1| PREDICTED: hypothetical protein [Vitis vinifera]
sp|A7NY33.1|PER4_VITVI RecName: Full=Peroxidase 4; Flags: Precursor
emb|CBI15844.1| unnamed protein product [Vitis vinifera]
Length = 321

Score = 204 bits (520), Expect = 4e-50
Identities = 94/124 (75%), Positives = 110/124 (88%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCT+FRARIYNETNI+++FA+TRQ SCP SGSGDNNLAPLDLQTPT+FDNYY+KNL+
Sbjct: 198 QARCTSF RARIYNETNIDSSFAKTRQASCPSASGSGDNNLAPLDLQTPTTFDNYYYKNLI 257

Query: 1987 QKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L+NGGSTDS V+ Y NP TF+SDF A MIKMGDI+PLTGS GEIRK+C
Sbjct: 258 NQKGLLHSDQVLYNGGSTDSTVKTYVNNPKFTSDFVAGMIKMGDITPLTGSEGEIRKSC 317

Query: 2167 RRIN 2178
++N
Sbjct: 318 GKVN 321

Score = 165 bits (417), Expect = 3e-38
Identities = 92/169 (54%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEK VCPGVVSCADILAI 1330
+ GCD S+LLDDTSSFTGE+ A PN+NS RG VIDNIKS VE VCPGVVSCADI+AIAA
Sbjct: 71 VNGCDASVLLDDTSSFTGEQTAVPNKNSIRGLNVIDNIKSQVESVCPGVVSCADIIAIAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W+VKLG
Sbjct: 131 RDSVVI-----LGGPDWDVKLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS S ANN IP PTS+L+ LIS+F A GLST+D+VALSG I
Sbjct: 148 RRDSKTASLSGANNIPPTSSLSNLISKFQAQGLSTRDMVALSGAHTI 196

Score = 90.5 bits (223), Expect = 1e-15
Identities = 44/70 (62%), Positives = 54/70 (77%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPFLFSSVKSTVQSAISKETRMGASLL 753
+S S + + L + L GS++AQLSTNFY +CP +F +VKS VQSA+SKE RMGASLL
Sbjct: 3 SSSFSIVVVALGVLALFAGSSSAQLSTNFYSKTCPKVFDTVKSGVQSAVSKERRMGASLL 62

Query: 754 RLFFHDCFVN 783
RLFFHDCFVN
Sbjct: 63 RLFFHDCFVN 72

>emb|CAD67479.1| peroxidase [Asparagus officinalis]
Length = 320

Score = 203 bits (516), Expect = 1e-49
Identities = 95/124 (76%), Positives = 109/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPSFDNYYFKNLV 1986
QARCTNFRA +YN+T+I+ FA+TRQ +CP TSGSGDNNLAPLDLQTP +FDN YFKNLV
Sbjct: 197 QARCTNFRAHVYNDTIDATFAKTRQSNCPSTSGSGDNNLAPLDLQTPVAFDNNYFKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQ+F+GGST+S V YST+P T+SSDF AAMIKMGDISPLTG +GEIRKNC
Sbjct: 257 SKKGLLHSDQQVFGGSTNSQVSTYSTPSTWSSDFVAAMIKMGDISPLTGKSGEIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKTN 320

Score = 169 bits (427), Expect = 2e-39
Identities = 92/169 (54%), Positives = 107/169 (63%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGS+LLDDTSSFTGEKNA PN+ S RGF+VID IK+AVE+ CPGVVSCADILA+ A
Sbjct: 70 VNGCDGSLLLDDTSSFTGEKNAIPNKGSVRGFDVIDKIKTAVEQACPGVVSCADILAVTA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV ++ G PTWNVKLG
Sbjct: 130 RDSVLLGG-----PTWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTASQS ANN IP PTS+L+ LIS+FSA GLS K++VAL G I
Sbjct: 147 RRDSRTASQSGANNIPPTSSLSNLISKFSAQGLSAKEMVALVGAHTI 195

Score = 80.1 bits (196), Expect = 1e-12
Identities = 42/73 (57%), Positives = 52/73 (71%)
Frame = +1

Query: 565 LTMASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
+ +SF S I L + + +++AQL+ NFY SCP LF ++KS VQSAIS E RMGA
Sbjct: 1 MASSSFKSLAPISLVSYV--RASSAQLTPNFYSSCPTLFPPTIKSVVQSAISSEKRMGA 58

Query: 745 SLLRRLFHDCFVN 783
SLLRRLFHDCFVN
Sbjct: 59 SLLRRLFHDCFVN 71

>ref|NP_196153.1| peroxidase, putative [Arabidopsis thaliana]
sp|Q9FLC0.1|PER52_ARATH RecName: Full=Peroxidase 52; Short=Atperox P52; AltName: Full=ATP49;
Flags: Precursor
dbj|BAB09977.1| peroxidase [Arabidopsis thaliana]
gb|AAL38746.1| putative peroxidase [Arabidopsis thaliana]
Length = 324

Score = 202 bits (513), Expect = 2e-49
Identities = 97/124 (78%), Positives = 107/124 (86%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RCTNFRARIYNETNI AFA TRQ++CPR SGSGD NLAPLD+ T SFDN YFKNL+
Sbjct: 201 QSRCTNFRARIYNETNINAAFATTRQRTCPRASGSGDGNLAPLDVTTAASFDNYYFKNLM 260

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ LFNNGGSTDSIVRGYS NP +F+SDF AAMIKMGDISPLTGS+GEIRK C
Sbjct: 261 TQRGLLHSDQVLFNGGSTDSIVRGYSNPNSSFNDFTAAMIKMGDISPLTGSNGEIRKVC 320

Query: 2167 RRIN 2178
R N
Sbjct: 321 GRN 324

Score = 187 bits (476), Expect = 5e-45
Identities = 104/169 (61%), Positives = 115/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTSSFTGE+NA PNRNSARGF VIDNIKSAVEK CPGVVSCADILAI AA
Sbjct: 74 VNGCDGSILLDDTSSFTGEQNAAPNRNSARGFNVIDNIKSAVEKACPGVVSCADILAI AA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 134 RDSV-----VALGGPNWNVKVG 150

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AAAN+ IPAPTS+L+QLIS FSA+GLST+D+VALSG I
Sbjct: 151 RRDARTASQAANSNIPAPTSLSQLISSFSAVGLSTRDMVALSGAHTI 199

Score = 78.2 bits (191), Expect = 5e-12
Identities = 38/66 (57%), Positives = 50/66 (75%), Gaps = 4/66 (6%)
Frame = +1

Query: 598 ICLALFVLIWGSAN----AQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR LFF 765
+ L + +L+ G N AQL+TNFY SCPNL S+V++ V+SA++ E RMGAS+LRLFF
Sbjct: 10 LVLVVTL LLQGDNNYVVEAQLTTNFYSTSCP NLLSTVQTAVKSAVNSEARMGASILRLFF 69

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 70 HDCFVN 75

>dbj|BAF27413.2| Os11g0112400 [Oryza sativa Japonica Group]
Length = 136

Score = 201 bits (510), Expect = 5e-49
Identities = 93/124 (75%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA +RQ CPR+SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 13 QARCTNFRAHIYNETNIDSGFAMSRQSGCPRSSGSGDNNLAPLDLQTPTVFENNYK NLV 72

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMI KMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 73 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMIKMGDITPLTGSNGEIRKNC 132

Query: 2167 RRIN 2178
RRIN
Sbjct: 133 RRIN 136

>ref|NP_001065568.1| Os11g0112400 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69372.1| TPA: class III peroxidase 130 precursor [Oryza sativa (japonica
cultivar-group)]
gb|ABA91159.1| Peroxidase 52 precursor, putative, expressed [Oryza sativa (japonica
cultivar-group)]
gb|EAZ00524.1| hypothetical protein OsI_22542 [Oryza sativa Indica Group]
gb|EAZ17186.1| hypothetical protein OsJ_32693 [Oryza sativa Japonica Group]
dbj|BAH01350.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 324

Score = 201 bits (510), Expect = 5e-49
Identities = 93/124 (75%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA +RQ CPR+SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 201 QARCTNFRAHIYNETNIDSGFAMSRQSGCPRSSGSGDNNLAPLDLQTPTVFENNYKLV 260

Query: 1987 QKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 261 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMKMGDITPLTGSNGEIRKNC 320

Query: 2167 RRIN 2178
RRIN
Sbjct: 321 RRIN 324

Score = 166 bits (419), Expect = 2e-38
Identities = 94/169 (55%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT+SFTGEK ANPN S RGFEVID IKSAVE +CPGVVSCADILAI AA
Sbjct: 74 VQGCDASLLDDTASFTGEKMANPNNGSVRGFEVIDAIKSAVETICPGVVSCADILAI AA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 134 RDSVAI-----LGGPSWDVKVG 150

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG+ I
Sbjct: 151 RRDSRTASLSGANNNIPPTSGLANLTSLFAAQGLSQKDMVALSGSHTI 199

Score = 75.5 bits (184), Expect = 3e-11
Identities = 35/75 (46%), Positives = 56/75 (74%)
Frame = +1

Query: 556 LSKLTMASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETR 735
+++ T ++ CS L + + + + + G ++AQLS +FY +SCP +F +VK +QSAI+ E R
Sbjct: 1 MAQPTSSARCS-LVVMVVVVLAVAGGSSAQLSPSFYSYSCPGVFDVAVKCGMQSAIANEKR 59

Query: 736 MGASLLRLFFHDCFV 780
+GAS++RLFFHDCFV
Sbjct: 60 IGASIVRLFFHDCFV 74

>gb|EAY79693.1| hypothetical protein OsI_34840 [Oryza sativa Indica Group]
Length = 329

Score = 199 bits (507), Expect = 1e-48
Identities = 93/124 (75%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA RQ CPR SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 206 QARCTNFRAHIYNETNIDSGFAMRRQSGCPRNSGSGDNNLAPLDLQTPTVFENNYKLV 265

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 266 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMIKMGDITPLTGSNGEIRKNC 325

Query: 2167 RRIN 2178
RRIN
Sbjct: 326 RRIN 329

Score = 166 bits (421), Expect = 1e-38
Identities = 94/169 (55%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDT+SFTGEK ANPN S RGFEVID IKSVE +CPGVVSCADILAIAA
Sbjct: 79 VQGCDASLLDDTASFTGEKTANPNNGSVRGFEVIDAIKSAVETICPGVVSCADILAIAA 138

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 139 RDSVAI-----LGGPSWDVKVG 155

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG+ I
Sbjct: 156 RRDSRTASLSGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGSHTI 204

Score = 70.1 bits (170), Expect = 1e-09
Identities = 31/61 (50%), Positives = 47/61 (77%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCF 777
+ + + + G + AQLS +FY SCP +F++VK +QSAI++E R+GAS++RFFHDCF
Sbjct: 19 VVVVVVLAVAGGSWAQLSPSFYSFSCPGVFNVAVKRGMQSAIAREKRIGASIVRFFHDCF 78

Query: 778 V 780
V
Sbjct: 79 V 79

>ref|NP_001065971.1| Os12g0112000 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69377.1| TPA: class III peroxidase 135 precursor [Oryza sativa (japonica
cultivar-group)]
gb|ABA96259.1| Peroxidase 52 precursor, putative, expressed [Oryza sativa (japonica
cultivar-group)]
dbj|BAF28990.1| Os12g0112000 [Oryza sativa Japonica Group]
gb|EAZ19424.1| hypothetical protein OsJ_34981 [Oryza sativa Japonica Group]
dbj|BAG91443.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 327

Score = 199 bits (507), Expect = 1e-48
Identities = 93/124 (75%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA RQ CPR SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 204 QARCTNFRAHIYNETNIDSGFAMRRQSGCPRNSGSGDNNLAPLDLQTPTVFENNYKLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 264 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMKMGDITPLTGSNGEIRKNC 323

Query: 2167 RRIN 2178
RRIN
Sbjct: 324 RRIN 327

Score = 164 bits (415), Expect = 5e-38
Identities = 93/169 (55%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT+SFTGEK ANPN S RGFEVID I KSAVE +CPGVVSCADILAI AA
Sbjct: 77 VQGCDA SLLDDTASFTGEKTANPNNGSVRGFEVIDAIKSAVETICPGVVSCADILAI AA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 137 RDSVAI-----LGGPSWDVKVG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A LS KD+VALSG+ I
Sbjct: 154 RRDSRTASLSGANNIPPTSGLANLTSLFAAQALSQKDMVALSGSHTI 202

Score = 72.8 bits (177), Expect = 2e-10
Identities = 32/63 (50%), Positives = 49/63 (77%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + + + + G + AQLS +FY +SCP +F++VK +QSAI++E R+GAS++RRLFHD
Sbjct: 15 LVVMVVVVLAVAGGSWAQLSPSFYSYSCPGVFNNAVKRGMQSAIAREKRIGASIVRRLFHD 74

Query: 772 CFV 780
CFV
Sbjct: 75 CFV 77

>ref|XP_002450132.1| hypothetical protein SORBIDRAFT_05g001000 [Sorghum bicolor]
gb|EES09120.1| hypothetical protein SORBIDRAFT_05g001000 [Sorghum bicolor]
Length = 331

Score = 199 bits (505), Expect = 2e-48
Identities = 93/124 (75%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA +YN+TNI+ FARTRQ CPRTSGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 208 QARCTNFRAHVYNDTNIDGTFARTRQSGCPRTSGSGDNNLAPLDLQTPTVFENNYKLV 267

Query: 1987 QKKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNNG+TD+ V+ Y ++ TF SDF MIKMGDI+PLTGSNG+IRKNC
Sbjct: 268 CKKGLLHSDQELFNNGATDAQVQSYISSQSTFFSDFVTGMKMGDITPLTGSNGQIRKNC 327

Query: 2167 RRIN 2178
R IN
Sbjct: 328 RMIN 331

Score = 160 bits (404), Expect = 1e-36
Identities = 92/169 (54%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LLDDT+SF GEK A PN S RGFVID +KSAVEKVCPGVVSCADILAIAA
Sbjct: 81 VQGCDASLLDDTASFQGEKMATPNNGSVRGFEVIDAVKSAVEKVCPGVVSCADILAIAA 140

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 141 RDSVVI-----LGGPSWDVKVG 157

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 158 RRDSTTASFSGANNNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 206

Score = 82.8 bits (203), Expect = 2e-13
Identities = 39/74 (52%), Positives = 55/74 (74%)
Frame = +1

Query: 559 SKLTMASFCRSLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRM 738
+K + + S L + L L ++ G+++AQLST+FY SCP ++ SVKS +QSAI+ E RM
Sbjct: 8 TKCSSCSASGLALLLLVMAAGTSSAQLSTSFYSSSCPGVYDSVKSAIQSAIATEQRM 67

Query: 739 GASLLRRLFHDCFV 780
GAS++RRLFHDCFV
Sbjct: 68 GASIVRRLFHDCFV 81

>gb|ACT35473.1| peroxidase 52 [Brassica rapa]
Length = 306

Score = 197 bits (500), Expect = 7e-48
Identities = 93/124 (75%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RCTNFR R+YNETNI AFA RQ+SCPR +GSGD NLAPLD+ + +FDN YFKNLV
Sbjct: 183 QSRCTNFRTRVYNETNINAAFATLRQRSCPRAAGSGDGNLAPLDVNSANTFDNSYFKNLV 242

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGSTDSIV GYS NP +FSSDF AAMIKMGDISPLTGS+GEIRK C
Sbjct: 243 AQRGLLHSDQELFNGGSTDSIVTGYSNPNSSSFSSDFTAAMIKMGDISPLTGSNGEIRKVC 302

Query: 2167 RRIN 2178
R N

Sbjct: 303 GRN 306

Score = 189 bits (481), Expect = 1e-45
Identities = 104/169 (61%), Positives = 115/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGE+NANPNRNSARGF VIDNIK+AVE CPGVVSCADILAI
Sbjct: 56 VNGCDGSILLDDTSSFTGEQANPNRNSARGFNVIDNIKTAVEAACPGVVSCADILAI 115

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 116 RDSVVL-----LGGPNWNVKVG 132

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IPAPTS+L+QLIS FSA+GLST+D+VALSG I
Sbjct: 133 RRDARTASQAAANNIPAPTSLSQLISSFSAVGLSTRDMVALSGAHTI 181

Score = 75.9 bits (185), Expect = 3e-11
Identities = 34/48 (70%), Positives = 41/48 (85%)
Frame = +1

Query: 640 AQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
AQL+TNFY SCPNL S+V+STV+SA+ + R GAS+LRLFFHDCFVN
Sbjct: 10 AQLTTFYSTSCPNNLSTVRSTVKS AVDSQPRTGASILRLLFFHDCFVN 57

>ref|XP_002441703.1| hypothetical protein SORBIDRAFT_08g000990 [Sorghum bicolor]
gb|EES15541.1| hypothetical protein SORBIDRAFT_08g000990 [Sorghum bicolor]
Length = 328

Score = 196 bits (498), Expect = 1e-47
Identities = 92/123 (74%), Positives = 105/123 (85%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
ARCTNFRA IYN+TNI+ +FAR+RQ CPRTSGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 206 ARCTNFRAHIYNDTNIDGSFARSRSQVCPRTSGSGDNNLAPLDLQTPVFNYYKNLVY 265

Query: 1990 KKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KKG+LHSDQ+LFNNGSTD+ V+ Y ++ F +DF MIKMGDI PLTGSNGEIRKNCR
Sbjct: 266 KKGILHSDQELFNNGSTDAQVQSYVSSQSAFFADFVTGMIKMGDIPLTGSNGEIRKNCR 325

Query: 2170 RIN 2178
RIN

Sbjct: 326 RIN 328

Score = 164 bits (415), Expect = 5e-38
Identities = 95/169 (56%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT SF GEK ANPN SARGFEVID IKS AV+KVC PGVVSCADILAI AA
Sbjct: 78 VQGCDASLLDDTPSFQGEKMANPNNGSARGFEVIDAIKS AVDKVC PGVVSCADILAI AA 137

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 138 RDSVVI-----LGGPSWDVKVG 154

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 155 RRDSRTASFSGANNIPPTSGLVNLTSLFAAQGLSQKDMVALSGAHTI 203

Score = 77.4 bits (189), Expect = 9e-12
Identities = 36/61 (59%), Positives = 50/61 (81%), Gaps = 2/61 (3%)
Frame = +1

Query: 604 LALFVLI--WGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR LFFHDCF 777
L L VL+ G+++AQL T+FY HSCP ++ +V+S +Q+AI+++E RMGAS+LRLFFHDCF
Sbjct: 18 LLLLVL LAGTGTSSAQLCTSFYSHSCPGVYDAVRSVLQAAIAREQRMGASILR LFFHDCF 77

Query: 778 V 780
V
Sbjct: 78 V 78

>ref|XP_002450133.1| hypothetical protein SORBIDRAFT_05g001010 [Sorghum bicolor]
gb|EES09121.1| hypothetical protein SORBIDRAFT_05g001010 [Sorghum bicolor]
Length = 328

Score = 196 bits (498), Expect = 1e-47
Identities = 89/124 (71%), Positives = 107/124 (86%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCTNFRA IYN+T+I +AFA+TRQ CP TSG+GDNNLAPLDLQTPT F+N Y+KNL+
Sbjct: 205 QARCTNFRAHIYNDTDINSAFAKTRQSGCPSTSGAGDNNLAPLDLQTPTVFENNYK NLL 264

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y + TF +DF MIKMGDI+PLTGSNG+IRKNC

Sbjct: 265 SKKGLLHSDQELFNGGATDTLVQSYVGSQSTFFTFDVTGMIKMGDITPLTGSNGQIRKNC 324

Query: 2167 RRIN 2178
RR+N

Sbjct: 325 RRVN 328

Score = 159 bits (401), Expect = 2e-36
Identities = 91/169 (53%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLDDT++F GEK A PN S RGFEVID +KSAVEKVCPGVVSCADILAI

Sbjct: 78 VQGCDASLLDDTATFQGEKMATPNNGSVRGFEVIDAVKSAVEKVCPGVVSCADILAI 137

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G

Sbjct: 138 RDSVVI-----LGGPSWDVKVG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I

Sbjct: 155 RRDSTTASFSGANNNIPPTSGLANLTSFAAQGLSQKDMVALSGAHTI 203

Score = 77.4 bits (189), Expect = 9e-12
Identities = 38/70 (54%), Positives = 52/70 (74%), Gaps = 1/70 (1%)
Frame = +1

Query: 574 ASFC SRLTICLALFVL-IWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
AS S + L L L + G+++AQLST FY +SCP ++ +VKS ++SAI+ E RMGAS+

Sbjct: 9 ASSSSAAALLLLLLALAVAGTSSAQLSTGFYSYSCPGVYGAVKSVMSAIANEKRMGASI 68

Query: 751 LRLFFHDCFV 780

+RLFFHDCFV

Sbjct: 69 VRLFFHDCFV 78

>gb|ABV24960.2| putative secretory peroxidase [Catharanthus roseus]
Length = 330

Score = 196 bits (498), Expect = 1e-47
Identities = 92/124 (74%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FRARIYNE+NIET+FARTRQ +CP +G+GDN+LAPLDLQ+P FD Y+KNL+

Sbjct: 207 QARCTVFRARIYNESNIETSFARTRQGNCLPTGNGDNLAPLDLQSPNGFDINYYKNLI 266

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+L+NGGST+S+V YS + F SDFAAAMIKMGDISPLTGSNGE+RKNC
Sbjct: 267 NKKGLLHSDQELYNGGSTNSLVEAYSKDTKAFYSDFAAAMIKMGDISPLTGSNGEVRKNC 326

Query: 2167 RRIN 2178
RR+N
Sbjct: 327 RRVN 330

Score = 164 bits (414), Expect = 7e-38
Identities = 92/169 (54%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCDGSILLDDTSS GEK A PN S RGF+V+DNIS VEKVCPGVVSCADILAI
Sbjct: 80 VQGCDGSILLDDTSSLRGEKTAGPNVGSVRGFDVVDNIKSDVEKVCPGVVSCADILAI 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W VK+G
Sbjct: 140 RDSV-----VALGGPSWKVKVG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS S AN+ IP PTSNL LIS F A+GLS KD+V LSG+ I
Sbjct: 157 RRDSKTASLSGANSRIPPPTSNLRLISSFQAVGLSAKDMVVLSGSHTI 205

Score = 72.4 bits (176), Expect = 3e-10
Identities = 37/77 (48%), Positives = 52/77 (67%), Gaps = 3/77 (3%)
Frame = +1

Query: 559 SKLTMASFCSRLTICLALFVL---IWGSANAQLSTNFYYHSCP NFLFSSVKSTVQSAISKE 729
S + +SF S I + + VL + S + QLS+ FY +CP +++++V+ V+SA+SKE
Sbjct: 4 SSSSSSSFSNFGIVIMVIVLSIIMRSCSGQLSSEFYSKTCPQVYNTVRKGVESAVSKE 63

Query: 730 TRMGASLLRLFFHDCFV 780
RMGASLLRL FHDCFV
Sbjct: 64 KRMGASLLRLHFHDCFV 80

>sp|P00434.3|PERP7_BRARA RecName: Full=Peroxidase P7; AltName: Full=TP7
Length = 296

Score = 196 bits (498), Expect = 1e-47
Identities = 93/124 (75%), Positives = 107/124 (86%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRSTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC NFRAR+YNETNI AFA RQ+SCPR +GSGD NLAPLD+ + TSFDN YFKNL+
Sbjct: 173 QSRCVNFRRARVYNETNINAAAFATLRQSRCPRAAGSGDANLAPLDINSATSFDNSYFKNLM 232

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ LFNGGSTDSIVRGYS +P +F+SDFAAAMIKMGDISPLTGS+GEIRK C
Sbjct: 233 AQRGLLHSDQVLFNGGSTDSIVRGYSNSPSSFNDFAAAMIKMGDISPLTGSSGEIRKVC 292

Query: 2167 RRIN 2178
+ N
Sbjct: 293 GKTN 296

Score = 179 bits (455), Expect = 1e-42
Identities = 99/169 (58%), Positives = 114/169 (67%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKCPGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGE+NA PNRNSARGF VI++IKSAVEK CPGVVSCADILAIAA
Sbjct: 46 VNGCDGSILLDDTSSFTGEQNAGPNRNSARGFTVINDIKSAVEKACPGVVSCADILAIAA 105

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 106 RDSV-----VQLGGPNWNVKVG 122

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDA+TASQ+AAAN+ IPAP+ +L+QLIS FSA+GLST+D+VALSG I
Sbjct: 123 RRDAKTASQAAANSNIPAPMSLSQLISSFSAVGLSTRDMVALSGAHTI 171

Score = 76.6 bits (187), Expect = 1e-11
Identities = 35/47 (74%), Positives = 41/47 (87%)
Frame = +1

Query: 643 QLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCFVN 783
QL+TNFY SCPNL S+VKS V+SA+S + RMGAS+LRLFFHDCFVN
Sbjct: 1 QLSTNFYSTSCPNNLSTVKSGVKS AVSSQPRMGASILRFFHDCFVN 47

>gb|AAD37423.1|AF149281_1 peroxidase 6 [Phaseolus vulgaris]
Length = 128

Score = 195 bits (495), Expect = 3e-47
Identities = 106/165 (64%), Positives = 116/165 (70%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKCPGVVSCADILAIAA 1330

+ GCDGSILLDDTSSFTGEKNA PN+NSARGF+VID IKSAVE+VCPGVVSCADILAIAA
Sbjct: 7 VNGCDGSILLDDTSSFTGEKNARPNKNSARGFDVIDKIKSAVEEVCPGVVSCADILAIAA 66

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGP+WNVKLG

Sbjct: 67 RDSVHIL-----GGPSWNVKLG 83

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+RTASQSAANNGIP PTSN+NQLISRF++LGLS KDLVALSG

Sbjct: 84 RRDSRTASQSAANNGIPPTSNVNLISRFSNLGLSPKDLVALSG 128

>ref|XP_002520835.1| Peroxidase 52 precursor, putative [Ricinus communis]
gb|EEF41544.1| Peroxidase 52 precursor, putative [Ricinus communis]
Length = 318

Score = 194 bits (494), Expect = 4e-47
Identities = 109/169 (64%), Positives = 115/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKCPGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGE+ A PNRNS RGFEVID+IKSAVEK CPGVVSCADILAIAA

Sbjct: 70 VNGCDGSILLDDTSSFTGEQTAVPNRNSVRGFEVIDSIKSAVEKACPGVVSCADILAIAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I+ GGP+WNVKLG

Sbjct: 130 RDSTAIL-----GGPSWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTAS SAANNGIPAPTSNLNQLISRFSALGLST+DLVALSG I

Sbjct: 147 RRDARTASLSAANNGIPAPTSNLNQLISRFSALGLSTRDLVALSGAHTI 195

Score = 193 bits (490), Expect = 1e-46
Identities = 93/124 (75%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR RIYN+TNI+++FA+TR+ +CP T G DNNLAPLDLQTPTSFDN YFKNL+

Sbjct: 197 QARCTNFRTRIYNDTIDSSFAQTRRSNCPSTGG--DNNLAPLDLQTPTSFDNYYFKNLL 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFN GSTDSIVR YS TF SDF A MIKMGDISPLTGS GEIRKNC

Sbjct: 255 VQKGLLHSDQELFNGGSTDSIVRTYSNGQSTFFSDFVAGMIKMGDISPLTGSQGEIRKNC 314

Query: 2167 RRIN 2178
++N

Sbjct: 315 GKVN 318

Score = 88.2 bits (217), Expect = 5e-15
Identities = 43/63 (68%), Positives = 50/63 (79%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDC 774
TI +L+ +NAQLSTNFY SCPNLFS+VK VQSAI++E RMGASL+RLFFHDC
Sbjct: 9 TIVTLSLLLVSISNAQLSTNFYSKSCPRLFSTVKPVVQSAINQEKRMGASLVRLFFHDC 68

Query: 775 FVN 783
FVN
Sbjct: 69 FVN 71

>ref|XP_002319968.1| predicted protein [Populus trichocarpa]
gb|EEE95891.1| predicted protein [Populus trichocarpa]
Length = 325

Score = 193 bits (491), Expect = 8e-47
Identities = 92/124 (74%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNETNI+++FA TRQ++CP GDN LAPLD+QTPTSFDN Y+KNL+
Sbjct: 202 QARCTSFARIYNETNIDSSFATTRQKNCPPGPKGDNKLAPLDVQTPTSFDNKYYKNLI 261

Query: 1987 QKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ LFNGGSTDS+VR YS+NP TFSSDF AMIKMGDI PLTGS GEIRK C
Sbjct: 262 SQKGLLHSDQVLFNGGSTDSLVRTYSSNPKTFSSDFVTAMIKMGDIDPLTGSQGEIRKIC 321

Query: 2167 RRIN 2178
+ N
Sbjct: 322 SKRN 325

Score = 160 bits (406), Expect = 6e-37
Identities = 91/170 (53%), Positives = 107/170 (62%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
++GCDGSILL+DTSSFTGE+ A PN NS RGF V+ IKS VEKVCPG+VSCADI+AIAA
Sbjct: 74 VKGCDGSILLEDTSSFTGEQTAGPNNNSVRGFNVVAKIKSQVEKVCPGIVSCADIVAIAA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I LGGP WNVKLG
Sbjct: 134 RDSTVI-----LGGPFWNVKLG 150

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS SAAN+G IP PTS L+ LI+RF++ GLS KD+VALSG+ I
Sbjct: 151 RRDSKTASLSAANSVIPPPTSTLSNLINRFNSKGLSVKDMVALSGSHTI 200

Score = 86.7 bits (213), Expect = 1e-14
Identities = 44/70 (62%), Positives = 55/70 (78%), Gaps = 1/70 (1%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGS-ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
+SF S + I F++I+ S ++AQLSTNFY SCP +F +VKS VQSA+SKE RMGASL
Sbjct: 5 SSFSSYMAIFTLAFLVIFTSHSSAQLSTNFYSKCPKVFVAVKSVVQSAVSKERRMGASL 64

Query: 751 LRLFFHDCFV 780
+RLFFHDCFV
Sbjct: 65 VRLFFHDCFV 74

>ref|NP_001151940.1| peroxidase 52 [Zea mays]
gb|ACG45093.1| peroxidase 52 precursor [Zea mays]
Length = 334

Score = 191 bits (486), Expect = 3e-46
Identities = 89/126 (70%), Positives = 106/126 (84%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSG--SGDNNLAPLDLQTPTSFDNYYFKN 1980
QARCTNFRA +YN+TNI+ +FARTRQ CPR+S SGDNNLAPLDLQTPT FDN Y+KN
Sbjct: 209 QARCTNFRAHVYNDTNIDGSFARTRQSGCPRSSSGSSGDNNLAPLDLQTP TVFDNYYKN 268

Query: 1981 LVQKKLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
LV KKLLHSDQ+LFNGG+TD++V+ Y++ F SDF M+KMGDI+PLTGS G+IRK
Sbjct: 269 LVCKKLLHSDQELFNGGATDALVQSYASGQSEFFSDFVTGMVKMGDITPLTGS GGQIRK 328

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 329 NCRRVN 334

Score = 162 bits (409), Expect = 3e-37
Identities = 93/169 (55%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LLDDT SF GEK ANPN S RGFEVID +KSAVEKVC PGVVSCADILAI
Sbjct: 82 VQGCDASLLDDTSPFQGEKMANPNNGSVRGFEVIDAVKSAVEKVC PGVVSCADILAI 141

Query: 1331 RDSVQIVSGGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGPTW+VK+G
Sbjct: 142 RDSVVIL-----GGPTWDVKVG 158

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 159 RRDSTTASFGANNIPPTSGLANLTSFAAQGLSQKDMVALSGAHTI 207

Score = 79.0 bits (193), Expect = 3e-12
Identities = 36/59 (61%), Positives = 47/59 (79%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
LAL + G+++AQLST FY SCP ++ +VKS VQSA++ E RMGAS++RLFFHDCFV
Sbjct: 24 LALLMAAAGTSSAQLSTGFYSSSCPGVYDAVKSVVQSAVASEQRMGASIVRLFFHDCFV 82

>ref|XP_002489046.1| hypothetical protein SORBIDRAFT_0246s002010 [Sorghum bicolor]
gb|EES20431.1| hypothetical protein SORBIDRAFT_0246s002010 [Sorghum bicolor]
Length = 320

Score = 190 bits (483), Expect = 7e-46
Identities = 88/124 (70%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR IYN+TN++ AFARTRQ CP TSG+GDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 197 QARCTNFRDHIYNDTNVDGAFARTRQSGCPSTSGTGDNNLAPLDLQTPTVFENDYYKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFNGG+TD++V+ Y ++ F +DF MIKMGDI+PLTGS GEIRKNC
Sbjct: 257 SNMGLLHSDQELFNGGATDALVQSYVSSQSAFFADFVTGMKMGDITPLTGSAGEIRKNC 316

Query: 2167 RRIN 2178
RRIN
Sbjct: 317 RRIN 320

Score = 155 bits (392), Expect = 2e-35
Identities = 90/169 (53%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKPCPGVVSCADILAIAA 1330
+QGCD S+LLDDT++F GEK A PN S RGFEVID KSAVE VCPGVVSCADILAIAA
Sbjct: 70 VQGCDASLLDDTATFQGEKMATPNNGSVRGFEVIDAAKSAVENVCPGVVSCADILAIAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 130 RDSVVI-----LGGPSWDVKVG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 147 RRDSTTASFGANNIPPTSGLANLTSFAAQGLSQKDMVALSGAHTI 195

Score = 73.9 bits (180), Expect = 1e-10
Identities = 38/70 (54%), Positives = 47/70 (67%)
Frame = +1

Query: 571 MASFCRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ L + L G++ AQLST FY SCP L+S+VK VQSAI E R+GAS+
Sbjct: 1 MAAQSIALWLLTTTLMALQAGTSWAQLSTGFYSSSCPGLYSAVKPVVQSAIDSEKRVGASI 60

Query: 751 LRLFFHDCFV 780
+RLFFHDCFV
Sbjct: 61 VRLFFHDCFV 70

>ref|XP_002441702.1| hypothetical protein SORBIDRAFT_08g000980 [Sorghum bicolor]
gb|EES15540.1| hypothetical protein SORBIDRAFT_08g000980 [Sorghum bicolor]
Length = 131

Score = 190 bits (483), Expect = 7e-46
Identities = 88/124 (70%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR IYN+TN++ AFARTRQ CP TSG+GDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 8 QARCTNFRDHIYNDTNVDGAFARTRQSGCPSTSGTGDNNLAPLDLQTPTVFENDYYKNLV 67

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFNGG+TD++V+ Y ++ F +DF MIKMGDI+PLTGS GEIRKNC
Sbjct: 68 SNMGLLHSDQELFNGGATDALVQSYVSSQSAFFADFVTGMIKMGDITPLTGSAGEIRKNC 127

Query: 2167 RRIN 2178
RRIN
Sbjct: 128 RRIN 131

>gb|AAA96137.1| peroxidase [Stylosanthes humilis]
Length = 136

Score = 190 bits (483), Expect = 7e-46

Identities = 87/124 (70%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FR IYN+T+I+ +FA+ RQ++CPR SG+GD+NLAPLDLQTPT F+N Y+KNL+

Sbjct: 13 QARCTSRFGHIYNDTIDPSFAKLKQKNCPRQSGTGDSNLAPLDLQTPHFENNYKLI 72

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS+V+ YS N F+SDF MIKMGD+ PLTGS GEIRKNC

Sbjct: 73 NKKGLLHSDQELFNGGSTDSLVTYKSNKAFTSDFVPGMIKMGDLLPLTGSKEIRKNC 132

Query: 2167 RRIN 2178

RR+N

Sbjct: 133 RRMN 136

>gb|AAL93151.1|AF485265_1 class III peroxidase [Gossypium hirsutum]
Length = 320

Score = 189 bits (480), Expect = 2e-45
Identities = 91/124 (73%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIYN+T I+T+FA+TR+ SCPRT GSGDNNLAPLDL TP SFD+ YF+NL+

Sbjct: 197 KARCLVFRNRIYNDTIIDTSFAKTRRSSCPRTSGSGDNNLAPLDLATPNSFDSKYFENLL 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS+V+ YS+N F SDF AAMIKMGDI PLTGSNGEIRKNC

Sbjct: 257 NKKGLLHSDQELFNGGSTDSLVTYSSNVKKFYSDFAAMIKMGDIKPLTGSNGEIRKNC 316

Query: 2167 RRIN 2178

+ N

Sbjct: 317 GKPN 320

Score = 160 bits (404), Expect = 1e-36
Identities = 92/170 (54%), Positives = 106/170 (62%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGE+ A PN S RGFEV+D IK+ VEKVCPCGVVSCADILAIAA

Sbjct: 69 VNGCDGSVLLDDTSSFTGEQTATPNNGSLRGFEVVDEIKAKVEKVCPCGVVSCADILAIAA 128

Query: 1331 RDSVQIVSGQTTNKNLTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W+VKLG

Sbjct: 129 RDSVVI-----LGGPDWDVKLG 145

Query: 1511 RRDARTASQSAANNGI-PAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS S AN+G+ P ++NL+QLIS F A GLSTKD+VALSG I
Sbjct: 146 RRDSKTASFSDANSGVLPPLGSANLSQLISLFAQQLSTKDMVALSGAHTI 195

Score = 76.6 bits (187), Expect = 1e-11
Identities = 34/60 (56%), Positives = 48/60 (80%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCPFLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
+ +++++ + AQLSTNFY SCP + S+V+ V++A+SKE R+GASLLRLLFFHDCFVN
Sbjct: 11 VGVWMMMGSGSYAQLSTNFYSKSCPVLSTVELVVETAVSKEQRLGASLLRLLFFHDCFVN 70

>emb|CAD67478.1| peroxidase [Asparagus officinalis]
Length = 301

Score = 188 bits (478), Expect = 3e-45
Identities = 87/124 (70%), Positives = 104/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT+FR IYN+ +I+ +FA RQ+ CPR SGSGD NLAPLDLQTPT+FDN Y+KNL+
Sbjct: 178 QARCTSFRGHIYNDADIDASFASLRQKICPRKSGSGDTNLAPLDLQTPTAFDNNYYKNLI 237

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFN G+TDS+V+ YS + G+F+SDF AMIKMGDISPLTGS GEIRK C
Sbjct: 238 NKKGLLHSDQELFNGGATDSLVSYSNSEGSFNSDFVKAMIKMGDISPLTGSKEIRKIC 297

Query: 2167 RRIN 2178
+IN
Sbjct: 298 SKIN 301

Score = 161 bits (407), Expect = 5e-37
Identities = 90/169 (53%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILL DT++F GE++A PN S RGF+VID IK+AVE CPGVVSCADILA+AA
Sbjct: 51 VNGCDGSILLADTANFRGEQHAGPNNGSVRGFKVIDKIKTAVENACPGVVSCADILAVAA 110

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W VKLG
Sbjct: 111 RDSVVI-----LGGPDWVKVKG 127

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDARTAS + ANN IP PTS+L+ LIS+F+A GLSTKD+VALSG I
Sbjct: 128 RRDARTASATLANNIPPTSSLSNLISKFAAQLSTKDMVALSGAHTI 176

Score = 82.4 bits (202), Expect = 3e-13
Identities = 37/52 (71%), Positives = 45/52 (86%)
Frame = +1

Query: 628 GSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783
GS++A LSTNFY SCP +FS++K +QSAI+KE RMGAS+LRLFHDCFVN
Sbjct: 1 GSSSAHLSTNFYSSSCPVKVFSTIKPVLQSAIAKEKRMGASILRRLFHDCFVN 52

>gb|AAR31108.1| peroxidase precursor [Quercus suber]
Length = 330

Score = 188 bits (477), Expect = 3e-45
Identities = 88/125 (70%), Positives = 107/125 (85%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSG-SGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT FR RIY + NI+++FA+TRQ CP+T+G GDN +APLDLQTPT+FDNYY+KNL
Sbjct: 205 QARCTVFRDRIYKDKNIDSSFAKTRQNKCPKTTGLPGDNKIAPLDLQTPTAFDNYYYKNL 264

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+++KGLL SDQQLFNGGSTDS+V+ YS + TF SDF AMIKMGDI PLTGS+GEIRKN
Sbjct: 265 IKEKGLLRSDQQLFNGGSTDSLVKKYSQDTKTFYSDFVNAMIKMGDIQPLTGSSGEIRKN 324

Query: 2164 CRRIN 2178
CR++N
Sbjct: 325 CRKVN 329

Score = 162 bits (409), Expect = 3e-37
Identities = 93/166 (56%), Positives = 103/166 (62%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDT +FTGEK A PN S R FEV+D IKS VEK CPGVVSCADILAIAA
Sbjct: 77 VNGCDGSILLDDTPTFTGEKTARPNNGSIRAFEVVDEIKSKVEKECPGVVSCADILAIAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I LGGP W+VKLG
Sbjct: 137 RDSVKI-----LGGPKWDVKLG 153

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD++TAS SAAN+G IP PTS L LI+RF A GLSTKD+VALSG

Sbjct: 154 RRDSKTASFAANSVIPPPTSTLGNLINRFKAKGLSTKDMVALSG 199

Score = 84.3 bits (207), Expect = 7e-14
Identities = 39/64 (60%), Positives = 51/64 (79%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ V+ G+++A+LSTNFY SCP +FS+V+S V SA+SK+ R GASLLRL FHD
Sbjct: 15 LIVSLAVLVIFTGNSSAKLSTNFYSKSCPVKFSTVQSVVHSAVSKQPRQGASLLRLHFHD 74

Query: 772 CFVN 783
CFVN
Sbjct: 75 CFVN 78

>gb|AAR31106.1| peroxidase precursor [Quercus suber]
Length = 330

Score = 187 bits (474), Expect = 8e-45
Identities = 87/125 (69%), Positives = 108/125 (86%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSG-SGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT FR RIY + NI+++FA+TRQ +CP+T+G GDN +APLDLQTPT+FDNYY+KNL
Sbjct: 205 QARCTVFRDRIYKDKNIDSSFAKTRQNTCPKTTGLPGDNKIAPLDLQTPTAFDNYYKKNL 264

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKN 2163
+++KGLL SDQQLFNGGSTDS+V+ YS + +F SDF AMIKMGDI PLTGS+GEIRKN
Sbjct: 265 IKQKGLLRSDQQLFNGGSTDSLVKKYSQDTKSFYSDFVNAMIKMGDIQPLTGSSGEIRKN 324

Query: 2164 CRRIN 2178
CR++N
Sbjct: 325 CRKVN 329

Score = 162 bits (410), Expect = 2e-37
Identities = 92/170 (54%), Positives = 105/170 (61%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDT +FTGEK A PN+ S RGFE +D IKS VEK CPGVVSCADILAIAA
Sbjct: 77 VNGCDGSVLLDDTPTFTGEKTAGPNKGSIRGFVFEVDEIKSKVEKECPGVVSCADILAIAA 136

Query: 1331 RDSVQIVSGQTTNKNLTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I LGGP W+VKLG
Sbjct: 137 RDSVKI-----LGGPKWDVKLG 153

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS AAN+G IP PTS L+ LI+RF A GLSTKD+VALSG I
Sbjct: 154 RRDSKTASLKAANSVIPPPTSTLSNLINRFKAKGLSTKDMVALSGAHTI 203

Score = 87.8 bits (216), Expect = 6e-15
Identities = 41/64 (64%), Positives = 52/64 (81%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ V+ G+++A+LSTNFY SCP +FS+V+S V SAISK+ R GASLLRL FHD
Sbjct: 15 LIVSLAVLVIFSGNSSAKLSTNFYKSCPVKVSTVQSVVHSAISKQPRQGASLLRRLFHD 74

Query: 772 CFVN 783
CFVN
Sbjct: 75 CFVN 78

>ref|NP_001131000.1| hypothetical protein LOC100192105 [Zea mays]
gb|ACF79421.1| unknown [Zea mays]
gb|ACL53914.1| unknown [Zea mays]
Length = 320

Score = 186 bits (473), Expect = 1e-44
Identities = 89/126 (70%), Positives = 107/126 (84%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG-DNNLAPLDLQTPTSFDNYYFKNL 1983
QARCTNFRA IYN+T+I+ AFARTRQ CP TSG+G DNNLAPLDLQTPT F+N Y++NL
Sbjct: 195 QARCTNFRAHIYNDTDIDAAFARTRQSGCPSTSGAGGDNNLAPLDLQTPTVFENNYRNL 254

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS-NGEIRK 2160
+ KKGLLHSDQ+LFNGG+TD++V+ Y + F +DF A MIKMGDI+PLTGS NG+IRK
Sbjct: 255 LAKKGLLHSDQELFNGGATDALVQSYVGSQSAFFADFVAGMIKMGDITPLTGSNNGQIRK 314

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 315 NCRRVN 320

Score = 160 bits (406), Expect = 6e-37
Identities = 92/169 (54%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKCPGVVSCADILAIAA 1330
+QGCD S+LLDDT SF GEK ANPN S RGFEVID +KSAVEK+CPGVVSCADILAIAA

Sbjct: 68 VQGCASLLDDTPSFQGEKMANPNNGSVRGFEVIDAVKSAVEKLCPGVVSCADILAIAA 127

Query: 1331 RDSVQIVSGGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGPTWNVKLG 1510
RDSV I+ GGPTW+VK+G

Sbjct: 128 RDSVVIL-----GGPTWDVKVG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I

Sbjct: 145 RRDSTTASFGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 193

Score = 81.6 bits (200), Expect = 5e-13
Identities = 37/65 (56%), Positives = 51/65 (78%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLF 765
+R L L + + G+++AQLST FY +SCP ++ +VKS +QSAI++E RMGAS+LRLFF

Sbjct: 4 TRAAATLLLLLALAGTSSAQLSTGFYSYSCPGVYGAVKSVMSAIAREKRMGASILRRLF 63

Query: 766 HDCFV 780

HDCFV

Sbjct: 64 HDCFV 68

>gb|AAD43561.1|AF155124_1 bacterial-induced peroxidase precursor [Gossypium hirsutum]
Length = 316

Score = 185 bits (470), Expect = 2e-44
Identities = 86/123 (69%), Positives = 104/123 (84%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
ARCT FR RIYN+TNI+ FA TR+ +CP + GDNNLAPLD+QTPT FDN YF+NLV

Sbjct: 196 ARCTTFRGRIYNDTNIDANFAATRRANCP--ASGGDNNLAPLDIQTPTFRFDNDYFRNLVA 253

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++VR YS NP TFS+DFAAAM+KMG+ISPLTG+ GEIR+NCR

Sbjct: 254 RRGLLHSDQELFNGGSQDALVRTYSNNPATFSADFAAAMVKMGNISPLTGTQGEIRRNCR 313

Query: 2170 RIN 2178

+N

Sbjct: 314 VVN 316

Score = 159 bits (403), Expect = 1e-36
Identities = 90/165 (54%), Positives = 101/165 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDT++FTGEKNA PNRNSARGFEVID IK+ VE C VSCADILA+AA
Sbjct: 68 VNGCDGSILLDDTATFTGEKNAVPNRNSARGFEVIDTIKTNVEAAC SATVSCADILALAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++ GGPTW V LG
Sbjct: 128 RDGVALL-----GGPTWQVPLG 144

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAANN IP+P +NL L S F+A GLST+DL ALSG
Sbjct: 145 RRDARTASQSAANNQIPSPFANLATLTSSFAAKGLSTRDLTALSG 189

Score = 76.6 bits (187), Expect = 1e-11
Identities = 35/62 (56%), Positives = 48/62 (77%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR LFFHDCF 777
+ L + +L +ANAQLS NFY SCPNL + V++ + A+++ETR+GAS+LRLFFHDCF
Sbjct: 8 VTLIVMLSCHAANAQLSPNFYASSCPNLQTIVRNAMSRVRETRIGASILR LFFHDCF 67

Query: 778 VN 783
VN
Sbjct: 68 VN 69

>gb|ACN33662.1| unknown [Zea mays]
Length = 320

Score = 184 bits (468), Expect = 4e-44
Identities = 88/126 (69%), Positives = 107/126 (84%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG-DNNLAPLDLQTPTSFDNYYFKNL 1983
QARCTNFRA IYN+T+I+ AFARTRQ CP TSG+G D+NLAPLDLQTPT F+N Y++NL
Sbjct: 195 QARCTNFRAHIYNDTDIDAAFARTRQSGCPSTSGAGGDSNLAPLDLQTPTVFENNYRNL 254

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS-NGEIRK 2160
+ KKGLLHSDQ+LFNGG+TD++V+ Y + F +DF A MIKMGDI+PLTGS NG+IRK
Sbjct: 255 LAKKGLLHSDQELFNGGATDALVQSYVGSQSAFFADFVAGMIKMGDITPLTGSNNGQIRK 314

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 315 NCRRVN 320

Score = 160 bits (406), Expect = 6e-37
Identities = 92/169 (54%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLDDT SF GEK ANPN S RGFVID +KSAVEK+CPGVVSCADILAI

Sbjct: 68 VQGCDASLLDDTPSFQGEKMANPNNGSVRGFEVIDAVKSAVEKLCPGVVSCADILAI 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGPTW+VK+G

Sbjct: 128 RDSVVIL-----GGPTWDVKVG 144

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I

Sbjct: 145 RRDSTTASFSGANNIPPTSGLANLTSFAAQGLSQKDMVALSGAHTI 193

Score = 81.6 bits (200), Expect = 5e-13
Identities = 37/65 (56%), Positives = 51/65 (78%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLF 765
+R L L + + G+++AQLST FY +SCP ++ +VKS +QSAI++E RMGAS+LRLFF

Sbjct: 4 TRAAATLLLLLALAGTSSAQLSTGFYSYSCPGVYGAVKSVMQSAIAREKRMGASILRRLF 63

Query: 766 HDCFV 780
HDCFV

Sbjct: 64 HDCFV 68

>emb|CBI25393.1| unnamed protein product [Vitis vinifera]
Length = 179

Score = 184 bits (466), Expect = 7e-44
Identities = 100/169 (59%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDTSSF GEKNA PN NS RGF+V+D+IKS VE CPGVVSCAD+LAI

Sbjct: 15 VNGCDGSVLLDDTSSFIGEKNAAPNANSVRGFVDDIKSKVETACPGVVSCADVLAI 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGP+WNVKLG

Sbjct: 75 RDSVVIL-----GGPSWNVKLG 91

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IP PTSNLNQLISRF ALGLST+DLVAL+G+ I

Sbjct: 92 RRDARTASQAANNSIPPPTSNLNLISRFAALGLSTRDLVALAGSHTI 140

Score = 57.8 bits (138), Expect = 7e-06
Identities = 24/31 (77%), Positives = 29/31 (93%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR 1899
QARCT+FRARIYNETNI+ +FA+TRQ +CPR
Sbjct: 142 QARCTSFARIYNETNIDNSFAKTRQSNCP 172

Score = 38.1 bits (87), Expect = 5.8
Identities = 16/16 (100%), Positives = 16/16 (100%)
Frame = +1

Query: 736 MGASLLRLLFFHDCFVN 783
MGASLLRLLFFHDCFVN
Sbjct: 1 MGASLLRLLFFHDCFVN 16

>gb|ACU23223.1| unknown [Glycine max]
Length = 328

Score = 182 bits (462), Expect = 2e-43
Identities = 86/124 (69%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR RIYN+TNI+ FA RQ+ CPRT+G+GDNNLA LD +TP FDN YFKNL+
Sbjct: 205 KARCTSFDRRIYNTNIDRTFALARQRRCPRTNGTGDNNLANLDFRTPNHFDNYYFKNLL 264

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GLL+SDQ LFNNGGSTDS+VR YS N F +DF AMI+MGDI PLTGS GEIRKNC
Sbjct: 265 IKRGLLNSDQVLFNGGSTDSLVRTYSQNNKAFDTDFVKAMIRMGDIKPLTGSQGEIRKNC 324

Query: 2167 RRIN 2178
RR+N
Sbjct: 325 RRVN 328

Score = 152 bits (383), Expect = 3e-34
Identities = 88/166 (53%), Positives = 100/166 (60%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCDGSILLDDT +F GEK A N NS RGFEVID IKS VEK+CPGVVSCADIL IA+

Sbjct: 77 VQGCDSILLDDTPTFQGEKTAANNNSVRGFEVIDAIKSEVEKICPGVSCADILDIAS 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W V+LG

Sbjct: 137 RDSVVL-----LGGPFWKVRLG 153

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+RTA+ +AAN G IP PTSNL LI+RF GLS +D+VALSG

Sbjct: 154 RRDSRTANFTAANTGVIPPTSNTLNLTRFRDQGLSARDMVALSG 199

Score = 87.0 bits (214), Expect = 1e-14
Identities = 39/77 (50%), Positives = 59/77 (76%)
Frame = +1

Query: 550 VCLSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKE 729
+ LS + +SF S + LA+ +L+ G+++A LS NFY +CPN+F++VKS V+SA+ +E

Sbjct: 1 MALSPIRSSSFSSSAIVALAVLLLLTGTSSANLSKNFYSKTCPNVFNTVKS VVKS AVVRE 60

Query: 730 TRMGASLLRLFFHDCFV 780
R+GAS++RLFFHDCFV

Sbjct: 61 PRIGASIVRLFFHDCFV 77

>emb|CAA71491.1| peroxidase [Spinacia oleracea]
Length = 323

Score = 182 bits (462), Expect = 2e-43
Identities = 84/123 (68%), Positives = 102/123 (82%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCTNFR IYN++NI+ FA TR+ SCPR +G+GD NLAP+D+QTP +FDN Y+KNLV

Sbjct: 201 ARCTNFRDHIYNDNSNIDPNAATRKAACPRPTGTGDFNLAPMDIQTPTNTFDNDYYKNLVA 260

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLLHSDQ+L+NGGS DS+V+ YSTN F DFAAAMI+MGD+ PLTG+NGEIR NCR

Sbjct: 261 KRGLLHSDQELYNGGSQDSLKMYSTNQALFFQDFAAAMIRMGDLKPLTGTNGEIRNNCR 320

Query: 2170 RIN 2178
IN

Sbjct: 321 VIN 323

Score = 123 bits (308), Expect = 1e-25
Identities = 74/166 (44%), Positives = 89/166 (53%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRN-SARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+ GCDGS+LLDDT + GEK A PNRN S RGFEVID IKS VE C G VSCADILA+A
Sbjct: 72 VNGCDGSVLLDDTPTSQGEKMAFPNRNNSIRGFEVIDATKSNVEAACSGTVSCADILALA 131

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD VQ++ G PTWNVKL
Sbjct: 132 ARDGVQLLGG-----PTWNVKL 148

Query: 1508 GRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRDARTA+ + AN +P + L L F+ L+ +++ ALSG
Sbjct: 149 GRRDARTANMTLANLNLPPGNAPLANLTELAFARQNLNIREMTALSG 194

Score = 66.6 bits (161), Expect = 2e-08
Identities = 32/60 (53%), Positives = 46/60 (76%), Gaps = 1/60 (1%)
Frame = +1

Query: 607 ALFVLIWGSANAQL-STNFYYHSCP NFLSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
++ +L+ G+++A L +FY SCPN+ V +T++ A+SKE RMGAS+LRLFFHDCFVN
Sbjct: 14 SIILLAGTSDAWLRKPHFYASSCPNVEQIVFNTMKQAVSKEPRMGASILRLLFFHDCFVN 73

>gb|ABK21858.1| unknown [Picea sitchensis]
Length = 326

Score = 180 bits (457), Expect = 7e-43
Identities = 86/124 (69%), Positives = 104/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCTNFR RI++E+NI+ +FAR RQ +CP T G D+NLAPLDL TPT+FDN Y+KNL
Sbjct: 205 QARCTNFRNRIHSESNI DLSFARARQANCPSTGG--DDNLAPLDLLTPTTFDNYYKNLE 262

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+++GLLHSDQQLFNGGSTD++V Y+T P FS DFA AM+KMG I PLTG+NGEIRKNC
Sbjct: 263 RRRGLLHSDQQLFNGGSTDNLVSFYTTYPIAFSIDFAVAMVKMGSI EPLTGNGEIRKNC 322

Query: 2167 RRIN 2178
R+IN
Sbjct: 323 RKIN 326

Score = 153 bits (386), Expect = 1e-34
Identities = 88/169 (52%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTS+F GEK A PN+NS RGFEVID IK+ VE CPGVVSCADI+AIAA
Sbjct: 78 VNGCDGSILLDDTSTFQGEKTAVPNKNSVRGFEVIDAIKTQVEAACPGVVSCADIVAIAA 137

Query: 1331 RDSVQIVSGQTTNKNLNL*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + LGGPTW V LG
Sbjct: 138 RDAV-----VQLGGPTWLVLLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ +P P SNL+ LIS F + GLS +DLVALSG+ I
Sbjct: 155 RRDSTTASLSAANSNLPPPASNLSALISSFQSHGLSIRDLVALSGSHTI 203

Score = 67.8 bits (164), Expect = 7e-09
Identities = 35/65 (53%), Positives = 42/65 (64%)
Frame = +1

Query: 589 RLTICLALFVLIWGSANAQLSTNFYYHSCP NFLSSVKSTVQSAISKETRMGASLLRRLFH 768
R +CL + V + + QL FY SCP+ FS V S V A++KE RMGASLLRL FH
Sbjct: 16 RSLLLCLLILVRL-SAVYGQLCPRFYDISCPSAFSIVNSVVTQAVAKEKRMGASLLRRLFH 74

Query: 769 DCFVN 783
DCFVN
Sbjct: 75 DCFVN 79

>emb|CAD67477.1| peroxidase [Asparagus officinalis]
Length = 315

Score = 179 bits (455), Expect = 1e-42
Identities = 82/124 (66%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT+FR+ IYN+++I+ +FA R+ +CP+ SGSGD NLAPLDLQTPT+FDN Y++NLV
Sbjct: 192 QARCTSFRRSHIYNDSDIDPSFATLRKSNCPKQSGSGDMNLAPLDLQTPTTFDNNYYRNLV 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGL+HSDQ+LFNGGSTDS+V+ YS G F S F MIKMGD+SPL GSNGEIRK C
Sbjct: 252 VKKGLMHSDQELFNGGSTDSLKSYSVSDGTGKFYSAFVEGMIKMGDVSPLVGSNGEIRKIC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 162 bits (409), Expect = 3e-37

Identities = 92/169 (54%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILL DT F GE++ANPN SARGF+VID IK+AVEK CPGVVSCADILAIAA

Sbjct: 65 VNGCDGSILLADTPHFVGEQHANPNRNSARGFKVIDRIKTAVEKACPGVVSCADILAIAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W+VKLG

Sbjct: 125 RDSVVI-----LGGPNWDVKLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+RTA+++AANN IP PTS+L L S F+A GLSTKD+VALSG I

Sbjct: 142 RRDSRTANKTAANNEIPPTSSLANLTSLFAAKGLSTKDMVALSGAHTI 190

Score = 82.8 bits (203), Expect = 2e-13
Identities = 40/64 (62%), Positives = 51/64 (79%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L I L+L ++ S+NAQLST FY +SCPN+F+++K +Q AI KE RMGAS+LRLFHD

Sbjct: 6 LAIILSLCIV---SSNAQLSTTFYSNSCPNVFTTIKPVLQHAIEKEKRMGASILRRLFHD 62

Query: 772 CFVN 783
CFVN

Sbjct: 63 CFVN 66

>emb|CAA62597.1| korean-radish isoperoxidase [Raphanus sativus]
Length = 315

Score = 179 bits (455), Expect = 1e-42
Identities = 89/124 (71%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RCTNFR RIYNETNI AFA RQ+SCPR + PLD+ +PTSFDN YFKNL+

Sbjct: 193 QSRCTNFRTRIYNETNINAAFATLRQKSCPRAAFRR-RKPQLDINSPTSFDNSYFKNLM 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ LFNNGGSTDSIVRGYS +P +F+SDFAAAMIKMGDISPLTGS+GEIRK C

Sbjct: 252 AQRGLLHSDQVLFNGGSTDSIVRGYSNSPSSFNDSFAAAMIKMGDISPLTGSSGEIRKVC 311

Query: 2167 RRIN 2178
R N

Sbjct: 312 GRN 315

Score = 176 bits (445), Expect = 2e-41
Identities = 99/169 (58%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKPCPGVVSCADILAI 1330
+ GCDGSILLDDTS FTGE+NA PNRNSARGF VIDNIKSAVEK CPGVVSCADILAI
Sbjct: 67 VNGCDGSILLDDTS-FTGEQNAGPNRNSARGFNVIDNIKSAVEKACPGVVSCADILAI 125

Query: 1331 RDSVQIVSGQTTNKNLNL*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 126 RDSV-----VQLGGPNWNVKVG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDA+TASQ+AAAN+ IPAP+ +L+QLIS F A+GLST+D+VALSG I
Sbjct: 143 RRDARTASQAAANSNIPAPSM SLSQLISSFRAVGLSTRDMVALSGAHTI 191

Score = 82.8 bits (203), Expect = 2e-13
Identities = 39/66 (59%), Positives = 49/66 (74%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLF 765
S + I + + L+ AQL+TNFY SCPNL S+VKS V+SA+S + RMGAS+LRLFF
Sbjct: 3 SNIAILLVIVITLLLQGGEAQLTTFYSTSCPNLLSTVKSGVKS AVSSQPRMGASILRRLF 62

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 63 HDCFVN 68

>gb|AC090366.1| peroxidase precursor [Triticum aestivum]
Length = 180

Score = 179 bits (454), Expect = 2e-42
Identities = 83/123 (67%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCTNFR IYN+TNI+ FAR+RQ CP +GS DNNLAPLDLQT T F+N+Y+KNLVQ
Sbjct: 58 ARCTNFRDHIYNDTNIDAGFARSRQSGCPHATGSRDNNLAPLDLQTLTVFENHYYKNLVQ 117

Query: 1990 KKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLLHSDQ+LFNGG+ D++VR Y + F DF MI MGDI+PLTGSNG+IR NCR
Sbjct: 118 KRGLLHSDQELFNNGAADALVREYVGSQS AFFQDFVEGMIMMGDITPLTGSNGQIRMNCR 177

Query: 2170 RIN 2178

RIN
Sbjct: 178 RIN 180

Score = 64.7 bits (156), Expect = 6e-08
Identities = 33/55 (60%), Positives = 38/55 (69%)
Frame = +2

Query: 1493 WNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
W VK+GRRD+ TAS + A N IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 1 WEVKMGRRDSTTASFNGAENNIPPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 55

>gb|ACN34270.1| unknown [Zea mays]
Length = 332

Score = 179 bits (453), Expect = 2e-42
Identities = 85/127 (66%), Positives = 103/127 (81%), Gaps = 3/127 (2%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG---DNNLAPLDLQTPTSFDNYFFK 1977
QARCTNFRA +YN+TNI+ AFAR R+ CP + SG DNNLAPLDLQTPT F+N Y++
Sbjct: 206 QARCTNFRAHVYNDTNIDGAFARARRSVCPAAASSGSGGDNNLAPLDLQTPTVFENDYYR 265

Query: 1978 NLVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSGEIR 2157
NLV +KGLLHSDQ+LFNG +TD+ V+ Y ++ F +DF A M+KMGDISPLTGSGEIR
Sbjct: 266 NLVCRKGLLHSDQELFNGAATDAQVQAYVSSQSAFFADVFAGMVKMGDISPLTGSSGEIR 325

Query: 2158 KNCRRIN 2178
KNCRRIN
Sbjct: 326 KNCRRIN 332

Score = 159 bits (401), Expect = 2e-36
Identities = 92/169 (54%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAREKVCPCGVVSCADILAIAA 1330
+QGCD S+LLDDT SF GEK A PN S RGFEVID IKSAV+K CPGVVSCADILAIAA
Sbjct: 79 VQGCDASLLDDTSPSQGEKMAKPNGSVRGFEVIDA IKSAVDKACPGVVSCADILAIAA 138

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W+VKLG
Sbjct: 139 RDSV-----VTLGGPNWDVKLG 155

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG I

Sbjct: 156 RRDSRTASFGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 204

Score = 76.6 bits (187), Expect = 1e-11
Identities = 35/61 (57%), Positives = 47/61 (77%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCF 777
+ LAL +++AQLST FY HSCP + +V+S +Q+AI+++E RMGAS+LRLFFHDCF
Sbjct: 19 LLLALLAAGTSTSSAQLSTGFYSHSCPGVHDAVRSVLQAAIAREQRMGASILRFFHDCF 78

Query: 778 V 780
V
Sbjct: 79 V 79

>gb|ACU24215.1| unknown [Glycine max]
Length = 329

Score = 178 bits (451), Expect = 4e-42
Identities = 85/124 (68%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR RIYN+TNI+ FA RQ+ CPRT+G+GDNNLA LD +TP FDN YFKNL
Sbjct: 206 KARCTSFDRRIYNQTNIDRTFALARQRRCPRTNGTGDNNLANLDFRTPNHFDNYYFKNLF 265

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GLL+ DQ LFNGGSTDS+VR YS N F DF AMI+MGDI PLTGS GEIRKNC
Sbjct: 266 IKRGLLNFDQVLFNGGSTDSLVRTYSQNKAFDFVVKAMIRMGDIKPLTGSQGEIRKNC 325

Query: 2167 RRIN 2178
RR+N
Sbjct: 326 RRVN 329

Score = 152 bits (383), Expect = 3e-34
Identities = 86/166 (51%), Positives = 102/166 (61%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCDGSILLDDT +F GEK A N NS RG+E+ID+IKS VEK+CPGVVSCADIL IA+
Sbjct: 78 VQGCDGSILLDDTPTFQGEKTAANNNSVRGYELIDDIKSKVEKICPGVVSCADILDIAS 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNV+LG
Sbjct: 138 RDSVVL-----LGGPFWNVRLG 154

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+R+A+ +AAN G IP PTSNL LI+RF GLS +D+VALSG
Sbjct: 155 RRDSRSANFTAANTGVIPPTSNTLNLI TRFQDQGLSARDMVALSG 200

Score = 80.1 bits (196), Expect = 1e-12
Identities = 39/78 (50%), Positives = 59/78 (75%), Gaps = 1/78 (1%)
Frame = +1

Query: 550 VCLSKLTMASFCSRLTIC-LALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISK 726
+ LS + ++F S I LA+ +L+ +++A LS NFY +CPN+F++VKS V+SA++K
Sbjct: 1 MALSPIRSSTFSSSSAIVTLAVLLLLTRTSSATLSKNFYSKTCPNVFNTVKS VVKS AVAK 60

Query: 727 ETRMGASLLRRLFHDCFV 780
E R+GAS++RRLFHDCFV
Sbjct: 61 EPRIGASIVRRLFHDCFV 78

>gb|AAB48184.1| peroxidase precursor [Linum usitatissimum]
Length = 323

Score = 178 bits (451), Expect = 4e-42
Identities = 83/123 (67%), Positives = 100/123 (81%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC +FR RIYNETNI+ +FA +++CP SGD+NLAPLDL+TPTSFDN Y+ NL++
Sbjct: 201 ARCVSFRDRIYNETNIDPSFASQSEENCPLAPNSGDDNLAPLDLKTPTSFDNYYNNLIE 260

Query: 1990 KKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
+KGLLHSDQ LFNNGSTDS+VR YS +P F++DFAAAM+KMGDI PLTGS GEIR C
Sbjct: 261 QKGLLHSDQVLFNNGSTDSLRSYSQSPKRFAADFAAAMVKMGDIKPLTGSQGEIRNVCS 320

Query: 2170 RIN 2178
R N
Sbjct: 321 RPN 323

Score = 143 bits (361), Expect = 1e-31
Identities = 82/170 (48%), Positives = 101/170 (59%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILL+DT SFTGE+ A PN S RG+ VI++IKS VE+VCPGVVSCADI+AIAA
Sbjct: 72 VNGCDGSILLEDDTSSFTGEQTAAPNNGSVRGYVIEDIKSKEVQCPGVVSCADIVAIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I GQ +W VK+G
Sbjct: 132 RDSTVIAGGQ-----SWEVKVG 148

Query: 1511 RRDARTASQSAANNGI-PAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS +AAN+G+ PAPTS+LN+LI F GLS D+V LSG+ I
Sbjct: 149 RRDSKTASFNAANSVLPAPTSSLNELIKSFGDQGLSANDMVVLSGSHTI 198

Score = 73.9 bits (180), Expect = 1e-10
Identities = 37/66 (56%), Positives = 45/66 (68%), Gaps = 2/66 (3%)
Frame = +1

Query: 592 LTICLALFVLIWGSANA--QLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
L CL L V + G+ QLST+FY SCP L +V+ V+SA+ KETR+ ASLLRL F
Sbjct: 8 LRSCLVLLVAVCGAGKCGWQLSTDFYSESCPMLMDTVRCEVESAVDKETRIAASLLRLHF 67

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 68 HDCFVN 73

>emb|CBI27506.1| unnamed protein product [Vitis vinifera]
Length = 266

Score = 177 bits (450), Expect = 5e-42
Identities = 89/125 (71%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RI+ N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 142 QARCVTFRDRIHDNGTNI DAGFASTRRRRCVPVDNGGDDNLAPLDL VTPNSFDNYYFKNL 201

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS + TFSSDFAAAM+KMGDI PLTGSNGEIRK
Sbjct: 202 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSRSTFSSDFAAAMVKMGDIDPLTGSNGEIRKL 261

Query: 2164 CRRIN 2178
C IN
Sbjct: 262 CNAIN 266

Score = 138 bits (347), Expect = 4e-30
Identities = 77/169 (45%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+QGCD SILLDD+++ EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 15 VQGCDA SILLDD SATI QSEKNAPNNNSVRGFEVIDNVK SQVESICPGVVSCADILAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDS S+ +GGPTW VKLG

Sbjct: 75 RDS-----SVA VGGPTWTVKLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P+ L++L+S FS+ GL+T+++VALSG+ I

Sbjct: 92 RRDSTTSGLSQA AANLPSFRDGLDKLVSLFSSKGLNTREMV ALSGSH TI 140

>ref|XP_002274550.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 320

Score = 177 bits (450), Expect = 5e-42
Identities = 89/125 (71%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RI+ N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL

Sbjct: 196 QARC VTRDRIHDNGT NIDAGFASTRRRRC PVDNGNGDDN LAPLDLVTPNSFDNYYFKNL 255

Query: 1984 VQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS + TFSSDFAAAM+KMGDI PLTGSNGEIRK

Sbjct: 256 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSRSTFSSDFAAAMV KMGDIDPLTGSNGEIRKL 315

Query: 2164 CRRIN 2178
C IN

Sbjct: 316 CNAIN 320

Score = 138 bits (347), Expect = 4e-30
Identities = 77/169 (45%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLDD+++ EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA

Sbjct: 69 VQGCDA SILLDD SATI QSEKNAPNNNSVRGFEVIDNVK SQVESICPGVVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDS S+ +GGPTW VKLG

Sbjct: 129 RDS-----SVA VGGPTWTVKLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P+ L++L+S FS+ GL+T+++VALSG+ I

Sbjct: 146 RRDSTTSGLSQA AANLPSFRDGLDKLVSLFSSKGLNTREMV ALSGSH TI 194

Score = 62.0 bits (149), Expect = 4e-07
Identities = 25/47 (53%), Positives = 38/47 (80%)
Frame = +1

Query: 640 AQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
AQLS+ FY ++CP S++++ +++A+S+E RM ASL+RL FHDCFV
Sbjct: 23 AQLSSKFYDNTCPKALSTIRTAIRTAVSRERRMAASLIRLHFHDCFV 69

>gb|ACN42168.1| peroxidase 1 [Sesuvium portulacastrum]
Length = 318

Score = 177 bits (449), Expect = 6e-42
Identities = 83/124 (66%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYN+++I +FA++ + +CP +G+GDNNLAPLD QTP FD+ YF+ LV
Sbjct: 195 QARCTNFRAHIYNDSINASFASKLNCPPKNGTGDNNLAPLDPQTPNKFHDHIYFQGLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KK LHSQ+L NG ST S ++ YSTNP FSSDF +MIKMGDI PLTGSNGEIRKNC
Sbjct: 255 NKKAPLHSDQELTNGASTSSWIQKYSTNPSLFSDFGSMIKMGDIKPLTGSNGEIRKNC 314

Query: 2167 RRIN 2178
RRIN
Sbjct: 315 RRIN 318

Score = 157 bits (398), Expect = 5e-36
Identities = 89/165 (53%), Positives = 105/165 (63%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS LLDDTSSF GEK+A+PN SARGFEVID IK+AVE+VCPGVVSCADILA+ A
Sbjct: 68 VNGCDGSNLLDDTSSFKGEKSASPNFQSARGFEVIDQIKAAVERVCPGVVSCADILAVTA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW+VKLG
Sbjct: 128 RDSV-----VGLGGPTWDVKLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTA+Q+AAAN+ IP +S+L++LIS F GL+ KDLVAL G
Sbjct: 145 RRDARTANQAAANSSIPPASSLSRLISSFQNGQLTIKDLVALYG 189

Score = 86.3 bits (212), Expect = 2e-14
Identities = 46/68 (67%), Positives = 55/68 (80%), Gaps = 2/68 (2%)
Frame = +1

Query: 586 SRLTICLAL-FVLIW-GSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRL 759
+RLT LAL FV+++ GS++AQL+TNFY SCP+LF V+ VQSAI KE RMGASLLRL
Sbjct: 2 ARLTCFLALAFVIVFVGSSSAQLTTNFYEKSCPHLFPVVRDQVQSAIRKEARMGASLLRL 61

Query: 760 FFHDCFVN 783
FHDCFVN
Sbjct: 62 HFHDCFVN 69

>ref|XP_002269058.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 319

Score = 177 bits (448), Expect = 8e-42
Identities = 88/125 (70%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP TSG GD+N+A LDL TP SFDN YFKNL
Sbjct: 195 QARCVTFRDRIYDNGTDIDAGFASTRRRRCPATSGDGDNNIAALDLVTPNSFDNYYFKNL 254

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTDSIV GYS +P TFSSDFA+AM+KMG+I PLTGS GEIRK
Sbjct: 255 IQKKGLLQSDQVLFSGGSTDSIVTGYSKSPSTFSSDFASAMVKGNIPLTGSAGEIRKL 314

Query: 2164 CRRIN 2178
C IN
Sbjct: 315 CSAIN 319

Score = 127 bits (318), Expect = 9e-27
Identities = 73/169 (43%), Positives = 94/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAREKVCVGVVSCADILAIAA 1330
+QGCD SILL+D+SS EKNA N NS RG++VID++KS VE +CPG+VSCADILA+AA
Sbjct: 68 VQGDASILLNDSSSIQSEKNAPNNLSVRYDVIDDKSEVESICPGIVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VSG PTW V LG
Sbjct: 128 RDASVAVSG-----PTWTVNLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P + L++LIS F + GLS +D+VALSG+ I

Sbjct: 145 RRDSTTSGLSQAATNLPNFSDDLRLISLFGSKGLSERDMVALSGSHTI 193

Score = 63.9 bits (154), Expect = 1e-07
Identities = 28/57 (49%), Positives = 42/57 (73%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRRLFHDFV 780
LF+ AQLS++FY ++CP S++++ V++A+S+E RM ASL+RL FHDFV
Sbjct: 12 LFIFSNMPCEAQLSSSFYDNTCPKALSTIRTAVRTAVSRERRMAASLIRLHFHDFV 68

>emb|CBI27505.1| unnamed protein product [Vitis vinifera]
Length = 302

Score = 177 bits (448), Expect = 8e-42
Identities = 88/125 (70%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP TSG GD+N+A LDL TP SFDN YFKNL
Sbjct: 178 QARCVTFRDRIYDNGTDIDAGFASTRRRRCPATSGDGDNNIAALDLVTPNSFDNYYFKNL 237

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTDSIV GYS +P TFSSDFA+AM+KMG+I PLTGS GEIRK
Sbjct: 238 IQKKGLLQSDQVLFSGGSTDSIVTGYSKSPSTFSSDFASAMVKGNIPLTGSAGEIRKL 297

Query: 2164 CRRIN 2178
C IN
Sbjct: 298 CSAIN 302

Score = 127 bits (318), Expect = 9e-27
Identities = 73/169 (43%), Positives = 94/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILATAA 1330
+QGCD SILL+D+SS EKNA N NS RG++VID++KS VE +CPG+VSCADILA+AA
Sbjct: 51 VQGCDASILLNDSSSIQSEKNAPNNLNSVRGYDVIDDVKSEVESICPGIVSCADILAVAA 110

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VSG PTW V LG
Sbjct: 111 RDASVAVSG-----PTWTVNLG 127

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P + L++LIS F + GLS +D+VALSG+ I
Sbjct: 128 RRDSTTSGLSQAATNLPNFSDDLRLISLFGSKGLSERDMVALSGSHTI 176

Score = 62.8 bits (151), Expect = 2e-07
Identities = 26/47 (55%), Positives = 39/47 (82%)
Frame = +1

Query: 640 AQLSTNFYHSCP NFLSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
AQLS++FY ++CP S++++ V++A+S+E RM ASL+RL FHDCFV
Sbjct: 5 AQLSSSFYDNTCPKALSTIRTAVRTAVSRERRMAASLIRLHFHDCFV 51

>emb|CAL25300.1| properoxidase [Picea abies]
Length = 310

Score = 176 bits (447), Expect = 1e-41
Identities = 81/124 (65%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARC NFRA IYNETNI++ ++ + Q CP T+GSGD+NL+PLD TPT+FD Y+ NL
Sbjct: 187 QARCVNFRAHIYNETNIDSTYSTLSQSKCPSTAGSGDSNLSPLDYVTP TAFDKNYYSNLK 246

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS V Y++N +F SDFAAAM+KMG+I PLTG++G+IRKNC
Sbjct: 247 SKKGLLHSDQELFNGGSTDSQVTTYASNQNSFFSDFAAAMVKMGNIKPLTGTSGQIRKNC 306

Query: 2167 RRIN 2178
R+ N
Sbjct: 307 RKPN 310

Score = 159 bits (401), Expect = 2e-36
Identities = 88/165 (53%), Positives = 103/165 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AA 1330
+ GCDGS+LLDD+S+ TGEK ANPN NSARGF+VID IKS VEK C GVVSCADILAI+A
Sbjct: 60 VNGCDGSVLLDDSSITITGEKTANPNANSARGFDVIDTIKSNEKACSGVVSCADILAI SA 119

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 120 RDSV-----VELGGPSWTVM LG 136

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+ TAS++ ANN IP PTS+L+ LIS F A GLSTK++VALSG
Sbjct: 137 RRDSTASKNGANNIPPTSSLSNLISLFAQGLSTKEMVALSG 181

Score = 69.7 bits (169), Expect = 2e-09
Identities = 32/51 (62%), Positives = 38/51 (74%)
Frame = +1

Query: 631 SANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFVN 783
+AN QLS+ FY SCP S VK+ V+ A++ E RMGASLLR L F H D C F V N
Sbjct: 11 TANGQLSSTFYAQCPTALS VVKA AVRQAVANEKRMGASLLR L F H D C F V N 61

>ref|XP_002269145.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 331

Score = 175 bits (444), Expect = 2e-41
Identities = 87/125 (69%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARC V T F R D R I Y G N G T N I D A G F A S T R R R R C P A D N G N G D D N L A P L D L V T P N S F D N N Y F K N L 266

Query: 1984 VQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS GEIRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGEIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 136 bits (343), Expect = 1e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGC DASILLDD SPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 63.5 bits (153), Expect = 1e-07
Identities = 32/72 (44%), Positives = 49/72 (68%), Gaps = 1/72 (1%)
Frame = +1

Query: 568 TMAFCSRLTICLA-LFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGA 744
T S S I +A L +L AQLS++FY ++CP+ S++++ +++A+S+E RM A
Sbjct: 9 TWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNTCPSALSTIRTAIRTAIVSRERRMAA 68

Query: 745 SLLRLLFFHDCFV 780
SL+RL FHDCFV
Sbjct: 69 SLIRLHFHDCFV 80

>gb|ACJ85500.1| unknown [Medicago truncatula]
Length = 229

Score = 174 bits (441), Expect = 5e-41
Identities = 99/169 (58%), Positives = 106/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTS+FTGEKNA PN+NS RGF+VIDNIK+AVE VCPGVVSCADILAIAA
Sbjct: 72 VNGCDGSILLDDTSNFTGEKNALPNKNSVRGFDVIDNIKTAVENVCPGVVSCADILAIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
DSV I+ G PTWNVKLG
Sbjct: 132 TDSVAILGG-----PTWNVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDA TASQS AN IP PTSNLN L S F +GLSTKDLVALSG I
Sbjct: 149 RRDATTASQSDANTAIPRPTSNLNLTSMFKNVGLSTKDLVALSGAHTI 197

Score = 95.1 bits (235), Expect = 4e-17
Identities = 49/68 (72%), Positives = 55/68 (80%), Gaps = 1/68 (1%)
Frame = +1

Query: 583 CSRLTI-CLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRL 759
CSR+T+ L LFVLI GS NAQLSTNFY +CP L S V+ VQSAISKE R+GAS+LRL
Sbjct: 6 CSRITMFSLVLFVLIIGSVNAQLSTNFYSKTCPKLSSIVQRQVQSAISKEARIGASILRL 65

Query: 760 FFHDCFVN 783
FFHDCFVN
Sbjct: 66 FFHDCFVN 73

Score = 43.1 bits (100), Expect = 0.18
Identities = 18/24 (75%), Positives = 21/24 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFART 1878
QA+CT FR RIYNETNI+T+FA T
Sbjct: 199 QAKCTTFRVRIYNETNIDTSFAST 222

>emb|CAN80097.1| hypothetical protein [Vitis vinifera]
Length = 331

Score = 173 bits (438), Expect = 1e-40
Identities = 86/125 (68%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYNGTNI DAGFASTRRRRCPADNGNGDDNLAPLDLVT P NSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS G IRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGXIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 136 bits (343), Expect = 1e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGC DASILLDDSP TIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 63.9 bits (154), Expect = 1e-07

Identities = 32/78 (41%), Positives = 52/78 (66%), Gaps = 8/78 (10%)
Frame = +1

Query: 571 MASFC SRLTICLA-LFVLIWG-----SANAQLSTNFYHSCP NLFSSVKSTVQSAISK 726
+A+ SR C++ F+L+ G AQLS++FY + CP+ S++++ +++A+S+
Sbjct: 3 LAAGSSRWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNXCPSALSTIRTAIRTAVSR 62

Query: 727 ETRMGASLLRLFFHDCFV 780
E RM ASL+RL FHDCFV
Sbjct: 63 ERRMAASLIRLHFHDCFV 80

>emb|CBI27503.1| unnamed protein product [Vitis vinifera]
Length = 357

Score = 172 bits (437), Expect = 2e-40
Identities = 85/121 (70%), Positives = 97/121 (80%), Gaps = 1/121 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYNGTNI DAGFASTRRRRC PADNGGDDNLAPLDLVTPNSFDNYYFKNL 266

Query: 1984 VQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS GEIRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGEIRKF 326

Query: 2164 C 2166
C
Sbjct: 327 C 327

Score = 136 bits (343), Expect = 1e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGCDASILLDDSP TIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 63.5 bits (153), Expect = 1e-07
Identities = 32/72 (44%), Positives = 49/72 (68%), Gaps = 1/72 (1%)
Frame = +1

Query: 568 TMAFCSRLTICLA-LFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
T S S I +A L +L AQLS++FY ++CP+ S++++ +++A+S+E RM A
Sbjct: 9 TWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNTCPSALSTIRTAIRTAVSRERRMAA 68

Query: 745 SLLRLLFFHDCFV 780
SL+RL FHDCFV
Sbjct: 69 SLIRLHFHDCFV 80

>emb|CBI27502.1| unnamed protein product [Vitis vinifera]
Length = 266

Score = 172 bits (437), Expect = 2e-40
Identities = 86/125 (68%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 142 QARCVTFRDRIYNGTNDAGFASTRRRRCPADNGGDDNLAPLDLVTNPSFDNYYFKNL 201

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS G IRK
Sbjct: 202 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGVIRKF 261

Query: 2164 CRRIN 2178
C IN
Sbjct: 262 CNVIN 266

Score = 136 bits (343), Expect = 1e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 15 VQGCDASILLDDSPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI* LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 75 RDA-----SVAVGGPTWTLKLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 92 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 140

>ref|XP_002269169.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 331

Score = 172 bits (437), Expect = 2e-40
Identities = 86/125 (68%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYNGTNIIDAGFASTRRRRCPADNGGDDNLAPLDLVTPNSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS G IRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFFSAMVKMGDIEPLIGSAGVIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 136 bits (343), Expect = 1e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGCDASILLDDSPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 64.7 bits (156), Expect = 6e-08
Identities = 32/78 (41%), Positives = 53/78 (67%), Gaps = 8/78 (10%)
Frame = +1

Query: 571 MASFCSRLTICLA-LFVLIWG-----SANAQLSTNFYHSCPNLFSSVKSTVQSAISK 726
+A+ SR C++ F+L+ G AQLS++FY ++CP+ S++++ +++A+S+

Sbjct: 3 LAAGSSRWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNACPSALSTIRTAIRTAIVSR 62

Query: 727 ETRMGASLLRLLFFHDCFV 780
E RM ASL+RL FHDCFV

Sbjct: 63 ERRMAASLIRLHFHDCFV 80

>gb|AA013838.1|AF405326_1 peroxidase 2 [Lupinus albus]
Length = 260

Score = 172 bits (437), Expect = 2e-40
Identities = 81/126 (64%), Positives = 102/126 (80%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG--DNNLAPLDLQTPTSFDNYYFKN 1980
+ARC+++R RIY++TNI+ FA++RQ++CPR S DNN+A LD +TPT FDN Y+KN

Sbjct: 135 KARCSSYRDRIYDDTNIDKLFKSRQRNCPRKSSGTVKDNNVAVLDFKTPTHFDNLYYKN 194

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ KKGLLHSDQ+LFNGGSTDS+V YS N F+SDF AMIKMG+I PLTGSNG+IRK

Sbjct: 195 LINKKGLLHSDQQLFNGGSTDSLVTTYSNNEKAFNSDFVTAMIKMGNIKPLTGSNGQIRK 254

Query: 2161 NCRRIN 2178
+CRR N

Sbjct: 255 HCRRAN 260

Score = 155 bits (392), Expect = 2e-35
Identities = 92/170 (54%), Positives = 102/170 (60%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTSSF GEK A PN NS RGFEVID IKS VE+ CPGVVSCADI+AIAA

Sbjct: 7 VNGCDGSILLDDTSSFRGEKTAPPNNNSVRGFEVIDAIKSKVEEACPGVVSCADIVAIAA 66

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I LGGP WNVK+G

Sbjct: 67 RDSTAI-----LGGPYWNVKVG 83

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS S A++G IP P S L+ LISRF A GLS KD+VALSG I

Sbjct: 84 RRDSKTASFSASSGVI PPPFSTLSNLISRFAQGLSIKDMVALS GAHTI 133

>gb|ABA96220.1| Cationic peroxidase 1 precursor, putative, expressed [Oryza sativa
(japonica cultivar-group)]

gb|EAY79691.1| hypothetical protein OsI_34838 [Oryza sativa Indica Group]

gb|EAZ19422.1| hypothetical protein OsJ_34979 [Oryza sativa Japonica Group]

Length = 291

Score = 172 bits (437), Expect = 2e-40
Identities = 78/124 (62%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 170 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYAFDNFYKLL 227

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AAM+KMG+I+P+TGS+G+IRKNC
Sbjct: 228 NKKGVLHSDQQLFNGGSADSQTTTYSNMATFFTFSAAMVKMGNINPITGSSGQIRKNC 287

Query: 2167 RRIN 2178
R++N
Sbjct: 288 RKNV 291

Score = 146 bits (369), Expect = 1e-32
Identities = 82/170 (48%), Positives = 98/170 (57%)
Frame = +2

Query: 1148 QMQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1327
++ GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ +E +CP VVSCADILA+A
Sbjct: 42 RIAGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAHIEGICPQVVSCADILAVA 101

Query: 1328 ARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
AR+SV + LGGPTW V+L
Sbjct: 102 ARESV-----VALGGPTWVVQL 118

Query: 1508 GRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
GRRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 119 GRRDSTTASLDTANNDIPAPTFDLGDLTKSFSNKGLSATDMIALSGAHTI 168

>tpe|CAH69378.1| TPA: class III peroxidase 136 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 317

Score = 172 bits (437), Expect = 2e-40
Identities = 78/124 (62%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 196 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYAFDNFYKLL 253

QARC R RIY N TNI+T FA TR++ CP +G+GD+NLAPLD+ TP SFDN YFKNL
Sbjct: 75 QARCVTVRDRIYDNGTNIIDTGFASRRRRCPVDNGNGDDNLAPLDVVTPNSFDNYYFKNL 134

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSS+FA+AM+KMGDI PL GS GEIRK

Sbjct: 135 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSEFASAMVKMGDIEPLLSAGEIRKI 194

Query: 2164 CRRIN 2178

C IN

Sbjct: 195 CNVIN 199

Score = 38.9 bits (89), Expect = 3.4
Identities = 22/42 (52%), Positives = 31/42 (73%)
Frame = +2

Query: 1532 SQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

SQ+AAAN +P+ L++LI FS+ GLST+D+VALSG+ I

Sbjct: 34 SQAAAN--LPSFRDGLDRLIPLFSSKGLSTRDMVALSGSHTI 73

>emb|CAH10839.1| peroxidase [Picea abies]
Length = 317

Score = 172 bits (436), Expect = 2e-40
Identities = 83/124 (66%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT FRARIYNE+NI+T+FA + + SCP S GDN L+PLDL TPT+FDN Y+ +L

Sbjct: 196 QARCTTFRARIYNESNIDTSFATSVKSSCP--SAGGDNTLSPLDLATPTTFDNKYITDLG 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

+KGLLHSDQQLF+GGST+S V YS N TF +DFAAAM+KMG+ISPLTG++G+IRKNC

Sbjct: 254 NRKGLLHSDQQLFSGGSTNSQVTTYSANQNTFFTFDFAAAMVKMGNISPLTGTSGQIRKNC 313

Query: 2167 RRIN 2178

R+ N

Sbjct: 314 RKAN 317

Score = 158 bits (400), Expect = 3e-36
Identities = 91/165 (55%), Positives = 100/165 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330

+ GCDGSILLDD S+FTGEK A PN NS RGF+VID IK+ VE C GVVSCADILAI A

Sbjct: 69 VNGCDGSILLDDNSTFTGEKTALPNANSVRGFDVIDTIKTQVEAACSGVVSCADILAIVA 128

Query: 1331 RDSVQIVSGGTTNKNLNLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG

Sbjct: 129 RDSV-----VQLGGPTWTVLLG 145

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+ TAS SAANN IP+P SNL+ LIS F+A GLSTKDLVALSG

Sbjct: 146 RRDSTTASLSAANNIPSPASNLSALISSFTAHLSTKDLVALSG 190

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/64 (48%), Positives = 41/64 (64%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHD 771
+ +C+ I +A+ QL++ FY CP S VK+ V A++ E RMGASLLRL FHD

Sbjct: 7 IVLCVLCISSINNAAHGQLTSTFYNKLCPTALSIVKAAVNKAVNNEKRMGASLLRHFHD 66

Query: 772 CFVN 783

CFVN

Sbjct: 67 CFVN 70

>ref|XP_002266365.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 328

Score = 172 bits (435), Expect = 3e-40
Identities = 81/124 (65%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT FR RIYNE NI+ +F + Q +CP S GDN L+PLD QTPT+FDN Y+ NLV

Sbjct: 207 QARCTTFRTRIYNEANIDASFKTSLQANCP--SSGGDNTLSPLDTQTPTTFDNAYYTNLV 264

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNGGSTD++V YST TF +DFA AM+KMG++SPLTG++G+IR NC

Sbjct: 265 NKKGLLHSDQQLFNGGSTDAVVNTYSTRSTTFFTFANAMVKMGNLSPLTGTSGQIRTNC 324

Query: 2167 RRIN 2178

R+ N

Sbjct: 325 RKTN 328

Score = 147 bits (372), Expect = 5e-33
Identities = 83/169 (49%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+ GCD SILLDDTS+FTGEK A PN NS RG+EV+D IKS +E CPGVVSCADILA+AA
Sbjct: 80 VNGCDASILLDDTSNFTGEKTAGPNANSVRGYEVVDTIKSQLEASCPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GP+W V+LG
Sbjct: 140 RDSV-----VALRGPSWVRLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ IPAPT NL+ LIS F+ G + +++VALSG+ I
Sbjct: 157 RRDSTTASLSAANSNIPAPTLNLSGLISAFTNKGFNAREMVALSGSHTI 205

Score = 76.3 bits (186), Expect = 2e-11
Identities = 35/52 (67%), Positives = 40/52 (76%)
Frame = +1

Query: 628 GSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783
G A+AQL+TNFY +CPN S +KS V SA+ E RMGASLLRL FHDCFVN
Sbjct: 30 GMASAQLTTFYAKTCPNALSIIKSAVNSAVKSEARMGASLLRRLFHDCFVN 81

>ref|NP_001106040.1| plasma membrane-bound peroxidase 2b precursor [Zea mays]
sp|A5H452.1|PER70_MAIZE RecName: Full=Peroxidase 70; AltName: Full=Plasma membrane-bound
peroxidase 2b; Short=pmPOX2b; Flags: Precursor
gb|ABN48843.1| plasma membrane-bound peroxidase 2b [Zea mays]
Length = 321

Score = 172 bits (435), Expect = 3e-40
Identities = 77/123 (62%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
A+C NFRA IYN+TN+ AFA R+ +CP +G+GD NLAPLD TPT+FDN Y+ NL+
Sbjct: 199 AQCKNFRAHIYNDTNVNAAFATLRRANCPAAAGNGDGNLAPLDTATPTAFDNAYYTNLLA 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQQLFNGG+TD +VR Y++ P FS DFAAAMI+MG+ISPLTG+ G+IR+ C
Sbjct: 259 QRGLLHSDQQLFNGGATDGLVRTYASTPRRFSRDFAAAMIRMGNISPLTGTGQGIARRACS 318

Query: 2170 RIN 2178
R+N
Sbjct: 319 RVN 321

Score = 140 bits (353), Expect = 8e-31

Identities = 80/169 (47%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+QGCDGS+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE VCPGVVSCADILA+AA

Sbjct: 71 VQGCDGSVLLNDTATFTGEQTANPNVGSIRFGVVDNIKAQVEAVCPGVVSCADILAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 131 RDSV-----VALGGPSWRVLLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS + AN+ +PAP+ +L L + F+ LS DLVALSG I

Sbjct: 148 RRDSTTASLALANSIDLPAASDLANLTAFAKKRSLRDLVALSGAHTI 196

Score = 68.2 bits (165), Expect = 5e-09
Identities = 34/72 (47%), Positives = 49/72 (68%)
Frame = +1

Query: 565 LTMASFCRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744

+ +SF S L++ + L + A+AQLS FY SCP +++K+ V +A+++E RMGA

Sbjct: 1 MASSSFTS-LSVMVLLCLAAAASASAQLSPTFYRSCPRALATIKA AVTAAVAQEARMGA 59

Query: 745 SLLRRLFHDCFV 780

SLLRL FHDCFV

Sbjct: 60 SLLRLHFHDCFV 71

>gb|EAY82023.1| hypothetical protein OsI_37207 [Oryza sativa Indica Group]
gb|EAZ17184.1| hypothetical protein OsJ_32691 [Oryza sativa Japonica Group]
Length = 291

Score = 171 bits (434), Expect = 3e-40
Identities = 78/124 (62%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRTSVSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+

Sbjct: 170 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYTFDNFYKLL 227

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

KKG+LHSDQQLFNGGS DS YS+N TF +DF+AA++KMG+I PLTGS+G+IRKNC

Sbjct: 228 NKKGVLHSDQQLFNGGSADSQTTYSNMATFFTFSSAAIVKMGNDPLTGSSGQIRKNC 287

Query: 2167 RRIN 2178

R++N

Sbjct: 288 RKNV 291

Score = 146 bits (368), Expect = 2e-32
Identities = 83/167 (49%), Positives = 95/167 (56%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ VE +CP VVSCADILA+AARD
Sbjct: 45 GCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAQVEGICPQVVSCADILAVAARD 104

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + GGPTW V+LGRR
Sbjct: 105 SVFAL-----GGPTWVVLGRR 121

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 122 DSTTASLDTANNDIPAPTLDLGLTKSFSNKGLSATDMIALSGAHTI 168

>gb|ABA91154.1| Cationic peroxidase 1 precursor, putative, expressed [Oryza sativa
(japonica cultivar-group)]
Length = 254

Score = 171 bits (434), Expect = 3e-40
Identities = 78/124 (62%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 133 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYTFDNFYKLL 190

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AA++KMG+I PLTGS+G+IRKNC
Sbjct: 191 NKKGVLSHSDQQLFNGGSADSQTTTYSSNMATFFTFSSAAIVKMGNDPLTGSSGQIRKNC 250

Query: 2167 RRIN 2178
R++N
Sbjct: 251 RKNV 254

Score = 148 bits (374), Expect = 3e-33
Identities = 84/169 (49%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
M+GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ VE +CP VVSCADILA+AA
Sbjct: 6 MKGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAQVEGICPQVVSCADILAVAA 65

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + GGPTW V+LG
Sbjct: 66 RDSVFAL-----GGPTWVWVQLG 82

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 83 RRDSTTASLDTANNDIPAPTLDLGDLTKSFSNKGLSATDMIALSGAHTI 131

>ref|NP_001065566.1| Os11g0112200 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69373.1| TPA: class III peroxidase 131 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF27411.1| Os11g0112200 [Oryza sativa Japonica Group]
Length = 317

Score = 171 bits (434), Expect = 3e-40
Identities = 78/124 (62%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 196 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTG--DNNISPLDASTPYTFDNFYKLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AA++KMG+I PLTGS+G+IRKNC
Sbjct: 254 NKKGV LHSDQQLFNGGSADSQTTTYSSNMATFFDFSAIIVKMGNDPLTGSSGQIRKNC 313

Query: 2167 RRIN 2178
R++N
Sbjct: 314 RKNV 317

Score = 146 bits (369), Expect = 1e-32
Identities = 83/169 (49%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ VE +CP VVSCADILA+AA
Sbjct: 69 VNGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAQVEGICPQVVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + GGPTW V+LG
Sbjct: 129 RDSVFAL-----GGPTWVWVQLG 145

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 146 RRDSTTASLDTANNDIPAPTLDLGDLTKSFSNKGLSATDMIALSGAHTI 194

Score = 74.7 bits (182), Expect = 6e-11
Identities = 36/67 (53%), Positives = 48/67 (71%)
Frame = +1

Query: 583 CSRLTICLALFVLIWGSANAQLSTNFYHSCPFLFSSVKSTVQSAISKETRMGASLLRLF 762
CS ++ A ++ +AQLS NFY SCPN S+++ V+SA++KE RMGASLLRL
Sbjct: 9 CSVIALLFAAHLV-----SAQLSANFYDKSCPFLSTIRTAVRSVAVAKENRMGASLLRLH 63

Query: 763 FHDCFVN 783
FHDCFVN
Sbjct: 64 FHDCFVN 70

>gb|EEE67815.1| hypothetical protein OsJ_25569 [Oryza sativa Japonica Group]
Length = 324

Score = 171 bits (433), Expect = 4e-40
Identities = 78/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAPLD TP +FDN Y+ NL+
Sbjct: 200 QAQCQNFDRRIYNETNIDSAFATQRQANCPRPTGSGDSNLAPLDTTTPNAFDNAYYSNLL 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 260 SNKGLLHSDQQLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQGIIRLSC 319

Query: 2167 RRIN 2178
++N
Sbjct: 320 SKVN 323

Score = 116 bits (290), Expect = 2e-23
Identities = 71/167 (42%), Positives = 86/167 (51%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AARD
Sbjct: 80 GCDASVLLSGQ-----EQNAGPNVGLRGSVIDNAKARVEAICNQTVSCADILAVAARD 134

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 135 SV-----VALGGPSWTVLLGRR 151

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 152 DSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 198

Score = 71.6 bits (174), Expect = 5e-10
Identities = 34/69 (49%), Positives = 46/69 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNTLFSVVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
Sbjct: 7 SLSLMLLVAAAMASVASAQLSATFYDTSCPNTLSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFVNVIY 792
HDCFV +
Sbjct: 67 HDCFVQASF 75

>ref|NP_001060628.1| Os07g0677200 [Oryza sativa (japonica cultivar-group)]
dbj|BAC83103.1| peroxidase [Oryza sativa Japonica Group]
dbj|BAF22542.1| Os07g0677200 [Oryza sativa Japonica Group]
dbj|BAG93342.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG96895.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 317

Score = 171 bits (433), Expect = 4e-40
Identities = 78/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAPLD TP +FDN Y+ NL+
Sbjct: 193 QAQCQNFRDRIYNETNIDSAFATQRQANCPRPTSGSGDNLAPLDTTTPNAFDNAYYSNLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 253 SNKGLLHSDQVLFNGGSADNTVRNFAFNAAAFSSAFTTAMVKMGNISPLTGTGQIRLSC 312

Query: 2167 RRIN 2178
++N
Sbjct: 313 SKVN 316

Score = 118 bits (296), Expect = 3e-24
Identities = 72/169 (42%), Positives = 88/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAIAA 1330

+QGCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AA
Sbjct: 71 VQGCDASVLLSGQ-----EQNAGPNVGLRGRFSVIDNAKARVEAICNQTVSCADILAVAA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 126 RDSV-----VALGGPSWTVLLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I

Sbjct: 143 RRDSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 191

Score = 71.2 bits (173), Expect = 6e-10
Identities = 34/65 (52%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNISSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F

Sbjct: 7 SLSLMLLVAAAMASVASAQLSATFYDTSCPINALSTIKSVITAAVNSEARMGASLLRLHF 66

Query: 766 HDCFV 780
HDCFV

Sbjct: 67 HDCFV 71

>tpe|CAH69353.1| TPA: class III peroxidase 111 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 323

Score = 171 bits (433), Expect = 4e-40
Identities = 78/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAPLD TP +FDN Y+ NL+

Sbjct: 199 QAQCQNFDRRIYNETNIDSAFATQRQANCPRTGSGDSNLAPLDTTTPNAFDNAYYSNLL 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C

Sbjct: 259 SNKGLLHSDQVLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTGQIRLSC 318

Query: 2167 RRIN 2178
++N

Sbjct: 319 SKVN 322

Score = 113 bits (283), Expect = 1e-22

Identities = 69/162 (42%), Positives = 84/162 (51%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AARD

Sbjct: 80 GCDASVLLSGQ-----EQNAGPNVGLRGSVIDNAKARVEAICNQT VSCADILAVAARD 134

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR

Sbjct: 135 SV-----VALGGPSWTVLLGRR 151

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALS 1642

D+ TAS++ AN +PAP+S+L +LI FS GL D+VALS

Sbjct: 152 DSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALS 193

Score = 71.6 bits (174), Expect = 5e-10
Identities = 34/69 (49%), Positives = 46/69 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F

Sbjct: 7 SLSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFVNVIY 792

HDCFV +

Sbjct: 67 HDCFVQASF 75

>emb|CBI27501.1| unnamed protein product [Vitis vinifera]
Length = 265

Score = 170 bits (431), Expect = 7e-40
Identities = 82/124 (66%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YN T+I+ FA TR++ CP +G+GD NLAPL+L TP SFDN YFKNL+

Sbjct: 142 QARCVTFRDRVYNGTDIDAGFASTRRRRCPADNGNGDANLAPLELVTPNSFDNYYFKNLI 201

Query: 1987 QKKGLLHSDQQLFNGGSTDIVRGYSTNPGTFSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q+KGLL SDQ LF+GGSTD+IV YS +P TF SDF+AM+KMGDI PLTGS G IRK C

Sbjct: 202 QRKGLLQSDQVLFSGGSTDTIVNEYSKPKTFRSDFASAMVKMGDIEPLTGSAGVIRKFC 261

Query: 2167 RRIN 2178

IN

Sbjct: 262 NVIN 265

Score = 134 bits (337), Expect = 6e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLDD+SS EKNA N NS RG+EVIDNIKS VE +CPGVVSCADI+A+AA
Sbjct: 15 VQGCDASILLDDSSSIQSEKNAPNNLSVRGYEVIDNIKSKVESICPGVVSCADIVAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VS GPTW VKLG
Sbjct: 75 RDASVAVS-----GPTWTVKLG 91

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P+ +L++L+S F + GLS +D+VALSG+ I
Sbjct: 92 RRDSTTSGLSLAATNLPSFRDSLDKLVSLFGSKLSARDMVALSGSHTI 140

>ref|XP_002269266.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 326

Score = 170 bits (431), Expect = 7e-40
Identities = 82/124 (66%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YN T+I+ FA TR++ CP +G+GD NLAPL+L TP SFDN YFKNL+
Sbjct: 203 QARCVTFRDRVYNGTDIDAGFASTRRRRCPADNGNGDANLAPLELVTPNSFDNYYFKNLI 262

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q+KGLL SDQ LF+GGSTD+IV YS +P TF SDF+A+AM+KMGDI PLTGS G IRK C
Sbjct: 263 QRKGLLQSDQVLFSGGSTDTIVNEYSKSPKTFRSDFASAMVKMGDIEPLTGSAGVIRKFC 322

Query: 2167 RRIN 2178
IN
Sbjct: 323 NVIN 326

Score = 134 bits (337), Expect = 6e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLDD+SS EKNA N NS RG+EVIDNIKS VE +CPGVVSCADI+A+AA
Sbjct: 76 VQGCDASILLDDSSSIQSEKNAPNNLSVRGYEVIDNIKSKVESICPGVVSCADIVAVAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

Sbjct: 136 RD+ VS GPTW VKLG
RDASVAVS-----GPTWTVKLG 152

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P+ +L++L+S F + GLS +D+VALSG+ I

Sbjct: 153 RRDSTTSGLSLAATNLPFRDSDLKLVSLFGSKGLSARDMVALSGSHTI 201

Score = 62.4 bits (150), Expect = 3e-07
Identities = 31/69 (44%), Positives = 46/69 (66%), Gaps = 1/69 (1%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGS-ANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLL 753
S S I LA+F+++ AQLS FY +CP +++++ V++A+S+E RM ASL+

Sbjct: 8 SCISPACIFLAVFLILSNMPCEAQLSPTFYDDTCPTALTIRTAVRTAVSRERRMAASLI 67

Query: 754 RLFFHDCFV 780
RL FHDCFV

Sbjct: 68 RLHFHDCFV 76

>ref|XP_002509730.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
gb|EEF51117.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
Length = 323

Score = 170 bits (431), Expect = 7e-40
Identities = 82/125 (65%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIYN ++I+ FA TR++ CP +G+GD NLA LDL TP SFDN YF+NL

Sbjct: 199 QARCLTRGRIYNNASDIDAGFASTRRRRQCPANNGNGDGNLAALDLVTPNSFDNYYFRNL 258

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTD+IV YS +P TFSSDFA+AM+KMGDI PLTGS GEIR+

Sbjct: 259 IQKKGLLQSDQVLFSGGSTDNIVNEYSRSPSTFSSDFASAMVKMGDIEPLTGSQGEIRRL 318

Query: 2164 CRRIN 2178
C +N

Sbjct: 319 CNVVN 323

Score = 141 bits (355), Expect = 5e-31
Identities = 79/169 (46%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILATAA 1330
+QGCDGSILLDDTSS TGEK A N NS RGF+VIDN K+ VE +CPG+VSCADI+A+AA
Sbjct: 72 VQGCDGSILLDDTSSMTGEKFARNNNNSVRGFQVIDNAKAQVESICPGIVSCADIVAVAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W VKLG
Sbjct: 132 RDA-----SVAVGGPSWTVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ +ASQ A+ +P T +L LIS F GLS +D+VALSG I
Sbjct: 149 RRDSTSASQRLADANLPGFTDSLESLSLFRKGLSARDMVALSGAHTI 197

Score = 74.7 bits (182), Expect = 6e-11
Identities = 33/67 (49%), Positives = 51/67 (76%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRL 759
F +R+ + + L VL ++AQLS+NFY ++CPN S++++ ++SA+S+E RM ASL+RL
Sbjct: 6 FFRNRMVLTIFLIVLSSMQSHAQLSSNFYDNTCPNALSTIRTAIRSAVSRERRMSASLRL 65

Query: 760 FFHDCFV 780
FHDCFV
Sbjct: 66 HFHDCFV 72

>emb|CBI18066.1| unnamed protein product [Vitis vinifera]
Length = 263

Score = 170 bits (430), Expect = 1e-39
Identities = 81/124 (65%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETNI+ +F + Q +CP S GDNNL+PLD ++PT+FDN YF NLV
Sbjct: 142 QARCTNFRDRLYNETNIDASFQSSLQANCP--SSGGDNNLSPLDTKSPTTFDNAYFTNLV 199

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLFNGGSTDS V YST TF +DFA A++KMG++SPLTG++G+IR NC
Sbjct: 200 NNKGLLHSDQQLFNGGSTDSQVTTYSTKSTFFTFDFANAIVKMGNSPLTGTSGQIRTNC 259

Query: 2167 RRIN 2178
R+ N
Sbjct: 260 RKTN 263

Score = 150 bits (379), Expect = 8e-34
Identities = 86/169 (50%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCD SILLDDTS+FTGEK A PN NS RGF+VID IKS VE CPGVVSCADILA+ A
Sbjct: 15 VNGCDASILLDDTSNFTGEKTAVPNANSVRGFVDITIKSQVESSCPGVVSCADILAVVA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 75 RDSV-----VALGGPSWTVRLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ IPAPT NL+ LIS FS G S ++VALSG+ I
Sbjct: 92 RRDSTTASLSTANS DIPAPTLNLSGLISSFSNKGFSANEMVALSGSHTI 140

>ref|XP_002268259.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 298

Score = 170 bits (430), Expect = 1e-39
Identities = 81/124 (65%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETNI+ +F + Q +CP S GDNNL+PLD ++PT+FDN YF NLV
Sbjct: 177 QARCTNFRDRLYNETNIDASFQSSLQANCP--SSGGDNNLSPLDTKSPPTFDNAYFTNLV 234

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLFNGGSTDS V YST TF +DFA A++KMG++SPLTG++G+IR NC
Sbjct: 235 NNKGLLHSDQQLFNGGSTDSQVTTYSTKSTFFTFDFANAIVKMGNSPLTGTSGQIRTNC 294

Query: 2167 RRIN 2178
R+ N
Sbjct: 295 RKTN 298

Score = 150 bits (380), Expect = 6e-34
Identities = 86/169 (50%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
++GCD SILLDDTS+FTGEK A PN NS RGF+VID IKS VE CPGVVSCADILA+ A
Sbjct: 50 VKGCDASILLDDTSNFTGEKTAVPNANSVRGFVDITIKSQVESSCPGVVSCADILAVVA 109

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 110 RDSV-----VALGGPSWTVRLG 126

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ IPAPT NL+ LIS FS G S ++VALSG+ I
Sbjct: 127 RRDSTTASLSTANS DIPAPTLNLSGLISSFSNKGFSANEMVALSGSHTI 175

Score = 71.2 bits (173), Expect = 6e-10
Identities = 32/49 (65%), Positives = 39/49 (79%)
Frame = +1

Query: 634 ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFV 780
A+AQL+TN+Y SCPN S +KS V +A++ E RMGASLLRL FHDCFV
Sbjct: 2 ASAQLTTNYSSCPNALSIIKSAVNTAVNNEARMGASLLRRLFHDCFV 50

>ref|XP_002299006.1| predicted protein [Populus trichocarpa]
gb|EEE83811.1| predicted protein [Populus trichocarpa]
Length = 322

Score = 170 bits (430), Expect = 1e-39
Identities = 82/125 (65%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N ++I+ FA TR+++CP SG+G+NNLAPLDL TP SFDN YF+NL
Sbjct: 198 QARCVTFRGRIYDNSSDIDAGFASTRRRNCPSASGNGNNLAPLDLVTPNSFDNYYFRNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q++GLL SDQ LF+G STDSIV YS NP FSSDFAAAM++MGDI PLTGS GEIR+
Sbjct: 258 IQRRLQSDQVLFSGQSTDSIVTEYSRNP SLFSSDFAAAMLRMGDIEPLTGSQGEIRRV 317

Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CSVVN 322

Score = 126 bits (317), Expect = 1e-26
Identities = 72/169 (42%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SI+LD++ S EK + N NS RGFEVID+ K+ VE +CPGVVSCADI A+AA
Sbjct: 71 VQGCDASIMLDNSPIDSEKFSFSNNNSIRGFEVIDDAKAQVESICPGVVSCADIAAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W V+LG
Sbjct: 131 RDA-----SVAVGGPSWTVRLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS+S A++ IP T++L LI F+ GLS +D+VALSG+ I
Sbjct: 148 RRDSTTASRSLADSDIPRATTSLVNLIGMFNGKGLSERDMVALSGSHTI 196

Score = 66.2 bits (160), Expect = 2e-08
Identities = 32/69 (46%), Positives = 47/69 (68%), Gaps = 4/69 (5%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSA----NAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLL 753
SRL++ +F L S+ AQLS+NFY +CPN +++++ ++ A+S E RM ASL+
Sbjct: 3 SRLSLACVVFSLFLISSCLPCQAQLSSNFYDSTCPNALTTIRTAIRRAVSSERRMAASLI 62

Query: 754 RLFFHDCFV 780
RL FHDCFV
Sbjct: 63 RLHFHDCFV 71

>ref|XP_002333334.1| predicted protein [Populus trichocarpa]
gb|EEE74658.1| predicted protein [Populus trichocarpa]
Length = 322

Score = 170 bits (430), Expect = 1e-39
Identities = 82/125 (65%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N ++I+ FA TR+++CP SG+G+NNLAPLDL TP SFDN YF+NL
Sbjct: 198 QARCVTFRGRIDNSSDIDAGFASTRRRNCPSASGNGNNLAPLDLVTNPSFDNYYFRNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q++GLL SDQ LF+G STDSIV YS NP FSSDFAAAM++MGDI PLTGS GEIR+
Sbjct: 258 IQRRGLLQSDQVLFSGQSTDSIVTEYSRNP SLFSSDFAAAMLRMGDIEPLTGSQGEIRRV 317

Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CSVVN 322

Score = 126 bits (316), Expect = 2e-26
Identities = 71/169 (42%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SI+LD++ S EK + N NS RGFEV+D+ K+ VE +CPGVVSCADI A+AA
Sbjct: 71 VQGCDASIMLDNPSIDSEKFSFSNNNSIRGFEVVDDAKAQVESICPGVVSCADIAAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W V+LG
Sbjct: 131 RDA-----SVAVGGPSWTVRLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS+S A++ IP T++L LI F+ GLS +D+VALSG+ I
Sbjct: 148 RRDSTTASRSLADSDIPRATTSVLNLI GMFNGKGLSERDMVALSGSHTI 196

Score = 66.2 bits (160), Expect = 2e-08
Identities = 32/69 (46%), Positives = 47/69 (68%), Gaps = 4/69 (5%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSA----NAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLL 753
SRL++ +F L S+ AQLS+NFY +CPN +++++ ++ A+S E RM ASL+
Sbjct: 3 SRLSLACVVFSLFLISSCLPCQAQLSSNFYDSTCPNALTTIRTAIRRAVSSERRMAASLI 62

Query: 754 RLFFHDCFV 780
RL FHDCFV
Sbjct: 63 RLHFHDCFV 71

>ref|XP_002285723.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 317

Score = 170 bits (430), Expect = 1e-39
Identities = 84/124 (67%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR+RIYNETNI+ AFA ++Q+ CP T G DNNL+ LD +T T FDN YF+NL
Sbjct: 195 KARCTSFRRSRIYNETNIDAAFATSKQKICPSTGG--DNNLSDLD-ETTTVFDNVYFRNLK 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQL+NGGSTDSIV YSTN TF +D A AMIKMG++SPLTG+NGEIR +C
Sbjct: 252 AKKGLLHSDQQLYNGGSTDSIVETYSTNSATFFTDVANAMIKMGNLSPLTGTNGEIRTDC 311

Query: 2167 RRIN 2178
++IN
Sbjct: 312 KKIN 315

Score = 155 bits (391), Expect = 3e-35
Identities = 85/167 (50%), Positives = 103/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD SILLDDT+SFTGEK A PN++S RG+EVID IKS VE +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILLDDTASFTGEKTAGPNKDSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW ++LGRR
Sbjct: 130 SV-----VALGGPTWTLQLGRR 146

Query: 1517 DARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN+ +P P S+L+ LISRFS G +TK++VALSGT I
Sbjct: 147 DSTTASLSTANS DLPASPDLSTLISRFSNKGFTTKEMVALSGTHTI 193

Score = 75.1 bits (183), Expect = 4e-11
Identities = 38/70 (54%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+NFY SCP S++++ V +A++KE RMGASL
Sbjct: 1 MASLSLFSLFCVFSFLL--GMAHAQLSSNFYASSCPKALSTIRAAVNNAVAKERRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>emb|CAA46916.1| peroxidase [Oryza sativa (japonica cultivar-group)]
prf||1909367A peroxidase
Length = 317

Score = 170 bits (430), Expect = 1e-39
Identities = 77/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAP+D TP +FDN Y+ NL+
Sbjct: 193 QAQCQNFDRRIYNETNIDSAFATQRQANCPRPTSGGDSNLAPVDTTTPNAFDNAYYSNLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 253 SNKGLLHSDQVLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQGI RLSL 312

Query: 2167 RRIN 2178
++N
Sbjct: 313 SKVN 316

Score = 118 bits (296), Expect = 3e-24
Identities = 72/169 (42%), Positives = 88/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AA

Sbjct: 71 VQGCDASVLLSGQ-----EQNAGPNVGLRGRFVIDNAKARVEAICNQTVSCADILAVAA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 126 RDSV-----VALGGPSWTVLLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 143 RRDSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 191

Score = 71.2 bits (173), Expect = 6e-10
Identities = 34/65 (52%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F

Sbjct: 7 SLSLMLLVAAAMASVASAQLSATFYDTSCPINALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFV 780
HDCFV

Sbjct: 67 HDCFV 71

>ref|XP_002319967.1| predicted protein [Populus trichocarpa]
gb|EEE95890.1| predicted protein [Populus trichocarpa]
Length = 312

Score = 169 bits (429), Expect = 1e-39
Identities = 82/120 (68%), Positives = 94/120 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q +C FRARIYNETNI+ +FA RQ+ CP T+G D+NLAPLD QTP FDN Y+KNL+

Sbjct: 191 QTKCKTFRARIYNETNIDKSFATMRQKMCPLTTG--DDNLAPLDFQTPNVFDNYYKNLI 248

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ LF+G STDS+VR YS NP F SFAAAM+KMGDI P TG+ GEIRK C

Sbjct: 249 HKKGLLHSDQVLFSGESTDSLVRTYSNPNDFISSDFAAAMVKMGDIDPRTGTRGEIRKCC 308

Score = 140 bits (352), Expect = 1e-30
Identities = 75/169 (44%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
++GCD SILL+DT++F GE+ A PN NS RG+ V+ IKS +EKVCPG+VSCADI+ IAA
Sbjct: 64 VKGCDASILLEDATATFKGEQGAGPNNSVRGYNVVAKIKSKLEKVCPCGIVSCADIVVIA 123

Query: 1331 RDSVQIVSGQTTNKNLNLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS ++ LGGP W VKLG
Sbjct: 124 RDS-----TVLLGGPYWKV KLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TA+ +AA+ +P+ TS ++QLI RF + GLS D+VALSG+ I
Sbjct: 141 RRDSKTANMNAASKSLPSDTSTVSQLIKRFKSKGLSATDMVALSGSHTI 189

Score = 84.3 bits (207), Expect = 7e-14
Identities = 40/63 (63%), Positives = 51/63 (80%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHD 771
+++ LAL ++ S++A LST+FY SCP LF +VKS VQSAI+KE RMGASL+RLFFHD
Sbjct: 2 VSVTLALLLIYTSSSSAHLSTDFYDKSCPQLFGTVKSVVQSAIAKERRMGASLVRLFFHD 61

Query: 772 CFV 780
CFV
Sbjct: 62 CFV 64

>gb|ABK24123.1| unknown [Picea sitchensis]
Length = 208

Score = 169 bits (427), Expect = 2e-39
Identities = 81/124 (65%), Positives = 100/124 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSVSGDNNLAPLDLQTPTSFNYYFKNLV 1986
+ARCT+FR IYN++NI+TA+A++ Q CPR+ G DN L+PLD QTPT F+N Y+KNLV
Sbjct: 87 KARCTFRDHIYNSNIDTAYAKSLQAKCPRSGG--DNRLSPLDYQTPTKFENNYKLV 144

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNG STDS+V YS N F +DFAAAMIKMG+I PLTGS G+IRKNC
Sbjct: 145 ARKGLLHSDQELFNGVSTDSLVTKYKSNLKLFEFNDFAAAMIKMGNIMPLTGSQGIIRKNC 204

Query: 2167 RRIN 2178
R+ N
Sbjct: 205 RKRN 208

Score = 91.7 bits (226), Expect = 4e-16
Identities = 54/124 (43%), Positives = 66/124 (53%)
Frame = +2

Query: 1274 VEKVC PGV VSCADILAI AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRT 1453
+EK C GVVSCADILA+AARDSV
Sbjct: 1 MEKACSGVVSCADILAVAARDSV----- 23

Query: 1454 FC*F*SI*LGGPTWNVKLGRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLV 1633
+ LGGPTW V LGRRD+ TA+++AAN IPAPT+NL L S+F A GLS +++V
Sbjct: 24 -----VTLGGPTWTVM LGRRDSGTANRTAANTNIPAPTANLANLTSKFGAQGLSKREMV 77

Query: 1634 ALSG 1645
LSG
Sbjct: 78 VLSG 81

>gb|AAA20473.1| peroxidase [Cenchrus ciliaris]
Length = 313

Score = 169 bits (427), Expect = 2e-39
Identities = 78/124 (62%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR IYN+TNI T FA + + +CPR +GSGD NLA LD TP +FDN YFKNL+
Sbjct: 190 QAQCLNFRDHIYNDTNINTGFASLKANCPRTGSGDGNLASLDTSTPYTFDNAYFKNLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGSTD+ VR +++NP FSS FAAAM+KM +SPLTGS G+IR C
Sbjct: 250 SQKGLLHSDQELFNGGSTDNVTRNFASNPSAFSSAFAAAMVKMASLSPLTGSQQIRLTC 309

Query: 2167 RRIN 2178
+ N
Sbjct: 310 SKAN 313

Score = 103 bits (258), Expect = 9e-20
Identities = 67/170 (39%), Positives = 85/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI A 1330
+QGCD S+LLD GE+ A PN S RGF+VI NIK+ VE +C VSCADILA+ A
Sbjct: 66 VQGCDASVLLDSG----GEQGAIPNAGSLRGFDVIANIKAQVEAICKQTVSCADILAVGA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
R SV + LGGP+W V LG
Sbjct: 122 RHSV-----VALGGPSWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTS--NLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ + S + AN+ +PA S NL+QLI F G + ++VALSG I
Sbjct: 139 RRDSTSGSAALANSDLPASRSFNLSQLIGSFDNKGFTATEMVALSGAHTI 188

Score = 73.2 bits (178), Expect = 2e-10
Identities = 39/70 (55%), Positives = 47/70 (67%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L + + A+AQLS FY SCPN S++KS V +A+ KE RMGASL
Sbjct: 1 MASSVSGLLMLCMAAV----ASAQLSATFYDTSCPNALSTIKSAVTA AVKKNRMGASL 56

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 57 LRLHFHDCFV 66

>gb|ABK23423.1| unknown [Picea sitchensis]
Length = 318

Score = 168 bits (426), Expect = 3e-39
Identities = 81/124 (65%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNE+NI+T+ A + CPRT G DN L+PLDL TP +FD +Y+ NL
Sbjct: 197 QARCTSFARIYNESNIDTSLATAVKPKCPRTGG--DNTLSPLDLATPITFDKHYYCNLR 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNGGSTDS V YSTN F +DFAAAM+ MG+I PLTG++G+IR+NC
Sbjct: 255 SKKGLLHSDQQLFNGGSTDSQVTTYSTNQNNFFTDFAAAMVMGNIKPLTGTSGQIRRNC 314

Query: 2167 RRIN 2178
R+ N
Sbjct: 315 RKS N 318

Score = 149 bits (377), Expect = 1e-33
Identities = 86/169 (50%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+ GCDGSILLDD S+FTGEK A PN NS RG++VID IK+ VE C GVVSCADI+AIAA
 Sbjct: 70 VNGCDGSILLDDNSTFTGEKTATPNNSVRYDVIDTIKTQVEAACSGVVSCADIVAIAA 129
 Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGPTWNVKLG 1510
 RDSV + LGGPTW V LG
 Sbjct: 130 RDSV-----VALGGPTWTVLLG 146
 Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ TAS +AAN+ IP+P SNL+ LIS F + LS KDLVALSG I
 Sbjct: 147 RRDSTTASFNAANSSIPSPASNLSTLISSFRSHNLSPKDLVALSGAHTI 195

Score = 66.6 bits (161), Expect = 2e-08
 Identities = 33/64 (51%), Positives = 44/64 (68%), Gaps = 2/64 (3%)
 Frame = +1

Query: 598 ICLALFVL--IWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
 I + LF++ I + QL++ FY SCP S V++ V+ A++KE RMGASLLRL FHD
 Sbjct: 8 IPIVLFIIICSIPNIVHGQLTSTFYSESCPRALSIVQAAVEQAVAKERRMGASLLRRLFHD 67

Query: 772 CFVN 783
 CFVN
 Sbjct: 68 CFVN 71

>ref|NP_001060629.1| Os07g0677300 [Oryza sativa (japonica cultivar-group)]
 sp|Q0D3N0.1|PER2_ORYSJ RecName: Full=Peroxidase 2; Flags: Precursor
 dbj|BAA03911.1| peroxidase [Oryza sativa Japonica Group]
 dbj|BAC79528.1| peroxidase [Oryza sativa Japonica Group]
 dbj|BAC83104.1| peroxidase [Oryza sativa Japonica Group]
 tpe|CAH69354.1| TPA: class III peroxidase 112 precursor [Oryza sativa (japonica
 cultivar-group)]
 dbj|BAF22543.1| Os07g0677300 [Oryza sativa Japonica Group]
 dbj|BAG93552.1| unnamed protein product [Oryza sativa Japonica Group]
 gb|EEE67816.1| hypothetical protein OsJ_25570 [Oryza sativa Japonica Group]
 Length = 314

Score = 168 bits (426), Expect = 3e-39
 Identities = 76/124 (61%), Positives = 99/124 (79%)
 Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
 QA+C NFR R+YNETNI+++FA + +CPR +GSGD+NLAPLD TP +FD+ Y+ NL+
 Sbjct: 191 QAQCQNFDRRLYNETNIDSSFATALKANCPRTGSGDSNLAPLDTTTPNAFDSAYYTNLL 250

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
 KLLHSDQ LFNGGSTD+ VR +S+N F+S F AAM+KMG+ISPLTG+ G+IR NC
 Sbjct: 251 SNKGLLHSDQVLFNGGSTDNTVRNFSSNTAAFNSAFTAAMVKMGNISPLTGTGQIRLNC 310

Query: 2167 RRIN 2178
 ++N
Sbjct: 311 SKVN 314

Score = 121 bits (303), Expect = 5e-25
Identities = 72/169 (42%), Positives = 89/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
 +QGCD S+LL E+NA PN S RGF V+DNIK+ VE +C VSCADILA+AA
Sbjct: 69 VQGCDA SVLLSGQ-----EQNAGPNAGSLRGNVVDNIKTQVEAICSQTVSCADILAVAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDSV + LGGP+W V LG
Sbjct: 124 RDSV-----VALGGPSWTVLLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ TA++S AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 141 RRDSTTANESQANTDLPAPSSSLAELIGNFSRKGLDVTDVMAVLSGAHTI 189

Score = 70.5 bits (171), Expect = 1e-09
Identities = 36/70 (51%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
 MAS S +++ L + + +A+AQLS FY SCPN S++KS V +A++ E RMGASL
Sbjct: 1 MAS-ASSVSLMLLVAAAMASAASAQLSATFYDTSCPNALSTIKSAVTA AVNSEPRMGASL 59

Query: 751 LRLFFHDCFV 780
 +RL FHDCFV
Sbjct: 60 VRLHFHDCFV 69

>gb|ACJ11762.1| class III peroxidase [Gossypium hirsutum]
 Length = 323

Score = 168 bits (425), Expect = 4e-39
Identities = 80/124 (64%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
 QARCT FR RIYNETNI++ FA + + +CP S GDN+L+PLD + TSFDN YFKNL
Sbjct: 202 QARCTTFRTRIYNETNIDSTFATSLRANCP--SNGGDNSLSPLDTSSTSF DNAYFKNLQ 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQLF+GGSTDS V YS+N G+F++DFA AM+KMG++SPLTG++G+IR NC
Sbjct: 260 GQKGLLHSDQQLFSGGSTDSQVNAYSSNLGSFTTDFANAMVKMGNLSPLTGTSGQIRTNC 319

Query: 2167 RRIN 2178
R+ N
Sbjct: 320 RKAN 323

Score = 152 bits (384), Expect = 2e-34
Identities = 87/169 (51%), Positives = 103/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDT++ TGEK A PN NSARGFEVID IKS VE +CPGVVSCADI+A+AA
Sbjct: 75 VNGCDGSILLDDTANMTGEKTAVPNSNSARGFEVIDTIKSQVESLCPGVVSCADIVAVAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 135 RDSV-----VALGGPSWIVLLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ IPAPT NL+ LI+ FS G + K++VALSG+ I
Sbjct: 152 RRDSTTASLSAANSNIPAPTLNLSGLITAFSNKGFTAKEMVALSGSHTI 200

Score = 72.0 bits (175), Expect = 4e-10
Identities = 39/75 (52%), Positives = 48/75 (64%)
Frame = +1

Query: 559 SKLTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRM 738
SK S R + + LF+L+ A AQLS+ FY +CP S++KS V SA+S E RM
Sbjct: 3 SKTCSPSNKLRFLLMVLFLLM-NMATAQLSSTFYSTTCPRALSTIKSAVNSAVSNEARM 61

Query: 739 GASLLRRLFHDCFVN 783
GASL RL FHDCFVN
Sbjct: 62 GASLPRLHFHDCFVN 76

>gb|ABK25962.1| unknown [Picea sitchensis]
Length = 323

Score = 168 bits (425), Expect = 4e-39
Identities = 79/124 (63%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986

QARC NFRA IYN+TNI + ++ + + CP T+GSGDNNL+PLD +PT+FD Y+ NL
Sbjct: 200 QARCFNFRAHIYNDTNILSTYSTSLRSKCPPTNGSGDNNLSPLDYVSPTAFDKNYYCNLK 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS V Y++N F SDFAAAM+KMG+I PLTG++G+IRKNC

Sbjct: 260 IKKGLLHSDQELFNGGSTDSQVTTYASNQNIFFSDFAAAMVKGNIKPLTGTSGQIRKNC 319

Query: 2167 RRIN 2178

R+ N

Sbjct: 320 RKPN 323

Score = 153 bits (387), Expect = 9e-35
Identities = 87/169 (51%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDD+S TGEK A PN NSARGF+VID IKS VEK C GVVSCADILAIAA

Sbjct: 73 VNGCDGSVLLDDSSKITGEKTAVPNANSARGFDVIDTIKSQVEKSCSGVVSCADILAIAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 133 RDSV-----VELGGPSWTVLLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS+S ANN IP PTS+L+++IS F A GLS K++VAL+G I

Sbjct: 150 RRDSTTASKSGANNIPPTSSLSKIIISLFQAQGLSAKEMVALAGAHTI 198

Score = 69.3 bits (168), Expect = 2e-09
Identities = 36/65 (55%), Positives = 45/65 (69%), Gaps = 4/65 (6%)
Frame = +1

Query: 601 CLALFVLIWGS----ANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFH 768
C+A+ V I S ++ QLS+ FY SCP S VK+ V+ A++KE RMGASLLRL FH

Sbjct: 10 CIAVMVFIICSIANLSHGQLSSTFYDKSCPAALS VVKA AVKQAVAKEQRMGASLLRLHFH 69

Query: 769 DCFVN 783

DCFVN

Sbjct: 70 DCFVN 74

>gb|EAZ05133.1| hypothetical protein OsI_27326 [Oryza sativa Indica Group]
Length = 324

Score = 168 bits (425), Expect = 4e-39
Identities = 77/124 (62%), Positives = 97/124 (78%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLA LD TP +FDN Y+ NL+
Sbjct: 200 QAQCQNFRDRIYNETNIDSAFATQRQANCPRTGSGDSNLAALDTPNAFDNAYYSNLL 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNNGS D+ VR ++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 260 SNKGLLHSDQVLFNNGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQQIRLSC 319

Query: 2167 RRIN 2178
++N
Sbjct: 320 SKVN 323

Score = 116 bits (290), Expect = 2e-23
Identities = 71/167 (42%), Positives = 86/167 (51%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCVGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AARD
Sbjct: 80 GCDASVLLSQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAARD 134

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 135 SV-----VALGGPSWTVLLGRR 151

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 152 DSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 198

Score = 71.6 bits (174), Expect = 5e-10
Identities = 34/69 (49%), Positives = 46/69 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
Sbjct: 7 SLSLMLLVAAAMASVASAQLSATFYDTSCPINALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFVNVIY 792
HDCFV +
Sbjct: 67 HDCFVQASF 75

>ref|NP_001046400.1| Os02g0240100 [Oryza sativa (japonica cultivar-group)]
Length = 335

Score = 168 bits (425), Expect = 4e-39
Identities = 74/123 (60%), Positives = 101/123 (82%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++C NFR R+YN+TNI+ AFA R++ CP GSGD++LAPLD QT FDN Y++NL+
Sbjct: 211 SQCANFRDRVYNDTNIDPAFAALRRRGCPAAPGSGDSSLAPLDAQTNVFDNAYYRNLLA 270

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++V+ YS+NP F++DFAAAMIKMG+I PLTG+ G+IR++CR
Sbjct: 271 QRGLLHSDQELFNGGSQDALVQQYSSNPALFAADFAAAMIKMGNIKPLTGAAGQIRRSR 330

Query: 2170 RIN 2178
+N
Sbjct: 331 AVN 333

Score = 134 bits (337), Expect = 6e-29
Identities = 80/171 (46%), Positives = 97/171 (56%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1324
+QGCD SILLDD +SF GEK A PN NS RG++VID IK VE +CPGVVSCADI+A+
Sbjct: 81 VQGCDASILLDDVPATSFVGEKTAFPNVNSVRGYDVIDQIKRNVLLCPGVVSCADIVAL 140

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 141 AARDSTAL-----LGGPSWAVP 157

Query: 1505 LRRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
LRRRD+ TAS SAAN+ +PAP+S+L LI+ F GLS +D+ ALSG I
Sbjct: 158 LRRRDSTTASLSAANSDLPAPSSDLATLIAGFGNKGLSPRDMTALSGAHTI 208

Score = 70.1 bits (170), Expect = 1e-09
Identities = 42/82 (51%), Positives = 52/82 (63%), Gaps = 4/82 (4%)
Frame = +1

Query: 547 LVCLSKLTMASFCSRLTICLALFVLIWGSANA----QLSTNFYHSCP NFLSSVKSTVQS 714
L+ + ++TMAS S CL F L+ +A A QLST FY SCP L V++TV
Sbjct: 1 LIKICEITMASRSS-WHCCLLAFFLLSSAAGAAYGQQLSTTFYAASCP TLQVVVRATVLG 59

Query: 715 AISKETRMGASLLRFFHDCFV 780
A+ E RMGASL+RFFHDCFV
Sbjct: 60 ALLAERRMGASLVRFFHDCFV 81

>gb|AAC49818.1| peroxidase [Oryza sativa Indica Group]
Length = 317

Score = 168 bits (425), Expect = 4e-39
Identities = 77/124 (62%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLA LD TP +FDN Y+ NL+
Sbjct: 193 QAQCQNFDRRIYNETNIDSAFATQRQANCPRTGSGDSNLAALDTPNAFDNAYYSNLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNNGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 253 SNKGLLHSDQVLFNNGSADNTRNFASNAAAFSSAFTTAMVKMGNISPLTGTQGIIRLSC 312

Query: 2167 RRIN 2178
++N
Sbjct: 313 SKVN 316

Score = 118 bits (296), Expect = 3e-24
Identities = 72/169 (42%), Positives = 88/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AA
Sbjct: 71 VQGCDASVLLSGQ-----EQNAGPNVGLRGFVIDNAKARVEAICNQTVSCADILAVAA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 126 RDSV-----VALGGPSWTVLLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 143 RRDSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 191

Score = 71.2 bits (173), Expect = 6e-10
Identities = 34/65 (52%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
Sbjct: 7 SSSLMLLVAAAMASVASAQLSATFYDTPSCPNALSTIKSVITA AVNSEARMGASLLRLLHF 66

Query: 766 HDCFV 780

HDCFV
Sbjct: 67 HDCFV 71

>dbj|BAD28869.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69272.1| TPA: class III peroxidase 30 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAG98261.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAF08314.2| Os02g0240100 [Oryza sativa Japonica Group]
Length = 327

Score = 168 bits (425), Expect = 4e-39
Identities = 74/123 (60%), Positives = 101/123 (82%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
++C NFR R+YN+TNI+ AFA R++ CP GSGD++LAPLD QT FDN Y++NL+
Sbjct: 203 SQCANFRDRVYNDTNIDPAFAALRRRGCPAAPGSGDSSLAPLDAQTNVFDNAYYRNLLA 262

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++V+ YS+NP F++DFAAAMIKMG+I PLTG+ G+IR++CR
Sbjct: 263 QRGLLHSDQELFNGGSQDALVQQYSSNPALFAADFAAAMIKMGNIKPLTGAAGQIRRSR 322

Query: 2170 RIN 2178
+N
Sbjct: 323 AVN 325

Score = 134 bits (337), Expect = 6e-29
Identities = 80/171 (46%), Positives = 97/171 (56%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1324
+QGCD SILLDD +SF GEK A PN NS RG++VID IK VE +CPGVVSCADI+A+
Sbjct: 73 VQGCASILLDDVPATSFVGEKTAFPNVNSVRGYDVIDQIKRNVELLCPGVVSCADIVAL 132

Query: 1325 AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 133 AARDSTAL-----LGGPSWAVP 149

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
LGRRD+ TAS SAAN+ +PAP+S+L LI+ F GLS +D+ ALSG I
Sbjct: 150 LGRRDSTTASLSAANSDL PAPSDDLATLIAGFGNKGLSPRDMTALSGAHTI 200

Score = 66.6 bits (161), Expect = 2e-08

Identities = 36/64 (56%), Positives = 42/64 (65%), Gaps = 4/64 (6%)
Frame = +1

Query: 601 CLALFVLIWGSANA----QLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFH 768
CL F L+ +A A QLST FY SCP L V++TV A+ E RMGASL+RLFFH
Sbjct: 10 CLLAFFLLSSAAGAAYGQQLSTTFYAASCPTLQVVVRATVLGALLAERRMGASLVRLFFH 69

Query: 769 DCFV 780
DCFV
Sbjct: 70 DCFV 73

>ref|XP_002274693.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 324

Score = 167 bits (424), Expect = 5e-39
Identities = 85/125 (68%), Positives = 96/125 (76%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP +G GD+NLA LDL TP SFDN YFKNL
Sbjct: 200 QARCVTFRDRIYDNGTDIDAGFASTRRRRCPADNGDGDNNLAALDLVTPNSFDNYYFKNL 259

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTDSIV YS N TFSSDFA AM+KMGDI PLTG+ GEIR+
Sbjct: 260 IQKKGLLQSDQVLFSGGSTDSIVSEYSKNRKTFSDFALAMVKMGDIEPLTGAAGEIREF 319

Query: 2164 CRRIN 2178
C IN
Sbjct: 320 CNAIN 324

Score = 136 bits (343), Expect = 1e-29
Identities = 76/169 (44%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLDD+SS EKNA N NSARG+EVI ++KS VE +CPG+VSCADILA+AA
Sbjct: 73 VQGCDASILLDDSSSIQSEKNAPNNLNSARGYEV IHDVKSQVESICPGIVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNLTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW VKLG
Sbjct: 133 RDA-----SVAVGGPTWTVKLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S ++ +P+ +L++LIS F + GLST+D+VALSG+ I
Sbjct: 150 RRDSTTSGLSQVSSNLPSFRDSLRLISLFGSKGLSTRDMVALSGSHTI 198

Score = 63.2 bits (152), Expect = 2e-07
Identities = 31/73 (42%), Positives = 46/73 (63%), Gaps = 3/73 (4%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGS---ANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMG 741
M S C + + VL+ S AQLS++FY ++CP S++++ + A+S+E RM
Sbjct: 1 MGSIAGNYGACIFVA VLLILSIMPCEAQLSSSFYDNTCPKALSTIRTATRKAVSRERRMA 60

Query: 742 ASLLR LFFHDCFV 780
ASL+RL FHDCFV
Sbjct: 61 ASLIRLHFHDCFV 73

>gb|EEC82680.1| hypothetical protein OsI_27324 [Oryza sativa Indica Group]
Length = 318

Score = 167 bits (424), Expect = 5e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+
Sbjct: 195 QAQCQNFDRRLYNETNIDAAFAAALKASCPRPTGSGDGNLAPLDTTTPTAFDNAYYTLL 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C
Sbjct: 255 SNKGLLHSDQVLFNGGAVDGGVRSYASGPSRFRDFAAAMVKMGNIAPLTGTGQGI RLVLC 314

Query: 2167 RRIN 2178
++N
Sbjct: 315 SKVN 318

Score = 130 bits (327), Expect = 9e-28
Identities = 73/165 (44%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AA
Sbjct: 68 VQGCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 128 RDSV-----VALGGPSWRVLLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645

RRD+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG
Sbjct: 145 RRDSTTASLALANSDLPPPSFDVANLTAAFAAKGLSQADMVALSG 189

Score = 64.3 bits (155), Expect = 8e-08
Identities = 32/63 (50%), Positives = 43/63 (68%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L +CLAL + G QLS FY SCP + +++ V++A+++E RMGASLLRL FHD
Sbjct: 9 LLLCLALAGSVSGQ---QLSATFYRSRCPRALAIIRAGVRAAVAQEPRMGASLLRRLFHD 65

Query: 772 CFV 780
CFV
Sbjct: 66 CFV 68

>ref|NP_001060626.1| Os07g0676900 [Oryza sativa (japonica cultivar-group)]
dbj|BAF22540.1| Os07g0676900 [Oryza sativa Japonica Group]
Length = 333

Score = 167 bits (424), Expect = 5e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+
Sbjct: 210 QAQCQNFRDRLYNETNIDAAFAAALKASCPRTSGSGDGNLAPLDTTPTAFDNAYYTLL 269

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C
Sbjct: 270 SNKGLLHSDQVLFNGGAVDGGQVRSYASGSPRFRDFAAAMVKMGNIAPLTGTQQGIRLVC 329

Query: 2167 RRIN 2178
++N
Sbjct: 330 SKVN 333

Score = 130 bits (327), Expect = 9e-28
Identities = 73/165 (44%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI AA 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AA
Sbjct: 83 VQGCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDSV + LGGP+W V LG
Sbjct: 143 RDSV-----VALGGPSWRVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG

Sbjct: 160 RRSTTASLALANSDLPPPSFDVANLTASFAAKGLSQADMVALSG 204

Score = 68.6 bits (166), Expect = 4e-09
Identities = 38/74 (51%), Positives = 50/74 (67%), Gaps = 1/74 (1%)
Frame = +1

Query: 562 KLTMASFCS-RLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRM 738
+LTMAS S L +CLAL + G QLS FY SCP + +++ V++A+++E RM
Sbjct: 13 RLTMASCLSVLLLLCLALAGSVSGQ---QLSATFYRSCPRALAIIRAGVRAAVAQEP RM 69

Query: 739 GASLLRRLFHDFCV 780
GASLLR L F H D C F V
Sbjct: 70 GASLLR L F H D C F V 83

>emb|CAH10840.1| peroxidase [Picea abies]
Length = 320

Score = 167 bits (424), Expect = 5e-39
Identities = 81/124 (65%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYNE+NI AFA + + +CP S GDN L+PLD+ TPT+FDN Y+ NL
Sbjct: 199 QSRCAFFRTRIYNESNINAAFATSVKPNCP--SAGGDNTLSPLDVVPTTFDNKYYSNLK 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGNGEIRKNC 2166
+KGLLHSDQQLFNGGSTDS V YSTN +F +DFAAAM+KMG+ISPLTG++G+IRKNC
Sbjct: 257 VQKGLLHSDQQLFNGGSTDSQVTTYSTNQNSFFTFDFAAAMVKMGNISPLTGTSQQIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKAN 320

Score = 151 bits (381), Expect = 5e-34
Identities = 87/169 (51%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDD ++FTGEK A PN NSARGF+VID IK+ VE C GVVSCADIL IAA

Sbjct: 72 VNGCDGSILLDDNATFTGEKTAGPNANSARGFDVIDTIKTQVEAACSGVWSCADILTIAA 131

Query: 1331 RDSVQIVSGQTTNKNLNLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS+ + L GPTW V LG

Sbjct: 132 RDSI-----VELQGPTWTVMLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAANN IP+P S+L+ LI+ F GLSTKDLVALSG I

Sbjct: 149 RRDSPTASLSAANNIPASSLSTLITSFQNHGLSTKDLVALSGAHTI 197

Score = 69.3 bits (168), Expect = 2e-09
Identities = 34/70 (48%), Positives = 46/70 (65%), Gaps = 5/70 (7%)
Frame = +1

Query: 589 RLTICLALFVLIWGS-----ANAQLSTNFYHSCPFLFSSVKSTVQSAISKETRMGASLL 753
R +C+ + ++ S N QLS+ FY SCP + S VK+ V+ A++KE RMGASL+

Sbjct: 4 RTLVCIGVMVLLCSININAVNGQLSSTFYAKSCPVRQSIKTVVKQAVAKEKRMGASLV 63

Query: 754 RLFFHDCFVN 783

RL FHDCFVN

Sbjct: 64 RLHFHDCFVN 73

>dbj|BAC83101.1| putative peroxidase precursor [Oryza sativa Japonica Group]
gb|EEE67813.1| hypothetical protein OsJ_25567 [Oryza sativa Japonica Group]
Length = 318

Score = 167 bits (424), Expect = 5e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+

Sbjct: 195 QAQCQNFDRRLYNETNIDAAFAAALKASCPRTGSGDGNLAPLDTTPTAFDNAYYTNLL 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C

Sbjct: 255 SNKGLLHSDQVLFNGGAVDQVRSYASGSPRRRDFAAAMVKMGNIAPLTGTGQIRLVC 314

Query: 2167 RRIN 2178

++N

Sbjct: 315 SKVN 318

Score = 130 bits (327), Expect = 9e-28
Identities = 73/165 (44%), Positives = 94/165 (56%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AA

Sbjct: 68 VQGCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 128 RDSV-----VALGGPSWRVLLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRD+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG

Sbjct: 145 RRDSTTASLALANSDLPPPSFDVANLTASFAAKGLSQADMVALSG 189

Score = 64.3 bits (155), Expect = 8e-08

Identities = 32/63 (50%), Positives = 43/63 (68%)

Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771

L +CLAL + G QLS FY SCP + +++ V++A+++E RMGASLLRL FHD

Sbjct: 9 LLLCLALAGSVSGQ---QLSATFYRSRCPRALAIRAGVRAAVAQEPRMGASLLRRLFHD 65

Query: 772 CFV 780

CFV

Sbjct: 66 CFV 68

>tpe|CAH69351.1| TPA: class III peroxidase 109 precursor [Oryza sativa (japonica
cultivar-group)]

Length = 322

Score = 167 bits (424), Expect = 5e-39

Identities = 77/124 (62%), Positives = 95/124 (76%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+

Sbjct: 199 QAQCQNFRDRLYNETNIDAAFAAALKASCPRTSGSGDGNLAPLDTTTPTAFDNAYYTPLL 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

KGLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C

Sbjct: 259 SNKGLLHSDQVLFNGGAVDQVRSYASGPSRFRDFAAAMVKMGNIAPLTGTGQIRLVC 318

Query: 2167 RRIN 2178

++N

Sbjct: 319 SKVN 322

Score = 128 bits (321), Expect = 4e-27
Identities = 72/163 (44%), Positives = 92/163 (56%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AARD
Sbjct: 74 GCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAARD 133

Query: 1337 SVQIVSQGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 134 SV-----VALGGPSWRVLLGRR 150

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
D+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG
Sbjct: 151 DSTTASLALANSDLPPPSFDVANLTASFAAKGLSQADMVALSG 193

Score = 64.3 bits (155), Expect = 8e-08
Identities = 32/63 (50%), Positives = 43/63 (68%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L +CLAL + G QLS FY SCP + +++ V++A+++E RMGASLLRL FHD
Sbjct: 9 LLLCLALAGSVSGQ---QLSATFYRSRCPRALAIRAGVRAAVAQEPRMGASLLRRLFHD 65

Query: 772 CFV 780
CFV
Sbjct: 66 CFV 68

>ref|XP_002451848.1| hypothetical protein SORBIDRAFT_04g008620 [Sorghum bicolor]
gb|EES04824.1| hypothetical protein SORBIDRAFT_04g008620 [Sorghum bicolor]
Length = 278

Score = 167 bits (423), Expect = 6e-39
Identities = 79/124 (63%), Positives = 100/124 (80%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSVSGG-DNNLAPLDLQTPTSFNYYFKNLV 1986
++C NFR IYN+T+I+ AFA RQ+SCP G+G D NLA LD+QT FDN Y++NL+
Sbjct: 153 SQCNFRGHIYNDTDIDAAFAALRQRSCPAAPGTGGDTNLAALDVQTLVFDNAYYRNL 212

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GLLHSDQ+LFNGGS D++VR YS+NP F+SDFAAAMIKMG+ISPLTG+ G+IR NC
Sbjct: 213 AKRGLLHSDQELFNGGSQDALVRQYSSNPALFASDFAAAMIKMGNISPLTGTAGQIRANC 272

Query: 2167 RRIN 2178
R +N
Sbjct: 273 RVVN 276

Score = 134 bits (338), Expect = 5e-29
Identities = 78/169 (46%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCDGSILLDD SF GEK A PN NS RGF+VID IK+ VE +CPGVVSCADI+A+AA
Sbjct: 25 VQGCDGSILLDDVGSFVGEKGAGPNVNSVRGFDVIDQIKTNVELICPGVVSCADIVALAA 84

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
R F + LGGP+W V LG
Sbjct: 85 R-----FGTFLLGGPSWAVPLG 101

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P+P S L L++ F GLS DL ALSG I
Sbjct: 102 RRDSTTASLTLANSIDLSPASGLATLVTAFGNKGLSPGDLTALSGAHTI 150

Score = 39.3 bits (90), Expect = 2.6
Identities = 17/22 (77%), Positives = 19/22 (86%)
Frame = +1

Query: 715 AISKETRMGASLLRFFHDCFV 780
A+ E RMGASL+RLFFHDCFV
Sbjct: 4 ALLAERRMGASLVRLFFHDCFV 25

>gb|ACN33811.1| unknown [Zea mays]
Length = 320

Score = 167 bits (423), Expect = 6e-39
Identities = 77/124 (62%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR IYN+TNI FA + + +CPR +GSGD NLAPLD TP SFDN Y+ NL+
Sbjct: 197 QAQCKNFRDHIYNDTNINQGFASSLKANCPRPTGSGDGNLAPLDTTTPYSFDNAYYSNLL 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGSTD+ VR +++N FSS FAAAM+KMG++SPLTGS G+IR C
Sbjct: 257 SQKGLLHSDQELFNGGSTDNVTRNFASNSAAFSSAFAAAMVKMGNLSPLTGSQQIRLTC 316

Query: 2167 RRIN 2178

+N
Sbjct: 317 STVN 320

Score = 118 bits (296), Expect = 3e-24
Identities = 72/171 (42%), Positives = 89/171 (52%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1324
+QGCD S+LL D ++ FTGE+ A PN S RGF+VI NIK+ VE VC VSCADILA+
Sbjct: 68 VQGCDAVLLADNAATGFTGEQGAAPNAGSLRGRFDVIANIKAQVEAVCKQTVSCADILAV 127

Query: 1325 AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDSV + LGGP+W V
Sbjct: 128 AARDSV-----VALGGPSWTVP 144

Query: 1505 LRRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
LRRRD+ TAS S AN+ +P P NL QLI+ F G + ++ LSG I
Sbjct: 145 LRRRDSTTASLSLANSIDLPPFFNLGQLITAFGNKGFTATEMATLSGAHTI 195

Score = 75.1 bits (183), Expect = 4e-11
Identities = 36/65 (55%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S ++ CL L + + A+AQLS FY SCPN S++K V +A+ KE RMGASLLRL F
Sbjct: 4 SSVSSCLLLLCLAAVASAQLSPTFYDSSCPNALSTIKI AVNAAVQKENRMGASLLRLHF 63

Query: 766 HDCFV 780
HDCFV
Sbjct: 64 HDCFV 68

>gb|ABR18139.1| unknown [Picea sitchensis]
Length = 327

Score = 167 bits (423), Expect = 6e-39
Identities = 83/124 (66%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR RIYNE+NI FA R+ +CP T G DNNLAPLDL TPT+FDN Y+ NL
Sbjct: 206 QARCTNFRNRIYNESNIALLFAGLRKANCPVTGG--DNNLAPLDLFTPTAFDNSYNNLQ 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ GLLHSDQQLF GGSTD+ V Y+ +P F +DFAAAM+KMG+I PLT +NGEIRKNC

Sbjct: 264 FQNGLLHSDQQLFKGGSTDNRVSFYAVHPDAFFNDFAAAMVKMGNIKPLTVNNGEIRKNC 323

Query: 2167 RRIN 2178
R+IN

Sbjct: 324 RKIN 327

Score = 162 bits (410), Expect = 2e-37
Identities = 91/169 (53%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTS+FTGEK ANPN NS RGF+VID IK+ VE C GVVSCADI+AIAA

Sbjct: 79 VNGCDGSILLDDTSTFTGEKTANPNNSVRGFDVIDTIKTQVEATCSGVVSCADIVAIAA 138

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG

Sbjct: 139 RDSV-----VQLGGPTWTVMGL 155

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ +AS+SAANN IP PTSNL+ LIS F A GL+T+D+VALSG+ I

Sbjct: 156 RRDSTSASKSAANNIPPTSNSALISFFQAQGLTTEDMVALSGSHTI 204

Score = 76.3 bits (186), Expect = 2e-11
Identities = 39/78 (50%), Positives = 52/78 (66%), Gaps = 4/78 (5%)
Frame = +1

Query: 562 KLTMASFCS---RLTICLALFVLIWG-SANAQLSTNFYHSCPNLFPSSVKSTVQSAISKE 729
++ MA F + R+ +C++L V++ S QL +FY SCPN+ S V S V A++KE

Sbjct: 3 RIVMAFFSTMGIRIIVCISLLVIVCSTSVYGGQLCPDFYDKSCPNVLSIVNSVVMQAVAKE 62

Query: 730 TRMGASLLRLLFFHDCFVN 783

RMGASLLRL FHDCFVN

Sbjct: 63 KRMGASLLRLLHFHDCFVN 80

>sp|A2YPX3.2|PER2_ORYSI RecName: Full=Peroxidase 2; Flags: Precursor
gb|AAC49821.1| peroxidase [Oryza sativa Indica Group]
gb|EEC82682.1| hypothetical protein OsI_27327 [Oryza sativa Indica Group]
Length = 314

Score = 167 bits (422), Expect = 8e-39
Identities = 75/124 (60%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFNYYFKNLV 1986

QA+C NFR R+YNETNI+++FA + +CPR +GSGD+NLAPLD TP +FD+ Y+ NL+
Sbjct: 191 QAQCQNFRDRLYNETNIDSSFATALKANCPRPTGSGDSNLAPLDTTTPNAFDSAYYTNLL 250

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGSTD+ VR +S+N F+S F AM+KMG+ISPLTG+ G+IR NC

Sbjct: 251 SNKGLLHSDQVLFNGGSTDNTVRNFSSNTAAFNSAFTVAMVKGNISPLTGTQGIIRLNC 310

Query: 2167 RRIN 2178
++N

Sbjct: 311 SKVN 314

Score = 121 bits (303), Expect = 5e-25
Identities = 72/169 (42%), Positives = 89/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGF V+DNIK+ VE +C VSCADILA+AA

Sbjct: 69 VQGCDAVLLSGQ-----EQNAGPNAGSLRGNVVDNIKTQVEAICSQTVSCADILAVAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 124 RDSV-----VALGGPSWTVLLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA++S AN +PAP+S+L +LI FS GL D+VALSG I

Sbjct: 141 RRDSTTANESQANTDLPAPSSSLAELIGNFSRKGLDVTDMDVALSGAHTI 189

Score = 70.5 bits (171), Expect = 1e-09
Identities = 36/70 (51%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S +++ L + + +A+AQLS FY SCPN S++KS V +A++ E RMGASL

Sbjct: 1 MAS-ASSVSLMLLVAAAMASAASAQLSATFYDTSCPNALSTIKSAVTA AVNSEPRMGASL 59

Query: 751 LRLFFHDCFV 780
+RL FHDCFV

Sbjct: 60 VRLHFHDCFV 69

>ref|XP_002461208.1| hypothetical protein SORBIDRAFT_02g042850 [Sorghum bicolor]
gb|EER97729.1| hypothetical protein SORBIDRAFT_02g042850 [Sorghum bicolor]
Length = 319

Score = 166 bits (421), Expect = 1e-38

Identities = 76/124 (61%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR IYN+TNI +AFA + + +CPR++GSGD NLAPLD TP FDN Y+ NL+

Sbjct: 196 QAQCQFFRDHIYNDTNINSAFATSLKANCPRTSGSGDGNLAPLDTTTPYKFDNAYYSNLL 255

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGSTD+ VR +++N FSS FAAAM+KMG++SPLTGS G+IR C

Sbjct: 256 NQKGLLHSDQELFNGGSTDNTVRNFASNSAAFSSAFAAAMVKMGNLSPLTGSQGGQIRLTC 315

Query: 2167 RRIN 2178

++N

Sbjct: 316 SKVN 319

Score = 118 bits (296), Expect = 3e-24
Identities = 71/171 (41%), Positives = 89/171 (52%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD S+LL D ++ FTGE+ A PN S RGF+VI NIK+ VE +C VSCADILA+

Sbjct: 67 VQGCDASVLLADNAATGFTGEGALPNAGSLRGFDVIANIKTQVEAICKQTVSCADILAV 126

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDSV + LGGP+W V

Sbjct: 127 AARDSV-----VALGGPSWTVP 143

Query: 1505 LRRRDARTASQSAANNGIPAPTSNQLISRFSALGLSTKDLVALSGTKHI 1657

LRRRD+ TAS S AN+ +P P+ NL QLI F G + ++ LSG I

Sbjct: 144 LRRRDSTTASLSLANSDLPPPSFNLEQLIKAFGNKGFTATEMATLSGAHTI 194

Score = 74.7 bits (182), Expect = 6e-11
Identities = 36/59 (61%), Positives = 43/59 (72%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
L LF+ + A+AQLS FY SCPN S++KS V +A+ KE RMGASLLRL FHDCFV

Sbjct: 9 LLLFLCLAAVASAQLSPTFYDTSCPNALSTIKSAVNAAVQKENRMGASLLRLLHFHDCFV 67

>ref|XP_002320417.1| predicted protein [Populus trichocarpa]
gb|EEE98732.1| predicted protein [Populus trichocarpa]
Length = 316

Score = 166 bits (421), Expect = 1e-38

Identities = 82/123 (66%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCT FR RIYN+TNI+ +FA TR+ SCP + GD LAPLD T T FDN Y+ NLV

Sbjct: 197 ARCTFRNRRIYNDTNIDASFATRRASCP--ASGGDATLAPLD-GTQTRFDNYYTNLVA 253

Query: 1990 KKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++VR YSTN TF+ DFAAAM+KMG+ISPLTG NGEIR+NCR

Sbjct: 254 RRGLLHSDQELFNNGSQDALVRTYSTNGATFARDFAAAMVKMGNISPLTGRNGEIRRNCR 313

Query: 2170 RIN 2178

+N

Sbjct: 314 VVN 316

Score = 157 bits (396), Expect = 9e-36
Identities = 89/165 (53%), Positives = 100/165 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDT++FTGEKNANPNRNSARGFEVID IK+ VE C VSCADILA+AA

Sbjct: 69 VNGCDGSILLDDTATFTGEKNANPNRNSARGFEVIDT IKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + GGP+W V LG

Sbjct: 129 RDGVVL-----RGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRDARTASQSAAN+ IP+P S+L LIS FSA GLS D+ ALSG

Sbjct: 146 RRDARTASQSAANSQIPSPASSLATLISMFSAKGLSAGDMTALSG 190

Score = 62.8 bits (151), Expect = 2e-07
Identities = 32/78 (41%), Positives = 45/78 (57%)
Frame = +1

Query: 550 VCLSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQS AISKE 729
+C+ L +SFCS AQLS FY +CPNL + V++ + A++ +

Sbjct: 10 LCVVPLLASSFCS-----AQLSATFYASTCPNLQTIVRNAMTGAVNGQ 52

Query: 730 TRMGASLLRLLFFHDCFVN 783

R+ AS+LRLFFHDCFVN

Sbjct: 53 PRLAASILRLLFFHDCFVN 70

>ref|NP_001130666.1| hypothetical protein LOC100191769 [Zea mays]

gb|ACF78975.1| unknown [Zea mays]
Length = 324

Score = 166 bits (421), Expect = 1e-38
Identities = 77/123 (62%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
++C NFRA IYN+T+I+ AFA RQ++CP G+GD++LAPLD+QT FDN Y++NL+
Sbjct: 200 SQCQNFRAHIYNDTDIDPAFASLRQRTCPAAPGTGDS SLAPLDVQTQLVFDNAYYRNLLA 259

Query: 1990 KKGLLHSDQQLFNNGSSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+G LL SDQ LFNNGS D++VR YS NP F+SDFA AMIKMG+ISPLTG+ G+IR NCR
Sbjct: 260 KRGLLRSDQALFNNGSQDALVRQYSANPALFASDFANAMIKMGNISPLTG TAGQIRANCR 319

Query: 2170 RIN 2178
+N
Sbjct: 320 VVN 322

Score = 134 bits (338), Expect = 5e-29
Identities = 77/169 (45%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCDGSILLDD SF GEK A PN NS RGF+VID IK+ VE +CPGVVSCADI+A+AA
Sbjct: 72 VQGCDGSILLDDVGSFVGEKGAGPNVNSLRGFDVIDQIKANVELICPGVVSCADIVALAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD + LGGP+W V LG
Sbjct: 132 RDGTFL-----LGGPSWAVPLG 148

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P+P S L L++ F GL DL ALSG I
Sbjct: 149 RRDSTTASLALANS DLPSPVSGLAALLAAFGNKGLGPGDLTALSGAHTI 197

Score = 63.9 bits (154), Expect = 1e-07
Identities = 36/72 (50%), Positives = 48/72 (66%), Gaps = 2/72 (2%)
Frame = +1

Query: 571 MASFCSRLTICLA--LFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
MASF + LA LF+L + QLS++FY +CP L V++T+ +A+ E RMGA
Sbjct: 1 MASFRTSWHCLLAACFL LASAAHQQLSSSFYAATCPTLELIVRTTMLTALLAERRMGA 60

Query: 745 SLLRLFFHDCFV 780
SL+RLFFHDCFV

Sbjct: 61 SLVRLFFHDCFV 72

>ref|NP_200648.1| peroxidase, putative [Arabidopsis thaliana]
sp|Q9LVL1.1|PER68_ARATH RecName: Full=Peroxidase 68; Short=Atperox P68; Flags: Precursor
dbj|BAA96931.1| peroxidase [Arabidopsis thaliana]
dbj|BAC42892.1| putative peroxidase [Arabidopsis thaliana]
gb|AAP40354.1| putative peroxidase [Arabidopsis thaliana]
Length = 325

Score = 166 bits (421), Expect = 1e-38
Identities = 82/124 (66%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RIYN TNI+ +FA +R++SCP +GSGDNN A LDL+TP FD YF LV
Sbjct: 202 QARCVTFRSRIYNSTNIDLSFALSRRRSCPAATGSGDNNAAILDRLTPEKFDGSYFMQLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
+GLL SDQ LFNGGSTDSIV YS + F DF AAMIKMGDISPLTGSNG+IR++C
Sbjct: 262 NHRGLLTSQVLFNGGSTDSIVVSYSRSVQAFYRDFVAAMIKMGDISPLTGSNGQIRRS 321

Query: 2167 RRIN 2178
RR N
Sbjct: 322 RRPN 325

Score = 144 bits (362), Expect = 7e-32
Identities = 85/170 (50%), Positives = 99/170 (58%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD SILLDDT SF GEK A PN NS RG+EVID IKS VE++CPGVVSCADILAI A
Sbjct: 74 VNGCDASILLDDTRSFLGEKTAGPNNNSVRGYEVIDAIKSRVERLCPGVVSCADILAITA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + +GG W+VKLG
Sbjct: 134 RDSVLL-----MGGRGWSVKLG 150

Query: 1511 RRDARTASQSAANNGI-PAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+G+ P PTS L+ LI+ F A GLS +D+VALSG I
Sbjct: 151 RRDSITASFSTANSGLVPPPTSTLDNLINLFRANGLSPRDMVALS GAHTI 200

Score = 73.2 bits (178), Expect = 2e-10
Identities = 36/66 (54%), Positives = 47/66 (71%), Gaps = 1/66 (1%)
Frame = +1

Query: 589 RLTICLALFVLIWGS-ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFF 765
R + LF+++ GS A AQL T+FY SCP+L +V+ VQ ++KE R+ ASLLRLLFF
Sbjct: 10 RAAFVLLLFVMLGSQAQAQLRDTFYSDSCPSLLPTVRRVVQREVAKERRIAASLLRLLFF 69

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 70 HDCFVN 75

>ref|XP_002338628.1| predicted protein [Populus trichocarpa]
gb|EEF10179.1| predicted protein [Populus trichocarpa]
Length = 183

Score = 166 bits (420), Expect = 1e-38
Identities = 83/124 (66%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR G NLAPLDL TP SFDN YFKNL+
Sbjct: 62 QAQCFTFRDRIYNASNIDAGFASTRKRRCPRAGGQA--NLAPLDLVTNSFDNYYFKNLM 119

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLL SDQ LFNGGSTDSIV YS NP FSSDFA+AMIKMGDI PLTGS G+IR+ C
Sbjct: 120 RNKGLLQSDQVLFNGGSTDSIVSEYSRNPAPKFSDFASAMIKMGDIRPLTGSAGQIRRIC 179

Query: 2167 RRIN 2178
+N
Sbjct: 180 SAVN 183

Score = 65.5 bits (158), Expect = 3e-08
Identities = 31/57 (54%), Positives = 43/57 (75%)
Frame = +2

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
+GGP+W VK GRRD+ TAS++ AN +PA L++LISRF GL+ +D+VALSG+
Sbjct: 1 VGGPSWAVKFGRRDSTASRTLANAELPAFFDRLDRLISRFAQKGLTARDMVALSGS 57

>ref|XP_002336344.1| predicted protein [Populus trichocarpa]
gb|EEE73229.1| predicted protein [Populus trichocarpa]
Length = 316

Score = 166 bits (420), Expect = 1e-38
Identities = 83/124 (66%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR G NLAPLDL TP SFDN YFKNL+
Sbjct: 195 QAQCFTFRDRIYNASNIDAGFASTRKRRCPRAGGQA--NLAPLDLVTNPSFDNYYFKNLM 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLL SDQ LFNGGSTDSIV YS NP FSSDFA+AMIKMGDI PLTGS G+IR+ C
Sbjct: 253 RNKGLLQSDQVLFNGGSTDSIVSEYSRNPAPKFSDFASAMIKMGDIRPLTGSAGQIRRIC 312

Query: 2167 RRIN 2178
+N
Sbjct: 313 SAVN 316

Score = 135 bits (339), Expect = 3e-29
Identities = 76/166 (45%), Positives = 97/166 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLD+TSS EK A N+NSARG+EVID K+ VEK+CPGVVSCADI+A+AA
Sbjct: 68 VQGDASILLDETSSIKSEKTAGANKNSARGYEVIDKAKAEVEKICPGVVSCADIIAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP+W VKLG
Sbjct: 128 RDA-----SAYVGGPSWAVKLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS + A +PA + +L +LISRF GL+ +D+VALSG+
Sbjct: 145 RRDSTTASPTLAITELPAFSDDLGRLISRFFQKGLTARDMVALSGS 190

Score = 63.5 bits (153), Expect = 1e-07
Identities = 26/50 (52%), Positives = 40/50 (80%)
Frame = +1

Query: 631 SANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
+ A+LS+ FY+ SCPN S++++ +++AI++E RM ASL+RL FHDCFV
Sbjct: 19 ACQAKLSSTFYHKSCPNAESAIRTAIRTAIRERRMAASLIRLHFHDCFV 68

>emb|CAA71493.1| peroxidase [Spinacia oleracea]
Length = 309

Score = 166 bits (420), Expect = 1e-38
Identities = 76/123 (61%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARC +FR IYN+T+I+ F TR+ +CP ++ +G+ NLAPLDLQ+PT FDN Y+KNL+
Sbjct: 187 ARCVSFRHHIYNDTDIDANFEATRKNVNCPLSNNTGNTNLAPLDLQSPKFDNSYYKNLIA 246

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLLHSDQ+L+NGGS D++V YS + F+ DF AA+IKMG+ISPLTGS+GEIRKNCR

Sbjct: 247 KRGLLHSDQELYNGGSQDALVTRYSKSNAAFKDFVAAIIKMGNISPLTGSSGEIRKNCR 306

Query: 2170 RIN 2178

IN

Sbjct: 307 FIN 309

Score = 131 bits (329), Expect = 5e-28
Identities = 79/170 (46%), Positives = 95/170 (55%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRN-SARGFEVIDNIKSAVEKVC PGVVSCADILAIA 1327
+ GCD S+LLDDTS+FTGEK A NRN S RGFVID+IK+ VE C VSCADILA+A

Sbjct: 58 VNGCDASLLDDTSTFTGEKTAISNRNNSVRGFVIDSIKTNVEASCKATVSCADILALA 117

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD V + LGGP+W V L

Sbjct: 118 ARDGVFL-----LGGPSWKVPL 134

Query: 1508 GRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

GRRDARTAS +AA N +P +S+L+ L + F+ GLS KD+ ALSG I

Sbjct: 135 GRRDARTASLTAATNNLPPASSSLSNLTLFNNKGLSPKDMTALSGAHTI 184

Score = 70.9 bits (172), Expect = 8e-10
Identities = 32/50 (64%), Positives = 39/50 (78%)
Frame = +1

Query: 634 ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783

+NAQLS+ Y SCPNL V+ T++ A+ KE RMGAS+LRLFFHDCFVN

Sbjct: 10 SNAQLSSKHYASSCPNLEKIVRKTMKQAVQKEQRMGASILRLLFFHDCFVN 59

>gb|AA53172.1| peroxidase [Populus alba x Populus tremula var. glandulosa]
Length = 316

Score = 166 bits (420), Expect = 1e-38
Identities = 81/123 (65%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARCT FR RIYN+TNI+ +FA TR+ SCP + GD LAPLD T T FDN Y+ NLV

Sbjct: 197 ARCTTFRNRIYNDTNIDASFATRRASCP--ASGGDATLAPLD-GTQTRFDNYYTNLVA 253

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++VR YSTN TF+ DFAAAM++MG+ISPLTG+NGEIR+NCR

Sbjct: 254 RRGLLHSDQELFNGGSQDALVRTYSTNGATFARDFAAAMVRMGNISPLTGTNGEIRRNCR 313

Query: 2170 RIN 2178
+N

Sbjct: 314 VVN 316

Score = 159 bits (402), Expect = 2e-36
Identities = 90/165 (54%), Positives = 101/165 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVWSCADILAI 1330
+ GCDGSILLDDT++FTGEKNANPNRNSARGFEVID IK+ VE C VSCADILA+AA

Sbjct: 69 VNGCDGSILLDDTATFTGEKNANPNRNSARGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG

Sbjct: 129 RDGVVL-----LGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAAN+ IP+P S+L LIS FSA GLS D+ ALSG

Sbjct: 146 RRDARTASQSAANSQIPSPASSLATLISMFSAKGLSAGDMTALSG 190

Score = 63.2 bits (152), Expect = 2e-07
Identities = 32/78 (41%), Positives = 45/78 (57%)
Frame = +1

Query: 550 VCLSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQS AISKE 729
+C+ L +SFCS AQLS FY +CPNL + V++ + A++ +

Sbjct: 10 LCIVPLLASSFCS-----AQLSATFYASTCPNLQTIVRNAMTGAVNGQ 52

Query: 730 TRMGASLLRLLFFHDCFVN 783
R+ AS+LRLFFHDCFVN

Sbjct: 53 PRLAASILRLLFFHDCFVN 70

>ref|XP_002509738.1| Lignin-forming anionic peroxidase precursor, putative [Ricin
communis]

gb|EEF51125.1| Lignin-forming anionic peroxidase precursor, putative [Ricin
communis]

Length = 320

Score = 166 bits (419), Expect = 2e-38
Identities = 80/125 (64%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIYN ++I+ FA TR+ CP SGSGD+NLAPLDL TP FDN YF+NL

Sbjct: 196 QAQCVTFRGRYNNASDIDAGFAATTRSQCPAASGSGDSNLAPLDLVTPNIFDNNYFRNL 255

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GG+TDSIV YS + FSSDFA+AM+KMG+ISPLTGS G+IR+

Sbjct: 256 IQKKGLLQSDQVLFSGGATDSIVNQYSRDSVSSDFASAMVKMGNISPLTGSQQIRRV 315

Query: 2164 CRRIN 2178

C +N

Sbjct: 316 CNVVN 320

Score = 137 bits (346), Expect = 5e-30
Identities = 77/169 (45%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCDGSILLDDT + TGEK A N NS RGF+VIDNIKS +E CPG+VSCADI+A+AA

Sbjct: 69 VQGCDGSILLDDTPTMTGEKTARNNANSVRGFVIDNIKSQLESRCPGIVSCADIVAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ GP+W+V LG

Sbjct: 129 RDA-----SVAASGPSWSVNLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS+S A++ +PA T +L++L S F + GLS +D+VALSG I

Sbjct: 146 RRDSTTASRSLADSNLPAFTDSLDRLTSLFGSKGLSQRDMVALSGAHTI 194

Score = 70.1 bits (170), Expect = 1e-09
Identities = 32/67 (47%), Positives = 49/67 (73%), Gaps = 2/67 (2%)
Frame = +1

Query: 586 SRLTICLALFVLIWGS--ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRL 759
SRL++ + ++I+ S AQLS+NFY ++CP+ S++K + +A+S+E RM ASL+RL

Sbjct: 3 SRLSLLCMVLMIFSSLPCQAQLSSNFYDNTCPSALSTIKGAISTAVSREQRMAASLIRL 62

Query: 760 FFHDCFV 780

FFHDCFV

Sbjct: 63 HFHDCFV 69

>ref|XP_002453592.1| hypothetical protein SORBIDRAFT_04g008630 [Sorghum bicolor]
gb|EES06568.1| hypothetical protein SORBIDRAFT_04g008630 [Sorghum bicolor]
Length = 321

Score = 165 bits (418), Expect = 2e-38
Identities = 76/123 (61%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A C +FR IYN+TN++ AFA RQ++CP SGSGD NLAPLD+QT FDN Y++NL+
Sbjct: 197 AECEDFRGHIYNDTNVDPFAALRQRNCPAESGSGDTNLAPLDVQTRYVFDNAYYRNLMV 256

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++V+ YST+PG F+S F AAMIKMG+I LTGS G+IR +CR
Sbjct: 257 RQGLLHSDQELFNGGSQDALVQQYSTDPGLFASHFVAAMIKMGNIGTLTGSQGGIRADCR 316

Query: 2170 RIN 2178
+N
Sbjct: 317 VVN 319

Score = 135 bits (339), Expect = 3e-29
Identities = 81/169 (47%), Positives = 92/169 (54%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCDGSILLDD SF GEK A PN S RG+EVID IK+ VE VCPGVVSCADI+A+AARD
Sbjct: 72 GCDGSILLDDAGSFVGEKTALPNA-SIRGYEVIDQIKANVEAVCPGVVSCADIVALAARD 130

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
++ GGPTW V LGRR
Sbjct: 131 GTVLL-----GGPTWAVPLGRR 147

Query: 1517 DARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHISH 1663
D+ TAS S AN+ IPAPT NL+ LI F GLS D+ ALSG I +
Sbjct: 148 DSTTASLSQANS DIPAPTLNLDLILAFGKKGLSPADMTALSGAHTIGY 196

Score = 60.8 bits (146), Expect = 8e-07
Identities = 34/70 (48%), Positives = 40/70 (57%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA L CL L + QL+ FY SCP L V++T+ AI + RMGASL
Sbjct: 1 MACSFRRLLHCLLALSCLSTAYGGQLTPTFYALSCPALEPIVRTTMTKAIINDRRMGASL 60

Query: 751 LRLFFHDCFV 780

LRLFFHDCFV
Sbjct: 61 LRLFFHDCFV 70

>gb|ACN60163.1| class III peroxidase [Tamarix hispida]
Length = 320

Score = 164 bits (415), Expect = 5e-38
Identities = 77/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNETNI ++FA++ Q +CP T G DNNL+PLD +PT+FD Y+ +L+
Sbjct: 199 QARCTSFARIYNETNINSSFAKSLQANCPSTGG--DNNLSPLDTSSPTTFDVGYYTDLI 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQL+NGGSTDS V YS++ TF +DF +MI MG+ISPLTGS G++R NC
Sbjct: 257 GQKGLLHSDQQLYNGGSTDSQVTSYSSSSSTFLTDFGTSMINMGNISPLTGSRGQVRTNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKTN 320

Score = 125 bits (313), Expect = 4e-26
Identities = 78/170 (45%), Positives = 89/170 (52%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGS-ILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIA 1327
+ GCD S + K A PN S RGF+V+D IKS VE VCPGVV CADILA+A
Sbjct: 71 VNGCDASGSIRRHCQLHRKRKTAQPNNGLRGFVVDTIKSKVESVCPGVVPCADILAVA 130

Query: 1328 ARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGG +W V L
Sbjct: 131 ARDSV-----VALGGKSWGVL 147

Query: 1508 GRRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
GRRD+ TAS SAAN GIPAPT NL+ LI+ FS +GLSTKDLV LSG I
Sbjct: 148 GRRDSTTASLSAANTGIPAPTLNLSGLITSFNSVGLSTKDLVVLGAHTI 197

>ref|XP_002450134.1| hypothetical protein SORBIDRAFT_05g001030 [Sorghum bicolor]
gb|EES09122.1| hypothetical protein SORBIDRAFT_05g001030 [Sorghum bicolor]
Length = 317

Score = 163 bits (413), Expect = 9e-38
Identities = 76/124 (61%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+E NI+T+ A + + +CP +G DNN++PLD TP FDN+Y+KNL+
Sbjct: 196 QARCVNFRDRIYSEANIDTSLATSLKTCNPKTG--DNNISPLDASTPYVFDNFYKKNLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N F +DF+ AM+KM +ISPLTGS+G+IRKNC
Sbjct: 254 NKKGVLHSDQQLFNGGSADSQTTTYSSNMAKFFTFSTAMLKMSNISPLTGSSGQIRKNC 313

Query: 2167 RRIN 2178
RR+N
Sbjct: 314 RRVN 317

Score = 147 bits (370), Expect = 9e-33
Identities = 81/165 (49%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGS+LLDDT +FTGEK A PN NS RGF+VID+IK+ +E++CP VVSCADI+A+AA
Sbjct: 69 VNGCDGSVLLDDTPTFTGEKTAVPNNSLRGFVIDSIKALERICPQVVSCADIVAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 129 RDSV-----VALGGPTWAVNLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+ TAS AANN IPAPT +L L FS GLS D++ALSG
Sbjct: 146 RRDSL TASLDAANNDIPAPTLDLTDLTKSFSNKGLSASDMIALSG 190

Score = 68.9 bits (167), Expect = 3e-09
Identities = 36/71 (50%), Positives = 47/71 (66%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS LALF ++QL+ NFY SCPN ++++ V+SA+++E RMGASL
Sbjct: 1 MASHKPLTCSVLALFFAA-SLVSSQLNANFYDKSCP NALYTIQTAVRS AVAREN RMGASL 59

Query: 751 LRLFFHDCFVN 783
LRL FHDCFVN
Sbjct: 60 LRLHFHDCFVN 70

>gb|AAC05277.1| peroxidase FLXPER4 [Linum usitatissimum]
Length = 305

Score = 163 bits (413), Expect = 9e-38
Identities = 81/124 (65%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYN+TNI+ AFA TR+ +CP+ +G+G N LAPLD TPT FDN Y+++LV
Sbjct: 185 QARCTTFRQRIYNDTNIDPAFATRRGNCPQ-AGAGAN-LAPLD-GTPTQFDNRYQDLV 241

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFN G+ D++VR YS N TF++DFAAAM++MG+ISPLTG+NGEIR NC
Sbjct: 242 ARRGLLHSDQELFNNGTQDALVRTYSNNAATFATDFAAAMVRMGNISPLTGNGEIRFNC 301

Query: 2167 RRIN 2178
RR N
Sbjct: 302 RRPN 305

Score = 144 bits (362), Expect = 7e-32
Identities = 80/169 (47%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGS+LLDDT++FTGEKNA PN+NS RGF++ID IK+ VE C VSCADILA+AA
Sbjct: 58 VNGCDGSLLLDDTATFTGEKNAGPNQNSVRGFDIIDT IKTRVEAACNATVSCADILALAA 117

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V +V GGPTW V LG
Sbjct: 118 RDGVVLV-----GGPTWTVPLG 134

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAAN IPAP S+L + + F+ GL+ +D+ LSG I
Sbjct: 135 RRDARTASQSAANAQIPAPGSSLGTITNLFTNKGLTARDVTILSGAHTI 183

Score = 65.1 bits (157), Expect = 4e-08
Identities = 29/55 (52%), Positives = 39/55 (70%)
Frame = +1

Query: 619 LIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
L+ S +AQL+ NFY SCP L + V++ + A++ E RM AS+LRL FHDCFVN
Sbjct: 5 LLASSGSAQLAANFYATSCPTLLTIVRNAMTQAVNSENMAASILRLHFHDCFVN 59

>ref|XP_002269343.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 331

Score = 163 bits (412), Expect = 1e-37

Identities = 81/125 (64%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP +G+GD+NLAPL+L TP SFDN YFKNL

Sbjct: 207 QARCVTFRDRIYDNGTDIDAGFASTRRRRCPANNGGDDNLAPLELVTPNSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+++KGLL SDQ LF+GGSTD+IV YS +P TF SDFA+AM+KMGDI LTGS G IRK

Sbjct: 267 IRRKGLLQSDQVLFSGGSTDTIVNEYSKSPKTFRSDFASAMVKMGDIEALTGSAGVIRKF 326

Query: 2164 CRRIN 2178

C IN

Sbjct: 327 CNVIN 331

Score = 132 bits (332), Expect = 2e-28
Identities = 76/169 (44%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLDD+SS EKNA N NS RG+EVIDNIKS VE +CPGVVSCADI+A+AA

Sbjct: 80 VQGCDA SILLDDSSSIQSEKNAPNNLNSVRGYEVIDNIKSKVESLCPGVVSCADIVAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VS GPTW V+LG

Sbjct: 140 RDASVAVS-----GPTWTVRLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ T+ S A +P+ +L++L+S F + GLS +D+VALSG+ I

Sbjct: 157 RRDSTTSGLSQAATNLPSFRDSLDKLVSLFGSKGLSARDMVALSGSHTI 205

Score = 63.5 bits (153), Expect = 1e-07
Identities = 31/69 (44%), Positives = 46/69 (66%), Gaps = 1/69 (1%)
Frame = +1

Query: 577 SFC SRLTICLALFVLIWGS-ANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753
S S I LA+F+++ A LS FY H+CP +++++ V++A+S+E RM ASL+

Sbjct: 12 SCISPACIFLAVFLILSNMPCEAHLSPTFYDHTCPRALTTIQTAVRTAVSRERRMAASLI 71

Query: 754 RLFFHDCFV 780

RL FHDCFV

Sbjct: 72 RLHFHDCFV 80

>gb|EAY85148.1| hypothetical protein OsI_06503 [Oryza sativa Indica Group]

Length = 323

Score = 163 bits (412), Expect = 1e-37
Identities = 74/123 (60%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
++C NFR RIYN+TNI+ AFA R+ CP GSGD +LAPLD T FDN Y++NL+
Sbjct: 199 SQCANFRDRIYNDTNIDPAFAALRRGGCPAAPGSGDTS LAPLDALTQNVFDNAYYRNLLA 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGS D++V+ YS+NP F++DFAAAMIKMG+I+PLTG+ G+IR++CR
Sbjct: 259 QRGLLHSDQVLFNGGSQDALVQQYSSNPALFAADFAAAMIKMGNINPLTGAAGQIRRSCR 318

Query: 2170 RIN 2178
+N
Sbjct: 319 AVN 321

Score = 139 bits (349), Expect = 2e-30
Identities = 80/171 (46%), Positives = 99/171 (57%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD SILLDD +SF GEK A PN NS RG++VID IK VE +CPGVVSCADI+A+
Sbjct: 69 VQGCDASILLDDVPATSFVGEKTAFPNVNSVRGYDVIDQIKRRVELLCPGVVSCADIVAL 128

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 129 AARDSTAL-----LGGPSWEVP 145

Query: 1505 LRRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
LRRRD+ TAS SAAN+ +PAP+S+L L++RF + GLS +D+ ALSG I
Sbjct: 146 LRRRDSTTASLSAANS DLPAPSSDLATLVARFGSKGLSPRDMTALSGAHTI 196

Score = 69.7 bits (169), Expect = 2e-09
Identities = 35/60 (58%), Positives = 41/60 (68%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
CL F L+ +A QLST FY SCP L V++TV S + E RMGASL+RLFFHDCFV
Sbjct: 10 CLLAFFLLSSAACGQLSTTFYAASCP TLQLVVRATV LSTLLAERRMGASLVR LFFHDCFV 69

>ref|XP_002269301.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 213

Score = 162 bits (411), Expect = 2e-37
Identities = 81/124 (65%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q RC FR RIYN T+I+ FA TR++ CP +G+GD NLAPL+L TP SFDN YFKNL+
Sbjct: 90 QGRCVTFRDRIYNGTDIDAGFASTRRRRCPADNGNGDANLAPLELVTPNSFDNYYFKNLI 149

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q+KGLL SDQ LF+GGSTDSIV YS +P TF SDF+AM+KMGDI PLT S G IRK
Sbjct: 150 QRKGLLQSDQVLFSGGSTDSIVNEYSKSPKTFRSDFASAMLKMGDIEPLTRSAGVIRKIFY 209

Query: 2167 RRIN 2178
IN
Sbjct: 210 NVIN 213

Score = 62.0 bits (149), Expect = 4e-07
Identities = 30/60 (50%), Positives = 42/60 (70%)
Frame = +2

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
+ GPTW VKLGRRD+ T+ S A +P+ +L++LIS F + GLS +D+VALSG+ I
Sbjct: 29 VSGPTWTVKLGRRDSTTSGLSLAATNLPSFRDSLKLI SLFGSKGLSARDMVALSGSHTI 88

>gb|AAD37428.1|AF149278_1 peroxidase 3 precursor [Phaseolus vulgaris]
Length = 324

Score = 162 bits (411), Expect = 2e-37
Identities = 78/126 (61%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG--DNNLAPLDLQTPTSFDNYYFKN 1980
+ARC + +RIYNE NIE+ FA+ RQ++CPR S DNN+APL+ +TP FDN Y+KN
Sbjct: 199 KARCAVYGSRIYNEKNIESLFAKARQKNCPRNSNGTPKDNNVAPLEFKTPNHFDNYYKN 258

Query: 1981 LVQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ KKGLLHSDQ LF+GGSTDS+VR YS + F SDF AMIKMG+I PLTGSNG+IR+
Sbjct: 259 LINKKGLLHSDQVLFDDGGSTDSLVRAYSNDQRAFESDFVTAMIKMGNIKPLTGSNGQIRR 318

Query: 2161 NCRRIN 2178
C R N
Sbjct: 319 LCGRPN 324

Score = 126 bits (317), Expect = 1e-26
Identities = 79/170 (46%), Positives = 93/170 (54%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+ GCDGS+LLD SS EK A PN S RG+EVID IKS VE +CPG+VSCADI+AIAA
Sbjct: 74 VNGCDGSVLLDGPSS---EKTAPPNDKSLRGYEVIDAIKSKVEALCPGIVSCADIVAIAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W VKLG
Sbjct: 131 RDSVNI-----LGGPFWKVKLG 147

Query: 1511 RRDARTA-SQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T Q A++ +P+P S+L+ LIS F GLS KD+VALSG I
Sbjct: 148 RRDSSTGFFQLASSGALPSPASSLDTLISSFKDQGLSAKDMVALSGAHTI 197

Score = 83.6 bits (205), Expect = 1e-13
Identities = 42/67 (62%), Positives = 50/67 (74%), Gaps = 1/67 (1%)
Frame = +1

Query: 586 SRLTICLALFVL-IWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLF 762
S T +A F L + GS++AQLS NFY CP + +VKS VQSA++KE RMGASLLRLF
Sbjct: 9 STTFAIAFFTLFLIGSSSAQLSENFYAKKCPKVLVAVKSVVQSAVAKEPRMGASLLRLF 68

Query: 763 FHDCFVN 783
FHDCFVN
Sbjct: 69 FHDCFVN 75

>ref|XP_002334243.1| predicted protein [Populus trichocarpa]
gb|EEF07510.1| predicted protein [Populus trichocarpa]
Length = 317

Score = 162 bits (410), Expect = 2e-37
Identities = 80/124 (64%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RI+++ NI+ FA TR++ CP D+ LAPLDL TP SFDN YFKNL+
Sbjct: 196 QAQCFTFRDRIHSDNNIDAGFASTRKRRCLVGS--DSTLAPLDLVT PNSFDNYYFKNLM 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
QKKGLL SDQ+LF+GGSTDSIV YS NP FSSDFA+AMIKMGDISPLTG+ G+IR+ C
Sbjct: 254 QKKGLLQSDQELFSGGSTDSIVSEYSRNP AKFSSDFASAMIKMGDISPLTGTAGQIRRIC 313

Query: 2167 RRIN 2178
+N

Sbjct: 314 SAVN 317

Score = 133 bits (335), Expect = 1e-28
Identities = 76/166 (45%), Positives = 95/166 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLD+TSS EK A N NS RG+EVID KS VEK+CPGVVSCADI+A+AA
Sbjct: 69 VQGC DASILLDETSSIQSEKTAGGNNSVRGYEVIDKAKSKVEKICPGVVSCADIIAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP+W VKLG
Sbjct: 129 RDA-----SAYVGGPSWAVKLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS + A +PA + +L +LISRF GL+ +D+VALSG+
Sbjct: 146 RR DSTTASPTLAITELPAFSDDLGRLISR FQQKGLTARDMVALSGS 191

Score = 62.0 bits (149), Expect = 4e-07
Identities = 28/57 (49%), Positives = 42/57 (73%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
LF+L + A+LS+ FY SCP S++++ +++AI++E RM ASL+RL FHDCFV
Sbjct: 13 LFLSTTACQAKLSSAFYDKSCPKAESAIRTAIRTAIARERRMAASLIRLHFHDCFV 69

>ref|XP_002438530.1| hypothetical protein SORBIDRAFT_10g021630 [Sorghum bicolor]
gb|EER89897.1| hypothetical protein SORBIDRAFT_10g021630 [Sorghum bicolor]
Length = 329

Score = 162 bits (409), Expect = 3e-37
Identities = 73/126 (57%), Positives = 100/126 (79%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS--GSGDNNLAPLDLQTPTSFDNYYFKN 1980
QARCT FR+RIY +TNI FA RQQ+CP+ S G+GD LAP+D++TP +FDN Y++N
Sbjct: 204 QARCTTFRSRIYGDTNINATFASLRQQTCPQASDGGAGDAALAPIDVRTPEAFDNAYYQN 263

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ ++GL HSDQ+LFNGGS D++V+ YS N F++DFA AM++MG ISPLTG+ GE+R
Sbjct: 264 LMARQGLFHSDQQLFNGGSQDALVKKYSGNAAMFAADFAKAMVRMG AISPLTGTQGEVRL 323

Query: 2161 NCRRIN 2178
+CR++N

Sbjct: 324 DCRKVN 329

Score = 141 bits (356), Expect = 4e-31
Identities = 79/165 (47%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA

Sbjct: 77 VNGCDASILLDDTATFTGEKNAGPNANSVRGYEVIDAIKTQEASCNATVSCADILALAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ GGPTW V LG

Sbjct: 137 RDAVNLL-----GGPTWTVYLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRDARTASQS AN +P P S+L L++ F GLS +D+ ALSG

Sbjct: 154 RRDARTASQSDANGNLPGPSLTLVTMFGNKGLSARDMTALSG 198

Score = 69.3 bits (168), Expect = 2e-09
Identities = 35/66 (53%), Positives = 48/66 (72%), Gaps = 2/66 (3%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQ--LSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFF 765
LT+ L +L+ G+A A LST+FY CPN+ S V++ + SA++ E RMGAS+LR+FF

Sbjct: 13 LTVAAVLSLLMAGAAAAGGLSTSFYSKCKPNVQSIVRAGMASAVAAEKRMGASILRMFF 72

Query: 766 HDCFVN 783

HDCFVN

Sbjct: 73 HDCFVN 78

>ref|XP_002281755.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 317

Score = 162 bits (409), Expect = 3e-37
Identities = 78/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD+QT FDN Y++NL+

Sbjct: 196 QAQCFTFRSRIYNDTNIDPNFAATRRSTCP-VSG-GNSNLAPLDIQTMNKFDNYYQNLN 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR YS N F DFAAAM+KM +ISPLTG+NGEIR NC

Sbjct: 254 TQRGLLHSDQELFNGGSQDALVRTYSANNALFFGDFAAAMVKMSNISPLTG+NGEIRSNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RVVN 317

Score = 152 bits (383), Expect = 3e-34
Identities = 85/169 (50%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACKATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 129 RDGVVL-----LGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTA+QSAANN +PAP +NL+ LIS F+A GL+ D+ ALSG+ I
Sbjct: 146 RRDARTANQSAANNDLPAPFANLSALISGFAAKGLNADDMTALSGSHTI 194

Score = 70.9 bits (172), Expect = 8e-10
Identities = 37/71 (52%), Positives = 47/71 (66%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPFLSSVKSTVQSAISKETRMGASL 750
MASF + + + VL S NAQLS NFY +CPN+ V+ + A+ +E RMGAS+
Sbjct: 1 MASFTNSFVFSIISVLAC-SINAQLSPNFYASTCPNVQKIVRVEMVQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>ref|XP_002437128.1| hypothetical protein SORBIDRAFT_10g021610 [Sorghum bicolor]
gb|EER88495.1| hypothetical protein SORBIDRAFT_10g021610 [Sorghum bicolor]
Length = 314

Score = 161 bits (408), Expect = 3e-37
Identities = 76/125 (60%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFART-RQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT FR+RIY +TNI +FA RQQ+CP++ G G NLAP+D+QTPT FD Y+ NL
Sbjct: 191 QARCTTFRSRIYGDTNINASF AAALRQQTCPQSGGDG--NLAPMDVQTPTRFDTDYNTNL 248

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ ++GL HSDQ+LFNGGS D++VR YS NP F+SDF AAMIKMG++ LTG+ G+IR+N
Sbjct: 249 LSQRGLFHSDQELFNGGSQDALVRQYSANPSLFNSDFMAAMIKMGVGLTGTAGQIRRN 308

Query: 2164 CRRIN 2178
CR +N
Sbjct: 309 CRVVN 313

Score = 134 bits (336), Expect = 8e-29
Identities = 80/169 (47%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCDGSILLD GEK A PN NSARGFEVID IK+ VE CPGVVSCADILA+AA
Sbjct: 68 VQGCDGSILLDAG----GEKTAGPNANSARGFEVIDTIKTNVEAACPGVVSCADILALAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD ++ G PTWNV LG
Sbjct: 124 RDGTNLLG-----PTWNVPLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P T++L LIS FS GLS +D+ ALSG I
Sbjct: 141 RRDSTTASASLANSNLPQSTASLGTLISLFSRQGLSARDMTALSGAHTI 189

Score = 71.6 bits (174), Expect = 5e-10
Identities = 36/60 (60%), Positives = 42/60 (70%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
CL L+ A+AQLST FY SCPNL S V+ + A+S + RMGASLLRFFHDCFV
Sbjct: 9 CLVAISLLSCVAHAQLSTTFYASSCPNLQSI VRRAMIQALSNDQRMGASLLRFFHDCFV 68

>ref|XP_002517727.1| Cationic peroxidase 1 precursor, putative [Ricinus communis]
gb|EEF44659.1| Cationic peroxidase 1 precursor, putative [Ricinus communis]
Length = 264

Score = 160 bits (406), Expect = 6e-37
Identities = 79/124 (63%), Positives = 100/124 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPSFDNYYFKNLV 1986
QARC FR R+YNETNI++A A + + CP T+GS D+NL+PLD +P FDN YFKNLV
Sbjct: 143 QARCLMFRGRLYNETNIDSALATSLKSDCP--TTGS--DDNLSPLDATSPVIFDINSYFKNLV 200

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLF+GGST+S V+ YST+P TF +DFA AMIKMG +SPLTG++G+IR +C
Sbjct: 201 NNGLLHSDQQLFSGGSTNSQVKTYSTDPFTFYADFANAMIKMGKLSPLTGTGQIRTDC 260

Query: 2167 RRIN 2178
R++N
Sbjct: 261 RKNV 264

Score = 140 bits (354), Expect = 6e-31
Identities = 80/170 (47%), Positives = 98/170 (57%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTS-SFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI A 1327
+ GCD S+LLDD S SFTGEK A PN NS RGF+VID IKS VE +CPGVVSCADILA+A
Sbjct: 15 VNGCDASVLLDDISPSTGEKTAGPNANSLRGFDVIDTIKSQVESICPGVVSCADILAVA 74

Query: 1328 ARDSVQIVSQGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGP+W V+L
Sbjct: 75 ARDSV-----VALGGPSWQVEL 91

Query: 1508 GRRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
GRRD+ TAS AAN +P+P +L+ LIS S G + K++VAL+G+ I
Sbjct: 92 GRRDSTTASYDAANTDLPSPMLDSDLISALSRKGFTAKEMVALAGSHTI 141

>ref|NP_001057822.1| Os06g0547400 [Oryza sativa (japonica cultivar-group)]
dbj|BAD54122.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69328.1| TPA: class III peroxidase 86 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAF19736.1| Os06g0547400 [Oryza sativa Japonica Group]
gb|EEC80780.1| hypothetical protein OsI_23305 [Oryza sativa Indica Group]
gb|EEE65851.1| hypothetical protein OsJ_21628 [Oryza sativa Japonica Group]
Length = 324

Score = 160 bits (406), Expect = 6e-37
Identities = 74/124 (59%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR+RIY E NI +FA RQQ+CPR+ G D NLAP D+QTP +FDN Y++NLV
Sbjct: 203 RAQCQFFRSRIYTERNINASFASLRQQTCPRSSG--DANLAPFDVQTPDAFDNAYYQNLV 260

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D +VR YSTNP FSSDF +AM+KMG++ P +G+ E+R NC
Sbjct: 261 SQRLLHSDQELFNGGSQDGLVRQYSTNPSQFSSDFVSAMVKMGNLLPSSGTATEVRLNC 320

Query: 2167 RRIN 2178
R++N
Sbjct: 321 RKNV 324

Score = 149 bits (375), Expect = 2e-33
Identities = 84/169 (49%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTS+FTGEK+A PN NSARGFEVID IK+ VE C VSCADILA+AA
Sbjct: 76 VNGCDGSILLDDTSTFTGEKSAGPNANSARGFEVIDAIKTQVEASCKATVSCADILALAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGPTWNVKLG 1510
RD V ++ GGPTW+V LG
Sbjct: 136 RDGVNLL-----GGPTWSVALG 152

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
R+D+RTASQSAAN+ +P P S+L LIS F GLS +D+ ALSG I
Sbjct: 153 RKDSRTASQSAANSNLPGPSLATLISMFGNQLSARDMTALSGAHTI 201

Score = 73.2 bits (178), Expect = 2e-10
Identities = 36/63 (57%), Positives = 47/63 (74%), Gaps = 1/63 (1%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQ-LSTNFYHSCPFLFSSVKSTVQSAISKETRMGASLLRRLFHDC 774
+ + + VL+ G+A AQ LS NFY +CPNL + V+S + SA+ E RMGAS+LRLFHDC
Sbjct: 15 VAVVVAVLLGGAAEAQQLSPNFYSRTCPLATIVRSGMASAVRTEPRMGASILRRLFHDC 74

Query: 775 FVN 783
FVN
Sbjct: 75 FVN 77

>ref|XP_002285724.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 318

Score = 160 bits (405), Expect = 8e-37
Identities = 78/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR IYN+T+I+ AFA ++Q+ CPR+ G D+NL+PLD T T FDN YF+ L
Sbjct: 196 KARCTSFRNHIYNDTDIDPAFAASKQKICPRSGG--DDNLSPLD-GTTTVFDNVYFRGLK 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ+L+NGGSTDSIV YS N TF D A AM+KMG+ISPLTG+NG+IR NC
Sbjct: 253 EKKGLLHSDQELYNGGSTDSIVETYSINTATFFRDVANAMVKMGNISPLTGNGQIRTNC 312

Query: 2167 RRIN 2178
R++N
Sbjct: 313 RKNV 316

Score = 155 bits (391), Expect = 3e-35
Identities = 86/167 (51%), Positives = 100/167 (59%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG+EVID IKS VE +CPGVVSCADI+A+AARD
Sbjct: 71 GCDASILLDDTATFTGEKTAGPNNNSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 130

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1516
SV + LGGPTW V+LGRR
Sbjct: 131 SV-----VALGGPTWTVRLGR 147

Query: 1517 DARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS SAA +P P NL+QLIS FS GL+TK++V LSGT I
Sbjct: 148 DSTTASFAARTDLPGNLNLSQLISAFSKKGLTTKEMVVLSGHTI 194

Score = 66.6 bits (161), Expect = 2e-08
Identities = 32/58 (55%), Positives = 41/58 (70%), Gaps = 1/58 (1%)
Frame = +1

Query: 610 LFVLIWGSANAQ-LSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFV 780
+F L+ G A+A LS NFY SCP ++++ V A++KE RMGASLLRL FHDCFV
Sbjct: 12 IFSLLGMAHAHYLSPNFYARSCPRLPTIRTAVNKAVAKEKRMGASLLRRLFHDCFV 69

>ref|XP_002521867.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
gb|EEF40503.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
Length = 326

Score = 160 bits (405), Expect = 8e-37
Identities = 83/125 (66%), Positives = 96/125 (76%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIY N T I+ FA TR++SCP G D NLAPLDL TP SFDN YFKNL

Sbjct: 204 QAQCFTFRDRIYSNGTEIDAGFASTRKRSCPAVGG--DANLAPLDLVTTPNSFDNNYFKNL 261

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ L +GGSTDSIV GYS +P TFSSDFA+AMIKMG+I PLTG+ G+IR+

Sbjct: 262 MQRKGLLESQILLSGGSTDSIVSGYSRSPSTFSSDFASAMIKMGIDPLTGTAGQIRRI 321

Query: 2164 CRRIN 2178
C IN

Sbjct: 322 CSAIN 326

Score = 137 bits (344), Expect = 9e-30
Identities = 75/165 (45%), Positives = 99/165 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLD+TS+ EK A PN++SARG+EVID K+ VEK+CPGVVSCADIL++AA

Sbjct: 77 IQGCDASVLLDETSTIESEKTALPNKDSARGYEVIDKAKTEVEKICPGVVSCADILSVAA 136

Query: 1331 RDSVQIVSGQTTNKNLTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDS S +GGP+W V LG

Sbjct: 137 RDS-----SAYVGGPSWTVMLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS++ AN+ +P+ L++LISRF + GLS +D+VALSG

Sbjct: 154 RRDSTTASRTLANSFELPSFKDGLDRLISRFSKGLSARDMVALSG 198

Score = 60.8 bits (146), Expect = 8e-07
Identities = 27/56 (48%), Positives = 44/56 (78%), Gaps = 1/56 (1%)
Frame = +1

Query: 616 VLIWGSA-NAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
+LI G+A +AQL++ FY CPN S+++++++I+ E RM ASL+RL FHDCF+

Sbjct: 22 LLILGTACHAQLTSTFYDSLCPNALSTIRTSIRNSIAAERRMAASLIRLHFHDCFV 77

>emb|CAH10841.1| peroxidase [Picea abies]
Length = 320

Score = 160 bits (405), Expect = 8e-37
Identities = 78/124 (62%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRTS GSGDNNLAPLDLQTPTSF DNNYFKNLV 1986
Q+RC FR RIYNE+NI AFA + + +CP S GDN L+PLD+ TP F+N Y+ NL

Sbjct: 199 QSRCAFFRTRIYNESNINAAFATSVKANCP--SAGGDNTLSPLDVVTPIKFNKYYGNLK 256

Query: 1987 QKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQLFNGGSTDS V YSTN +F +DFAAAM+KM +ISPLTG++G+IRKNC
Sbjct: 257 IQKGLLHSDQQLFNGGSTDSQVTAYSTNQNSFFTFDFAAAMVKMSNISPLTGTSGQIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKAN 320

Score = 154 bits (388), Expect = 7e-35
Identities = 89/169 (52%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGSILLDD ++FTGEK A PN NSARGF+VID IK+ VE C GVVSCADIL IAA
Sbjct: 72 VSGCDGSILLDDNATFTGEKTAGPNANSARGFDVIDTIKTQVEAACSGVVSCADILTIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GPTW V LG
Sbjct: 132 RDSV-----VELQGPTWTVMLG 148

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAANN IP+P S+L+ LIS F GLSTKDLVALSG I
Sbjct: 149 RRDSTTASLSAANNIPSPASSLSALISSFKGHGLSTKDLVALSGAHTI 197

Score = 62.8 bits (151), Expect = 2e-07
Identities = 33/70 (47%), Positives = 43/70 (61%), Gaps = 5/70 (7%)
Frame = +1

Query: 589 RLTICLALFVLIWGSAN-----AQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLL 753
R +C+ + + S N QLS+ FY SCP S VK V+ A++KE RMGASL+
Sbjct: 4 RNLICIGIMAVFVCSININAVSGQLSSTFYDKSCPRAQSIVKRVVKQALAKEKRMGASLV 63

Query: 754 RLFHDFCFVN 783
RL FHDFCV+
Sbjct: 64 RLHFHDFCFVS 73

>gb|EEE67814.1| hypothetical protein OsJ_25568 [Oryza sativa Japonica Group]
Length = 135

Score = 160 bits (404), Expect = 1e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFDN Y+ NL+
Sbjct: 12 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTPYSFDNAYYSNLL 71

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PLTGS G+IR +C
Sbjct: 72 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLTGSQQIRLSC 131

Query: 2167 RRIN 2178
++N
Sbjct: 132 SKVN 135

>tpe|CAH69352.1| TPA: class III peroxidase 110 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 313

Score = 160 bits (404), Expect = 1e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFDN Y+ NL+
Sbjct: 190 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTPYSFDNAYYSNLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PLTGS G+IR +C
Sbjct: 250 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLTGSQQIRLSC 309

Query: 2167 RRIN 2178
++N
Sbjct: 310 SKVN 313

Score = 127 bits (319), Expect = 7e-27
Identities = 74/175 (42%), Positives = 94/175 (53%)
Frame = +2

Query: 1118 AS*ILMSKH*QMCGDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV 1297
AS + + H GCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C
Sbjct: 53 ASLLRLHFHDFVGCDA SVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQT 112

Query: 1298 VSCADILAI AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI* 1477
VSCADILA+AARDSV +
Sbjct: 113 VSCADILAVAARDSV-----VA 129

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALS 1642
LGGP+W V LGRRD+ TAS +ANN +P P +L LI F G S D+VALS

Sbjct: 130 LGGPSWTVGLGRDSTTASMSANNDLPPFFDLENLIKAFGDKGFSVTDMVALS 184

Score = 67.0 bits (162), Expect = 1e-08
Identities = 31/62 (50%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC
Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRLATIKSAVTAAVNNEPRMGASLLRLLHFHDC 63

Query: 775 FV 780
FV
Sbjct: 64 FV 65

>ref|NP_001060627.1| Os07g0677100 [Oryza sativa (japonica cultivar-group)]
dbj|BAC83102.1| peroxidase [Oryza sativa Japonica Group]
dbj|BAF22541.1| Os07g0677100 [Oryza sativa Japonica Group]
dbj|BAG95220.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 315

Score = 160 bits (404), Expect = 1e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFDN Y+ NL+
Sbjct: 192 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTPYFDNAYYSNLL 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR ++N FSS F++AM+KM ++ PLTGS G+IR +C
Sbjct: 252 SNKGLLHSDQVLFNGNSTDNTVRNFAFNRAAFSSAMVKMANLGPLTGSQQGQIRLSC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 132 bits (331), Expect = 3e-28
Identities = 74/169 (43%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C VSCADILA+AA
Sbjct: 65 VQGCDASVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQTVSCADILAVAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 125 RDSV-----VALGGPSWTVGLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS +ANN +P P +L LI F G S D+VALSG I
Sbjct: 142 RRSTTASMDSANNDLPPPFDFLENLIKAFGDKGFSVTDMVALSGAHTI 190

Score = 67.0 bits (162), Expect = 1e-08
Identities = 31/62 (50%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASLLRRLFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC
Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTAANNNEPRMGASLLRRLFHDC 63

Query: 775 FV 780
FV
Sbjct: 64 FV 65

>gb|ABD66594.1| peroxidase [Litchi chinensis]
Length = 234

Score = 159 bits (403), Expect = 1e-36
Identities = 88/169 (52%), Positives = 103/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTS+F GEK A PN NS RGF V+D IK+ +EK CPGVVSCAD+LAIAA
Sbjct: 4 VDGCDGSLLDDTSTFVGEKTAVPNNNSVRGFNVVDQIKAKLEKACPGVVSCADLLAIAA 63

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 64 RDSV-----VHLGGPSWTVRLG 80

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS++ AN IP PTSNL+ LIS FSA GLS KDLVALSG I
Sbjct: 81 RRDSKTASRALANTSIPPPTSNSALISSFSAQGLSLKDLVALSGAHTI 129

Score = 113 bits (283), Expect = 1e-22
Identities = 54/98 (55%), Positives = 69/98 (70%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARCT+FR IYN+TNI+++FA + ++ CPR+ DN LA LD QTP FD Y+ NL++
Sbjct: 132 ARCTSFRGHIYNDTNIDSSFAMSLRRKCPRSGN--DNALANLDRQTPFCFDKLYYDNLK 189

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAA 2103
KKGLLHSDQ+LF GGS D V+ Y+ N F DFA A

Sbjct: 190 KKGLLHSDQELFKGGSADPFVKKYANNTSAFFKDFAGA 227

>emb|CBI19219.1| unnamed protein product [Vitis vinifera]
Length = 446

Score = 159 bits (403), Expect = 1e-36
Identities = 81/138 (58%), Positives = 105/138 (76%), Gaps = 1/138 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR IYN+T+I+ AFA ++Q+ CPR+ G D+NL+PLD T T FDN YF+ L

Sbjct: 194 KARCTFRNHIYNDTIDPAFAASKQKICPRSGG--DDNLSPLD-GTTTVFDNVYFRGLK 250

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ+L+NGGSTDSIV YS N TF D A AM+KMG+ISPLTG+NG+IR NC

Sbjct: 251 EKKGLLHSDQELYNGGSTDSIVETYSINTATFFRDVANAMVKMGNISPLTGNGQIRTNC 310

Query: 2167 RRIN*F-DSVLNIKGPTH 2217

R+I + + I+ PT+

Sbjct: 311 RKIQCIGPTPIEIRNPTN 328

Score = 155 bits (391), Expect = 3e-35
Identities = 86/167 (51%), Positives = 100/167 (59%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG+EVID IKS VE +CPGVVSCADI+A+AARD

Sbjct: 69 GCDASILLDDTATFTGEKTAGPNNNSVRGYEVIDTIKQVESLCPGVVSCADIVAVAARD 128

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V+LGRR

Sbjct: 129 SV-----VALGGPTWTVRLGRR 145

Query: 1517 DARTASQAANNGIPAPTSNLSRFSALGLSTKDLVALSGTKHI 1657

D+ TAS SAA +P P NL+QLIS FS GL+TK++V LSGT I

Sbjct: 146 DSTTASFAARTDLPGNLNSQLISAFSKKGLTTKEMVVLSGHTI 192

Score = 65.1 bits (157), Expect = 4e-08
Identities = 31/57 (54%), Positives = 40/57 (70%), Gaps = 1/57 (1%)

Frame = +1

Query: 610 LFVLIWGSANAQ-LSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777
+F L+ G A+A LS NFY SCP +++++ V A++KE RMGASLLRL FHDCF
Sbjct: 12 IFSLLLGMAHAHYLSPNFYARSCPRLPTIRTAVNKAVAKEKRMGASLLRLLHFHDCF 68

>ref|XP_002334317.1| predicted protein [Populus trichocarpa]
gb|EEF08174.1| predicted protein [Populus trichocarpa]
Length = 224

Score = 159 bits (403), Expect = 1e-36
Identities = 80/124 (64%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR D LAPLDL TP SFDN YFKNL+
Sbjct: 103 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGS--DATLAPLDLVTNPSFDNYYFKNLM 160

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS+G+IR+ C
Sbjct: 161 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPFRFRSDFGSAMIKMGDIGLLTGSSGQIRRIC 220

Query: 2167 RRIN 2178
+N
Sbjct: 221 SAVN 224

Score = 99.4 bits (246), Expect = 2e-18
Identities = 59/140 (42%), Positives = 77/140 (55%)
Frame = +2

Query: 1229 NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARDSVQIVSGQTTNKNTLN*I IKLYIS 1408
NSARG+ VID K+ VEK+CPGVVSCADI+A+AARD+
Sbjct: 2 NSARGYNVIDKAKTEVEKICPGVVSCADIIA VAARDA----- 38

Query: 1409 KLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQL 1588
S +GGP++ VKLGRRD+ TAS++ AN +PA +L L
Sbjct: 39 -----SAYVGGPSYAVKLGRRDSTASRTLANAELPAFFESLES L 78

Query: 1589 ISRFSALGLSTKDLVALSGT 1648
ISRF GL+ +D+VALSG+
Sbjct: 79 ISRFQKKGLTARDMVALSGS 98

>emb|CAN73051.1| hypothetical protein [Vitis vinifera]
Length = 297

Score = 159 bits (403), Expect = 1e-36
Identities = 77/124 (62%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD+QT FDN Y++NL

Sbjct: 176 QAQCFTFRSRIYNDTNIDPNFAATRRSTCP-VSG-GNSNLAPLDIQTMNKFNDNKYYENLE 233

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++VR YS N F DFAAAM+KM +ISPLTG+NGEIR NC

Sbjct: 234 AQRGLFHSDQELFNGGSQDALVRAYSANNALFFXDFAAAMVKMSNISPLTGTNGEIRSNC 293

Query: 2167 RRIN 2178
R +N

Sbjct: 294 RVVN 297

Score = 151 bits (382), Expect = 4e-34
Identities = 85/169 (50%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA

Sbjct: 49 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACNATVSCADILALAA 108

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG

Sbjct: 109 RDGVVL-----LGGPSWTVPLG 125

Query: 1511 RRDARTASQAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTA+QSAANN +PAP +NL+ LIS F+A GL+ D+ ALSG+ I

Sbjct: 126 RRDARTANQSAANNLPPFANLSALISGFAAKGLNADDMTALSGSHTI 174

Score = 62.4 bits (150), Expect = 3e-07
Identities = 28/49 (57%), Positives = 36/49 (73%)
Frame = +1

Query: 637 NAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783
N +LS NFY +CPN+ V+ + A+ +E RMGAS+LRLFHDCFVN

Sbjct: 2 NYKLSPNFYASTCPNVQKIVRVEMVQAVIREPRMGASILRRLFHDCFVN 50

>gb|EEE67818.1| hypothetical protein OsJ_25573 [Oryza sativa Japonica Group]
Length = 323

Score = 159 bits (402), Expect = 2e-36

Identities = 72/123 (58%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC FR R+YNETNI+ AFA + +CP T GSGD NLAPLD TPT+FDN Y++NL+

Sbjct: 200 ARCRGFRTRLYNETNIDAAFAAALKANCPATPGSGDGNLAPLDTTTPTAFDNAYYRNLLS 259

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KGLLHSDQ+LF+ GSTD+ VR +++++ F + FA AM+KMG+ISPLTG+ G+IR C

Sbjct: 260 NKGLLHSDQELFSNGSTDNTVRSFASSAAAFGAATAMVKMGNISPLTGTGQIRLICS 319

Query: 2170 RIN 2178

+N

Sbjct: 320 AVN 322

Score = 94.7 bits (234), Expect = 5e-17
Identities = 68/168 (40%), Positives = 85/168 (50%), Gaps = 1/168 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD SILL E+NA PN S RG++VID+IK+ +E VC VSCADIL +AARD

Sbjct: 79 GCDASILLAGN-----ERNAAPNF-SVRGYDVIDSIKTQIEAVCKQTVSCADILTVAARD 132

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W+V LGRR

Sbjct: 133 SV-----VALGGPSWSVPLGRR 149

Query: 1517 DARTASQSAANNGIPAP-TSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ A+ +A AP T +L QLIS +++ GLS DLVALSG I

Sbjct: 150 DSTGAATAAQVISSLAPSTDSLAQLISAYASKGLSATDLVALSGAHTI 197

Score = 67.8 bits (164), Expect = 7e-09
Identities = 39/70 (55%), Positives = 46/70 (65%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L L L+ +A A LS FY SCP S +KSTV +A++ E RMGASL

Sbjct: 1 MAS-ASSLGLLLMLAALV-STATAHLSPTFYDTSCPRAMSIKSTVTA AVNNEPRMGASL 58

Query: 751 LRLFFHDCFV 780

LRL FHDCFV

Sbjct: 59 LRLHFHDCFV 68

>gb|EEE56633.1| hypothetical protein OsJ_06032 [Oryza sativa Japonica Group]

Length = 303

Score = 159 bits (402), Expect = 2e-36
Identities = 74/123 (60%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
A+C FR IYN+TN++ FA R++ CP SGSGD+NLAPLD T +FDN Y+++LV
Sbjct: 179 AQCQFFRGRHIYNDTNVDPLFAAERRRRCPAASGSGDSNLAPLDDMTALAFDNAYYRDLVG 238

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D V+ YST+P F+ DF AAMIKMG I PLTG+ G+IRKNCR
Sbjct: 239 RRGLLHSDQELFNGGSQDERVKKYSTDPDLFAGDFVAAMIKMGKICPLTGAAGQIRKNCR 298

Query: 2170 RIN 2178
+N
Sbjct: 299 VVN 301

Score = 95.9 bits (237), Expect = 2e-17
Identities = 48/70 (68%), Positives = 54/70 (77%), Gaps = 2/70 (2%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD SILLDD S F GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+
Sbjct: 80 VQGDASILLDDVPSKGFVGEKTAGPNTNSIRGYEVIDKIKANVEAACPGVVSCADILAL 139

Query: 1325 AARDSVQIVS 1354
AAR+ V +VS
Sbjct: 140 AAREGVNLVS 149

Score = 60.5 bits (145), Expect = 1e-06
Identities = 34/76 (44%), Positives = 47/76 (61%), Gaps = 7/76 (9%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANA-----QLSTNFYHSCPNLFSSVKSTVQSAISKET 732
+S +R + LAL + + SA A ++ ++Y SCP L + V+ T+ SAI E
Sbjct: 5 SSTTTRFCLLLALVLPMISSAAAGDDALPLPMTPSYRKSCTPLEAIVRGTMLSAIKAER 64

Query: 733 RMGASLLRLLFFHDCFV 780
RMGAS+LRLFFHDCFV
Sbjct: 65 RMGASILRLLFFHDCFV 80

>ref|XP_002281731.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 317

Score = 159 bits (402), Expect = 2e-36
Identities = 76/124 (61%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD++T FDN Y++NL+
Sbjct: 196 QAQCFTFRSRIYNDTNIDPNFAATRRSTCP-VSG-GNSNLAPLDIRTMNRFDNIIYQNLN 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TRRGLLHSDQELFNGGSQDALVRTYNANNALFFRDFAAAMVKMSNISPLTGTNGEIRSNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RVVN 317

Score = 151 bits (381), Expect = 5e-34
Identities = 85/169 (50%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 129 RDGV-----VQLGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAANN IP+P ++L+ LIS F+A GL+ +D+ ALSG+ I
Sbjct: 146 RRDARTASQSAANNEIPSPLASLSALISGFAAKGLNARDMTALSGSHTI 194

Score = 71.6 bits (174), Expect = 5e-10
Identities = 35/71 (49%), Positives = 49/71 (69%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MASF + + ++ L+ S N QLS NFY +CPN+ + V+ ++ A+ +E RMGAS+
Sbjct: 1 MASFTNSFVV-FSII SLLACSLNQLSPNFYASTCPNVQNI VVRVAMRQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>gb|EAZ05136.1| hypothetical protein OsI_27329 [Oryza sativa Indica Group]
Length = 338

Score = 159 bits (402), Expect = 2e-36
Identities = 72/123 (58%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC FR R+YNETNI+ AFA + +CP T GSGD NLAPLD TPT+FDN Y++NL+
Sbjct: 215 ARCRGFRTRLYNETNIDAAFAAALKANCPATPGSGDGNLAPLDTTPTAFDNAYYRNLLS 274

Query: 1990 KKGLLHSDQQLFNGGSTDIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KGLLHSDQ+LF+ GSTD+ VR ++++ F + FA AM+KMG+ISPLTG+ G+IR C
Sbjct: 275 NKGLLHSDQELFNSGSTDNTVRSFASSAAAFGAATAMVKMGNISPLTGTQGGIRLICS 334

Query: 2170 RIN 2178
+N
Sbjct: 335 AVN 337

Score = 96.7 bits (239), Expect = 1e-17
Identities = 69/169 (40%), Positives = 86/169 (50%), Gaps = 1/169 (0%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
QGCD SILL E+NA PN S RG++VID+IK+ +E VC VSCADIL +AAR
Sbjct: 93 QGCDASILLAGN-----ERNAAPNF-SVRGYDVDSIKTQIEAVCKQTVSCADILTVAAR 146

Query: 1334 DSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGP+W+V LGR
Sbjct: 147 DSV-----VALGGPSWSVPLGR 163

Query: 1514 RDARTASQSAANNGIPAP-TSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RD+ A+ +A AP T +L QLIS +++ GLS DLVALSG I
Sbjct: 164 RDSTGAATAAQVISSLAPSTDSLAQLISAYASKGLSATDLVALSGAHTI 212

Score = 69.3 bits (168), Expect = 2e-09
Identities = 45/93 (48%), Positives = 55/93 (59%), Gaps = 1/93 (1%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L L L+ +A A LS FY SCP S +KSTV +A++ E RMGASL
Sbjct: 1 MAS-ASSLGLLLMLAALV-STATAHLSPTFYDTSCPRAMSIKSTVTAAVNNEPRMGASL 58

Query: 751 LRLFFHDCFVNV-IYLHLLPLTYKYAKLTYSSS 846

LRL FHDCFV +L P+ + Y L SS
Sbjct: 59 LRLHFHDCFVQARFHLTNHPVFFFYFDLMPKSS 91

>ref|NP_001046402.1| Os02g0240500 [Oryza sativa (japonica cultivar-group)]
dbj|BAD28874.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69270.1| TPA: class III peroxidase 28 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAF08316.1| Os02g0240500 [Oryza sativa Japonica Group]
Length = 334

Score = 159 bits (402), Expect = 2e-36
Identities = 74/123 (60%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSVSGSDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C FR IYN+TN++ FA R++ CP SGSGD+NLAPLD T +FDN Y+++LV
Sbjct: 210 AQCQFFRGHIYNDTNVDPLFAAERRRRCPAASGSGSDNLAPLDDMTALAFDNAYYRDLVG 269

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D V+ YST+P F+ DF AAMIKMG I PLTG+ G+IRKNCR
Sbjct: 270 RRGLLHSDQELFNGGSQDERVKKYSTDPDLFAGDFVAAMIKMGKICPLTGAAGQIRKNCR 329

Query: 2170 RIN 2178
+N
Sbjct: 330 VVN 332

Score = 134 bits (336), Expect = 8e-29
Identities = 76/173 (43%), Positives = 96/173 (55%), Gaps = 2/173 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1324
+QGCD SILLDD S F GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+
Sbjct: 80 VQGCASILLDDVPSKGFVGEKTAGPNTNSIRGYEVIDKIKANVEAACPCGVVSCADILAL 139

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AAR+ V + LGGP+W V
Sbjct: 140 AAREGVNL-----LGGPSWEVP 156

Query: 1505 LRRRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHISH 1663
LRRRD+ TAS+S A++ +P P+S+L L++ F GL+ +D+ ALSG I +
Sbjct: 157 LRRRDSTTASKSEADSDLPGPSSSLADLVAAFGKKGLAPRDMTALSGAHTIGY 209

Score = 60.5 bits (145), Expect = 1e-06

Identities = 34/76 (44%), Positives = 47/76 (61%), Gaps = 7/76 (9%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANA-----QLSTNFYHSCPNLFSSVKSTVQSAISKET 732
+S +R + LAL + + SA A ++ ++Y SCP L + V+ T+ SAI E
Sbjct: 5 SSTTRFCLLLALVLPMISSAAAGDDALPLPMTPSYYRKSCPTLEAIVRGTMLSAIKAER 64

Query: 733 RMGASLLRRLFHDCFV 780
RMGAS+LRLFHDCFV
Sbjct: 65 RMGASILRRLFHDCFV 80

>ref|NP_001060630.1| Os07g0677400 [Oryza sativa (japonica cultivar-group)]
gb|AAC49820.1| peroxidase [Oryza sativa Indica Group]
dbj|BAC79530.1| peroxidase [Oryza sativa Japonica Group]
dbj|BAD30310.1| peroxidase [Oryza sativa Japonica Group]
tpe|CAH69355.1| TPA: class III peroxidase 113 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF22544.1| Os07g0677400 [Oryza sativa Japonica Group]
Length = 314

Score = 159 bits (402), Expect = 2e-36
Identities = 72/123 (58%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
ARC FR R+YNETNI+ AFA + +CP T GSGD NLAPLD TPT+FDN Y++NL+
Sbjct: 191 ARCRGFRTRLYNETNIDAAFAAALKANCPATPGSGDGNLAPLDTTPTAFDNAYRNLLS 250

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KGLLHSDQ+LF+ GSTD+ VR ++++ F + FA AM+KMG+ISPLTG+ G+IR C
Sbjct: 251 NKGLLHSDQELFNSGSTDNTVRSFASAAAFGAATAMVKMGNISPLTGTGQIRLICS 310

Query: 2170 RIN 2178
+N
Sbjct: 311 AVN 313

Score = 97.1 bits (240), Expect = 1e-17
Identities = 69/170 (40%), Positives = 87/170 (51%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVSCADILAI AA 1330
+QGCD SILL E+NA PN S RG++VID+IK+ +E VC VSCADIL +AA
Sbjct: 68 VQGCDASILLAGN-----ERNAAPNF-SVRGYDVIDSIKTQIEAVCKQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNLNL*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W+V LG

Sbjct: 122 RDSV-----VALGGPSWSVPLG 138

Query: 1511 RRDARTASQSAANNGIPAP-TSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+ +A AP T +L QLIS +++ GLS DLVALSG I

Sbjct: 139 RRDSTGAATAAQVISSLAPSTDSLAQLISAYASKGLSATDLVALSGAHTI 188

Score = 67.8 bits (164), Expect = 7e-09
Identities = 39/70 (55%), Positives = 46/70 (65%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L L L+ +A A LS FY SCP S +KSTV +A++ E RMGASL

Sbjct: 1 MAS-ASSLGLLLMLAALV-STATAHLSPTFYDTS CPRAMSIIKSTVTA AVNNEPRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV

Sbjct: 59 LRLHFHDCFV 68

>emb|CAA59487.1| peroxidase [Triticum aestivum]
gb|ACF08093.1| class III peroxidase [Triticum aestivum]
Length = 319

Score = 159 bits (401), Expect = 2e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+TAF A + + +CPR +GSGD++LAPLD TP +FDN Y++NL+

Sbjct: 196 QAQCQNFDRRLYNETNIDTAFATSLRANCPRPTGSGDSSLAPLDTTTPNAFDNAYYRNL M 255

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGNGEIRKNC 2166
+KGLLHSDQ L N G T +VR YS+ F+ DF AAM+ MG+ISPLTG+ G++R +C

Sbjct: 256 SQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNRFRAAMVSMGNISPLTGTQQVRLSC 315

Query: 2167 RRIN 2178
R+N

Sbjct: 316 SRVN 319

Score = 131 bits (329), Expect = 5e-28
Identities = 76/169 (44%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SILL DT++FTGE+ A PN S RG VIDNIK+ VE VC VSCADILA+AA

Sbjct: 69 VQGCASILLSDTATFTGEQAGPNAGSIRGMNVIDNIKAQVEAVCTQTVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNLNL*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 129 RDSV-----VALGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P P+ ++ L + F+A GLS D+VALSG I

Sbjct: 146 RRDSTTASLSLANSDLPPPSFDVANLTANFAAKGLSVTDMVALSGAHTI 194

Score = 60.5 bits (145), Expect = 1e-06
Identities = 35/73 (47%), Positives = 44/73 (60%), Gaps = 1/73 (1%)
Frame = +1

Query: 565 LTMASFCs-RLTICLALFVLIWGSANAQLSTNFYHSCPFLFSSVKSTVQSAISKETRMG 741
+ MAS S L +CLA ++AQLS FY SCP + ++ V +A+ E RMG

Sbjct: 3 MAMASSLSVLLLLCLA-----APSSAQLSPRFYARSCPRAQAIIRRGVAAAVRSERRMG 56

Query: 742 ASLLRRLFHDCFV 780

ASLLRL FHDCFV

Sbjct: 57 ASLLRRLFHDCFV 69

>gb|AAB02554.1| cationic peroxidase [Stylosanthes humilis]
Length = 320

Score = 159 bits (401), Expect = 2e-36
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYNE+NI+ ++A++ Q +CP S GD+NL+P D+ TP FDN Y+ NL

Sbjct: 198 QARCTTFRTRIYNESNIDPSYAKSLQGNCP--SVGGDSNLSPFDVTPNKFNDAYYINLK 255

Query: 1987 QKKGLLHSDQQLFNGG-STDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
KKGLLH+DQQLFNGG STDS V YS N TF++DF AMIKMG++SPLTG++G+IR N

Sbjct: 256 NKKGLLHADQQLFNGGSTDSQVTAYSNNAATFNTDFGNAMIKMGNLSPLTGTSGQIRTN 315

Query: 2164 CRRIN 2178

CR+ N

Sbjct: 316 CRKTN 320

Score = 152 bits (384), Expect = 2e-34
Identities = 85/169 (50%), Positives = 103/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLDDTS+FTGEK A PN NSARGF+VID IKS VE +CPGVVSCADILA+AA
Sbjct: 71 VQGCDASVLLDDTSTFTGEKTAFPNVNSARGFDVIDTIKSQVESLCPGVVSCADILALAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+WNV+LG
Sbjct: 131 RDSV-----VALGGPSWNVQLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS ++AN+ +P P+ NL+ LIS FS G + K+LV LSG I
Sbjct: 148 RRDSTTASLNSANSDLPGPSFNLSGLISAFSKKGFTAKELVTLGAHTI 196

Score = 75.1 bits (183), Expect = 4e-11
Identities = 35/62 (56%), Positives = 45/62 (72%), Gaps = 1/62 (1%)
Frame = +1

Query: 598 ICLALFVLI-WGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDC 774
+C +F+ + G + QLS+NFY CPN S++KS V SA+SKE R+GASLLRL FHDC
Sbjct: 10 VCFIIFMCLNIGLGGQLSSNFYATKCPNALSTIKSAVNSAVSKEARLGASLLRHFHDC 69

Query: 775 FV 780
FV
Sbjct: 70 FV 71

>sp|P16147.2|PERX_LUPPO RecName: Full=Peroxidase
emb|CAA36066.1| peroxidase [Lupinus polyphyllus]
prf||1805332A peroxidase:ISOTYPE=basic isozyme
Length = 158

Score = 159 bits (401), Expect = 2e-36
Identities = 79/124 (63%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+ C F+ RIYN+TNI+T FA +RQ +CP ++G G+ NLAPLD TP FDN Y+K+LV
Sbjct: 36 QSECQFFKTRINNDTNIDTNFATSRQANCPFSAG-GETNLAPLDSLTPNRFDNYYKDLV 94

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+GLLHSDQ LFNGGS D++VR YSTN F SDFAAA++KM ISPLTG GEIRKNC
Sbjct: 95 SNRGLLHSDQVLFNGGSQDTLVRTYSTNNVFFSDFAAAIKMSKISPLTG IAGEIRKNC 154

Query: 2167 RRIN 2178
R IN
Sbjct: 155 RVIN 158

>dbj|BAA77389.1| peroxidase 3 [Scutellaria baicalensis]
Length = 318

Score = 159 bits (401), Expect = 2e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYN+TNI AFA + +CPR+ G DNNLAPLD +P F+N Y++NL+
Sbjct: 197 QARCTTFRGRIYNDTNINGAFATGLRANCPRSGG--DNNLAPLDNVSPARFNNDYYRNL 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+GLLHSDQ+LFN G+ D+ VR YSTN F +DFA AM+KM ++SPLTG+NG+IR+NC
Sbjct: 255 GLRGLLHSDQELFNNGTADAQVRAYSTNSAAFFNDFANAMVKMSNLSPLTGNGQIRRNC 314

Query: 2167 RRIN 2178
RR N
Sbjct: 315 RRTN 318

Score = 135 bits (341), Expect = 2e-29
Identities = 76/169 (44%), Positives = 94/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGKKNANPNRNSARGFEVIDNIKSAREKVCVGVVSCADILAI 1330
+ GCD S+LLDD + FTGK A PN NS RGF+VIDNIK+ VE CP +VSC+DIL++AA
Sbjct: 70 VNGCDASVLLDDRTGFTGKTAGPNANSLRGFVIDNIKTLVEGSCPNIVSCSDILSVAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V V GGP+W V LG
Sbjct: 130 RDGVVAV-----GGPSWAVALG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS +AAN IP P NLN LI+ FS G + +++VALSG+ I
Sbjct: 147 RRDSTTASLNAANTQIPGPGLNLNALITSFSNKGFTAREMVALSGSHTI 195

Score = 87.4 bits (215), Expect = 8e-15
Identities = 42/71 (59%), Positives = 53/71 (74%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MASF S + L L +L+ G +NAQLS NFY +CPNL + +++ V SA+S +TRMGASL
Sbjct: 1 MASFVSEFSTRMLVLLLIGVSNAQLSANFYNTTCPNLLTIIRNAVNSAVSSDTRMGASL 60

Query: 751 LRLFFHDCFVN 783

LRL FHDCFVN
Sbjct: 61 LRLHFHDCFVN 71

>ref|XP_002461207.1| hypothetical protein SORBIDRAFT_02g042840 [Sorghum bicolor]
gb|EER97728.1| hypothetical protein SORBIDRAFT_02g042840 [Sorghum bicolor]
Length = 318

Score = 158 bits (400), Expect = 3e-36
Identities = 73/124 (58%), Positives = 93/124 (75%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++C NFRA IYN+TN+ AFA R+ SCP +G GD NL PLD T T+FDN Y+ NL+
Sbjct: 195 SQCKNFRAHIYNDTNVNAFATLRKVSPPAAAGDGDGNTPLDTATSTAFDNAYYTNLLS 254

Query: 1990 KKGLLHSDQQLFN-GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ GLLHSDQQLFN GG+TD +VR Y++ P F+ DF AAMI+MG+ISPLTG G+IR+ C
Sbjct: 255 RSGLLHSDQQLFNFGGGATDGLVRYASTPTRFNRDFTAAMIRMGNISPLTGRQGQIRAC 314

Query: 2167 RRIN 2178
R+N
Sbjct: 315 SRVN 318

Score = 138 bits (347), Expect = 4e-30
Identities = 79/169 (46%), Positives = 98/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE VCPGVVSCADILA+AA
Sbjct: 67 VQGCDASVLLNDTATFTGEQTANPNVGSIRGFGVVDNIKAQVEAVCPGVVSCADILAVAA 126

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 127 RDSV-----VALGGPSWRVLLG 143

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +PAP+ +L L + F+ LS DLVALSG I
Sbjct: 144 RRDSTTASLALANSPLPAPSLDLANLTAFAKKRSLRSDLVALSGAHTI 192

Score = 67.0 bits (162), Expect = 1e-08
Identities = 30/49 (61%), Positives = 38/49 (77%)
Frame = +1

Query: 634 ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780

A+AQLS FY SCP +++KS V +A+++E RMGASLLRL FHDCFV
Sbjct: 19 ASAQLSATFYRSRCPRALATIksAVTAAVAQEP RMGASLLRLHFHDCFV 67

>gb|EEC82684.1| hypothetical protein OsI_27330 [Oryza sativa Indica Group]
Length = 309

Score = 158 bits (400), Expect = 3e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+
Sbjct: 187 QAQCSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTNNL 244

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C
Sbjct: 245 SNKGLLHSDQVLFNGGSTDNTVRNFASNAAAFSSAFATAMVNMGNIPKGTNGQIRLSC 304

Query: 2167 RRIN 2178
++N
Sbjct: 305 SKVN 308

Score = 102 bits (254), Expect = 2e-19
Identities = 64/167 (38%), Positives = 85/167 (50%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI AARD 1336
GCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AARD
Sbjct: 67 GCDASVLLSGN-----EQDAPPNKDSL RGYGVIDS IKAQIETVCNQT VSCADILTVAARD 121

Query: 1337 SVQIVSQGTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V LGRR
Sbjct: 122 SV-----VALGGPTWTVPLGRR 138

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ AS + A + +P T++L +L+ F+ GLS D+VALSG I
Sbjct: 139 DSTGASAALAI SDLP PFTASLQELVDAFAKGLSVTDMVALSGAHTI 185

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/61 (54%), Positives = 43/61 (70%), Gaps = 2/61 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC

Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIKSAVTAAVNSEPRMGASLLRLHFHDC 65

Query: 775 F 777
F

Sbjct: 66 F 66

>gb|AAW52720.1| peroxidase 6 [Triticum monococcum]
Length = 322

Score = 158 bits (400), Expect = 3e-36
Identities = 73/123 (59%), Positives = 95/123 (77%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLVQ 1989
++C NFR IYN TNI+ AFA R+++CP + +GD NLAP D+QT FDN Y++NLV

Sbjct: 199 SQCLNFRDHIYNGTNIDPAFATLRKRTCPAQAPNGDKNLAPFDVQTQLLFDNAYYRNLVA 258

Query: 1990 KKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLL+SDQ LFNNGS D++VR Y NP F+SDF AMIKMG+I+PLTG+ G+IR+NCR

Sbjct: 259 KRGLLNSDQVLFNNGSQDALVRQYVANPALFASDFVTAMIKMGNINPLTGTAGQIRRNCR 318

Query: 2170 RIN 2178
+N

Sbjct: 319 VVN 321

Score = 131 bits (329), Expect = 5e-28
Identities = 76/169 (44%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCDGSILLDD SF GEK A PN +S RG+EVID IK VE +CPG+VSCADI A+AA

Sbjct: 71 VQGCDGSILLDDVGSFVGEKTAFPNVDSVRGYEVIDEIKKNVELLCPGIVSCADIAALAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD + LGGP+W+V LG

Sbjct: 131 RDGTFL-----LGGPSWSVPLG 147

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +PAP+ +L LI F LS +DL ALSG I

Sbjct: 148 RRDSTTASLTEANSDLPAPSLSLGLLIKAFDCKQLSPQDLTALSGAHTI 196

Score = 64.3 bits (155), Expect = 8e-08
Identities = 33/60 (55%), Positives = 39/60 (65%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNISSVVKSTVQSAISKETRMGASLLRRLFHDCFV 780
CL L+ SA QLS +FY SCP L V++T+ A+ E RMGASLLRL FHDCFV
Sbjct: 12 CLLALFLLSSSAYGQLSPSYAKSCPTLQLIVRATMIKALLAERRMGASLLRRLFHDCFV 71

>gb|AAQ55292.1| class III peroxidase GvPx2b [Vitis vinifera]
Length = 255

Score = 158 bits (400), Expect = 3e-36
Identities = 76/124 (61%), Positives = 100/124 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR IYN+T+I+ AFA ++Q+ CPR+ G D+NL+PLD T T FDN YF+ L
Sbjct: 135 KARCTFRNHIYNDTIDPFAASKQKICPRSGG--DDNLSPLD-GTTTVFDNVYFRGLE 191

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ L+NGGSTDS+V+ YS + TF +D A AM++MGDISPLTG+NG+IR NC
Sbjct: 192 EKKGLLHSDQVLYNGGSTDSLVTYSIDTATFFTDVANAMVRMGDISPLTGNGQIRTNC 251

Query: 2167 RRIN 2178
R++N
Sbjct: 252 RKNV 255

Score = 147 bits (372), Expect = 5e-33
Identities = 83/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLD T++FTGEK A PN NS RG+EVID IKS V +CPGVVSCADI+A+AARD
Sbjct: 10 GCDASILLDGTATFTGEKTAGPNNNSVRGYEVIDTIKSQVGS LCPGVVSCADIVAVAARD 69

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV I+ GGPTW V+LGRR
Sbjct: 70 SVVIL-----GGPTWTVRLGRR 86

Query: 1517 DARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS SAA +P P +L+QLIS FS GL+TK++V LSGT I
Sbjct: 87 DSTTASFAAGTDLPGPNLSLSQLISAFSKKGLTTKEMVVLSTGHTI 133

>gb|AAF65464.2|AF247700_1 peroxidase POC1 [Oryza sativa Indica Group]
Length = 311

Score = 158 bits (400), Expect = 3e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+

Sbjct: 189 QAQCSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTLL 246

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C

Sbjct: 247 SNKGLLHSDQVLFNNGSTDNTVRNFASNAAAFSSAFATAMVNMGNIAPKTGTTNGQIRLSC 306

Query: 2167 RRIN 2178
++N

Sbjct: 307 SKVN 310

Score = 104 bits (260), Expect = 5e-20
Identities = 65/169 (38%), Positives = 87/169 (51%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AA

Sbjct: 67 VQGCDASVLLSGN-----EQDAPPNKDSL RGYGVIDS IKAQIEAVCNQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG

Sbjct: 122 RDSV-----VALGGPTWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ AS + A + +P T++L +L+ F+ GLS D+VALSG I

Sbjct: 139 RRDSTGASAALAI SDLPPTASLQELVDAFAKKGLSVTDMVALSGAHTI 187

Score = 68.2 bits (165), Expect = 5e-09
Identities = 34/62 (54%), Positives = 44/62 (70%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC

Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIIKSAVTA AVNSEPRMGASLLR LHFHDC 65

Query: 775 FV 780
FV

Sbjct: 66 FV 67

>ref|XP_002311022.1| predicted protein [Populus trichocarpa]
gb|EEE88389.1| predicted protein [Populus trichocarpa]

Length = 319

Score = 158 bits (399), Expect = 4e-36
Identities = 79/124 (63%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR + + LAPLDL TP SFDN YFKNL+
Sbjct: 197 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGSN--STLAPLDLVTPNSFDNYYFKNLM 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS G+IR+ C
Sbjct: 255 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPAPFKSDFGSAMIKMGDIGLLTGSAGQIRRIC 314

Query: 2167 RRIN 2178
+N
Sbjct: 315 SAVN 318

Score = 126 bits (316), Expect = 2e-26
Identities = 74/166 (44%), Positives = 94/166 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SILLD+T S EK A N NSARG+ VID K+ VEK+CPGVVSCADI+A+AA
Sbjct: 70 VQGCDASILLDETLSIQSEKTALGNLNSARGYNVIDKAKTEVEKICPGVVSCADIIAVAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RD+ S +GGP++ VKLG
Sbjct: 130 RDA-----SAYVGGPSYAVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGT 1648
RRD+ TAS++ AN +PA +L LISRF GL+ +D+VALSG+
Sbjct: 147 RRDSTTASRTLANAELPAFFESLES LISRFQKKGLTARDMVALSGS 192

Score = 62.4 bits (150), Expect = 3e-07
Identities = 28/57 (49%), Positives = 40/57 (70%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
+ L+ + AQLS FY SCPN S++++ ++SAI+ + RM ASL+RL FHDCFV
Sbjct: 14 MLFLLNTACQAQLSPAFYDSSCPNAISAIRTAIRSAIASDRRMAASLIRLHFHDCFV 70

>gb|EEE67819.1| hypothetical protein OsJ_25574 [Oryza sativa Japonica Group]
Length = 309

Score = 158 bits (399), Expect = 4e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+
Sbjct: 187 QACSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTNNL 244

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C
Sbjct: 245 SNKGLLHSDQVLFNNGSTDNTVRNFASNAAEFSSAFATAMVNMGNAPKTGTNGQIRLSC 304

Query: 2167 RRIN 2178
++N
Sbjct: 305 SKVN 308

Score = 102 bits (254), Expect = 2e-19
Identities = 64/167 (38%), Positives = 85/167 (50%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCVGVVSCADILAI AARD 1336
GCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AARD
Sbjct: 67 GCDASVLLSGN-----EQDAPPNKDSL RGYGVIDS IKAQIEAVCNQTVSCADILTVAARD 121

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V LGRR
Sbjct: 122 SV-----VALGGPTWTVPLGRR 138

Query: 1517 DARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ AS + A + +P T++L +L+ F+ GLS D+VALSG I
Sbjct: 139 DSTGASAALAI SDLPPTASLQELVDAFAKGLSVTDMVALSGAHTI 185

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/61 (54%), Positives = 43/61 (70%), Gaps = 2/61 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC
Sbjct: 6 CISLLVVVALATAASAQLSATFYDTS CPRAMSIKSAVTA AVNSEPRMGASLLR LHFHDC 65

Query: 775 F 777
F
Sbjct: 66 F 66

>ref|NP_001147216.1| LOC100280824 [Zea mays]
gb|ACG26145.1| peroxidase 52 precursor [Zea mays]
Length = 318

Score = 158 bits (399), Expect = 4e-36
Identities = 72/124 (58%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIY +T+I +FA RQQ+CPR+ G G NLAP+D+QTP FD YF NL+
Sbjct: 196 QARCTTFRGRIYGD TDINASFAALRQQTCPRSGGDG--NLAPIDVQTPVRFDTAYFTNLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++VR YS + F++DF AAMI+MG++ LTG+ G+IR+NC
Sbjct: 254 SRRGLFHSDQELFNGGSQDALVRQYSASASLNFADVAAMIRMGNVGVLGTAGQIRRNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RNVN 317

Score = 134 bits (338), Expect = 5e-29
Identities = 83/169 (49%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGKKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCDGSILLD GEK A PN NS RGFEVID IK VE CPGVVSCADILA+AA
Sbjct: 73 VQGCDGSILLDAG----GEKTAGPNLSVRGFEVIDT IKRNVEAACPGVVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD TNL LGGPTW+V LG
Sbjct: 129 RDG-----TNL-----LGGPTWSVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P PT++L LIS F GLS +D+ ALSG I
Sbjct: 146 RRDSTTASASLANSNLPPPTASLGT LISLFRQGLSPRDMTALSGAHTI 194

Score = 73.2 bits (178), Expect = 2e-10
Identities = 40/75 (53%), Positives = 49/75 (65%)
Frame = +1

Query: 556 LSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETR 735
+ +L MAS L CL + L+ A+AQLS FY SCPNL S V++ + A+ E R
Sbjct: 1 MQQLAMAS--PTLMQCLVVVSLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVGSEQR 58

Query: 736 MGASLLRRLFHDCFV 780
MGASLLRRLFHDCFV
Sbjct: 59 MGASLLRRLFHDCFV 73

>ref|NP_001060631.1| Os07g0677500 [Oryza sativa (japonica cultivar-group)]
dbj|BAC79531.1| peroxidase POC1 [Oryza sativa Japonica Group]
dbj|BAD30311.1| peroxidase POC1 [Oryza sativa Japonica Group]
tpe|CAH69356.1| TPA: class III peroxidase 114 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF22545.1| Os07g0677500 [Oryza sativa Japonica Group]
Length = 311

Score = 158 bits (399), Expect = 4e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+
Sbjct: 189 QAQCSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTNNL 246

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C
Sbjct: 247 SNKGLLHSDQVLFNNGSTDNTRNFASNAEFSSAFATAMVMGNIAPKTG TNGQIRLSC 306

Query: 2167 RRIN 2178
++N
Sbjct: 307 SKVN 310

Score = 104 bits (260), Expect = 5e-20
Identities = 65/169 (38%), Positives = 87/169 (51%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AA
Sbjct: 67 VQGCDA SVLLSGN-----EQDAPPNKDSL RGYGVIDS IKAQIEAVCNQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNLNLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 122 RDSV-----VALGGPTWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ AS + A + +P T++L +L+ F+ GLS D+VALSG I
Sbjct: 139 RRDSTGASAA LAISDLPPFTASLQELVDAFAKKGLSVTDMVALSGAHTI 187

Score = 68.2 bits (165), Expect = 5e-09
Identities = 34/62 (54%), Positives = 44/62 (70%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC
Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIKSAVTAAVNSEPRMGASLLRLLHFHDC 65

Query: 775 FV 780
FV
Sbjct: 66 FV 67

>pdb|1SCH|A Chain A, Peanut Peroxidase
pdb|1SCH|B Chain B, Peanut Peroxidase
Length = 294

Score = 158 bits (399), Expect = 4e-36
Identities = 76/124 (61%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CT FR RIYNE+NI+ +A++ Q +CP S GD NL+P D+ TP FDN Y+ NL
Sbjct: 173 QAQCTAFRTRIYNESNIDPTYAKSLQANCP--SVGGDTNLSPFDVTPNKFVNAYYINLR 230

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS V YS N TF++DF AMIKMG++SPLTG++G+IR NC
Sbjct: 231 NKKGLLHSDQQLFNGVSTDSQVTAYSNNAATFNTDFGNAMIKMGNLSPLTGTSGQIRTNC 290

Query: 2167 RRIN 2178
R+ N
Sbjct: 291 RKTN 294

Score = 152 bits (385), Expect = 2e-34
Identities = 87/169 (51%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDTS+FTGEK A PN NS RGFEVID IKS VE +CPGVVSCADILA+AA
Sbjct: 46 VQGCDASVLLDDTSNFTGEKTAGPNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVAA 105

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGG +WNV LG
Sbjct: 106 RDSV-----VALGGASWNVLLG 122

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S+AN+ +PAP NL+ LIS FS G +TK+LV LSG I

Sbjct: 123 RRDSTTASLSSANSDLPAFFNLSGLISAFSNKGFTTKELVTLGAHTI 171

Score = 68.9 bits (167), Expect = 3e-09
Identities = 31/45 (68%), Positives = 36/45 (80%)
Frame = +1

Query: 646 LSTNFYHSCP NFLSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
LS+NFY CPN S++KS V SA++KE RMGASLLRL FHDCFV
Sbjct: 2 LSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLR LHFHDCFV 46

>sp|P22195.2|PER1_ARAHY RecName: Full=Cationic peroxidase 1; AltName: Full=PNPC1; Flags:
Precursor
gb|AAB06183.1| cationic peroxidase [Arachis hypogaea]
Length = 316

Score = 158 bits (399), Expect = 4e-36
Identities = 76/124 (61%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CT FR RIYNE+NI+ +A++ Q +CP S GD NL+P D+ TP FDN Y+ NL
Sbjct: 195 QAQCTAFRTRIYNESNIDPTYAKSLQANCP--SVGGDTNLSFPDVTTPNKFDNAYYINLR 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS V YS N TF++DF AMIKMG++SPLTG++G+IR NC
Sbjct: 253 NKKGLLHSDQQLFNGVSTDSQVTAYSNNAATFNTDFGNAMIKMGNLSPLTGTSGQIRTNC 312

Query: 2167 RRIN 2178
R+ N
Sbjct: 313 RKTN 316

Score = 152 bits (385), Expect = 2e-34
Identities = 87/169 (51%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSTFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LLDDTS+FTGEK A PN NS RGFEVID IKS VE +CPGVVSCADILA+AA
Sbjct: 68 VQGCDASVLLDDTSNFTGEKTAGPNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGG +WNV LG
Sbjct: 128 RDSV-----VALGGASWNVLLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS S+AN+ +PAP NL+ LIS FS G +TK+LV LSG I
Sbjct: 145 RRDSTTASLSSANSDDLPAFFNLSGLISAFSNKGFTTKELVTLGSAHTI 193

Score = 77.0 bits (188), Expect = 1e-11
Identities = 35/57 (61%), Positives = 44/57 (77%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYHSCP NFLSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
+F+ + G +AQLS+NFY CPN S++KS V SA++KE RMGASLLRL FHDCFV
Sbjct: 12 IFMCLIGLGSACLSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLRLHFHDCFV 68

>gb|ACU22965.1| unknown [Glycine max]
Length = 322

Score = 157 bits (398), Expect = 5e-36
Identities = 78/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI+++FA + Q +CP S GD+NLAPLD T FDN YFK+L
Sbjct: 202 QAKCSTFRTRIYNETNIDSSFATSLQANCP--SVGGDSNLAPLDSNQNT-FDNAYFKDLQ 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLH+DQ LFNGGSTDS V GY+++P +F++DFA AM+KMG+ISPLTGS+GEIR NC
Sbjct: 259 SQKGLLHTDQVLFNGGSTDSQVNGYASDPSSFNTDFANAMVKMGNISPLTGSSGEIRTNC 318

Query: 2167 RRIN 2178
+ N
Sbjct: 319 WKTN 322

Score = 134 bits (338), Expect = 5e-29
Identities = 78/165 (47%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKS AVEKVC PGVVSCADILAIAA 1330
+QGCD S+LL+DTSSFTGE+ A N NS RGF VIDNIKS VE +CPGVVSCADIL +AA
Sbjct: 75 VQGCDASVLLNDTSSFTGEQTAAGNVNSIRFGVIDNIKSQVESLCPGVVSCADILTVAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 135 RDSV-----VALGGPSWTVQLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS S+AN+ +P +L QL F GL+T ++VALSG

Sbjct: 152 RRDSTTASLSSANSDLPRFDLSLQQLSDNFQNKGLTTAEMVALSG 196

Score = 76.6 bits (187), Expect = 1e-11
Identities = 40/75 (53%), Positives = 51/75 (68%), Gaps = 5/75 (6%)
Frame = +1

Query: 571 MASFC SRLT-----ICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETR 735
MAS C +T I LF+ G +++QLS++FY +CPN S++KS V SA+S E R
Sbjct: 1 MASSCF SMTPIFKIRFFLFLCFIGISSQLSSDFYSTTCPNALSTIKSAVDSAVSNEAR 60

Query: 736 MGASLLR LFFHDCFV 780
MGASLLRL FHDCFV
Sbjct: 61 MGASLLR LHFHDCFV 75

>ref|XP_002311955.1| predicted protein [Populus trichocarpa]
gb|EEE89322.1| predicted protein [Populus trichocarpa]
Length = 187

Score = 157 bits (398), Expect = 5e-36
Identities = 79/124 (63%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR + + LAPLDL TP SFDN YFKNL+
Sbjct: 65 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGSN--STLAPLDLVT PNSFDNYYFKNLM 122

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS G+IR+ C
Sbjct: 123 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPFRSDFGSAMIKMGDIGLLTGSAGQIRRIC 182

Query: 2167 RRIN 2178
+N
Sbjct: 183 SAVN 186

Score = 63.2 bits (152), Expect = 2e-07
Identities = 31/57 (54%), Positives = 43/57 (75%)
Frame = +2

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
+GGP++ VKLGRRD+ TAS++ AN +PA +L LISRF GL+ +D+VALSG+
Sbjct: 4 VGGPSYAVKLGRRDSTASRTLANAELPAFFESLESISR FQKKGLTARDMVALSGS 60

>gb|AAM61588.1| peroxidase [Arabidopsis thaliana]

Length = 316

Score = 157 bits (398), Expect = 5e-36
Identities = 76/124 (61%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYN +NI+T+FA +++++CP TSGSGDN A LD+++P FD+ ++K L+
Sbjct: 193 RAQCVTFRNRIYNASNIDTSFAISKRRNCPATSGSGDNKKANLDVRSPDRFDHGFYKQLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLL SDQ LFN G TDS+V YS N F DFA AMIKMGDISPLTGSNG+IR+NC
Sbjct: 253 SKKGLLTSQVLFNNGPTDSLVIAYSHNLNAFYRDFARAMIKMGDISPLTGSNGQIRQNC 312

Query: 2167 RRIN 2178
RR N
Sbjct: 313 RRPN 316

Score = 150 bits (378), Expect = 1e-33
Identities = 85/170 (50%), Positives = 103/170 (60%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDT SF GEK + P+ NS RGFEVID IK VEK+CPG+VSCADILAI A
Sbjct: 65 VNGCDGSLLLDDTSPFLGEKTSGPSNNSVRGFEVIDKIKFKVEKMCPGIVSCADILAITA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGP TWNVKLG 1510
RDSV + LGGP W+VKLG
Sbjct: 125 RDSVLL-----LGGPGWSVKLG 141

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA+ +AAN+G IP P + L+ LI+RF A GLST+D+VALSG+ I
Sbjct: 142 RRDSTTANFAAANSVIPPITTLNLRNFKAQGLSTRDMVALSGSHTI 191

Score = 72.8 bits (177), Expect = 2e-10
Identities = 32/62 (51%), Positives = 46/62 (74%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777
+ L + +++ + AQL+ +FY SCP+LF V+ V+ A+++E RMGASLLRLLFFHDCF
Sbjct: 5 VLLMMIMMLASQSEAQLNRDFYKESCPSLFLVRRRVVKRAVAREPRMGASLLRLLFFHDCF 64

Query: 778 VN 783
VN
Sbjct: 65 VN 66

>ref|NP_200647.1| peroxidase, putative [Arabidopsis thaliana]
sp|Q9LVL2.1|PER67_ARATH RecName: Full=Peroxidase 67; Short=Atperox P67; AltName: Full=ATP44;
Flags: Precursor
dbj|BAA96930.1| peroxidase [Arabidopsis thaliana]
Length = 316

Score = 157 bits (398), Expect = 5e-36
Identities = 76/124 (61%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRSTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYN +NI+T+FA +++++CP TSGSGDN A LD+++P FD+ ++K L+
Sbjct: 193 RAQCVTFRNRIYNASNIDTSFAISKRRNCPATSGSGDNKKANLDVRSPDRFDHGFYKQLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLL SDQ LFN G TDS+V YS N F DFA AMIKMGDISPLTGSNG+IR+NC
Sbjct: 253 SKKGLLTSQVLFNNGPTDSLVIAYSHNLNAFYRDFARAMIKMGDISPLTGSNGQIRQNC 312

Query: 2167 RRIN 2178
RR N
Sbjct: 313 RRPN 316

Score = 149 bits (377), Expect = 1e-33
Identities = 85/170 (50%), Positives = 102/170 (60%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAIAA 1330
+ GCDGS+LLDDT SF GEK + P+ NS RGFEVID IK VEK+CPG+VSCADILAI A
Sbjct: 65 VNGCDGSLLDDTSPFLGEKTSGPSNNSVRGFEVIDKIKFKVEKMC PGIVSCADILAITA 124

Query: 1331 RDSVQIVSGQTTNKNLTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W+VKLG
Sbjct: 125 RDSVLL-----LGGPGWSVKLG 141

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA+ +AAN+G IP P + L+ LI+RF A GLST+D+VALSG I
Sbjct: 142 RRDSTTANFAAANSVIPPPIITLNLINRFKAQGLSTRDMVALSGAHTI 191

Score = 72.8 bits (177), Expect = 2e-10
Identities = 32/62 (51%), Positives = 46/62 (74%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777

+ L + +++ + AQL+ +FY SCP+LF V+ V+ A+++E RMGASLLRLLFFHDCF
Sbjct: 5 VLLMMIMMLASQSEAQLNRDFYKESCPSLFLVRRVVKRAVAREPRMGASLLRLLFFHDCF 64

Query: 778 VN 783

VN

Sbjct: 65 VN 66

>ref|XP_002460939.1| hypothetical protein SORBIDRAFT_02g037840 [Sorghum bicolor]
gb|EER97460.1| hypothetical protein SORBIDRAFT_02g037840 [Sorghum bicolor]
Length = 325

Score = 157 bits (397), Expect = 7e-36
Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C N++ARIYN+ NI AFA + + CP G G N APLD TP +FDN Y+ +LV

Sbjct: 204 QAQCQNYQARIYNDANINAAFAASLRAGCPAGGGGGAN--APLDASTPNAFDNAYYGDV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGSTD +VR Y+ + FSSDFAAAM+KMG I +TGS+GE+R+NC

Sbjct: 262 AQQGLLHSDQELFNGGSTDGLVRSYAASSARFSSDFAAAMVKMGIGVITGSSGEVRRNC 321

Query: 2167 RRIN 2178
RR+N

Sbjct: 322 RRVN 325

Score = 139 bits (349), Expect = 2e-30
Identities = 76/165 (46%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+QGCD S+LLDDT +FTGEK+A PN S RGF VID IK+ +E +CP VSCADILA+AA

Sbjct: 77 VQGCDAVLLDDTGNFTGEKSAGPNAGSLRFGVIDTIKALLEALCPRTVSCADILAVAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG

Sbjct: 137 RDSV-----VALGGPSWTVQLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS S AN +P+P S+L+ L++ F+ GLS+ D+VALSG

Sbjct: 154 RRDSTTASLSTANTDLPSPASSLSTLLAAFARKGLSSTDMVALSG 198

Score = 64.7 bits (156), Expect = 6e-08

Identities = 30/65 (46%), Positives = 43/65 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S+L++ + + +A AQLS FY SCP ++K+ V++A+ + RMGASLLRL F
Sbjct: 13 SKLSVLILALATVVAARAQLSPTFYASSCPAALVTIKTAVRAALVLDRRMGASLLRLHF 72

Query: 766 HDCFV 780
HDCFV
Sbjct: 73 HDCFV 77

>ref|XP_002334018.1| predicted protein [Populus trichocarpa]
gb|EEE77880.1| predicted protein [Populus trichocarpa]
Length = 307

Score = 157 bits (397), Expect = 7e-36
Identities = 79/124 (63%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR + LAPLDL TP SFDN YFKNL+
Sbjct: 186 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGSNA--TLAPLDLVTPNSFDNYYFKNLM 243

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS G+IR+ C
Sbjct: 244 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPFRSDFGSAMIKMGDIGLLTGSAGQIRRIC 303

Query: 2167 RRIN 2178
+N
Sbjct: 304 SAVN 307

Score = 127 bits (319), Expect = 7e-27
Identities = 74/166 (44%), Positives = 95/166 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SILLD+T+S EK A N NSARG+ VID K+ VEK+CPGVVSCADI+A+AA
Sbjct: 59 VQGCDASILLDETTSIQSEKTALGNLNSARGYNVIDKAKTEVEKICPGVVSCADIIAVAA 118

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP++ VKLG
Sbjct: 119 RDA-----SAYVGGPSYAVKLG 135

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS++ AN +PA +L LISRF GL+ +D+VALSG+
Sbjct: 136 RRDSTTASRTLANAELPAFFESLESISRFFQKKGLTARDMVALSGS 181

Score = 60.5 bits (145), Expect = 1e-06
Identities = 27/50 (54%), Positives = 36/50 (72%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
+ AQLS FY SCPN S++ + ++SAI+ + RM ASL+RL FHDCFV
Sbjct: 10 ACQAQLSPA FYDSSCPN ALSAIGTAIRSAIASDRRMAASLIRLHFHDCFV 59

>gb|EAY85151.1| hypothetical protein OsI_06506 [Oryza sativa Indica Group]
Length = 335

Score = 157 bits (397), Expect = 7e-36
Identities = 73/123 (59%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
A+C FR IYN+TN++ FA R++ CP SGSGD+NLAPLD T +FDN Y+++LV
Sbjct: 211 AQCQFFRGIHYNDTNVDPLFAAERRRRCPAASGSGDNLAPLDDMTALAFDNAYYRDLVG 270

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D V+ YST+P F+ DF AAMIKMG I PLTG+ G+IRKNCR
Sbjct: 271 RRGLLHSDQELFNGGSQDERVKKYSTDPDLFAGDFVAAMIKMGKICPLTGAAGQIRKNCR 330

Query: 2170 RIN 2178
++
Sbjct: 331 VVS 333

Score = 138 bits (347), Expect = 4e-30
Identities = 76/171 (44%), Positives = 95/171 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AA 1330
+QGCD SILLDD F GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+AA
Sbjct: 83 VQGCDASILLDDVQGFVGEKTAGPNANSIRGYEVIDKIKANVEAACPGVVSCADILALAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LG GPTWNVKLG 1510
R+ V + LGGP+W V LG
Sbjct: 143 REGVNL-----LGGPSWEVPLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHISH 1663
RRD+ TAS+S A++ +P P+S+L LI+ F GL+ +D+ ALSG I +
Sbjct: 160 RRDSTTASKSEADSLPGPSSSLADLIAAFGKKGLAPRDMTALSGAHTIGY 210

Score = 58.2 bits (139), Expect = 5e-06
Identities = 26/45 (57%), Positives = 34/45 (75%)
Frame = +1

Query: 646 LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRRLFHDCFV 780
++ ++Y SCP L + V+ T+ SAI E RMGAS+LRLFHDCFV
Sbjct: 39 MTPSYRKSQCPTLEAIVRGTMVSAIKAERRMGASILRRLFHDCFV 83

>emb|CAH10842.1| peroxidase [Picea abies]
Length = 320

Score = 157 bits (397), Expect = 7e-36
Identities = 77/124 (62%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYNE+NI AFA + + +CP S GDN L+PLD+ T FDN Y+ NL
Sbjct: 199 QSRCAFFRTRIYNESNINAAFATSVKANCP--SAGGDNTLSPLDVVTSIKFDNKYYGNLK 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQLFNGG TDS V YSTN +F +DFAAAM+KM +ISPLTG++G+IRKNC
Sbjct: 257 IQKGLLHSDQQLFNGGPTDSQVTAYSTNQNSFFTFDFAAAMVKMSNISPLTGTSGQIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKAN 320

Score = 151 bits (382), Expect = 4e-34
Identities = 88/169 (52%), Positives = 98/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDD ++FTGEK A PN NSARGF+VID IK+ VE C GVVSCADIL IAA
Sbjct: 72 VNGCDGSILLDDNATFTGEKTAGPNANSARGFDVIDTIKTQVEAACSGVVSCADILTIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GPTW V LG
Sbjct: 132 RDSV-----VELQGPTWTVMGL 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP+P S+L+ LIS F GLSTKDLVALSG I
Sbjct: 149 RRDSTTASLSDANNIPSPASSLSALISSFKGHGLSTKDLVALSGAHTI 197

Score = 65.5 bits (158), Expect = 3e-08
Identities = 34/70 (48%), Positives = 43/70 (61%), Gaps = 5/70 (7%)
Frame = +1

Query: 589 RLTICLALFVLIWGSAN-----AQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLL 753
R +C+ + + S N QLS+ FY SCP S VK V+ A++KE RMGASL+
Sbjct: 4 RTLLCIGVMAVFCVSININAVSGQLSSTFYDKSCPRAQSIVKRVVQAVAKEKRMGASLV 63

Query: 754 RLFHDCFVN 783
RL FHDCFVN
Sbjct: 64 RLHFHDCFVN 73

>emb|CBI22007.1| unnamed protein product [Vitis vinifera]
Length = 425

Score = 157 bits (396), Expect = 9e-36
Identities = 75/121 (61%), Positives = 97/121 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD++T FDN Y++NL+
Sbjct: 196 QAQCFTFRSRIYNDTNIDPNFAATRRSTCP-VSG-GNSNLAPLDIRTMNRFDNIIYYQNL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TRRGLLHSDQELFNGGSQDALVRTYNANNALFFRDFAAAMVKMSNISPLTGTNGEIRSNC 313

Query: 2167 R 2169
R
Sbjct: 314 R 314

Score = 151 bits (381), Expect = 5e-34
Identities = 85/169 (50%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDT IKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 129 RDGV-----VQLGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAANN IP+P ++L+ LIS F+A GL+ +D+ ALSG+ I

Sbjct: 146 RRDARTASQSAANNEIPSPLASLSALISGFAAKGLNARDMTALSGSHTI 194

Score = 71.6 bits (174), Expect = 5e-10
Identities = 35/71 (49%), Positives = 49/71 (69%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MASF + + ++ L+ S N QLS NFY +CPN+ + V+ ++ A+ +E RMGAS+
Sbjct: 1 MASFTNSFVV-FSIIISLLACSLINGQLSPNFYASTCPNVQNIIVRVAMRQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>ref|XP_002283995.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 316

Score = 157 bits (396), Expect = 9e-36
Identities = 76/124 (61%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYNETN++ AFA+++Q+ CP T G D NL+ LD +T T FD YFK+L+
Sbjct: 195 KAQCIKFRYRIYNETNVDAFAKSKQKICPWTGG--DENLSDLD-ETTTVFDTVYFKDLI 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YST+ TF +D A AM+KMG++SPLTG++GEIR NC
Sbjct: 252 EKKGLLHSDQQLYNGNSTDSMVETYSTDSTFFFTDVANAMVKMGNSPLTGTGDEIRTNC 311

Query: 2167 RRIN 2178
R+IN
Sbjct: 312 RKIN 315

Score = 148 bits (374), Expect = 3e-33
Identities = 82/167 (49%), Positives = 101/167 (60%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILLDDTANFTGEKTAGPNNNSLRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V++GRR
Sbjct: 130 SV-----VALGGPTWTVQMGRR 146

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN +PAPTS+L+ L S FS G +T+++VALSGT I
Sbjct: 147 DSTTASLSTANADLPAPTSDDLVLTSLSFNKGFTTQEMVALSGHTI 193

Score = 74.3 bits (181), Expect = 7e-11
Identities = 38/70 (54%), Positives = 48/70 (68%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPFLSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS NFY SCP S++++ V +A++KE RMGASL
Sbjct: 1 MASLSLFSFFCMFSFLL--GMAHAQLSPNFYASSCPRALSTIRTAVNNAVAKERRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>emb|CAN81400.1| hypothetical protein [Vitis vinifera]
Length = 317

Score = 157 bits (396), Expect = 9e-36
Identities = 75/124 (60%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C F +RIYN+TNI+ FA TR+ +CP SG G++NLAPLD++T FDN Y++NL+
Sbjct: 196 QAQCFTFXSRIYNDTNIDPNFAATTRSTCP-VSG-GNSNLAPLDIRTMNRFDNIIYYQNL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TRRGLLHSDQELFNGGSQDALVRTYNANNALFFRDFAAAMVKMSNISPLTGTNGEIRSNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RVVN 317

Score = 150 bits (380), Expect = 6e-34
Identities = 84/169 (49%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W + LG
Sbjct: 129 RDGV-----VQLGGPSWTIPLG 145

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAANN IP+P ++L+ LIS F+A GL+ +D+ ALSG+ I
Sbjct: 146 RRDARTASQSAANNEIPSPLASLSALISGFAAKGLNARDMTALSGSHTI 194

Score = 71.6 bits (174), Expect = 5e-10
Identities = 35/71 (49%), Positives = 49/71 (69%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MASF + + ++ L+ S N QLS NFY +CPN+ + V+ ++ A+ +E RMGAS+
Sbjct: 1 MASFTNSFVV-FSIISLLACSLNGQLSPNFYASTCPNVQNIWRVAMRQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>emb|CAN63655.1| hypothetical protein [Vitis vinifera]
Length = 272

Score = 157 bits (396), Expect = 9e-36
Identities = 76/124 (61%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYNETN++ AFA+++Q+ CP T G D NL+ LD +T T FD YFK+L+
Sbjct: 151 KAQCIKFRYRIYNETNVDAAFKSKQKICPWTGG--DENLSDLD-ETTTVFDTVYFKDLI 207

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YST+ TF +D A AM+KMG++SPLTG++GEIR NC
Sbjct: 208 EKKGLLHSDQQLYNGNSTDSMVETYSTDTTFFTDVANAMVKGMLSPLTGTGDEIRTNC 267

Query: 2167 RRIN 2178
R+IN
Sbjct: 268 RKIN 271

Score = 150 bits (379), Expect = 8e-34
Identities = 83/168 (49%), Positives = 102/168 (60%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AAR 1333

Sbjct: 25 QGCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AAR
QGCDASILLDDTANFTGEKTAGPNNNSLRGYDVIDTIKSMESLCPGVVSCADIVAVAAAR 84

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGPTW V++GR

Sbjct: 85 DSV-----VALGGPTWTVQMGR 101

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RD+ TAS S AN +PAPTS+L+ L S FS G +T+++VALSGT I

Sbjct: 102 RDSTTASLSTANADLPAPTSDDLVLTSLSFKGFTTQEMVALSGTHTI 149

>gb|AAA20472.1| peroxidase [Cenchrus ciliaris]
Length = 307

Score = 156 bits (395), Expect = 1e-35
Identities = 75/125 (60%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT FR RIY +TNI+ +FA +QQ+CPR+ G G NLAP+D QTP FDN Y+ NLV

Sbjct: 188 QARCTTFRGRIYGDNTIDASFAALQQQTCPRSGGDG--NLAPIDAQTPARFDNAYYTNLV 245

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSN-GEIRKN 2163
++GL HSDQ+LFNGGS D++VR YS++P F+SDF AAMIKMG+I G+N G++R+N

Sbjct: 246 SRRGLFHSDQELFNGGSQDALVRQYSSSPSQFNSDFVAAMIKMGNI----GANAGQVRRN 301

Query: 2164 CRRIN 2178
CR +N

Sbjct: 302 CRVVN 306

Score = 108 bits (271), Expect = 3e-21
Identities = 71/168 (42%), Positives = 83/168 (49%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SIL S GEK+A PN NS RG+EVID IK VE CPGVVSCA I+ +AA

Sbjct: 68 VQGCDASIL----SRSGGEKSAGPNANSVRGYEVIDTIKKNVEAACPGVVSCATIVPLAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
R ++ G PTWNV LG

Sbjct: 124 RPGPNLLGG-----PTWNVPLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKH 1654
RRD+ TA S AN +P PTS L LIS F LS +D++ALSG H

Sbjct: 141 RRDSTTAMLSLANQLPPPTS-LGTLISLFGG-RLSARDMIALSGAHH 186

Score = 73.6 bits (179), Expect = 1e-10
Identities = 35/60 (58%), Positives = 44/60 (73%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
CL L+ +A+QLST FY SCPNL + V++ + A+S E RMGAS+LRLFFHDCFV
Sbjct: 9 CLLAISLLSFTAHAQLSTTFYASSCPNLQTVVRAAMTQAVSSEPRMGASILRFFHDCFV 68

>gb|ACF08096.1| class III peroxidase [Triticum aestivum]
Length = 313

Score = 156 bits (394), Expect = 1e-35
Identities = 72/126 (57%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI + FA + + +CP+ +GSGD NLA LD+ TP SFDN Y+ NL
Sbjct: 188 QAQCQNFRDRLYNETNINSGFATSLKANCPQPTGSGDRNLANDVSTPYSFDNAYYSNLK 247

Query: 1987 QKKGLLHSDQQLF--NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+KGLLHSDQ LF GG TD+ V +++NP FSS FA+AM+KMG++SPLTGS G++R
Sbjct: 248 SQKGLLHSDQVLFVTGGTDNTVNNFASNPAAFSSAFASAMVKGMLNSPLTGSQQQVRL 307

Query: 2161 NCRRIN 2178
+C ++N
Sbjct: 308 SCSKVN 313

Score = 101 bits (252), Expect = 4e-19
Identities = 64/169 (37%), Positives = 83/169 (49%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGFVID+IK+ +E +C VSCADIL +AA
Sbjct: 66 VQGCDAVLLSGM-----EQNAFPNVMSLRGFVIDSIKAKLETMCKQTVSCADILTVAA 120

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 121 RDSV-----VALGGPSWTVPLG 137

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P P +L L F G + D+VALSG I
Sbjct: 138 RRDSTNANEAVANSDLPPFFDLVNLTSFGDKGFTVTDMLVALSGAHTI 186

Score = 72.4 bits (176), Expect = 3e-10
Identities = 36/72 (50%), Positives = 50/72 (69%)
Frame = +1

Query: 565 LTMASFC SRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGA 744
+ +S + L +CLA+ +A+AQLS FY +CPN +++KS V +A++KE RMGA
Sbjct: 1 MASSSLSAVLLLCLAV-----AASAQLSPTFYDTTCPNALATI KSAVTA AVNKENRMGA 54

Query: 745 SLLR LFFHDCFV 780
SLLRL FHDCFV
Sbjct: 55 SLLR LHFHDCFV 66

>ref|XP_002461211.1| hypothetical protein SORBIDRAFT_02g042870 [Sorghum bicolor]
gb|EER97732.1| hypothetical protein SORBIDRAFT_02g042870 [Sorghum bicolor]
Length = 321

Score = 156 bits (394), Expect = 1e-35
Identities = 74/125 (59%), Positives = 95/125 (76%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR-TSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR IYN+TNI +AFA + Q +CPR +GSGD+ LAPLD +PT+FDN YF NL
Sbjct: 196 QAQCRFFRDHIYNDTNINS AFAASLQANCP RPANGSGDSTLAPLDAASPTAFDNAYFSNL 255

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMI KMGDISPLTGSNGEIRKN 2163
+ KGLLHSDQQLFNGGSTDS VR ++++ FS+ FA AM+ MG+I+P TGS G+IR
Sbjct: 256 MSHKGLLHSDQQLFNGGSTDSTVRSFASSASAFSNAFATAMVNMGN IAPKTGSQQGIRVT 315

Query: 2164 CRRIN 2178
C ++N
Sbjct: 316 CSKVN 320

Score = 121 bits (303), Expect = 5e-25
Identities = 71/165 (43%), Positives = 88/165 (53%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTG EKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD S+LL DT SFTGE+ A PN+NS RGF VID+IK+ VE VC VSCADILA+AA
Sbjct: 69 VDGCDASVLLADTGSFTGEQGAIPNKNSLRGFSVIDSIKTQVEAVCNQTVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V +G
Sbjct: 129 RDSV-----VALGGPSWTVLVG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRD+ TAS+ A +P P+ +L L F+ LS D+VALSG
Sbjct: 146 RRDSTTASKDNAERDLPPPSFDLANLTRSFANKNLSVTDMVALSG 190

Score = 71.2 bits (173), Expect = 6e-10
Identities = 33/66 (50%), Positives = 47/66 (71%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPFLFSSVKSTVQSAISKETRMGASLLRLFF 765
SRL++ + + + +A AQLS+ FY SCP +++KS V +A++ E RMGASLLRL F
Sbjct: 5 SRLSLLVAILALATAATAQLSSTFYDTSCP KALATI KSAVTA AVNNEARMGASLLRLHF 64

Query: 766 HDCFVN 783
HDCFV+
Sbjct: 65 HDCFVD 70

>sp|Q02200.1|PERX_NICSY RecName: Full=Lignin-forming anionic peroxidase; Flags: Precursor
gb|AAA34050.1| anionic peroxidase [Nicotiana glauca]
Length = 322

Score = 156 bits (394), Expect = 1e-35
Identities = 82/125 (65%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIY N T+I+ FA TR++ CP+ +G NLAPLDL TP FDN YFKNL
Sbjct: 200 QAQCFLFRDRIYSNGTDIDAGFASTRRRQCPQEGENG--NLAPLDLVTPNQFDNYYFKNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LFNGGSTD+IV YS + FSSDFAAAMIKMGDISPL+G NG IRK
Sbjct: 258 IQKKGLLQSDQVLFNGGSTDNIVSEYSNSARAFSSDFAAAMIKMGDISPLSGQNGIIRKV 317

Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CGSVN 322

Score = 134 bits (337), Expect = 6e-29
Identities = 76/169 (44%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLD+T S EK A PN SARGF +I++ K VEK+CPGVVSCADIL +AA
Sbjct: 73 VQGCDASILLDETPSIESEKTALPNLGSARGFGIIEDAKREVEKICPGVVSCADILTVAA 132

Query: 1331 RDSVQIVSGQTTNKNLTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510

Sbjct: 133 RD+ S +GGP+W VKLG
RDA-----SAAVGGPSWTVKLG 149

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ A +P P LN+LIS F++ GLST+D+VALSG I

Sbjct: 150 RRDSTTASKTLAETDLPFPDPLNRLISSFASKGLSTRDMVALSGAHTI 198

Score = 64.7 bits (156), Expect = 6e-08
Identities = 32/68 (47%), Positives = 47/68 (69%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR 756
SF ++ I +L +L +AQLS FY ++CPN ++++++V+ AIS E RM ASL+R
Sbjct: 7 SFRAKAAI-FSLLLLSCMQCHAQLSATFYDNTCPNALNTIRTSVRQAISSERRMAASLIR 65

Query: 757 LFFHDCFV 780
L FHDCFV
Sbjct: 66 LHFHDCFV 73

>ref|XP_002437129.1| hypothetical protein SORBIDRAFT_10g021620 [Sorghum bicolor]
gb|EER88496.1| hypothetical protein SORBIDRAFT_10g021620 [Sorghum bicolor]
Length = 313

Score = 155 bits (393), Expect = 2e-35
Identities = 73/124 (58%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR+RIY +TNI +FA RQQ+CP++ G G NLA +D QTPT FD Y+ NL+
Sbjct: 191 QARCTTFRSRIYGD TNINASFAALRQQTCPQSGGDG--NLASIDEQTPTRFDTDYYTNLM 248

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++VR YS + F+SDF AAMIKMG++ LTG+ G+IR+NC
Sbjct: 249 LQRGLFHSDQELFNGGSQDALVRQYSASSSLFNSDFVAAMIKMGNVGLTGTAGQIRRNC 308

Query: 2167 RRIN 2178
R +N
Sbjct: 309 RVVN 312

Score = 128 bits (322), Expect = 3e-27
Identities = 76/169 (44%), Positives = 90/169 (53%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVS CADILAIAA 1330

+QGCDGSILLD GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+AA
Sbjct: 68 VQGCDGSILLDAG----GEKTAGPNANSVRGYEVIDTIKTNVEAACPGVVSCADILALAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGP TWNVKLG 1510
R+ ++ G PTWNV LG

Sbjct: 124 REGTNLLGG-----PTWNVPLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P T++L LIS F GLS +D+ ALSG I

Sbjct: 141 RRDSTTASASLANSLPPATASLGLTSLFGRQGLSARDMTALSGAHSI 189

Score = 69.7 bits (169), Expect = 2e-09
Identities = 35/60 (58%), Positives = 41/60 (68%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFV 780
CL L+ A+ AQLST FY SCP L S V+ + A+S + RMGASLLRRLFHDCFV

Sbjct: 9 CLVAISLLSCVAHAQLSTTFYASSCPKLSIVRKAMIQALSNDQRMGASLLRRLFHDCFV 68

>gb|AAW52718.1| peroxidase 4 [Triticum monococcum]
Length = 313

Score = 155 bits (393), Expect = 2e-35
Identities = 72/126 (57%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI + FA + + +CP+ +GSGD NLA LD+ TP SFDN Y+ NL

Sbjct: 188 QAQCQNFDRRLYNETNINSGFATSLKANCPQPTGSGDRNLANLDVSTPYSFDNAYYSNLK 247

Query: 1987 QKKGLLHSDQQLF--NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+KGLLHSDQ LF GG TD+ V +++NP FSS FA+AM+KMG++SPLTGS G++R

Sbjct: 248 SQKGLLHSDQVLFVTGTGGTDNTVNNFASNPAAFSSAFASAMVKMGNLSPLTGSQGVRI 307

Query: 2161 NCRRIN 2178
+C ++N

Sbjct: 308 SCSKVN 313

Score = 104 bits (260), Expect = 5e-20
Identities = 66/169 (39%), Positives = 84/169 (49%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGFEVID+IK+ +E +C VSCADIL +AA

Sbjct: 66 VQGCDAVLLSGM-----EQNAIPNVMSLRGFEVIDSIKAQLETMCKQTVSCADILTVAA 120

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 121 RDSV-----VALGGPSWTVPLG 137

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+++AANN +P P +L L F G + D+VALSG I

Sbjct: 138 RRDSTNANEEAANLPPPFDFLVNLTQSFQDKGFTVTDMAVALSGAHTI 186

Score = 72.4 bits (176), Expect = 3e-10
Identities = 36/72 (50%), Positives = 50/72 (69%)
Frame = +1

Query: 565 LTMASFCRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
+ +S + L +CLA+ +A+AQLS FY +CPN +++KS V +A++KE RMGA

Sbjct: 1 MASSSLSAVLLLCLAV-----AASAQLSPTFYDTTCPNALATIKAHTAANVKNRMGA 54

Query: 745 SLLRLLFFHDCFV 780

SLLRL FHDCFV

Sbjct: 55 SLLRLHFHDCFV 66

>gb|ACI03401.1| peroxidase 1 [Litchi chinensis]
Length = 318

Score = 155 bits (392), Expect = 2e-35
Identities = 87/169 (51%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTS+F GEK A PN S RGF V+D IK+ +EK CPGVVSCAD+LAIAA

Sbjct: 69 VNGCDGSLLDDTSTFVGEKTAVPNNISVRGFNVVDQIKAKLEKACPGVVSCADLLAIAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG

Sbjct: 129 RDSV-----VHLGGPSWKVRLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ AN IP PTSNL+ LIS FSA GLS KDLVALSG+ I

Sbjct: 146 RRDSTTASRALANTSIPPPTSNSALISSFSAQGLSLKDLVALSGSHTI 194

Score = 150 bits (379), Expect = 8e-34
Identities = 70/123 (56%), Positives = 91/123 (73%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCT+FR +YN+TNI+++FA++ ++ CPR+ DN LA LD QTP FD Y+ NL++
Sbjct: 197 ARCTSFRGHVYNDTNIDSSFAQSLRRKCPRSGN--DNVLANLDRQTPFCFDKLYDNLLK 254

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KKGLLHSDQQLF GGS D V+ Y+ N F DFA AM+KMG+I PLTG G+IR NCR
Sbjct: 255 KKGLLHSDQQLFKGGSADPFVKKYANNTSAFFKDFAGAMVKMGNIKPLTGRAGQIRINCR 314

Query: 2170 RIN 2178
++N
Sbjct: 315 KVN 317

Score = 63.9 bits (154), Expect = 1e-07
Identities = 31/50 (62%), Positives = 34/50 (68%)
Frame = +1

Query: 634 ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
AN QL NFY +CP S V V +AI ETR+GASLLRL FHDCFVN
Sbjct: 21 ANGQLCPNFYESTCPQALSIVHKGVAIAIKNETRIGASLLRLLFHDCFVN 70

>ref|XP_002284007.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 316

Score = 155 bits (392), Expect = 2e-35
Identities = 76/124 (61%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C+ FR RIYNETNI+ FA ++Q CP S GD NL+ LD +T T FDN YF NL+
Sbjct: 195 KAQCSKFRDRIYNETNIDATFATSKQAICP--SSGDENLSDLD-ETTTVFDNVYFTNLI 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YS + TF +D A+AM+KMG++SPLTG++GEIR NC
Sbjct: 252 EKKGLLHSDQQLYNGNSTDSMVETYSNDSTTFFTDVASAMVKMGNLSPLTGTGDEIRTNC 311

Query: 2167 RRIN 2178
R IN
Sbjct: 312 RAIN 315

Score = 151 bits (381), Expect = 5e-34
Identities = 83/167 (49%), Positives = 102/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
 GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD
 Sbjct: 70 GCDASILLDDTANFTGEKTAGPNNNSVRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
 SV + LGGPTW V+LGRR
 Sbjct: 130 SV-----VALGGPTWTVQLGRR 146

Query: 1517 DARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
 D+ TAS S AN+ +PAPTS+L+ LIS FS G +T+++V LSGT I
 Sbjct: 147 DSTTASFSTANS DLPAPTS DLDALISLFSNKGFTTQEMVVLSGHTI 193

Score = 70.9 bits (172), Expect = 8e-10
 Identities = 35/70 (50%), Positives = 50/70 (71%)
 Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASL 750
 MAS C+ F+L G A+AQLS+++Y SCP+ S++++ V +A++ E+RMGASL
 Sbjct: 1 MASLSLFSLFCMFSFLL--GMAHAQLSSDYSSSCPSALSTIQTAVNNAVADES RMGASL 58

Query: 751 LRLFFHDCFV 780
 LRL FHDCFV
 Sbjct: 59 LRLHFHDCFV 68

>ref|XP_002323054.1| predicted protein [Populus trichocarpa]
 gb|EEF04815.1| predicted protein [Populus trichocarpa]
 Length = 317

Score = 155 bits (392), Expect = 2e-35
 Identities = 74/124 (59%), Positives = 94/124 (75%)
 Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
 QARCT F RI NETNI+++F + Q C T NN PLD+ +PTSFD+ Y++NL+
 Sbjct: 199 QARCTTFLTRINNETNIDSSFKTSTQAQCQNT-----NNFVPLDVTSPSFD SAYSRRNLL 253

Query: 1987 QKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
 +KGLLHSDQQLF+GGSTD+ VR YS+N F +DFA AMIKMG++SPLTG+NG+IR NC
 Sbjct: 254 NQKGLLHSDQQLFSGGSTDAQVRAYSSNQAAFRTDFANAMIKMGNLSPLTG TNGQIRTNC 313

Query: 2167 RRIN 2178
 R+ N
 Sbjct: 314 RKAN 317

Score = 119 bits (297), Expect = 3e-24
Identities = 73/170 (42%), Positives = 93/170 (54%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+ GCD S+LLD GEK A N NS RGFEVID+IK+ +E CPGVVSCADIL++AA
Sbjct: 76 VNGCDASVLLDG-----GEKTAPANTNSLRGFEVIDSIKTQLESSCPGVVSCADILSVAA 130

Query: 1331 RDSVQIVSGQTTNKNLNL*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 131 RDSV-----VALGGPSWVQVQLG 147

Query: 1511 RRDARTA-SQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA S S NN +P+P +++ LIS FS G + K++VALSG+ I
Sbjct: 148 RRDSATAGSVSDVNNNVPSPALSVSGLISAFSNGFTAKEMVALSGSHTI 197

Score = 79.0 bits (193), Expect = 3e-12
Identities = 37/57 (64%), Positives = 46/57 (80%)
Frame = +1

Query: 613 FVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783
F+L+ G A+AQL++NFY SCP++ S +KS V SA+S E RMGASLLRL FHFDCFVN
Sbjct: 21 FLLLVGVASAQLASNFYGTSCPSVLSVIKSAVDSAVSNEARMGASLLRRLFHDCFVN 77

>gb|EEC82681.1| hypothetical protein OsI_27325 [Oryza sativa Indica Group]
Length = 313

Score = 155 bits (392), Expect = 2e-35
Identities = 70/124 (56%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFD Y+ NL+
Sbjct: 190 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTPYSFDTAYYSNLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PL GS G+IR +C
Sbjct: 250 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLIGSQGQIRLSC 309

Query: 2167 RRIN 2178
++N
Sbjct: 310 SKVN 313

Score = 129 bits (325), Expect = 1e-27

Identities = 73/167 (43%), Positives = 91/167 (54%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C VSCADILA+AARD

Sbjct: 65 GCDASVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQTVSCADILAVAARD 124

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR

Sbjct: 125 SV-----VALGGPSWTVGLGRR 141

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ TAS +ANN +P P +L LI F G S D+VALSG I
Sbjct: 142 DSTTASMDSANNDLPPPFDFLENLIKAFGDKGFSVTDMVALSGAHTI 188

Score = 65.5 bits (158), Expect = 3e-08
Identities = 30/61 (49%), Positives = 43/61 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR LFFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC

Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTCPRALATI KSAVTA AVNNEPRMGASLLR LHFHDC 63

Query: 775 F 777
F

Sbjct: 64 F 64

>gb|EAZ01280.1| hypothetical protein OsI_23303 [Oryza sativa Indica Group]
Length = 327

Score = 155 bits (392), Expect = 2e-35
Identities = 73/124 (58%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA +Q+CP+ SG GD NLAP D QTP +FDN YFKNLV

Sbjct: 205 RARCLMFRGRIYGEANINATFAAALRQTCPQ-SGGGDGNLAPFDDQTPDAFDNAYFKNLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N G F+ DFA AM+KMG + P G+ E+R NC

Sbjct: 264 AQRGLLHSDQELFNGGSQDALVRKYAGNAGMFAGDFAKAMVKMGLMPAAGTPTEVRLNC 323

Query: 2167 RRIN 2178
R++N

Sbjct: 324 RKNV 327

Score = 135 bits (339), Expect = 3e-29
Identities = 74/165 (44%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IKS VE C GVVSCADI+A+A+
Sbjct: 78 VNGCDASILLDDTPTFTGEKNAGANINSVRGYEVIDAIKSQVEAACKGVVSCADIVALAS 137

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 138 RDAVNLLGG-----PTWNVQLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
R+D+RTAS +AAN +P P S+ L++ F+ GLS +++ ALSG
Sbjct: 155 RKDSRTASGTAANANLPGPASSGASLVAAFAGKGLSAREMTALSG 199

Score = 67.0 bits (162), Expect = 1e-08
Identities = 30/51 (58%), Positives = 39/51 (76%)
Frame = +1

Query: 631 SANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFVN 783
+A A LST FY +CP + + V+S V A++KE RMGAS++RLFFHDCFVN
Sbjct: 29 AAKAGLSTKIFYAKTC PGVDTIVRSVVAQAVAKEPRMGASII RLFFHDCFVN 79

>gb|AA Y89058.1| class III peroxidase [Phelipanche ramosa]
Length = 325

Score = 155 bits (392), Expect = 2e-35
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
Q+RC FR+RIY N T+I+ FA TR++ CP+T G DNNLAPLDL TP SFDN YF+NL
Sbjct: 203 QSRCFLFRSRIYSNGTDIDPNFASTRRRRQCPQTGG--DNNLAPLDLVT PNSFDNYYFRNL 260

Query: 1984 VQKKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNNGST+++V YS NP F++DFA+AM++M +I PL GSNG IR+
Sbjct: 261 IQRKGLLES DQVLFNNGSTNALVTSYSNNPRLFATDFASAMVRMSEIQPLLGSNGI IRRV 320

Query: 2164 CRRIN 2178
C IN
Sbjct: 321 CNVIN 325

Score = 124 bits (311), Expect = 6e-26
Identities = 70/169 (41%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD+ + EK+A PN NS RG++VI+ K VE +CP VSCADI+A+AA
Sbjct: 76 VQGCDASILLDDSPTIQSEKSAGPNVNSVRGYDIETAKREVESICPRNVSCADIVALAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW VKLG
Sbjct: 136 RDA-----SVAVGGPTWTVKLG 152

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA+ + AN +P+P ++L LI+ F GLS D+VALSG+ I
Sbjct: 153 RRDSTTANPNEANTDLPSPFASLQTLITAFDDKGLSETDMVALSGSHTI 201

Score = 61.2 bits (147), Expect = 6e-07
Identities = 31/71 (43%), Positives = 46/71 (64%), Gaps = 3/71 (4%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGS---ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGAS 747
S S LT+ ++ +L+ S AQLS FY CPN S++++++ A++ E RM AS
Sbjct: 6 SINLLTLTISSLILLSITPCQAQLSPTFYDICSIPNALSTIRTSIRRAVAEERRMAAS 65

Query: 748 LLRLFFHDCFV 780
L+RL FHDCFV
Sbjct: 66 LIRLHFHDCFV 76

>gb|AAW52719.1| peroxidase 5 [Triticum monococcum]
Length = 259

Score = 155 bits (392), Expect = 2e-35
Identities = 72/126 (57%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI + FA + + +CP+ +GSGD NLA LD+ TP SFDN Y+ NL
Sbjct: 134 QAQCLNFRDRLYNETNINSGFATSLKANCPQPTGSGDRNLANLDVLTPTSFDNAYYSNLK 193

Query: 1987 QKKGLLHSDQQLF--NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+KGLLHSDQ LF GG TD+ V +++NP FSS FA+AM+KMG++SPLTGS G++R
Sbjct: 194 SQKGLLHSDQVLFVTGTGGTDNTVNNFASNPAAFSSAFASAMVKMGNLSPLTGSQQQVRL 253

Query: 2161 NCRRIN 2178
+C ++N

Sbjct: 254 SCSKVN 259

Score = 101 bits (252), Expect = 4e-19
Identities = 64/169 (37%), Positives = 83/169 (49%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LL E+NA PN S RGF EVID+IK+ +E +C VSCADIL +AA
Sbjct: 12 VQGC DASVLLSGM-----EQNAFPNVMSLRGF EVIDSIKAKLETMCKQTVSCADILTVAA 66

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 67 RDSV-----VALGGPSWTVPLG 83

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P P +L L F G + D+VALSG I
Sbjct: 84 RRSTNANEAVANS DLP P P P FDLVNLQSF GDKGFTV TDMVALSGAHTI 132

>gb|AAC49819.1| peroxidase [Oryza sativa Indica Group]
Length = 315

Score = 155 bits (392), Expect = 2e-35
Identities = 70/124 (56%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFD Y+ NL+
Sbjct: 192 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAAALD TTPYSFD TAYYSNLL 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PL GS G+IR +C
Sbjct: 252 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLIGSQGQIRLSC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 132 bits (331), Expect = 3e-28
Identities = 74/169 (43%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C VSCADILA+AA
Sbjct: 65 VQGC DASVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQTVSCADILAVAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 125 RDSV-----VALGGPSWTVGLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS +ANN +P P +L LI F G S D+VALSG I
Sbjct: 142 RRDSTTASMDSANNDLPPPFDFLENLIKAFGDKGFSVTDMVALSGAHTI 190

Score = 67.0 bits (162), Expect = 1e-08
Identities = 31/62 (50%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSATSKETRMGASLLRRLFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC
Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTA AVNNEPRMGASLLRRLFHDC 63

Query: 775 FV 780
FV
Sbjct: 64 FV 65

>dbj|BAD97435.1| peroxidase [Pisum sativum]
Length = 318

Score = 155 bits (392), Expect = 2e-35
Identities = 80/125 (64%), Positives = 91/125 (72%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q C FR RIYNETNI+T FA R+ +CP S GD NLAPLD TPT+FDN Y+ +L+
Sbjct: 196 QTECQFFRNRIYNETNIDTNFATLRKSNCP--SSGGDTNLAPLDSVTPTTFDNYYNDLI 253

Query: 1987 QKKGLLHSDQQLFNG-GSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
KGLLHSDQ LFNG GS S+VR YS N F DFAAAMIK+ ISPLTG+NGEIRKN
Sbjct: 254 ANKGLLHSDQALFNGVGSQVSLVRTYSRNTVAFKRDFAAAMIKLSRISPLTGTNGEIRKN 313

Query: 2164 CRRIN 2178
CR +N
Sbjct: 314 CRLVN 318

Score = 141 bits (355), Expect = 5e-31
Identities = 82/169 (48%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILATAA 1330
+ GCDGSILLDDT++FTGEK+A PN NSARGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDGSILLDDTATFTGEKSAGPNINSARGFEVIDTIKTNVEASCNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD + ++ GGPTW V LG
Sbjct: 129 RDGIFLL-----GGPTWMVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAAN+ IP P+S+L L + F GL+ DL LSG I
Sbjct: 146 RRDARTASQSAANSQIPGPSSDLATLTTMFRNKGLTLNDLTVLSGAHTI 194

Score = 73.9 bits (180), Expect = 1e-10
Identities = 38/71 (53%), Positives = 52/71 (73%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+F +L + L++ L+ S NAQL NFY +CP+L + V++T+ SAI E R+GAS+
Sbjct: 1 MATFI-KLFVLSIISLLACSTNAQLINNFYATTCPSLQTIVRNTMISAIKTEARIGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>ref|NP_001057821.1| Os06g0547100 [Oryza sativa (japonica cultivar-group)]
dbj|BAD54117.1| putative bacterial-induced peroxidase precursor [Oryza sativa
Japonica Group]
tpe|CAH69329.1| TPA: class III peroxidase 87 precursor [Oryza sativa (japonica
cultivar-group)]
gb|EAZ37289.1| hypothetical protein OsJ_21627 [Oryza sativa Japonica Group]
Length = 327

Score = 155 bits (392), Expect = 2e-35
Identities = 73/124 (58%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA +Q+CP+ SG GD NLAP D QTP +FDN YFKNLV
Sbjct: 205 RARCLMFRGRIYGEANINATFAAALRQTC PQ-SGGGDGNLAPFDDQTPDAFDNAYFKNLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N G F+ DFA AM+KMG + P G+ E+R NC
Sbjct: 264 AQRGLLHSDQELFNGGSQDALVRKYAGNAGMFAGDFAKAMVKMGLMPAAGTPTEVRLNC 323

Query: 2167 RRIN 2178
R++N

Sbjct: 324 RKVN 327

Score = 134 bits (338), Expect = 5e-29
Identities = 74/165 (44%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IKS VE C GVVSCADI+A+A+
Sbjct: 78 VNGCDASILLDDTLTFTGEKNAGANINSVRGYEVIDAIKSQVEAACKGVVSCADIVALAS 137

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 138 RDAVNLLGG-----PTWNVQLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
R+D+RTAS +AAN +P P S+ L++ F+ GLS +++ ALSG
Sbjct: 155 RKDSRTASGTAANLPGPASSGASLVAAFAGKLSAREMTALSG 199

Score = 64.7 bits (156), Expect = 6e-08
Identities = 29/51 (56%), Positives = 38/51 (74%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPFLSSVKSTVQSAISKETRMGASLLRRLFHDFVFN 783
+A A LS FY +CP + + V+S V A++KE RMGAS++RRLFHDFVFN
Sbjct: 29 AAKAGLSIKFYAKTCPGVDTIVRSVVAQAVAKEPRMGASIRRLFHDFVFN 79

>emb|CBI19220.1| unnamed protein product [Vitis vinifera]
Length = 373

Score = 155 bits (391), Expect = 3e-35
Identities = 85/167 (50%), Positives = 103/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1336
GCD SILLDDT+SFTGEK A PN++S RG+EVID IKS VE +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILLDDTASFTGEKTAGPNKDSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW ++LGRR
Sbjct: 130 SV-----VALGGPTWTLQLGRR 146

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN+ +P P S+L+ LISRFS G +TK++VALSGT I
Sbjct: 147 DSTTASLSTANSIDLPGPASDLSTLISRFSNKGFTTKEMVALSGTHTI 193

Score = 128 bits (321), Expect = 4e-27
Identities = 64/95 (67%), Positives = 76/95 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR+RIYNETNI+ AFA ++Q+ CP T G DNNL+ LD +T T FDN YF+NL
Sbjct: 195 KARCTSFRRSRIYNETNIDAAFATSKQKICPSTGG--DNNLSLDL-ETTTVFDNVYFRNLK 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSD 2091
KKGLLHSDQQL+NGGSTDSIV YSTN TF +D
Sbjct: 252 AKKGLLHSDQQLYNGGSTDSIVETYSTNSATFFTD 286

Score = 75.1 bits (183), Expect = 4e-11
Identities = 38/70 (54%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCP NFLSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+NFY SCP S++++ V +A++KE RMGASL
Sbjct: 1 MASLSLFLFCVFSFLL--GMAHAQLSSNFYASSCPKALSTIRAAVNNAVAKERRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>gb|ACN30737.1| unknown [Zea mays]
Length = 260

Score = 155 bits (391), Expect = 3e-35
Identities = 73/127 (57%), Positives = 97/127 (76%), Gaps = 3/127 (2%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF NL+
Sbjct: 134 RAQCKNCRARIYNDTDIDASFAASLRASCPAQAGAGDGALEPLDGSTPDAFDNAYFGNLL 193

Query: 1987 QKKGLLHSDQQLF---NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIR 2157
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GEIR
Sbjct: 194 SQRGLLHSDQALFGGGGGATDGLVSAAYASNAGQWADFAAAMVKMGSISPLTGTGEIR 253

Query: 2158 KNCRIN 2178
NCRIN
Sbjct: 254 VNCRRVN 260

Score = 145 bits (365), Expect = 3e-32
Identities = 82/164 (50%), Positives = 96/164 (58%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILA+AAR
Sbjct: 8 QGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAV AAR 67

Query: 1334 DSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV LGGP+W V LGR
Sbjct: 68 DSVAQ-----LGGPSWAVPLGR 84

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 85 RDATTASASLANS DLPGPTSSLNGLLNAFSNKGLSSTD MVALSG 128

>gb|ACG40622.1| peroxidase 2 precursor [Zea mays]
Length = 342

Score = 155 bits (391), Expect = 3e-35
Identities = 73/127 (57%), Positives = 97/127 (76%), Gaps = 3/127 (2%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF NL+
Sbjct: 216 RAQCKNCRARIYNDTDIDASFAASLRASCPAQAGAGDGALEPLDGSTPDADFNDAYFGNLL 275

Query: 1987 QKKGLLHSDQQLF---NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIR 2157
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GEIR
Sbjct: 276 SQRGLLHSDQALFGGGGGGATDGLVSAAYASNAGQWADFAAAMVKMGSISPLTGT DGEIR 335

Query: 2158 KNCRRIN 2178
NCRN+N
Sbjct: 336 VNCRRVN 342

Score = 145 bits (366), Expect = 3e-32
Identities = 82/165 (49%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI A 1330
+QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILA+AA
Sbjct: 89 VQGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAV AA 148

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL G 1510

Sbjct: 149 RDSV-----LGGP+W V LG
RDSVAQ-----LGGPSWAVPLG 165

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG

Sbjct: 166 RRDATTASASLANSDLPGPTSSLNGLLNAFNSKGLSSTDMVALSG 210

Score = 57.8 bits (138), Expect = 7e-06
Identities = 32/67 (47%), Positives = 41/67 (61%), Gaps = 1/67 (1%)
Frame = +1

Query: 583 CSRLTICLALFVLIWGSANAQLSTNFYH-SCPNLFSSVKSTVQSAISKETRMGASLLRL 759
C L + LAL +AQLS+ YY SCP ++++ V +A+ E RMGASLLRL
Sbjct: 24 CGLLVLALALATTA-AVGSAQLSSESYYDASCPAALLTIRTAVSTAVLLEPRMGASLLRL 82

Query: 760 FFHDCFV 780
FFHDCFV
Sbjct: 83 HFHDCFV 89

>emb|CAN83972.1| hypothetical protein [Vitis vinifera]
Length = 290

Score = 154 bits (390), Expect = 4e-35
Identities = 76/124 (61%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C+ FR RIYNETNI+ FA ++Q CP S GD NL+ LD T T FDN YF NL+
Sbjct: 169 KAQCSKFRDRIYNETNIDATFATSKQAICP--SSGGDENLSDLXTT-TXFDNVYFTNLI 225

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YS + TF +D A+AM+KMG++SPLTG++GEIR NC
Sbjct: 226 EKKGLLHSDQQLYNGNSTDSMVETYSNDSTFFFTDVASAMVKMGNLSPLTGTGDEIRTNC 285

Query: 2167 RRIN 2178
R IN
Sbjct: 286 RAIN 289

Score = 135 bits (340), Expect = 3e-29
Identities = 81/186 (43%), Positives = 101/186 (54%), Gaps = 18/186 (9%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFE-----VIDNIKSAVE 1279
QGCD SILLDDT++FTGEK A PN NS RG++ + IKS +E

Sbjct: 25 QGCDASILLDDTANFTGEKTAGPNNNSXRGYDSSNCGSDWYPLCIRVVTCTENTIKSQME 84
Query: 1280 KVCPGVVSCADILAI AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC 1459
+CPGVVSCADI+A+AARDSV
Sbjct: 85 SLCPGVVSCADIVAVAARDSV----- 105
Query: 1460 *F*SI*LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVAL 1639
+ LGGPTW V+LGRRD+ TAS S AN+ +PAPTS+L+ LIS FS G +T+++V L
Sbjct: 106 ----VALGGPTWTVQLGRRDSTASFSTANS DLPAPTS DLDALISLFSNKGF TQEMVVL 161
Query: 1640 SGT KHI 1657
SGT I
Sbjct: 162 SGT HTI 167

>ref|XP_002509737.1| Lignin-forming anionic peroxidase precursor, putative [Ricin
communis]
gb|EEF51124.1| Lignin-forming anionic peroxidase precursor, putative [Ricin
communis]
Length = 322

Score = 154 bits (389), Expect = 6e-35
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIYN ++I+ FA TR+ +CP+T G+G NLAPLDL TP +FDN Y+ NL
Sbjct: 200 QAQCVTFRDRIYNNASDIDPDFAATRRGNCPTGGNG--NLAPLDLVTPNNFDNNYYSNL 257
Query: 1984 VQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ K+GLL SDQ LF+GGSTDSIV YST+ +F SDFAAAM+KMG+ISPLTG+ GEIR+
Sbjct: 258 IAKRGLLASDQILFSGGSTDSIVNEYSTDSSSFSDFAAAMVKGNI SPLTGTQGEIRRI 317
Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CSAVN 322

Score = 131 bits (330), Expect = 4e-28
Identities = 75/169 (44%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCDGS+LL DT +FTGEK+A N NS RG VID+ K+ VE +CPG+VSCADILA+AA
Sbjct: 73 VQGCDGSVLLVDTPFTFTGEKSARNNANSIRGENVIDDAKAQVESICPGIVSCADILAVAA 132
Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ GGP+W V LG

Sbjct: 133 RDA-----SVAAGGPSWTVNLG 149

Query: 1511 RRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P + LN+LIS FS GL+ +D+VALSG I

Sbjct: 150 RRDSTTASLAQANSDLPGFSDPLNRLISLFSKGLNERDMVALSGAHTI 198

Score = 68.9 bits (167), Expect = 3e-09
Identities = 36/73 (49%), Positives = 49/73 (67%), Gaps = 3/73 (4%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGS---NAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMG 741
MAS S + L +F +I S+ AQLS+NFY ++CPN +++KS + +AI E RM

Sbjct: 1 MASRLSFACMILTIFFIINYSSLPCQAQLSSNFYDNTCPNALTTIKSAIDAAIESEQRMA 60

Query: 742 ASLLRRLFHDCFV 780
ASL+RL FHDCFV

Sbjct: 61 ASLIRLHFHDCFV 73

>ref|XP_002268412.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 318

Score = 154 bits (389), Expect = 6e-35
Identities = 75/123 (60%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C F+ RIYNE+NI+ AFAR RQ +CP GD LAPLD T FD YF NLV+

Sbjct: 199 AQC�FFKNRIYNESNIDPAFARARQSTCP--PNGGDTKLAPLD-PTAARFDTGYFTNLVK 255

Query: 1990 KKGLLHSDQQLFNGGSTDIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGSTD++V+ YSTN G FS+DFA +M+KMG+I PLTG G+IR NCR

Sbjct: 256 RRGLLHSDQALFNGGSTDTLVKTYSTNFGAFSADFAKSMVKMGNIKPLTGKKGQIRVNCR 315

Query: 2170 RIN 2178
++N

Sbjct: 316 KVN 318

Score = 136 bits (343), Expect = 1e-29
Identities = 82/166 (49%), Positives = 97/166 (58%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC-PGVVSCADILAI 1327
+ GCD SILLD TS+ EKNA N NSARGF V+D+IKS V+KVC VVSCADILA+A

Sbjct: 70 VNGCDASILLDATSTIDSEKNAGANANSARGFNVDIKSQVDKVCGRPVVSCADILAVA 129

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGP+W V+L
Sbjct: 130 ARDSV-----VALGGPSWTVQL 146

Query: 1508 GRRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRD+ TAS++ ANN IP+P +L LI+RFS GL TKDLVALSG
Sbjct: 147 GRRDSTTASRTDANNIPSPFMDLPALITRFSNQLDTKDLVALSG 192

Score = 66.6 bits (161), Expect = 2e-08
Identities = 35/69 (50%), Positives = 42/69 (60%), Gaps = 3/69 (4%)
Frame = +1

Query: 586 SRLTICLALFVLI---WGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR 756
SR +CL FVL +A LS FY CP ++K V++A+ KE RMGASLLR
Sbjct: 3 SRSLLCLYAFVLFSLATADFSAAALSPYFYNKVCPKALPTIKRVVEAAVQKEKRMGASLLR 62

Query: 757 LFFHDCFVN 783
L FHDCFVN
Sbjct: 63 LHFHDCFVN 71

>dbj|BAD36900.1| peroxidase [Lotus japonicus]
Length = 143

Score = 154 bits (389), Expect = 6e-35
Identities = 73/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC+ FR+RIY+E NI+ A+AR+ Q CPRTSG GD+NL+P+D TP FD+ Y++NL+
Sbjct: 21 QSRCSLFRSRIYSEQNIDPAYARSLQGQCPRTSGVGDNSLSPIDT-TPNFFDSTYYRNL 79

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GL HSDQQLFNGGSTDS V Y++NP F DFA AM+KMG++ LTG+ G+IRK C
Sbjct: 80 NKRGLFHSDQQLFNGGSTDSKVSQYASNPLFRIDFANAMVKGMLGTLGTGQIRKVC 139

Query: 2167 RRIN 2178
+N
Sbjct: 140 SSVN 143

>gb|ACN26131.1| unknown [Zea mays]
Length = 323

Score = 154 bits (388), Expect = 7e-35
Identities = 71/124 (57%), Positives = 93/124 (75%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR RIYN+ NI FA RQQ+CP G D LAP+D+QTP +FDN Y+KNL+
Sbjct: 202 QARCATFRNRIYNDGNINATFASLRQQTCPLAGG--DAALAPIDVQTPEAFDNAYYKNLM 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++V+ YS N F++DFA AM++MG ISPLT + GE+R +C
Sbjct: 260 ARQGLFHSDQELFNGGSQDALVKKYSNAAMFTADFAKAMVRMGAI SPLTATQGEVRLDC 319

Query: 2167 RRIN 2178
R++N
Sbjct: 320 RKNV 323

Score = 140 bits (353), Expect = 8e-31
Identities = 79/165 (47%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 75 VNGCDASILLDDTATFTGEKNAGPNANSVRGYEVIDAIKARVEASCNATVSCADILALAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + LGGP+W V LG
Sbjct: 135 RDAVNL-----LGGPSWTVYLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQS AN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 152 RRDARTASQSDANANLPGPGSSLATLVTMFGNKLSARDMTALSG 196

Score = 67.8 bits (164), Expect = 7e-09
Identities = 36/73 (49%), Positives = 47/73 (64%), Gaps = 4/73 (5%)
Frame = +1

Query: 577 SFCSRLTICLALF----VLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
S S + CL L VL +A LST+FY CP++ S V++ V SA++ E RMGA
Sbjct: 4 SAASSVVRCLQLLTVA AVLAGAAAGGLSTSFYSKCPDVQSIVRAGVASAVAAEKRMGA 63

Query: 745 SLLRLLFFHDCFVN 783
S+LR+FFHDCFVN
Sbjct: 64 SILRMFFHDCFVN 76

>gb|ACF08094.1| class III peroxidase [Triticum aestivum]
Length = 321

Score = 153 bits (387), Expect = 9e-35
Identities = 70/124 (56%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR+R+YNETNI+ AFA + + +CPRT+ SG+++LAPLD TP FDN Y+ NL+
Sbjct: 198 QSQCRRFFRSRLYNETNIDAAFATSLKANCPRRTSSGNSSLAPLDTTTPNGFDNAYYSNLM 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L N G T +VR YS+ F+ DFAAAM++MG+ISPLTG+ G+IR +C
Sbjct: 258 SQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNRFDAAMVRMGNISPLTGAQQGIRLSC 317

Query: 2167 RRIN 2178
R+N
Sbjct: 318 SRVN 321

Score = 132 bits (332), Expect = 2e-28
Identities = 76/165 (46%), Positives = 93/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL DT++FTGE+ A PN S RG VIDNIK+ VE VC VSCADILA+AA
Sbjct: 71 VQGCDASVLLSDTATFTGEQGAAPNARSIRGMNVIDNIKAQVEAVCRQTVSCADILAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 131 RDSV-----VALGGPSWTVPLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS S AN+ +PAP+ +L L + F+A GLS D+VALSG
Sbjct: 148 RRDSTTASLSLANSIDLPAFDFLANLTANFAAKGLSVTDMVALSG 192

Score = 65.5 bits (158), Expect = 3e-08
Identities = 32/63 (50%), Positives = 41/63 (65%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L++ L L + SA+ LS FY SCP +++KS V +A+ E RMGASLLRL FHD
Sbjct: 9 LSVLLLLCLAAAASAPPLSPQFYAKSCPRALATIksAVTAAVRSEPRMGASLLRLHFHD 68

Query: 772 CFV 780
CFV
Sbjct: 69 CFV 71

>ref|XP_002509733.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus communis]
gb|EEF51120.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus communis]
Length = 321

Score = 153 bits (387), Expect = 9e-35
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIYN ++I+ FA TR+ +CP+T G+G NLAPLDL TP +FDN Y+ NL
Sbjct: 199 QAQCVTFRDRIYNNASDIDPDFAAATRRGNCPQTGGNG--NLAPLDLVTNNFDNNYYSNL 256

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ K+G LL SDQ LF+GGSTDSIV YST+ +F SDFAAAM+KMG+ISPLTG+ GEIR+
Sbjct: 257 MAKRGLLASDQILFSGGSTDSIVNEYSTDSSSFSDFAAAMVKGNISPLTGTQGEIRRL 316

Query: 2164 CRRIN 2178
C +N
Sbjct: 317 CSAVN 321

Score = 131 bits (330), Expect = 4e-28
Identities = 75/169 (44%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAIAA 1330
+QGCDGS+LL DT +FTGEK+A N NS RG VID+ K+ VE +CPG+VSCADILA+AA
Sbjct: 72 VQGCDGSVLLVDTPFTFTGEKSARNNANSIRGENVIDDAKAQVESICPGIVSCADILAVAA 131

Query: 1331 RDSVQIVSGQTTNKNLNLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ GGP+W V LG
Sbjct: 132 RDA-----SVAAGGPSWTVNLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P + LN+LIS FS GL+ +D+VALSG I
Sbjct: 149 RRDSTTASLAQANSDLPGFSDPLNRLISLFSKGLNERDMVALSGAHTI 197

Score = 67.4 bits (163), Expect = 9e-09
Identities = 35/72 (48%), Positives = 48/72 (66%), Gaps = 2/72 (2%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSA--NAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
MAS S + L +F + S+ AQLS+NFY ++CPN +++KS + +AI E RM A

Sbjct: 1 MASHLSFACMILTIFIPNYSSLQQAQLSSNFYDNTCPNALTTIKSAIDAAIESEQRMAA 60

Query: 745 SLLRLLFFHDCFV 780
SL+RL FHDCFV

Sbjct: 61 SLIRLHFHDCFV 72

>ref|XP_002319407.1| predicted protein [Populus trichocarpa]
gb|EEE95330.1| predicted protein [Populus trichocarpa]
Length = 302

Score = 153 bits (387), Expect = 9e-35
Identities = 72/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YNET++++ A + + +CP T D++L+ LD TP +FDN YFKNL

Sbjct: 181 QARCLLFRNRVYNETSLLDSTLATSLSKSNCPNTGS--DDSLSSLDATTPVTFDINSYFKNLA 238

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLF+GG+TDS V+ YS N TF +DFA+AM+KMG ISPLTGS+G+IR NC

Sbjct: 239 NNKGLLHSDQQLFSGGTTDSQVKTYINSATFYADFASAMVKMGSISPLTGSDDGQIRTNC 298

Query: 2167 RRIN 2178
++N

Sbjct: 299 AKVN 302

Score = 147 bits (372), Expect = 5e-33
Identities = 83/180 (46%), Positives = 105/180 (58%)
Frame = +2

Query: 1118 AS*ILSKH*QMCGCDGSILLDDTSSFTGKKNANPNRNSARGFEVIDNIKSAVEKVC PGV 1297
AS + + H QGCD S+LLDDTSSFTGK A PN NS RG++VID IKS +E +CPGV

Sbjct: 43 ASLLRLLHFHDCFQGCDAVLLDDTSSFTGKTAGPNANSLRGYDVIDTIKSLQLESICPGV 102

Query: 1298 VSCADILAI AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI* 1477
VSCADILA+AARDSV +

Sbjct: 103 VSCADILAVAARDSV-----VA 119

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
L GP+W V+LGRRD+ TAS AAN+ +P+P +L+ LI+ FS G + K++VALSG+ I

Sbjct: 120 LSGPSWTVQLGRRDSTTASLGAANS DLP S PLMDLSDLITSFSNKGFTAKEMVALSGSHTI 179

Score = 65.5 bits (158), Expect = 3e-08
Identities = 30/54 (55%), Positives = 39/54 (72%)

Frame = +1

Query: 616 VLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCF 777
+L+ G +AQLST FY +CP S++++ V A+ KE RMGASLLRL FHDCF
Sbjct: 1 MLLGLVHAQLSTTFYATTCPKALSTIRTAVLKAVVKEHRMGASLLRRLFHDCF 54

>dbj|BAA77388.1| peroxidase 2 [Scutellaria baicalensis]
Length = 325

Score = 153 bits (387), Expect = 9e-35
Identities = 78/126 (61%), Positives = 97/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
Q++C NFRARIY N ++IE FA TR++ CP+ GSGD+NLAPLDL TP SFDN Y++NL
Sbjct: 201 QSQCGNFRARIYSNGSDIEANFASTRRRQCPQ-DGSGDSNLAPLDLVTPNSFDNYYRNL 259

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAIKMGDISPL-TGSNGEIRK 2160
V ++GLL SDQ L +GG TD+IV YS+NP TF+SDF A MIKMG+I PL G NG IR+
Sbjct: 260 VARRGLLQSDQVLLSGGETDAIVTSYSSNPATFASDFANAMIKMGEIQPLQLGQNGIIRR 319

Query: 2161 NCRRIN 2178
C +N
Sbjct: 320 TCGAVN 325

Score = 140 bits (353), Expect = 8e-31
Identities = 75/165 (45%), Positives = 98/165 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLD+TS+ EK A PN S RGF+VID K+AVE++CPGVVSCADIL +AA
Sbjct: 74 VQGCDASILLDETSTIQSEKTAGPNAGSVRGFQVIDAAKTAVERLCPGVVSCADILTAA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W V+LG
Sbjct: 134 RDA-----SVAVGGPSWTVRLG 150

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TA+++ AN +P PTS L QLI+RF A GL+ +++VALSG
Sbjct: 151 RRDSTTANRAQANTDLPGPTSTLTQLITRFDAKGLNAREMVALSG 195

Score = 63.9 bits (154), Expect = 1e-07
Identities = 30/68 (44%), Positives = 44/68 (64%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR 756
SF +I +L + AQLS FY +CPN S+++++ A+S E RM ASL+R
Sbjct: 7 SFRPIFSIAALVLLTLVPSEAQLSATFYDSTCPNAVSTIRTSIRQAVSAERRMAASLIR 66

Query: 757 LFFHDCFV 780
L FHDCFV
Sbjct: 67 LHFHDCFV 74

>gb|ACF08095.1| class III peroxidase [Triticum aestivum]
Length = 321

Score = 153 bits (386), Expect = 1e-34
Identities = 69/124 (55%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
Q++C FR+R+YNETNI+ AFA + + +CPR++GSG+++LAPLD TP FDN Y+ NL+
Sbjct: 198 QSQCRFFRSRLYNETNIDAAFAASLKANCPSTGSGNSSLAPLDTNTPNGFDNAYYSNLM 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L N G T +VR YS+ F+ DFA AM++MG+ISPLTG+ G+IR +C
Sbjct: 258 SQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNRFVAVMVRMGNISPLTGAQQQIRLSC 317

Query: 2167 RRIN 2178
R+N
Sbjct: 318 SRVN 321

Score = 132 bits (332), Expect = 2e-28
Identities = 76/165 (46%), Positives = 93/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAIAA 1330
+QGCD S+LL DT++FTGE+ A PN S RG VIDNIK+ VE VC VSCADILA+AA
Sbjct: 71 VQGCDAVLLSDTATFTGEQGAAPNARSIRGMNVIDNIKAQVEAVCRQTVSCADILAVAA 130

Query: 1331 RDSVQIVSGQTTNKNLNLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 131 RDSV-----VALGGPSWTVPLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+ TAS S AN+ +PAP+ +L L + F+A GLS D+VALSG
Sbjct: 148 RRDSTTASLSLANSIDLAPSFDLANLTANFAAKGLSVTDMVALSG 192

Score = 67.8 bits (164), Expect = 7e-09
Identities = 33/63 (52%), Positives = 42/63 (66%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L++ L L + SA+ QLS FY SCP +++KS V +A+ E RMGASLLRL FHD
Sbjct: 9 LSVLLLLCLAAAASASPQLSPQFYAKSCPRALATIKSAVTA AVRSEPRMGASLLRRLFHD 68

Query: 772 CFV 780
CFV
Sbjct: 69 CFV 71

>gb|EAZ01279.1| hypothetical protein OsI_23302 [Oryza sativa Indica Group]
Length = 318

Score = 153 bits (386), Expect = 1e-34
Identities = 68/124 (54%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RI+ + N++ AFA RQQ+CP++ G D+ LAP+D+QTP +FDN Y+ NLV
Sbjct: 197 QARCATFRSRIFGDGNVDAFAALRQQACPQSGG--DSTLAPIDVQTPDAFDNAYYANLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+K+GL HSDQ+LFNGGS D++VR Y+ N G F++DFA AM++MG + P G+ E+R NC
Sbjct: 255 KKQGLFHSDQELFNGGSQDALVRKYAGNAGMFAADFAKAMVRMGALLPAAGTPTEVRLNC 314

Query: 2167 RRIN 2178
R++N
Sbjct: 315 RKNV 318

Score = 140 bits (354), Expect = 6e-31
Identities = 78/165 (47%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGKKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD SILLDDT++FTGKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 70 VNGCDASILLDDTANFTGKKNAGPNANSVRGYEVIDAIKTQVEASCNATVSCADILALAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ GGPTW ++LG
Sbjct: 130 RDAVNLL-----GGPTWTMQLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRDA TASQSAAN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 147 RRDALTASQAANGNLPGPSDLATLVTFMGKGLSPRDMTALSG 191

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/71 (43%), Positives = 46/71 (64%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ + + + + G+A QLST +Y CPN+ S V++ + A++ E RMGAS+
Sbjct: 1 MATQWVLVVVAVMAVLFAGGAAGGQLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRMGASI 60

Query: 751 LRLFFHDCFVN 783
LR+FFHDCFVN
Sbjct: 61 LRMFFHDCFVN 71

>ref|NP_001046392.1| Os02g0236600 [Oryza sativa (japonica cultivar-group)]
dbj|BAD27598.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69269.1| TPA: class III peroxidase 27 precursor [Oryza sativa (japonica cultivar-group)]
gb|EAY85140.1| hypothetical protein OsI_06495 [Oryza sativa Indica Group]
gb|EAZ22363.1| hypothetical protein OsJ_06021 [Oryza sativa Japonica Group]
dbj|BAH01530.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 321

Score = 152 bits (385), Expect = 2e-34
Identities = 82/169 (48%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAIAA 1330
+ GCD S+LLDD+S+ TGEKNA PN NS RGFEVID+IKS VE CPG VSCADILA+AA
Sbjct: 73 VNGCDASVLLDDSSSTITGEKNAGPNANSLRGFEVIDSIKSQVEAACPGTVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++ GGPTW V+LG
Sbjct: 133 RDGVNLL-----GGPTWAVQLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD RTASQSAAN+ +P+P+S+ L+S F++ GL ++D+VALSG I
Sbjct: 150 RRDTRTASQSAANSLPSPSSAAALVSAFASKGLDSRDMVALSGAHTI 198

Score = 151 bits (382), Expect = 4e-34
Identities = 72/123 (58%), Positives = 89/123 (72%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARC FRAR+YN+TNI FA R+Q CP + GD NLAPLD + FDN YF+NL+
Sbjct: 201 ARCATFRARVYNDTNISPGFAVRRRQVCP--ASGGDGNLAPLDALSSVRFDNGYFRNLMG 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
+ GLLHSDQ+LFNGG DSI + Y+ N FS DF A++KMG+ISPLTGS+GE+R NCR

Sbjct: 259 RFGLLHSDQELFNGGPVDSIAQQYAANGAAFSRDFVTAVVKMGNISPLTGSSGEVRSNCR 318

Query: 2170 RIN 2178
+ N

Sbjct: 319 KPN 321

Score = 68.2 bits (165), Expect = 5e-09
Identities = 33/66 (50%), Positives = 47/66 (71%), Gaps = 1/66 (1%)
Frame = +1

Query: 589 RLTICLALFVLIW-GSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLF 765
R+ + +A+ L+ G AQL+ +Y SCP+L S V+S + +A+ +E RMGAS+LRLFF

Sbjct: 9 RMVVVVAIAALVAPGEVAAQLTPTYDGCPSLQSIVRSAMAAVQQEPRMGASILRRLF 68

Query: 766 HDCFVN 783
HDCFVN

Sbjct: 69 HDCFVN 74

>gb|EAZ37287.1| hypothetical protein OsJ_21626 [Oryza sativa Japonica Group]
Length = 309

Score = 152 bits (385), Expect = 2e-34
Identities = 68/124 (54%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RI+ + N++ AFA RQQ+CP++ G D LAP+D+QTP +FDN Y+ NLV

Sbjct: 188 QARCATFRSRIFGDGNVDAAFALRQQACPQSGG--DTLAPIDVQTPDAFDNAYYANLV 245

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+K+GL HSDQ+LFNGGS D++VR Y+ N G F++DFA AM++MG + P G+ E+R NC

Sbjct: 246 KKQGLFHSDQELFNGGSQDALVRKYAGNAGMFAADFAKAMVRMGALLPAAGTPTEVRLNC 305

Query: 2167 RRIN 2178
R++N

Sbjct: 306 RKNV 309

Score = 122 bits (307), Expect = 2e-25
Identities = 73/165 (44%), Positives = 87/165 (52%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGKKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGKNA PN NS RG+EVID IK+ VE C VSCADILA+AA

Sbjct: 70 VNGCDASILLDDTANFTGKKNAGPNANSVRGYEVIDAIKTQVEASCNATVSCADILALAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + LG

Sbjct: 130 RDAVNL-----LG 137

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRDA TASQSAAN +P P S+L L++ F GLS +D+ ALSG

Sbjct: 138 RRDALTASQSAANGNLPGPSDLATLVTMFGNKGLSPRDMTALSG 182

Score = 66.6 bits (161), Expect = 2e-08

Identities = 31/71 (43%), Positives = 46/71 (64%)

Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750

MA+ + + + G+A QLST +Y CPN+ S V++ + A++ E RMGAS+

Sbjct: 1 MATQWVVLVVAVMAVLFAGGAAGQLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRMGASI 60

Query: 751 LRLFFHDCFVN 783

LR+FFHDCFVN

Sbjct: 61 LRMFFHDCFVN 71

>gb|ABD47726.1| peroxidase [Eucalyptus globulus subsp. globulus]

Length = 258

Score = 152 bits (385), Expect = 2e-34

Identities = 73/123 (59%), Positives = 92/123 (74%)

Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989

ARCT+FR RIYN++NI+T+FA Q CP+ D+ L LD+QTPT FDN Y+ NL+Q

Sbjct: 138 ARCTSFRGRIYNDNSNIDTSFAHKLQNICPKIGN--DSVLQRLDIQTPTFFDNLYYHLLQ 195

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169

KKGLLHSDQ+LFNG S DS+V+ Y+ + G F DFA AMIKM I P GS+G+IRKNCR

Sbjct: 196 KKGLLHSDQELFNGSSVDSL VKKYACDTGKFFRDFAKAMIKMSKIKPPKGSSGQIRKNCR 255

Query: 2170 RIN 2178

++N

Sbjct: 256 KVN 258

Score = 152 bits (383), Expect = 3e-34
Identities = 85/169 (50%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD SILLDDT SF GEK A PN NS RGFEVID IK+++EK CPGVVSCADI+A+AA
Sbjct: 10 VNGCDASILLDDTPSFVGEKTAAPNNNSVRGFEVIDRIKASLEKECPGVVSCADIVALAA 69

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 70 RDSV-----VHLGGPSWTVSLG 86

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
R+D+ TAS+S AN IP PTSNL+ LI+ F+A GLS K++VALSG+ I
Sbjct: 87 RKDSITASRSLANTSIPPPTS NLSALITSFAAQGLSVKNMVALSGSHTI 135

>ref|NP_001057820.1| Os06g0546500 [Oryza sativa (japonica cultivar-group)]
dbj|BAD54114.1| putative bacterial-induced peroxidase precursor [Oryza sativa
Japonica Group]
tpe|CAH69330.1| TPA: class III peroxidase 88 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF19734.1| Os06g0546500 [Oryza sativa Japonica Group]
dbj|BAG93666.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 318

Score = 152 bits (385), Expect = 2e-34
Identities = 68/124 (54%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RI+ + N++ AFA RQQ+CP++ G D LAP+D+QTP +FDN Y+ NLV
Sbjct: 197 QARCATFRSRIFGDGNVDAFAALRQQACPQSGG--DTTLAPIDVQTPDAFDNAYYANLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+K+GL HSDQ+LFNGGS D++VR Y+ N G F++DFA AM++MG + P G+ E+R NC
Sbjct: 255 KKQLFHSDQELFNGGSQDALVRKYAGNAGMFAADFAKAMVRMGALLPAAGTPTEVRLNC 314

Query: 2167 RRIN 2178
R++N
Sbjct: 315 RKNV 318

Score = 142 bits (357), Expect = 3e-31
Identities = 79/165 (47%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 70 VNGCDASILLDDTANFTGEKNAGPNANSVRGYEVIDAIKTQEASCNATVSCADILALAA 129

Query: 1331 RDSVQIVSQGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ GGPTW V+LG
Sbjct: 130 RDAVNLL-----GGPTWTVQLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDA TASQSAAN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 147 RRDALTASQSAANGNLPGPSDLATLVMTFGNKGLSPRDMTALSG 191

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/71 (43%), Positives = 46/71 (64%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ + + + + G+A QLST +Y CPN+ S V++ + A++ E RMGAS+
Sbjct: 1 MATQWVLVVAVMAVLFAGGAAGGQLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRMGASI 60

Query: 751 LRLFFHDCFVN 783
LR+FFHDCFVN
Sbjct: 61 LRMFFHDCFVN 71

>ref|XP_002438534.1| hypothetical protein SORBIDRAFT_10g021650 [Sorghum bicolor]
gb|EER89901.1| hypothetical protein SORBIDRAFT_10g021650 [Sorghum bicolor]
Length = 325

Score = 152 bits (384), Expect = 2e-34
Identities = 71/124 (57%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+++C FR+RIY E+NI +FA RQ++CPR+ G D LAP D+QTP FDN Y++NLV
Sbjct: 204 RSQCQFFRSRIYTESNINASFALRQKTCPRSGG--DATLAPFDVQTPDGFNAYYQNLV 261

Query: 1987 QKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNNGS D++VR YSTN FS+DF +AMIKMG++ P +G+ E+R NC
Sbjct: 262 AQKGLLHSDQELFNNGSQDALVRQYSTNANQFSADFVSAMIKMGNLMPSSGTPTEVRLNC 321

Query: 2167 RRIN 2178
R+ N
Sbjct: 322 RKTN 325

Score = 143 bits (360), Expect = 1e-31
Identities = 81/169 (47%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+ GCDGSILLDDTS+FTGEK A PN NS RGFEVID IK+ VE C VSCADILA+AA

Sbjct: 77 VNGCDGSILLDDTSTFTGEKGAGPNANSVRGFEVIDAIKTKVEASCKATVSCADILALAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++ GGPTW+V LG

Sbjct: 137 RDGVNLL-----GGPTWSVPLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

R+D+RTASQS AN+ +P P S+L LI F GLS +D+ ALSG I

Sbjct: 154 RKDSRTASQSLANSNLPGPSLATLIRMFNGQLSARDMTALSGAHTI 202

Score = 68.9 bits (167), Expect = 3e-09
Identities = 39/78 (50%), Positives = 54/78 (69%), Gaps = 7/78 (8%)
Frame = +1

Query: 571 MASFCR----LTICLALFV--LIWGSANAQ--LSTNFYHSCP NLFSSVKSTVQSAISKE 729
MA+F R L++ A+ V L G+A+AQ LS NFY +CPN+ + V+ + SA++ E

Sbjct: 1 MATFTCRSM AFLSLAAAVLVALLTAGAADAQKLSPNFYSKTCPNVATIVRQQMASAVAAE 60

Query: 730 TRMGASLLRLFFHDCFVN 783

RMGAS+LR+FFHDCFVN

Sbjct: 61 KRMGASILRMFFHDCFVN 78

>ref|NP_001140437.1| hypothetical protein LOC100272496 [Zea mays]
gb|ACF83840.1| unknown [Zea mays]
Length = 263

Score = 152 bits (384), Expect = 2e-34
Identities = 72/129 (55%), Positives = 97/129 (75%), Gaps = 5/129 (3%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF +L+

Sbjct: 135 RAQCKNCRARIYNDTIDASFAASLRASCPAQAGAGDGALEPLDGSTPDAFDNAYFGDLL 194

Query: 1987 QKKGLLHSDQQLF-----NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGE 2151
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GE

Sbjct: 195 SQRGLLHSDQALFGGGGGGGGATDGLVSAYASNAGQWGADFAAAMVKMGSISPLTGTGDE 254

Query: 2152 IRKNCRRIN 2178

IR NCRR+N

Sbjct: 255 IRVNCRRVN 263

Score = 145 bits (366), Expect = 3e-32
Identities = 83/164 (50%), Positives = 96/164 (58%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILAI AAR
Sbjct: 9 QGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAI AAR 68

Query: 1334 DSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV LGGP+W V LGR
Sbjct: 69 DSVAQ-----LGGPSWAVPLGR 85

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 86 RDATTASASLANSDLPGPTSSLNGLLNAFSNKGLSSTDMVALSG 129

>gb|ACF82414.1| unknown [Zea mays]
Length = 349

Score = 152 bits (384), Expect = 2e-34
Identities = 72/129 (55%), Positives = 97/129 (75%), Gaps = 5/129 (3%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF +L+
Sbjct: 221 RAQCKNCRARIYNDTDIDASFAASLRASCPAQAGAGDGALEPLDGSTPDAFDNAYFGDLL 280

Query: 1987 QKKGLLHSDQQLF-----NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGE 2151
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GE
Sbjct: 281 SQRGLLHSDQALFGGGGGGGATDGLVSAYASNAGQWGADFAAAMVKMGDISPLTGTGDGE 340

Query: 2152 IRKNCRRIN 2178
IR NCRR+N
Sbjct: 341 IRVNCRRVN 349

Score = 145 bits (367), Expect = 2e-32
Identities = 83/165 (50%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILAI AA
Sbjct: 94 VQGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAI AA 153

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV LGGP+W V LG
Sbjct: 154 RDSVAQ-----LGGPSWAVPLG 170

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 171 RRDATTASASLANSDLPGPTSSLNGLLNAFNSKGLSSTDMVALSG 215

Score = 57.4 bits (137), Expect = 9e-06
Identities = 36/92 (39%), Positives = 51/92 (55%), Gaps = 1/92 (1%)
Frame = +1

Query: 508 TPFQSNNT*STKLVCLSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYH-SCPNL 684
TP + + +++ LS+ C L + LAL +AQLS+ YY SCP
Sbjct: 4 TPLECDMAPAASRNKHLRSWPLPRCGLLVLVLALAATA-AVGSAQLSSEDYYDASCPAA 62

Query: 685 FSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
++++ V +A+ E RMGASLLRL FHDCFV
Sbjct: 63 LLTIRTAVSTAVLLEPRMGASLLRLLHFHDCFV 94

>dbj|BAF19735.2| Os06g0547100 [Oryza sativa Japonica Group]
Length = 353

Score = 152 bits (383), Expect = 3e-34
Identities = 72/122 (59%), Positives = 89/122 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA +Q+CP+ SG GD NLAP D QTP +FDN YFKNLV
Sbjct: 205 RARCLMFRGRIYGEANINATFAAALRQTCPQ-SGGGDGNLAPFDDQTPDAFDNAYFKNLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N G F+ DFA AM+KMG + P G+ E+R NC
Sbjct: 264 AQRGLLHSDQELFNGGSQDALVRKYAGNAGMFAGDFAKAMVKMGGLMPAAGTPTEVRLNC 323

Query: 2167 RR 2172
R+
Sbjct: 324 RK 325

Score = 134 bits (338), Expect = 5e-29
Identities = 74/165 (44%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IKS VE C GVVSCADI+A+A+
Sbjct: 78 VNGCDASILLDDTLTFTGEKNAGANINSVRGYEVIDAIKSQVEAACKGVVSCADIVALAS 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 138 RDAVNLLGG-----PTWNVQLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
R+D+RTAS +AAN +P P S+ L++ F+ GLS +++ ALSG
Sbjct: 155 RKDSRTASGTAANANLPGPASSGASLVAFAAGKLSAREMTALSG 199

Score = 64.7 bits (156), Expect = 6e-08
Identities = 29/51 (56%), Positives = 38/51 (74%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
+A A LS FY +CP + + V+S V A++KE RMGAS++RLFFHDCFVN
Sbjct: 29 AAKAGLSIKFYAKTCPGVDTIVRSVVAQAVAKEPRMGASIIRLFFHDCFVN 79

>ref|XP_002438533.1| hypothetical protein SORBIDRAFT_10g021640 [Sorghum bicolor]
gb|EER89900.1| hypothetical protein SORBIDRAFT_10g021640 [Sorghum bicolor]
Length = 318

Score = 151 bits (382), Expect = 4e-34
Identities = 71/124 (57%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA RQQ+CP+T G G NLAP D QTP +FDN Y+ NLV
Sbjct: 197 RARCVRFRGRIYGEPNINATFAAVRQQTCPQTGGDG--NLAPFDDQTPDAFDNAYYANLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGG+ D++VR YS N F++DFA AM+KMG ++P G+ E+R NC
Sbjct: 255 ARRGLLHSDQELFNGGTQDALVRKYSNGRMFANFAKAMVKMGLLAPAAGTPTEVRLNC 314

Query: 2167 RRIN 2178
R++N
Sbjct: 315 RKNV 318

Score = 136 bits (342), Expect = 2e-29
Identities = 75/165 (45%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI AA 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IK+ VE C VSCADI+A+A+
Sbjct: 70 VNGCDASILLDDTPTFTGEKNAGANVNSVRGYEVIDAIKTQVEAACKATVSCADIVALAS 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 130 RDAVNLLGG-----PTWNVQLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
R D+RTASQSAAN +P P S+ L++ F+A GLS +D+ ALSG
Sbjct: 147 RTDSRTASQSAANANLPGPGSSAASLVAFAAKGLSARDMTALSG 191

Score = 66.2 bits (160), Expect = 2e-08
Identities = 29/63 (46%), Positives = 43/63 (68%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDC 774
++ L + + + +LST FY SCP + + V+S A++KE RMGAS++RLFFHDC
Sbjct: 9 SVALLTLLCLLLTCHGKLS TKFYAKSCP GVA AIVRSVTAQAVAKEPRMGAS IIRLFFHDC 68

Query: 775 FVN 783
FVN
Sbjct: 69 FVN 71

>gb|ACE00594.1| lignin biosynthetic peroxidase [Leucaena leucocephala]
Length = 316

Score = 151 bits (382), Expect = 4e-34
Identities = 76/124 (61%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q +C FR RIYNE NI+ +FA TR+ +CPRT G NLAPLD TP FDN Y+K+LV
Sbjct: 196 QGQC NFFRNRIYENNIIDPSFAATRRATCPRTGGG--INLAPLDF-TPNRFDNYYKDLV 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ FNGGS D+IVR YSTN F DFA AM+KM I+PLTGS GEIRK+C
Sbjct: 253 NRRGLFHSDQVFFNGGSQDAIVRAYSTNSVLFFGDFAFAMVKMSSITPLTGSQGEIRKDC 312

Query: 2167 RRIN 2178
R +N
Sbjct: 313 RVVN 316

Score = 126 bits (317), Expect = 1e-26

Identities = 77/169 (45%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD ILLDDT+SFTGEKNA PN+ SARG+EVID IK+ VE C G VSCADILA+AA

Sbjct: 70 VNGCDAGILLDDTASFTGEKNAGPNQ-SARGYEVIDAIKTNVEAACRGTVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
++ V LGGP L

Sbjct: 129 QEGVTQ-----LGGPHGQYHLA 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDARTASQS AN+ IP P+S L+ LIS F+A GL+ +++ LSG I

Sbjct: 146 RRDARTASQSKANSEIPGPSSSELSTLISMFAAKGLNAREMTVLSGAHSI 194

Score = 80.1 bits (196), Expect = 1e-12
Identities = 37/71 (52%), Positives = 52/71 (73%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS + L++ L S+NAQLS NFY SCPN+ + V++T++ A+++E R+GAS+

Sbjct: 1 MASLTHFFLLALSVL SLFASSNAQLSPNFYARSCPNVRAIVRNTMRQALAREARLGASI 60

Query: 751 LRLFFHDCFVN 783

LRLFFHDCFVN

Sbjct: 61 LRLFFHDCFVN 71

>emb|CBI19221.1| unnamed protein product [Vitis vinifera]
Length = 441

Score = 151 bits (381), Expect = 5e-34
Identities = 83/167 (49%), Positives = 102/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AAD

Sbjct: 68 GCDASILLDDTANFTGEKTAGPNNNSVRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 127

Query: 1337 SVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V+LGRR

Sbjct: 128 SV-----VALGGPTWTVQLGRR 144

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ TAS S AN+ +PAPTS+L+ LIS FS G +T+++V LSGT I
Sbjct: 145 DSTTASFSTANS DLPAPTSDDLALISLFSNKGFTTQEMVVLSGHTI 191

Score = 83.2 bits (204), Expect = 2e-13
Identities = 45/84 (53%), Positives = 55/84 (65%)
Frame = +1

Query: 1867 FARTRQQSCPRTSGSDNNLAPLDLQTPSTFDNYFKNLVQKKGLLHSDQQLFNGGSTDS 2046
F RT+ + R GD+NL+PLD +T T F YF++L +KKGLLHSDQQL+N GSTDS
Sbjct: 357 FFRTKGITVIRIESGGDDNLSPLD-KTTTVFYAYFRDLKEKKGLLHSDQQLYNDGSTDS 415

Query: 2047 IVRGYSTNPGTFSSDFAAAMIKMG 2118
IV YS N TF D AM+ G
Sbjct: 416 IVESYSINSATFFRDVTNAMVLDG 439

Score = 69.3 bits (168), Expect = 2e-09
Identities = 34/69 (49%), Positives = 49/69 (71%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+++Y SCP+ S++++ V +A++ E+RMGASL
Sbjct: 1 MASLSLFLFCMFSFLL--GMAHAQLSSDYSSSCPSALSTIQTAVNNAVADES RMGASL 58

Query: 751 LRLFFHDCF 777
LRL FHDCF
Sbjct: 59 LRLHFHDCF 67

Score = 42.7 bits (99), Expect = 0.23
Identities = 17/30 (56%), Positives = 23/30 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCP 1896
+A+C+ FR RIYNETNI+ FA ++Q CP
Sbjct: 193 KAQCSKFRDRIYNETNIDATFATSKQAICP 222

Score = 38.1 bits (87), Expect = 5.8
Identities = 17/30 (56%), Positives = 22/30 (73%)
Frame = +2

Query: 1556 IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
+P PT NL+QL+S FS G +TK+ V LSG
Sbjct: 302 LPGPTLNLSQLVSAFNSKGFTTKETVVLSG 331

>ref|XP_002451846.1| hypothetical protein SORBIDRAFT_04g008590 [Sorghum bicolor]
gb|EES04822.1| hypothetical protein SORBIDRAFT_04g008590 [Sorghum bicolor]
Length = 325

Score = 151 bits (381), Expect = 5e-34
Identities = 83/169 (49%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDD+++ TGEKNA PN NS RGFEVID IKS VE CPG VSCADILA+AA
Sbjct: 75 VQGCDA SVLLDD SATLTGEKNAAPNANSLRGFEVIDAIKSQVEAACPGTVSCADILALAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++S GPTW V+LG
Sbjct: 135 RDGVNLLS-----GPTWAVQLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD RTASQSAAN+ +P+P+S+ L+S F++ GL ++DLVALSG I
Sbjct: 152 RRDRTRTASQAANSNLPSPSSAAALVSAFASKGLDSRDLVALSGAHTI 200

Score = 147 bits (372), Expect = 5e-33
Identities = 70/123 (56%), Positives = 87/123 (70%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
ARC +FR+RIYN++NI FA R+Q C SG D NLAPLD + FDN YF++LV
Sbjct: 203 ARCASFRRSRIYNDNINAGFAAKRKQICGPGSGGTDGNLAPLDAMSSVKFDNGYFRDLVS 262

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
+ GLLHSDQ+LF G DS+ Y+ N FSSDF A++KMG+ISPLTGS+GEIR NCR
Sbjct: 263 QFGLLHSDQELFGAGVVDSVTARYARNGAAFSSDFVTAIVKMGNISPLTGSSGEIRANCR 322

Query: 2170 RIN 2178
+ N
Sbjct: 323 KPN 325

Score = 66.6 bits (161), Expect = 2e-08
Identities = 34/62 (54%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDC 774
T+ +A V + G+ QLS FY SCPNL S V+S + +A+ +E RMGAS+LRLFHDC
Sbjct: 15 TVAVACVVAL-GAMAQQLSPTFYDASCPNLQSIIVRSGMAAAVQQEPRMGASILRRLFHDC 73

Query: 775 FV 780

FV
Sbjct: 74 FV 75

>emb|CAL25299.1| properoxidase [Picea abies]
Length = 341

Score = 151 bits (381), Expect = 5e-34
Identities = 86/169 (50%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
++GCDGSILLDDTSSFTGEK ANPNRNS RGF V+D IKS +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTGEKTANPNRNSVRGFGVVDQIKSELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F GL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGNSTHTLETKFKRQGLNVVDLVALSQAHTI 208

Score = 122 bits (305), Expect = 3e-25
Identities = 65/132 (49%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFARLYNQTVNGKSDPTLDTTYLKHLRAVCPQT-GTDDNQTTPLDPVTPIKFDID 269

Query: 1969 YFKNLVQKKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142
Y+ N+V KGLL SDQ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNNVAGKLLASDQILYSTKGSRTVGLVESYSTSMHAFFKQFAASMIKMGINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N
Sbjct: 330 HGEIRKNCRRMN 341

Score = 62.4 bits (150), Expect = 3e-07
Identities = 37/71 (52%), Positives = 45/71 (63%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ----LSTNFYHSCPFLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE RM AS

Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPKAQAIKSVVEDAVRKEARMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV

Sbjct: 73 LLRLHFHDCFV 83

>emb|CBI15847.1| unnamed protein product [Vitis vinifera]
Length = 263

Score = 150 bits (380), Expect = 6e-34
Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986
Q+RC FR RIYN+ NI+++FA + + +CP T G D+NL+ LD +P FDN YFKNLV

Sbjct: 142 QSRCLVFRDRIYNDNIDSSFAESLKSNCPTDG--DDNLSALDDTSPVIFDNGYFKNLV 199

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFN GSTDS V Y+++ +F DF AAM+KMG+ISPLTG+ G+IR NC

Sbjct: 200 DNKGLLHSDQELFNGGSTDSQVSSYASSATSFYKDFTAAMVKMGNISPLTGTKGQIRVNC 259

Query: 2167 RRIN 2178
R+IN

Sbjct: 260 RKIN 263

Score = 150 bits (378), Expect = 1e-33
Identities = 85/169 (50%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDT++FTGEK A PN +S RGFEVID+IKS VE VCPGVV+CADILA+AA

Sbjct: 15 VNGCDGSILLDDTANFTGEKTAGPNADSVRGFEVIDDIKSRVESVCPGVVTCADILAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V+LG

Sbjct: 75 RDSV-----VALGGPTWTVQLG 91

Query: 1511 RRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S A IP+P +L+ LIS FS G S K++VALSG+ I

Sbjct: 92 RRDSTTASISDAETDIPSPALDLDLISAFSDKGFSAKEMVALSGSHTI 140

>ref|XP_002451850.1| hypothetical protein SORBIDRAFT_04g008650 [Sorghum bicolor]
gb|EES04826.1| hypothetical protein SORBIDRAFT_04g008650 [Sorghum bicolor]
Length = 323

Score = 150 bits (380), Expect = 6e-34
Identities = 73/124 (58%), Positives = 92/124 (74%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRSTG-SGDNNLAPLDLQTPTSFDNYYFKNLV 1986
A+C +R+RIY++ NI FA T + +C T G S D NLA LD+QT FDN YF NL+

Sbjct: 200 AQCKTYRSRIYSDANINKQFANTLKGNC SATQGGSTDTNLAGLDVQTQVVF DNAYFGNLM 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ+LFNGGS D++V+ Y +PG F+S F AMIKMG+ISPLTGS G+IR NC

Sbjct: 260 KKGLLHSDQELFNGGSQDALVQQYDADPGLFASHFVTAMIKMGNISPLTGSQQGIRANC 319

Query: 2167 RRIN 2178
R+N

Sbjct: 320 GRVN 323

Score = 139 bits (350), Expect = 2e-30
Identities = 77/166 (46%), Positives = 99/166 (59%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDT-SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIA 1327
+QGCD SILLDD +F GEKNA PN NS G++VI+NIK+AVE CPGVVSCADI+A+A

Sbjct: 71 VQGC DASILLDDVPGTFVGEKNAGPNANSVLGYDV INNIKTAVEANCPGVVSCADIVALA 130

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD V ++ GGPTW+V L

Sbjct: 131 ARDGVNLL-----GGPTWSVSL 147

Query: 1508 GRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRD+ TASQS AN+ +P+P S+L+ LI+ F++ GL+ D+ ALSG

Sbjct: 148 GRRDSTTASQS QANS DLPSPASSLSTLIAAFASKGLNATDMTALSG 193

Score = 64.3 bits (155), Expect = 8e-08
Identities = 33/56 (58%), Positives = 41/56 (73%), Gaps = 1/56 (1%)
Frame = +1

Query: 616 VLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISK-ETRMGASLLRLLFFHDCFV 780
+L+ +A QLST+FY SCP+L S+V+S V I+ RMGASLLRLLFFHDCFV

Sbjct: 16 ILLSSAAYGQLSTSFYDTSCPSLESTVRSVSVGVINNGNRRRMGASLLRLLFFHDCFV 71

>ref|XP_002276796.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 1225

Score = 150 bits (380), Expect = 6e-34

Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYN+ NI+++FA + + +CP T G D+NL+ LD +P FDN YFKNLV

Sbjct: 1104 QSRCLVFRDRIYNDNDIDSSFAESLKSNCPTDG--DDNLSALDDTSPVIFDNGYFKNLV 1161

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFN GSTDS V Y+++ +F DF AAM+KMG+ISPLTG+ G+IR NC

Sbjct: 1162 DNKGLLHSDQELFNGGSTDSQVSSYASSATSFYKDFTAAMVKMGNISPLTGTKGQIRVNC 1221

Query: 2167 RRIN 2178

R+IN

Sbjct: 1222 RKIN 1225

Score = 150 bits (378), Expect = 1e-33
Identities = 85/169 (50%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDT++FTGEK A PN +S RGFEVID+IKS VE VCPGVV+CADILA+AA

Sbjct: 977 VNGCDGSILLDDTANFTGEKTAGPNADSVRGFEVIDDIKSRVESVCPGVVTCADILAVAA 1036

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V+LG

Sbjct: 1037 RDSV-----VALGGPTWTVQLG 1053

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS S A IP+P +L+ LIS FS G S K++VALSG+ I

Sbjct: 1054 RRDSTTASISDAETDIPSPALDLDLISAFSDKGFSAKEMVALSGSHTI 1102

Score = 62.8 bits (151), Expect = 2e-07
Identities = 27/52 (51%), Positives = 37/52 (71%)
Frame = +1

Query: 628 GSANAQLSTNFYYHSCP NFLSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783

G ++ LS+ FY CP S++++ V +A++ E RMGASLLRL FHDCFVN

Sbjct: 927 GVVSSGLSSTFYSAKCPKALSTIRTAVNTAVANENRMGASLLRLLHFHDCFVN 978

>gb|EAZ22364.1| hypothetical protein OsJ_06022 [Oryza sativa Japonica Group]
Length = 282

Score = 150 bits (380), Expect = 6e-34
Identities = 71/124 (57%), Positives = 92/124 (74%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV

Sbjct: 160 RASCNVFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 217

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC

Sbjct: 218 AGAGLLHSDQELFNNGPVDSVVQLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 277

Query: 2167 RRIN 2178

R++N

Sbjct: 278 RKVN 281

Score = 78.6 bits (192), Expect = 4e-12

Identities = 38/65 (58%), Positives = 46/65 (70%), Gaps = 1/65 (1%)

Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNR-NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
GCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAI AAR

Sbjct: 78 GCDASVLLDDTPAAPGEGKVGPNVAVGSTTVFDLVDTIKAQVEAVCPATVSCADVLAIAAR 137

Query: 1334 DSVQI 1348

DSV +

Sbjct: 138 DSVNL 142

Score = 61.2 bits (147), Expect = 6e-07

Identities = 28/63 (44%), Positives = 40/63 (63%)

Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD

Sbjct: 14 LLLLLAVALAARARAQLSPGFYSASCP TVHGVVRQVMSQAVMNDTRAGAAVLRRLFYHD 73

Query: 772 CFV 780

CFV

Sbjct: 74 CFV 76

>gb|EAY85141.1| hypothetical protein OsI_06496 [Oryza sativa Indica Group]
Length = 326

Score = 150 bits (380), Expect = 6e-34

Identities = 71/124 (57%), Positives = 92/124 (74%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV
Sbjct: 204 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC
Sbjct: 262 AGAGLLHSDQELFNNGPVDSVQVLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 119 bits (298), Expect = 2e-24
Identities = 68/164 (41%), Positives = 89/164 (54%), Gaps = 1/164 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNR-NSARGFEVIDNIKSAVEKVCVGVVSCADILAI AAR 1333
GCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAI AAR
Sbjct: 78 GCDASVLLDDTPAAPGEKGVGPNAIGSTTVFDLVDTIKAQVEAVCPATVSCADVLAIAAR 137

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGP+W V LGR
Sbjct: 138 DSVNL-----LGGPSWAVPLGR 154

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RDA + S+SA + +P P ++++ L+S F+A GLS++DL ALSG
Sbjct: 155 RDALSPSRSAVSTDLPGPEADISALVSFAAKGLSSRDLAALSG 198

Score = 61.2 bits (147), Expect = 6e-07
Identities = 28/63 (44%), Positives = 40/63 (63%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD
Sbjct: 14 LLLLLAVALALAAARARAQLSPGFYSASCPTVHGVVRQVMSQAVMNDTRAGAAVLRRLFYHD 73

Query: 772 CFV 780
CFV
Sbjct: 74 CFV 76

>tpe|CAH69268.1| TPA: class III peroxidase 26 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 326

Score = 150 bits (380), Expect = 6e-34
Identities = 71/124 (57%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV
Sbjct: 204 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC
Sbjct: 262 AGAGLLHSDQELFNNGPVDSVVQLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 112 bits (281), Expect = 2e-22
Identities = 65/166 (39%), Positives = 88/166 (53%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNR--NSARGFEVIDNIKSAVEKVC PGVVSCADILAIA 1327
+QGCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAIA
Sbjct: 76 VQGCDAVLLDDTPAAPGEKGVGPNAVSTTVFDLVDTIKAQVEAVCPATVSCADVLAIA 135

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
R + + LGGP+W V L
Sbjct: 136 GRR-----RVQLGGPSWAVPL 152

Query: 1508 GRRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRDA + S+SA + +P P ++++ L+S F+A GLS++DL ALSG
Sbjct: 153 GRRDALSPRSVSTDLPGPEADISALVSAFAAKGLSSRDLAALSG 198

Score = 61.2 bits (147), Expect = 6e-07
Identities = 28/63 (44%), Positives = 40/63 (63%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD
Sbjct: 14 LLLLLAVALAARARAQLSPGFYSASCTVHGVVRQVMSQAVMNDTRAGAVALRRLFYHD 73

Query: 772 CFV 780
CFV
Sbjct: 74 CFV 76

>ref|NP_001046393.1| Os02g0236800 [Oryza sativa (japonica cultivar-group)]
dbj|BAD27599.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
dbj|BAD29072.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
dbj|BAF08307.1| Os02g0236800 [Oryza sativa Japonica Group]
dbj|BAG91008.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG94336.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG96877.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 326

Score = 150 bits (380), Expect = 6e-34
Identities = 71/124 (57%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV
Sbjct: 204 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC
Sbjct: 262 AGALLHSDQELFNNGPVDSVVQLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKVN 325

Score = 119 bits (298), Expect = 2e-24
Identities = 68/164 (41%), Positives = 89/164 (54%), Gaps = 1/164 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNR-NSARGFEVIDNIKSAVEKVCVPGVVSCADILAI AAR 1333
GCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAI AAR
Sbjct: 78 GCDASVLLDDTPAAPGEKGVGPNAVSTTVFDLVDTIKAQVEAVCPATVSCADVLAIAAR 137

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGP+W V LGR
Sbjct: 138 DSVNL-----LGGPSWAVPLGR 154

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RDA + S+SA + +P P ++++ L+S F+A GLS++DL ALSG
Sbjct: 155 RDALSPRSRAVSTDLPGPEADISALVSFAAKGLSSRDLAALSG 198

Score = 61.2 bits (147), Expect = 6e-07

Identities = 28/63 (44%), Positives = 40/63 (63%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD
Sbjct: 14 LLLLLAVALALAAARARAQLSPGFYSASCPTVHGVVRQVMSQAVMNDTRAGAAVLRLFVHD 73

Query: 772 CFV 780
CFV
Sbjct: 74 CFV 76

>gb|ABK22680.1| unknown [Picea sitchensis]
Length = 341

Score = 150 bits (379), Expect = 8e-34
Identities = 85/169 (50%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
++GCDGSILLDDTSSFTGEK ANPN+NS RGF V+D IK +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTGEKTANPNKNSVRGFGVVDQIKCELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F LGL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGNSTHQ TLETKFKRLGLNVVDLVALSGAHTI 208

Score = 122 bits (305), Expect = 3e-25
Identities = 64/132 (48%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFARLYNQTVNGNHDP TLDTTYLKQLRAVCPQT-GTDDNQ TPLDPVTPIKFDIN 269

Query: 1969 YFKNLVQKKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142
Y+ N+V KGLL SD+ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDEILYSTKGSRTVGLVESYSTSTHAFFKQFAASMIKMGINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N
Sbjct: 330 HGEIRKNCRRMN 341

Score = 62.4 bits (150), Expect = 3e-07
Identities = 37/71 (52%), Positives = 45/71 (63%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ---LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE RM AS
Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPKAQAIKSVVEDAVRKEARMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV
Sbjct: 73 LLRLHFHDCFV 83

>emb|CAN61440.1| hypothetical protein [Vitis vinifera]
Length = 262

Score = 150 bits (379), Expect = 8e-34
Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYN+ NI+++FA + + +CP T G D+NL+ LD +P FDN YFKNLV
Sbjct: 141 QSRLVFRDRIYNDNIDSSFAESLKSNCPTDG--DDNLSALDDTSPVIFDNGYFKNLV 198

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFN GSTDS V Y+++ +F DF AAM+KMG+ISPLTG+ G+IR NC
Sbjct: 199 DNKGLLHSDQELFNGGSTDSQVSSYASSATSFYKDFXAAMVKMGNISPLTGTKGQIRVNC 258

Query: 2167 RRIN 2178
R+IN
Sbjct: 259 RKIN 262

Score = 150 bits (378), Expect = 1e-33
Identities = 85/168 (50%), Positives = 101/168 (60%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
+GCDGSILLDDT++FTGEK A PN +S RGFEVID+IKS VE VCPGVV+CADILA+AAR
Sbjct: 15 KGCDSILLDDTANFTGEKTAGPNADSVRGFEVIDDIKSRVESVCPGVVTCADILAVAAR 74

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGPTW V+LGR
Sbjct: 75 DSV-----VALGGPTWTVQLGR 91

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RD+ TAS S A IP+P +L+ LIS FS G S K++VALSG+ I
Sbjct: 92 RDSTTASISDAETDIPSPALDLDLISAFSDKGFSKEMVALSGSHTI 139

>gb|AAC31550.1| peroxidase PXC2 precursor [Avena sativa]
Length = 313

Score = 150 bits (379), Expect = 8e-34
Identities = 71/126 (56%), Positives = 97/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPR-TSGSGDNNLAPLDLQTPTSFDNYYFKN 1980
QA+C NFR+RIY +TNI AFA + Q +CP+ T GSGD++LAPLD +TP +FDN Y+ N
Sbjct: 187 QAQCKNFRSRIYGGDTNINAAFATSLQANCPQATGGSGDSSLAPLDTKTPNAFDNSYNN 246

Query: 1981 LVQKKLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRK 2160
L+ +KLLHSDQ LFN G+TD+ VR ++++ F+ F AMIKMG+ISPLTG+ G+IR
Sbjct: 247 LLSQKLLHSDQVLFNNGTDTNVRNFASSASAFTGAFTTAMIKMGNISPLTGTGQGI 306

Query: 2161 NCRRIN 2178
+C ++N
Sbjct: 307 SCSKVN 312

Score = 105 bits (261), Expect = 4e-20
Identities = 69/167 (41%), Positives = 84/167 (50%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCVGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDNIK+ VE VC VSC DILA+AARD
Sbjct: 69 GCDASVLLSGN-----EQNAAPNAGSLRGFSVIDNIKTQVEAVCKQTVSCDDILAVAARD 123

Query: 1337 SVQIVSQGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 124 SV-----VALGGPSWTVPLGRR 140

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ +A+ + + +PAPTS+L QL + FS L T D+VALSG I
Sbjct: 141 DSTSATGNTGD--LPAPTSLSLAQLQAASFKNLDTTDMVALSGAHTI 185

Score = 65.5 bits (158), Expect = 3e-08
Identities = 32/64 (50%), Positives = 45/64 (70%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR LFF 765
S +++ + L L +A+AQLS+ FY SCP +++KS V +A+S + RMGASLLRL F

Sbjct: 5 SCISLRVMLVALAATAASAQLSSTFYDTSCPALATIKSGVAAVSSDRRMGASLLRLHF 64

Query: 766 HDCF 777
HDCF

Sbjct: 65 HDCF 68

>gb|AAC31551.1| peroxidase PXC6 precursor [Avena sativa]
Length = 314

Score = 150 bits (379), Expect = 8e-34
Identities = 71/126 (56%), Positives = 97/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPR-TSGSGDNNLAPLDLQTPTSFDNYYFKN 1980
QA+C NFR+RIY +TNI AFA + Q +CP+ T GSGD++LAPLD +TP +FDN Y+ N
Sbjct: 188 QAQCKNFRSRIYGGDTNINAAFATSLQANCPQATGGSGDSSLAPLDTKTPNAFDNSYNN 247

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ +KGLLHSDQ LFN G+TD+ VR ++++ F+ F AMIKMG+ISPLTG+ G+IR
Sbjct: 248 LLSQKGLLHSDQVLFNNGTTDNTVRNFASSASAFTGAFTTAMIKMGNISPLTGTQQQIRL 307

Query: 2161 NCRIN 2178
+C ++N

Sbjct: 308 SCSKVN 313

Score = 94.0 bits (232), Expect = 9e-17
Identities = 68/168 (40%), Positives = 82/168 (48%), Gaps = 1/168 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCVGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDNIK+ VE VC VSCADILA+AARD
Sbjct: 69 GCDASVLLSGN-----EQNAAPNAGSLRGSVIDNIKTQVEAVCKQTVSCADILAVAARD 123

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGP-TWNVKLGR 1513
SV + LGGP V LGR
Sbjct: 124 SV-----VALGGPFLEQVPLGR 140

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RD+ +A+ + + +PAPTS+L QL + FS L T +VALSG I
Sbjct: 141 RDSTSATGNTGD--LPAPTSSLAQLAAFSKKNLDTTGMVALSGAHTI 186

Score = 65.5 bits (158), Expect = 3e-08
Identities = 32/64 (50%), Positives = 45/64 (70%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFF 765
S +++ + L L +A+AQLS+ FY SCP +++KS V +A+S + RMGASLLRL F
Sbjct: 5 SCISLRVMLVALAATAASAQLSSTFYDTSCKALATIKSGVAAAVSSDRRMGASLLRLHF 64

Query: 766 HDCF 777
HDCF
Sbjct: 65 HDCF 68

>emb|CAA71492.1| peroxidase [Spinacia oleracea]
Length = 315

Score = 149 bits (375), Expect = 2e-33
Identities = 81/165 (49%), Positives = 101/165 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDTS+F GEK A PN+NS RGF+ +D+IK+++EK CPGVVSCADILAIA+
Sbjct: 66 VNGCDGSILLDDTSTFRGEKTAIPKNNSVRGFKAVDSIKASLEKACPGVVSCADILAIA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + GGPTW V+LG
Sbjct: 126 RDAV-----VQYGGPTWQVRLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TA++SAAN IPAP+ NL L S F+ +GLS KD+V LSG
Sbjct: 143 RRDSL TANRSAANAFIPAPSFNLRNLTSSFTTVGLSFKDMVVLSG 187

Score = 133 bits (335), Expect = 1e-28
Identities = 66/124 (53%), Positives = 93/124 (75%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
ARCT+FR I+N+TNI AFA++ Q+ CP+ SG+G L PLD QT FD+ Y++NL+
Sbjct: 194 ARCTSFRPHIHNDTNINAFAKSLQKKCPQ-SGNG-KVLQPLDYQTKFRFDDKYYQNLV 251

Query: 1990 KKGLLHSDQQLFNGGST-DSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQL++G + D+ VR Y++ G F +F +MI+MG+I PLTG++G+IR+NC
Sbjct: 252 KKGLLHSDQQLYSGNNNADAYVRKYASKQGEFFQEFGNSMIRMGNIKPLTGTHGQIRRNC 311

Query: 2167 RRIN 2178
R+ N
Sbjct: 312 RKS N 315

Score = 64.3 bits (155), Expect = 8e-08
Identities = 29/51 (56%), Positives = 34/51 (66%)
Frame = +1

Query: 631 SANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
+ N QLS NFY +CPN VK + I KE R+GAS+LRL FHDCFVN
Sbjct: 17 TVNGQLSPNFYSSTCPNALRIVKQGIKRIKKEARVGASILRLLHFHDCFVN 67

>ref|NP_001054096.1| Os04g0651000 [Oryza sativa (japonica cultivar-group)]
emb|CAE04507.2| OSJNBb0059K02.17 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69299.1| TPA: class III peroxidase 57 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF16010.1| Os04g0651000 [Oryza sativa Japonica Group]
dbj|BAG98582.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 319

Score = 149 bits (375), Expect = 2e-33
Identities = 82/169 (48%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+ GCDGS+LLDDT++ TGEKNA PN+NS RGFV+D+IKS +E C VVSCADILA+AA
Sbjct: 70 VNGCDGSVLLDDTAAITGEKNAKPNKNSLRGFVVDIKSQLEDACEQVSCADILAVAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW+V+LG
Sbjct: 130 RDSV-----VALGGPTWDVELG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 147 RRDGTTASLDAANNDLPPPTSDLADLIKFSDFKGLTASDMIALSGAHTI 195

Score = 148 bits (373), Expect = 4e-33
Identities = 68/124 (54%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 197 QARCTNFRGRLYNETNLATLATSCLKPSCPNTG-GDDNTAPLDPATSYVFDNFYRNLL 255

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G++R NC
Sbjct: 256 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQVRVNC 315

Query: 2167 RRIN 2178
R++N

Sbjct: 316 RKNV 319

Score = 74.7 bits (182), Expect = 6e-11
Identities = 34/70 (48%), Positives = 52/70 (74%), Gaps = 1/70 (1%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLL 753
++ ++ +C A+ L++ + +AQLST+FY +CP+ ++S V+ A+SKE+RMGASLL
Sbjct: 2 AYSRQIFVCSAMAALLFSAVVSAQLSTDFYDETCPDALDIIESAVRDAVSKESRMGASLL 61

Query: 754 RLFFHDCFVN 783
RL FHDCFVN
Sbjct: 62 RLHFHDCFVN 71

>ref|XP_002308244.1| predicted protein [Populus trichocarpa]
gb|EEE91767.1| predicted protein [Populus trichocarpa]
Length = 321

Score = 149 bits (375), Expect = 2e-33
Identities = 71/123 (57%), Positives = 95/123 (77%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C F+ RIYNETNI+ FAR R+ +CPRT G D+NLAPL+ TP+ FD Y+ +L++
Sbjct: 202 AQCFTEKDRYNETNIDPKFARERKLTCPRTGG--DSNLAPLN-PTPSYFDARYYNDLLK 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GL HSDQ LFNGGSTDS+V+ YS+N F +DFA +M+KMG+I+PLTG G+ R NCR
Sbjct: 259 KRGLFHSDQALFNGGSTDSLKAYSSNAKAFWTFANSMVKMGNINPLTGKQGQTRLNCR 318

Query: 2170 RIN 2178
++N
Sbjct: 319 KVN 321

Score = 135 bits (339), Expect = 3e-29
Identities = 82/166 (49%), Positives = 93/166 (56%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC-PGVVSCADILAIA 1327
+ GCD SILLD TS+F EKNANPN NS RGFEVID IK V+K C VVSCADILA+A
Sbjct: 73 VNGCDASILLDDTSAFDSEKNANPNINSIRGFEVIDRIKLEVDKACGRPVVSCADILAVA 132

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGPTW V+L

Sbjct: 133 ARDSV-----VALGGPTWAVQL 149

Query: 1508 GRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRD+ TAS++ ANN IPAP +L LI F GL+ KDLV LSG

Sbjct: 150 GRRDSTTASKTTANNDIPAPFMDLPDLIINFKKHGLNKKDLVVLVLSG 195

Score = 64.3 bits (155), Expect = 8e-08
Identities = 34/76 (44%), Positives = 47/76 (61%)
Frame = +1

Query: 556 LSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETR 735
++ L + S S L + LAL S++ LS N+Y + CP ++K V++A+ E R

Sbjct: 1 MASLGIFSLISTLFLVLALATT--ASSSKGLSPNYDYVCPKALPTIKRVVEAAVYNERR 58

Query: 736 MGASLLRRLFHDCFVN 783
MGASLLRL FHDCFVN

Sbjct: 59 MGASLLRLHFHDCFVN 74

>emb|CBI19222.1| unnamed protein product [Vitis vinifera]
Length = 255

Score = 148 bits (374), Expect = 3e-33
Identities = 82/167 (49%), Positives = 101/167 (60%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD

Sbjct: 17 GCDASILLDDTANFTGEKTAGPNNNSLRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 76

Query: 1337 SVQIVSQGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V++GRR

Sbjct: 77 SV-----VALGGPTWTVMGRR 93

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN +PAPTS+L+ L S FS G +T+++VALSGT I

Sbjct: 94 DSTTASLSTANADLPAPTSDDLVLTSLSFNKGFTTQEMVALSGTHTI 140

Score = 126 bits (317), Expect = 1e-26
Identities = 62/106 (58%), Positives = 82/106 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPSFDNYYFKNLV 1986
+A+C FR RIYNETN++ AFA+++Q+ CP T G D NL+ LD +T T FD YFK+L+

Sbjct: 142 KAQCIFRYRIYNETNVDAAFKSKQKICPWTGG--DENLSDLD--ETTTVFDTVYFKDLI 198

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDI 2124
+KKGLLHSDQQL+NG STDS+V YST+ TF +D A AM+KMG++
Sbjct: 199 EKKGLLHSDQQLYNGNSTDSMVETYSTDSTFFFTDVANAMVKMGNL 244

>ref|XP_002467656.1| hypothetical protein SORBIDRAFT_01g031740 [Sorghum bicolor]
gb|EER94654.1| hypothetical protein SORBIDRAFT_01g031740 [Sorghum bicolor]
Length = 344

Score = 148 bits (374), Expect = 3e-33
Identities = 83/165 (50%), Positives = 98/165 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILA+AA
Sbjct: 92 VQGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAVAA 151

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV LGGP+W+V LG
Sbjct: 152 RDSVAQ-----LGGPSWSVPLG 168

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDA TAS S AN+ +P PTSNLN L++ FS GLS+ D+VALSG
Sbjct: 169 RRDATTASASLANSDLPGPTSNLNGLLNAFNSKGLSSTDMVALSG 213

Score = 143 bits (361), Expect = 1e-31
Identities = 69/126 (54%), Positives = 95/126 (75%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCP-RTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
+A+C N R+RIYN+T+I+ +A + + SCP + G+ D L PLD TP +FDN YF NL
Sbjct: 219 RAQCKNIRSRIYNDTIDATYAASLRASCPAQAGGASDGALEPLDDATPDAFDNAYFGNL 278

Query: 1984 VQKKGLLHSDQQLFNGG-STDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+ ++GLLHSDQ LF GG +TD +V Y+++ + SDFAAAM+KMG+ISPLTG++GEIR
Sbjct: 279 LSQRGLLHSDQALFGGGGATDGLVSTYASSADQWGSDFAAAMVKMGNISPLTGTGDEIRV 338

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 339 NCRRVN 344

Score = 55.5 bits (132), Expect = 4e-05
Identities = 29/65 (44%), Positives = 42/65 (64%), Gaps = 5/65 (7%)
Frame = +1

Query: 601 CLALFVLIWGSA----NAQLSTNFYYH-SCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
CL + ++ +A +AQLS+ YY SCP +++++ V +A+ + RMGASLLRL F
Sbjct: 28 CLLILIVALAAAAVASAQLSSEDYYDASCPAALFTIRTAVSTAVLLDRRMGASLLRLHF 87

Query: 766 HDCFV 780
HDCFV
Sbjct: 88 HDCFV 92

>gb|EEE61812.1| hypothetical protein OsJ_16433 [Oryza sativa Japonica Group]
Length = 1129

Score = 148 bits (374), Expect = 3e-33
Identities = 82/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCDGS+LLDDT++ TGEKNA PN+NS RGF EV+D+IKS +E C VVSCADILA+AARD
Sbjct: 78 GCDGSVLLDDTAAITGEKNAKPNKNSLRGF EVVDDIKS QLEDACEQVVSCADILAVAARD 137

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW+V+LGRR
Sbjct: 138 SV-----VALGGPTWDVELGRR 154

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 155 DGTASLDAANNDLPPPTS LADLIKFSFKGLTASDMIALSGAHTI 201

Score = 134 bits (336), Expect = 8e-29
Identities = 63/115 (54%), Positives = 82/115 (71%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 203 QARCTNFRGRLYNETNLDATLATS LKPCPNPTG-GDDNTAPLDPATSYVFDNFYRNL 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGE 2151
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G+
Sbjct: 262 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQ 316

Score = 69.7 bits (169), Expect = 2e-09
Identities = 31/49 (63%), Positives = 40/49 (81%)
Frame = +1

Query: 637 NAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783
+AQLST+FY +CP+ ++S V+ A+SKE+RMGASLLRL FHDCFVN
Sbjct: 11 SAQLSTDFYDETCPDALDIIESAVRDAVSKESRMGASLLRRLFHDCFVN 59

>gb|EEC78144.1| hypothetical protein OsI_17703 [Oryza sativa Indica Group]
Length = 325

Score = 148 bits (374), Expect = 3e-33
Identities = 82/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCDGS+LLDDT++ TGEKNA PN+NS RGFEV+D+IKS +E C VVSCADILA+AARD
Sbjct: 78 GCDGSVLLDDTAAITGEKNAKPNKNSLRGFEVVDDIKSQLEDACEQVVSCADILAVAARD 137

Query: 1337 SVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW+V+LGRR
Sbjct: 138 SV-----VALGGPTWDVELGRR 154

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 155 DGTASLDAANNDLPPTS LADLIKSFSDKGLTASDMIALSGAHTI 201

Score = 148 bits (373), Expect = 4e-33
Identities = 68/124 (54%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 203 QARCTNFRGRLYNETNL DATLATS LKPCPNPTG-GDDNTAPLDPATSYVFDNFYRNL 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G++R NC
Sbjct: 262 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQVRVNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 70.1 bits (170), Expect = 1e-09
Identities = 31/49 (63%), Positives = 41/49 (83%)
Frame = +1

Query: 637 NAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783

+AQLST+FY +CP+ ++S V++A+SKE+RMGASLLRL FHDCFVN
Sbjct: 11 SAQLSTDFYDETCPDALDIIESAVRAAVSKESRMGASLLRLHFHDCFVN 59

>emb|CAJ86184.1| H0212B02.16 [Oryza sativa (indica cultivar-group)]
emb|CAJ86323.1| OSIGBa0113E10.6 [Oryza sativa (indica cultivar-group)]
Length = 337

Score = 148 bits (374), Expect = 3e-33
Identities = 82/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCDGS+LLDDT++ TGEKNA PN+NS RGFEV+D+IKS +E C VVSCADILA+AARD
Sbjct: 90 GCDGSVLLDDTAAITGEKNAKPNKNSLRGFEVVDDIKSQLEDACEQVSCADILAVAARD 149

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW+V+LGRR
Sbjct: 150 SV-----VALGGPTWDVELGRR 166

Query: 1517 DARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 167 DGTASLDAANNDLPPTS LADLIKSFSDKGLTASDMIALSGAHTI 213

Score = 148 bits (373), Expect = 4e-33
Identities = 68/124 (54%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 215 QARCTNFRGRLYNETNLDATLATS LKPCPNPTG-GDDNTAPLDPATSYVFDNFYRNL 273

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G++R NC
Sbjct: 274 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQVRVNC 333

Query: 2167 RRIN 2178
R++N
Sbjct: 334 RKNV 337

Score = 75.1 bits (183), Expect = 4e-11
Identities = 34/70 (48%), Positives = 53/70 (75%), Gaps = 1/70 (1%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSA-NAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753

++ ++ +C A+ L++ + +AQLST+FY +CP+ ++S V++A+SKE+RMGASLL
Sbjct: 2 AYSRQIFVCSAMAALLFSAVVSAQLSTDFYDETCPDALDIIESAVRAAVSKESRMGASLL 61

Query: 754 RLFFHDCFVN 783

RL FHDCFVN

Sbjct: 62 RLHFHDCFVN 71

>gb|EAZ22372.1| hypothetical protein OsJ_06030 [Oryza sativa Japonica Group]
Length = 257

Score = 148 bits (374), Expect = 3e-33
Identities = 69/123 (56%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989

A CTNFRA IYN+ NI+ +FA R+++CP + +GD NLAPLD+QT +FDN Y+ NL+

Sbjct: 135 ALCTNFRAHIYNDANIDPSFAALRRRACPAAPNGDTNLAPLDVQTQNAFDNAYYGNTLV 194

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169

++GLLHSDQ LFNGGS D++VR Y+ NP F++DFA AM+KMG+I S+GE+R +CR

Sbjct: 195 RRGLLHSDQVLFNGGSQDALVRQYAANPALFAADFAKAMVKMGNIG--QPSDGEVRCDCR 252

Query: 2170 RIN 2178

+N

Sbjct: 253 VVN 255

Score = 93.6 bits (231), Expect = 1e-16
Identities = 46/68 (67%), Positives = 53/68 (77%), Gaps = 2/68 (2%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324

+QGCD SILLDD + F GEK A PN NS RG+EVID IK+ VE VCPGVVSCADI+A+

Sbjct: 69 VQGCDASILLDDVPATGFVGEKTAAPNNSVIRGYEVIDQIKANVEDVCPGVVSCADIVAL 128

Query: 1325 AARDSVQI 1348

AARDS +

Sbjct: 129 AARDSTAL 136

Score = 70.1 bits (170), Expect = 1e-09
Identities = 34/59 (57%), Positives = 43/59 (72%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780

L +F L+ A+ QLST++Y SCP++ V +TV SAI E RMGASL+RLFFHDCFV

Sbjct: 11 LLVFFLLSDDASGQLSTSYYADSCPSVEKVVHATVASAIQAERRMGASLIRLFFHDCFV 69

>ref|NP_001046401.1| Os02g0240300 [Oryza sativa (japonica cultivar-group)]
dbj|BAD28871.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69271.1| TPA: class III peroxidase 29 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAF08315.1| Os02g0240300 [Oryza sativa Japonica Group]
dbj|BAG90221.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG96858.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 321

Score = 148 bits (374), Expect = 3e-33
Identities = 68/123 (55%), Positives = 95/123 (77%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++CTNFRA IYN+ NI+ +FA R+++CP + +GD NLAPLD+QT +FDN Y+ NL+
Sbjct: 199 SQCTNFRAHIYNDANIDPSFAALRRRACPAAPNGDTNLAPLDVQTQNAFDNAYYGNNLV 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGS D++VR Y+ NP F++DFA AM+KMG+I S+GE+R +CR
Sbjct: 259 RRGLLHSDQQLFNGGSQDALVRQYAANPALFAADFAKAMVKMGNIG--QPSDGEVRCDCR 316

Query: 2170 RIN 2178
+N
Sbjct: 317 VVN 319

Score = 137 bits (344), Expect = 9e-30
Identities = 79/168 (47%), Positives = 95/168 (56%), Gaps = 2/168 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1324
+QGCD SILLDD + F GEK A PN NS RG+EVID IK+ VE VCPGVVSCADI+A+
Sbjct: 69 VQGCASILLDDVPATGFVGEKTAAPNNSVRGYEVIDQIKANVEDVCPGVVSCADIVAL 128

Query: 1325 AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 129 AARDSTAL-----LGGPSWAVP 145

Query: 1505 LGRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
LGR D+ TAS+S AN+ +P P SNL LI+RF GLS +D+ ALSG+
Sbjct: 146 LGRCDSTTASRSEANSDLPGPGSNLTMLIARFGNKGLSPRDMTALSGS 193

Score = 70.1 bits (170), Expect = 1e-09
Identities = 34/59 (57%), Positives = 43/59 (72%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
L +F L+ A+ QLST++Y SCP++ V +TV SAI E RMGASL+RLFFHDCFV
Sbjct: 11 LLVFFLLSDDASGQLSTSYADSCPSVEKVVHATVASAIQAERRMGASLIRLFFHDCFV 69

>gb|ABK21983.1| unknown [Picea sitchensis]
Length = 341

Score = 148 bits (373), Expect = 4e-33
Identities = 84/169 (49%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
++GCDGSILLDDTSSFTGEK ANPN+NS RGF V+D IK +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTGEKTANPNKNSVRGFGVVDQIKCELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F GL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGPNSTHQ TLETKFKRQGLNVVDLVALSGAHTI 208

Score = 121 bits (304), Expect = 4e-25
Identities = 64/132 (48%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTP T SFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFKARLYNQTVNGKPDPTLDTTYLKQLRAVCPQT-GTDDNQ TPLDPVTPIKFDID 269

Query: 1969 YFKNLVQKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142
Y+ N+V KGLL SD+ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDEILYSTKGSRTVGLVESYSTSTHAFFKQFAASMIKMGINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N
Sbjct: 330 HGEIRKNCRRMN 341

Score = 62.4 bits (150), Expect = 3e-07

Identities = 37/71 (52%), Positives = 45/71 (63%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ----LSTNFYHSCPNLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE RM AS
Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPQAIIKSVVEDAVRKEARMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV
Sbjct: 73 LLRLHFHDCFV 83

>ref|XP_002461210.1| hypothetical protein SORBIDRAFT_02g042860 [Sorghum bicolor]
gb|EER97731.1| hypothetical protein SORBIDRAFT_02g042860 [Sorghum bicolor]
Length = 313

Score = 148 bits (373), Expect = 4e-33
Identities = 70/124 (56%), Positives = 93/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+NF IYN+TNI+ AFA + Q +CP SG +LAPLD TPT+FDN Y+ NL+
Sbjct: 191 QAQCSNFDNHIYNDTNIDAAFATSLQANCP---ASGSTSLAPLDTMPTTFDNDYYTNLM 247

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFN GSTDS V ++++ F+S F AAM+KMG++SPLTG++GEIR C
Sbjct: 248 SQKGLLHSDQELFNGGSTDSTVSNFASSASAFTSAFTAAMVKMGNLSPLTGTGEIRLAC 307

Query: 2167 RRIN 2178
+N
Sbjct: 308 GIVN 311

Score = 123 bits (309), Expect = 1e-25
Identities = 76/169 (44%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LL+DTS GE+++ PN+ S R F+VID+IK+ VE VCPGVVSCADILA+AA
Sbjct: 68 VHGCDGSVLLNDTS---GEQSSPPNKGSLRRFDVIDSIKAQVEAVCPGVVSCADILAVAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNV 1510
RDSV + LGGP+W V LG
Sbjct: 125 RDSV-----VALGGPSWTVLLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + +PAPTS+L QL+S FS L D+VALSG I
Sbjct: 142 RRDS-TASFPSETDLPAPTSLLQLLSLFSNKNLDATDMVALS GAHTI 189

Score = 68.2 bits (165), Expect = 5e-09
Identities = 34/63 (53%), Positives = 44/63 (69%), Gaps = 2/63 (3%)
Frame = +1

Query: 601 CLALFVL--IWGSANAQLSTNFYYHSCPNI FSSVKSTVQSAISKETRMGASLLRLFFHDC 774
CLA V + A+AQLS+ FY SCPN S++KS V +A+ +E R GASLLR+ FHDC
Sbjct: 7 CLAFLVAAAVASVASAQLSSTFYDTS CPNALSTIKSGVDAAVMQEARTGASLLRMHFHDC 66

Query: 775 FVN 783
FV+
Sbjct: 67 FVH 69

>emb|CBI18065.1| unnamed protein product [Vitis vinifera]
Length = 413

Score = 147 bits (372), Expect = 5e-33
Identities = 83/169 (49%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDTS+FTGEK A PN NS RG+EV+D IKS +E CPGVVSCADILA+AA
Sbjct: 15 VNGCDASILLDDTSNFTGEKTAGPNANSVRGYEVVDTIKSQLEASCPGVVSCADILAVAA 74

Query: 1331 RDSVQIVSGQT TNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GP+W V+LG
Sbjct: 75 RDSV-----VALRGPSWVRLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRF SALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ IPAPT NL+ LIS F+ G + +++VALSG+ I
Sbjct: 92 RRDSTTASLSAANSNIPAPTLNLSGLISAFTNKGFNAREMVALSGSHTI 140

Score = 136 bits (343), Expect = 1e-29
Identities = 66/101 (65%), Positives = 77/101 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCT FR RIYNE NI+ +F + Q +CP S GDN L+PLD QTPT+FDN Y+ NLV
Sbjct: 142 QARCTTFRTRIYNEANIDASFKTSLQANCP--SSGGDNTLSPLDTQTPTTFDNAYYTNLV 199

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMI 2109
KKGLLHSDQQLFNGGST++V YST TF +DFA AM+
Sbjct: 200 NKKGLLHSDQQLFNGGSTDAVVNTYSTRSTTFFTFDFANAMM 240

Score = 106 bits (265), Expect = 1e-20
Identities = 64/139 (46%), Positives = 77/139 (55%), Gaps = 1/139 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC-PGVVSCADILAIA 1327
+ GCD SILLD TS+ EKNA N NSARGF V+D+IKS V+KVC VVSCADILA+A
Sbjct: 309 VNGCDASILLDATSTIDSEKNAGANANSARGFNVVDDIKSQVDKVCGRPVVSCADILAVA 368

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGP+W V+L
Sbjct: 369 ARDSV-----VALGGPSWTVQL 385

Query: 1508 GRRDARTASQSAANNNGIPA 1564
GRRD+ TAS++ ANN IP+
Sbjct: 386 GRRDSTTASRTDANNNIPS 404

Score = 68.2 bits (165), Expect = 5e-09
Identities = 40/89 (44%), Positives = 49/89 (55%), Gaps = 4/89 (4%)
Frame = +1

Query: 529 NT*STKLVCL-SKLTMASFCSRLTICLALFVLI---WGSANAQLSTNFYHSCPNLFSSV 696
NT ST+ + A SR +CL FVL +A LS FY CP ++
Sbjct: 222 NTYSTRSTTFFTFDFANAMMASRLLCLYAFVLFSLATADFSAAALSPYFYNKVCPKALPTI 281

Query: 697 KSTVQSAISKETRMGASLLRRLFHDFVN 783
K V++A+ KE RMGASLLRL FHDFVN
Sbjct: 282 KRVVEAAVQKEKRMGASLLRRLFHDFVN 310

>gb|ACF08091.1| class III peroxidase [Triticum aestivum]
Length = 316

Score = 147 bits (372), Expect = 5e-33
Identities = 69/125 (55%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSVSGSDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD TP +FDN Y+ NL
Sbjct: 191 QAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTPNAFDNAYYTNL 250

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAAMIKMGDISPLTGSNGEIRKN 2163
+ ++GLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +
Sbjct: 251 MSQRGLLHSDQVLFNNDTDTNVRNFASNPAAFSSAFTTAMIKMGNIAPKTGTGGQIRLS 310

Query: 2164 CRRIN 2178

C R+N
Sbjct: 311 CSRVN 315

Score = 94.4 bits (233), Expect = 7e-17
Identities = 63/170 (37%), Positives = 85/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILATAIAA 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 68 VQGCDAVLLSGM-----EQNAIPNAGSLRFGVIDSIKTQIEAICNQTVSCADILTVAA 122

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 123 RDSV-----VALGGPSWTVPLG 139

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSAL-GLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P S+ ++L + F GL+T D+VA SG I
Sbjct: 140 RRDSIDANEAEANSDLPGFNSSRSELEAAFLRKGLNTVDMVAPSGAHTI 189

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/62 (53%), Positives = 44/62 (70%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPFLSSVKSTVQSAISKETRMGASLLRRLFHDC 774
C++L VL+ +A+ QLS FY SCP +++KS V +A+S + RMGASLLRL FHDC
Sbjct: 7 CISLVVLVALATAASGQLSPTFYDTSCPRALATIKSGVMAAVSSDPRMGASLLRRLFHDC 66

Query: 775 FV 780
FV
Sbjct: 67 FV 68

>gb|EAY85149.1| hypothetical protein OsI_06504 [Oryza sativa Indica Group]
Length = 135

Score = 147 bits (372), Expect = 5e-33
Identities = 69/123 (56%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++CTNFRA IYN+ NI+ +FA R+++CP + +GD NLAPLD+QT FDN Y+ NL+
Sbjct: 13 SQCTNFRAHIYNDANIDPSFAALRRRACPAAPNGDNLAPLDVQTQNLFDNAYYGNLLV 72

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNNGS D++VR Y+ NP F++DFA AM+KMG+I S+GE+R +CR

Sbjct: 73 RRGLLHSDQVLFNGGSQDALVRQYAANPALFAADFAKAMVKGNI--QPSDGEVRCDCR 130

Query: 2170 RIN 2178
IN

Sbjct: 131 FIN 133

>gb|AAW52716.1| peroxidase 2 [Triticum monococcum]
Length = 316

Score = 147 bits (372), Expect = 5e-33
Identities = 69/125 (55%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD TP +FDN Y+ NL

Sbjct: 191 QAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTPNAFDNAYYTNL 250

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAIKMGDISPLTGSNGEIRKN 2163
+ ++GLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +

Sbjct: 251 MSQRGLLHSDQVLFNNDTTDNTVRNFASNPAAFSSAFTTAMIKMGNIAPKTGTQQQIRLS 310

Query: 2164 CRRIN 2178
C R+N

Sbjct: 311 CSRVN 315

Score = 97.1 bits (240), Expect = 1e-17
Identities = 64/170 (37%), Positives = 86/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA

Sbjct: 68 VQGCDA SVLLSGM-----EQNAIPNAGSLRGGVIDSIKTQIEAICNQTVSCADILTVAA 122

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 123 RDSV-----VALGGPSWTVPLG 139

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSAL-GLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P S+ ++L + F GL+T D+VALSG I

Sbjct: 140 RRDSIDANEAEANS DLPGFNSRSELEAAFLRKGLNTVDMVALSGAHTI 189

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/62 (53%), Positives = 44/62 (70%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDC 774
C++L VL+ +A+ QLS FY SCP +++KS V +A+S + RMGASLLRL FHDC
Sbjct: 7 CISLVVLVALATAASGQLSPTFYDTSCPRALATIKSGVMAAVSSDPRMGASLLRLLHFHDC 66

Query: 775 FV 780
FV
Sbjct: 67 FV 68

>gb|AAA32972.1| peroxidase [Hordeum vulgare]
Length = 315

Score = 147 bits (372), Expect = 5e-33
Identities = 70/125 (56%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI TA+A + + +CP+T GSGD +LA LD T +FDN Y+ NL
Sbjct: 190 QAQCSTFRARIYGGDTNINTAYAASLRANCPQTVGSGDGLANLDTTTANTFDNAYYTNL 249

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ +KGLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +
Sbjct: 250 MSQKGLLHSDQVLFNDDTTDNTVRNFASNPAAFSSAFTTAMIKMGNIAPKTGTQQGIRLS 309

Query: 2164 CRRIN 2178
C R+N
Sbjct: 310 CSRVN 314

Score = 95.9 bits (237), Expect = 2e-17
Identities = 64/170 (37%), Positives = 84/170 (49%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 67 VQGCDAVLLSGM-----EQNAIPNAGSLRGGVIDSIKTQIEAICKQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 122 RDSV-----VALGGPSWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRF-SALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN +P S+ +L + F GL+T D+VALSG I
Sbjct: 139 RRDSIDANENEANTDLPGFNSSRAEAAFLKKGGLNTVDMVALSGAHTI 188

Score = 65.5 bits (158), Expect = 3e-08
Identities = 31/59 (52%), Positives = 42/59 (71%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
L + V + +A+AQLS FY SCP +++KS V +A++ + RMGASLLR L FHDCFV
Sbjct: 9 LLVLVALVTAASAQLSPTFYDTSCPRALATIKSGVMAAVTSDPRMGASLLR LHFHDCFV 67

>emb|CBI22008.1| unnamed protein product [Vitis vinifera]
Length = 154

Score = 147 bits (371), Expect = 7e-33
Identities = 82/163 (50%), Positives = 97/163 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 25 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACKATVSCADILALAA 84

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 85 RDGVVL-----LGGPSWTVPLG 101

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVAL 1639
RRDARTA+QSAANN +PAP +NL+ LIS F+A GL+ D+ AL
Sbjct: 102 RRDARTANQSAANNLPPFANLSALISGFAAKGLNADDMTAL 144

Score = 43.5 bits (101), Expect = 0.14
Identities = 18/23 (78%), Positives = 21/23 (91%)
Frame = +1

Query: 715 AISKETRMGASLLR LFFHDCFVN 783
A+ +E RMGAS+LRLFFHDCFVN
Sbjct: 4 AVIREPRMGASILR LFFHDCFVN 26

>gb|ACD70388.1| class III peroxidase [Triticum aestivum]
Length = 316

Score = 147 bits (371), Expect = 7e-33
Identities = 70/124 (56%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR RIYNETNI+TAF A + + +CPR+ G DN+LAPLD TP FDN Y+ NL+
Sbjct: 194 QSQCRRFFRDRIYNETNIDTAFATSLRANCPRSGG--DNSLAPLDGTGPNGF DNAYYTNLM 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ LFNGG D+ VR +S++ TF+S F AMI MG+I+P TG+ G+IR C
Sbjct: 252 SQKGLLHSDQVLFNGGGADNTVRSFSSAATFNSAFTTAMINMGNIAPKTGTGGQIRLVC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 127 bits (320), Expect = 6e-27
Identities = 76/169 (44%), Positives = 89/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGKKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGS+LL DT SF GE+ A PN NS RG VIDNIK+ VE VC VSCADILA+AA
Sbjct: 67 VDGCDGSVLLADTGSFIGEQGAAPNNNSIRGMNVIDNIKTQVEAVCKQTVSCADILAVAA 126

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 127 RDSV-----VALGGPTWTVLLG 143

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ A N +P PT +L L + F LS D+VALSG I
Sbjct: 144 RRDSTTASKTNAENDLPPPTFDLQNLTTFLGKQLSMTDMVALSGAHTI 192

Score = 70.1 bits (170), Expect = 1e-09
Identities = 34/63 (53%), Positives = 46/63 (73%), Gaps = 2/63 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDC 774
CL L VL+ +A+AQLS+ FY SCPN +++K+ V +A+ E RMGASL+RL FHDC
Sbjct: 6 CLGLVVLVAMASAASAQLSSTFYDTSCPNALATIKAGVTA AVQNEARMGASLVRLHFHDC 65

Query: 775 FVN 783
FV+
Sbjct: 66 FVD 68

>gb|ABF48527.1| cell wall peroxidase [Capsicum annuum]
gb|ABG73021.1| cell wall peroxidase [Capsicum annuum]
Length = 322

Score = 147 bits (370), Expect = 9e-33
Identities = 79/125 (63%), Positives = 91/125 (72%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIY N T+I+ FA TR++ CP+ +G NLAPLDL TP DN YFKNL
Sbjct: 200 QAQCFLFRDRIYSNGTDIDAGFASTRRRRCQEDQNG--NLAPLDLVTPNQLDNNYFKNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
Q+KGLL SDQ L +GGSTD IV YS +P F+SDFAAAMI+MGDISPLTGSNG IR
Sbjct: 258 RQRKGLLQSDQVLLSGGSTDDIVLEYSNSPRAFASDFAAAMIRMGDISPLTGSNGIIRTV 317

Query: 2164 CRRIN 2178
C IN
Sbjct: 318 CGAIN 322

Score = 127 bits (320), Expect = 6e-27
Identities = 71/169 (42%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLD+T + EK A PN S RG+ +I++ K +EK CPG+VSCADILA+AA
Sbjct: 73 VQGCDASILLDETPTIVSEKTALPNLGSVRGYIIEDAKRELEKTC PGIVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ +V GGP+W VKLG
Sbjct: 133 RDASTLV-----GGPSWTVKLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + A +P P L +LIS F+ GLST+D+VALSG+ I
Sbjct: 150 RRDSTTASHTLAETDLPGPFDP LTRLISGFAKKGLSTRDMVALSGSHSI 198

Score = 62.8 bits (151), Expect = 2e-07
Identities = 28/58 (48%), Positives = 41/58 (70%)
Frame = +1

Query: 607 ALFVLIWGSANAQLSTNFYHSCPNLFSVVKSTVQSAISKETRMGASLLRFFHDCFV 780
+L +L +AQLS+ FY +CPN +++++ +V+ A+S E RM ASL+RL FHDCFV
Sbjct: 16 SLVLLCSMQCHAQLSSTFYDRACP NALNTIRKSVRQAVSAERRMAASLIRLHFHDCFV 73

>gb|ACF08092.1| class III peroxidase [Triticum aestivum]
Length = 316

Score = 146 bits (369), Expect = 1e-32
Identities = 68/125 (54%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD TP +FDN Y+ NL
Sbjct: 191 QAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTPNAFDNAYYTNL 250

Query: 1984 VQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ ++GLLHSDQ LFN +TD+ VR +++NP FS+ F AMIKMG+I+P TG+ G+IR +
Sbjct: 251 MSQRGLLHSDQVLFNNDTTDNTVRNFASNPAAFSNAFTTAMIKMGNIAPKTGTQQGIRLS 310

Query: 2164 CRRIN 2178
C R+N
Sbjct: 311 CSRVN 315

Score = 97.1 bits (240), Expect = 1e-17
Identities = 64/170 (37%), Positives = 86/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 68 VQGCDAVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICNQTVSCADILTVAA 122

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 123 RDSV-----VALGGPSWTVPLG 139

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSAL-GLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P S+ ++L + F GL+T D+VALSG I
Sbjct: 140 RRDSIDANEAEANSDLPGFNSSRSELEAAFLRKGLNTVDMVALSGAHTI 189

Score = 65.5 bits (158), Expect = 3e-08
Identities = 33/62 (53%), Positives = 43/62 (69%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDC 774
C++L VL+ +A QLS FY SCP +++KS V +A+S + RMGASLLRL FHDC
Sbjct: 7 CISLVVLVALATAAAGQLSPTFYDTSCPRALATIKSGVMAAVSSDPRMGASLLRLLHFHDC 66

Query: 775 FV 780
FV
Sbjct: 67 FV 68

>gb|ACN37032.1| unknown [Zea mays]
Length = 314

Score = 146 bits (369), Expect = 1e-32

Identities = 68/124 (54%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C +F IYN+TNI AFA + + +CP SG ++LAPLD TPT+FDN Y+ NL+

Sbjct: 193 QAQCLSFNDHIYNDTNINPAFAMSLRTNCP---ASGSSSLAPLDAMTPTAFDNAYYTLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFN GS DS V ++ N F+S FA AM+KMG++SPLTGS G++R NC

Sbjct: 250 SQRGLLHSDQELFNNGSADSTVSSFAANAAFTSAFATAMVKMGNLSPLTGSQGGVVRINC 309

Query: 2167 RRIN 2178

R+N

Sbjct: 310 WRVN 313

Score = 115 bits (287), Expect = 4e-23
Identities = 72/170 (42%), Positives = 93/170 (54%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRN-SARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+QGCD S+LL+DTS GE+N PN+ + RGF+V D+IK+ VE VCPG+VSCADILA+A

Sbjct: 69 VQGCDAVLLNDTS---GEQNQIPNQLNPRGFDVFDSEIKAQVEAVCPGIVSCADILAVA 125

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD V + LGGP+W V L

Sbjct: 126 ARDGV-----VALGGPSWTVAL 142

Query: 1508 GRRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

GRRD+ TAS A + +P PTS+L QL+ +S L+ D+VALSG I

Sbjct: 143 GRRDS-TASFPAQTSDLPPPTSSLQQLLRAYSCKNLNQTDMVALSQAHTI 191

Score = 66.6 bits (161), Expect = 2e-08
Identities = 35/70 (50%), Positives = 50/70 (71%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ S L + L + V++ A+AQLS+ FY SCP+ S++ S V +A+++E R+GASL

Sbjct: 1 MAASASCL-LSLLVVVLAALASAQLSSTFYDTSCPSALSTISSGVTAAVAQEARVGASL 59

Query: 751 LRLFFHDCFV 780

LRL FHDCFV

Sbjct: 60 LRLHFHDCFV 69

>sp|P27337.1|PER1_HORVU RecName: Full=Peroxidase 1; Flags: Precursor

emb|CAA41294.1| peroxidase [Hordeum vulgare]
Length = 315

Score = 146 bits (369), Expect = 1e-32
Identities = 69/125 (55%), Positives = 93/125 (74%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD T +FDN Y+ NL
Sbjct: 190 QAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTANTFDNAYYTNL 249

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ +KGLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +
Sbjct: 250 MSQKGLLHSDQVLFNDDTTDNTVRNFASNPAAFSSSFTTAMIKMGNIAPKTGTQQGIRLS 309

Query: 2164 CRRIN 2178
C R+N
Sbjct: 310 CSRVN 314

Score = 95.9 bits (237), Expect = 2e-17
Identities = 64/170 (37%), Positives = 84/170 (49%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVWSCADILAI AA 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 67 VQGCDASVLLSGM-----EQNAIPNAGSLRGGFVIDSIKTQIEAICKQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 122 RDSV-----VALGGPSWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRF-SALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN +P S+ +L + F GL+T D+VALSG I
Sbjct: 139 RRDSIDANENEANTDLPGFNSRAELEAAFLKKGGLNTVDMVALSGAHTI 188

Score = 65.5 bits (158), Expect = 3e-08
Identities = 31/59 (52%), Positives = 42/59 (71%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
L + V + +A+AQLS FY SCP +++KS V +A++ + RMGASLLRL FHDCFV
Sbjct: 9 LLVLVALVTAASAQLSPTFYDTSCPRALATIKSGVMAAVTSDPRMGASLLR LHFHDCFV 67

>gb|ABV24961.1| peroxidase [Catharanthus roseus]

Length = 135

Score = 146 bits (368), Expect = 2e-32
Identities = 82/170 (48%), Positives = 98/170 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEKNA PN+ S RGFEVID IKS +E +CPGVVSCADILA+AA
Sbjct: 8 VNGCDGSVLLDDTSSFTGEKNARPNKGLRGFEVIDTIKSQLETICPGVVSCADILAVAA 67

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W V+LG
Sbjct: 68 RDSV-----VALGGPAWIVELG 84

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHIS 1660
RRD+ TAS S A IP P +L +++ FS G S K++VALSG I+
Sbjct: 85 RRDSTTASLSDAEANIPFPRMDLTDILTAFSNKGFSKEMVALSGAHTIT 134

>emb|CAL25298.1| properoxidase [Picea abies]
Length = 341

Score = 146 bits (368), Expect = 2e-32
Identities = 84/169 (49%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
++GCDGSILLDDTSSFT EK ANPNRNS RGF V+D IK +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTREKTANPNRNSVRGFGVVDQIKCELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F GL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGPNSTHQTLTKFKRQGLNVVDLVALSGAHTI 208

Score = 121 bits (303), Expect = 5e-25
Identities = 64/132 (48%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFKARLYNQTVNGKPDPTLDTTYLKLHRAVCPQT-GTDDNQTTPLDPVTPIRFDIN 269

Query: 1969 YFKNLVQKKLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142

Y+ N+V KGLL SD+ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDEILYSTKGSRTVGLVESYSTSTHAFFKQFAASMIKMGINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N

Sbjct: 330 HGEIRKNCRRMN 341

Score = 59.7 bits (143), Expect = 2e-06
Identities = 36/71 (50%), Positives = 44/71 (61%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ----LSTNFYHSCPNLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE M AS
Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPKAQAIKSVVEDAVRKEAGMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV
Sbjct: 73 LLRLHFHDCFV 83

>gb|ACF08089.1| class III peroxidase [Triticum aestivum]
Length = 149

Score = 146 bits (368), Expect = 2e-32
Identities = 70/124 (56%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR RIYNETNI TAFa + + +CPR+ G DN+LAPLD TPT+FDN Y+ NL+
Sbjct: 27 QSQCRFFRDRIYNETNIGTAFATSLRANCPRSGG--DNSLAPLDGTPTAFDNAYYTLM 84

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ LFNGG D+ V ++++ TF+S F AMI MG+I+P TG+ G+IR C
Sbjct: 85 SKKGLLHSDQVLFNGGGADNTVMSFASSAATFNSAFTTAMINMGNIAPKTGTQQQIRLVC 144

Query: 2167 RRIN 2178
++N
Sbjct: 145 SKVN 148

Database: /usr/local/blast/db/blastlibs/nr
Posted date: Feb 13, 2010 7:16 AM
Number of letters in database: 3,559,509,877
Number of sequences in database: 10,432,217

Lambda K H
0.318 0.134 0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 10432217

Number of Hits to DB: 15,045,157,324

Number of extensions: 301983811

Number of successful extensions: 641055

Number of sequences better than 10.0: 1970

Number of HSP's gapped: 638318

Number of HSP's successfully gapped: 6610

Length of query: 910

Length of database: 3,559,509,877

Length adjustment: 146

Effective length of query: 764

Effective length of database: 2,036,406,195

Effective search space: 1555814332980

Effective search space used: 1555814332980

Neighboring words threshold: 12

Window for multiple hits: 40

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 33 (17.3 bits)

BLASTn Output of the 3' Border Sequences Flanking the Insert in Soybean Event DAS-68416-4 against GenBank Nucleotide Collection (nt/nr)

BLASTN 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Query= 68416_3_border
(1082 letters)

Database: /usr/local/blast/db/blastlibs/nt
10,930,266 sequences; 30,212,464,392 total letters

Searching..... done

Sequences producing significant alignments:	Score	E
	(bits)	Value
gb AC235472.1 Glycine max strain Williams 82 clone GM_WBc0099F2...	64	2e-06
emb AM473070.1 Vitis vinifera contig VV78X025151.6, whole genom...	48	0.11
gb AC233130.7 Solanum lycopersicum strain Heinz 1706 chromosome...	46	0.42
gb CP001633.1 Francisella tularensis subsp. tularensis NE061598...	46	0.42
ref XM_002426020.1 Pediculus humanus corporis synaptonemal comp...	46	0.42
emb AJ749949.2 Francisella tularensis subsp. tularensis SCHU S4...	46	0.42
gb AC235129.1 Glycine max strain Williams 82 clone GM_WBa0052I0...	46	0.42
tpg BK006741.1 TPA: TPA_reasm: Francisella tularensis subsp. ho...	46	0.42
ref XM_001336009.2 PREDICTED: Danio rerio hypothetical LOC10000...	46	0.42
gb CP000915.1 Francisella tularensis subsp. mediasiatica FSC147...	46	0.42
gb AC206008.3 Pongo abelii BAC clone CH276-282M20 from chromoso...	46	0.42
gb AC216474.1 Populus trichocarpa clone POP081-J22, complete se...	46	0.42
ref XM_001713455.1 Guillardia theta hypothetical protein (orf43...	46	0.42
gb CP000803.1 Francisella tularensis subsp. holarctica FTNF002-...	46	0.42
ref XM_001479242.1 PREDICTED: Mus musculus similar to MK-5 type...	46	0.42
emb AM457942.2 Vitis vinifera contig VV78X124814.1, whole genom...	46	0.42
emb AM446264.2 Vitis vinifera contig VV78X146694.5, whole genom...	46	0.42
gb CP000608.1 Francisella tularensis subsp. tularensis WY96-341...	46	0.42
ref NM_001110031.1 Danio rerio zgc:136903 (zgc:136903), mRNA >g...	46	0.42
emb AM485714.1 Vitis vinifera, whole genome shotgun sequence, c...	46	0.42
gb CP000439.1 Francisella tularensis subsp. novicida U112, comp...	46	0.42
emb CT027756.10 Zebrafish DNA sequence from clone DKEY-95F11 in...	46	0.42
gb CP000437.1 Francisella tularensis subsp. holarctica OSU18, c...	46	0.42
emb AM286280.1 Francisella tularensis subsp. tularensis strain ...	46	0.42
gb DQ681941.1 Synthetic construct Francisella tularensis clone ...	46	0.42

gb	AC151347.2	Xenopus (Silurana) tropicalis clone ISB-394A6, co...	46	0.42
gb	AC125096.3	Mus musculus BAC clone RP24-181K19 from chromosom...	46	0.42
gb	AC131109.3	Mus musculus BAC clone RP23-362M7 from chromosome...	46	0.42
dbj	AK137657.1	Mus musculus adult female vagina cDNA, RIKEN ful...	46	0.42
emb	CR690313.2	Tetraodon nigroviridis full-length cDNA	46	0.42
gb	AC026100.19	Homo sapiens 3 BAC RP11-449F7 (Roswell Park Canc...	46	0.42
gb	AF165818.4	Guillardia theta nucleomorph chromosome 1, comple...	46	0.42
emb	BX548071.7	Zebrafish DNA sequence from clone DKEY-25L23 in ...	46	0.42
emb	BX537275.8	Zebrafish DNA sequence from clone DKEYP-120E12 i...	46	0.42
emb	BX537269.8	Zebrafish DNA sequence from clone DKEY-181H1 in ...	46	0.42
dbj	AP005846.2	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.42
emb	AM233362.1	Francisella tularensis subsp. holarctica LVS com...	46	0.42
gb	AC151343.2	Xenopus (Silurana) tropicalis clone ISB-373E17, c...	46	0.42
gb	AC155316.6	Mus musculus BAC clone RP23-181P9 from chromosome...	46	0.42
ref	XM_733026.1	Plasmodium chabaudi chabaudi hypothetical prote...	46	0.42
emb	AL935040.6	Zebrafish DNA sequence from clone CH211-176L21, ...	46	0.42
emb	FP236458.5	Zebrafish DNA sequence from clone CH73-374P12, c...	44	1.7
emb	AL844509.2	Plasmodium falciparum 3D7 chromosome 13	44	1.7
emb	AL844508.1	Plasmodium falciparum 3D7 chromosome 9	44	1.7
dbj	AP010895.1	Solanum lycopersicum DNA, chromosome 8, clone: C...	44	1.7
gb	CP001110.1	Pelodictyon phaeoclathratiforme BU-1, complete ge...	44	1.7
ref	XM_001740672.1	Entamoeba dispar SAW760 F-box/leucine rich r...	44	1.7
ref	XM_001712135.1	Hemiselms andersenii hypothetical protein (...)	44	1.7
gb	CP000881.1	Hemiselms andersenii chromosome 1, complete sequ...	44	1.7
dbj	AB270792.1	Malus x domestica MdSFB9-alpha, S9-RNase, MdSFB...	44	1.7
ref	XM_001350114.1	Plasmodium falciparum 3D7 hypothetical prote...	44	1.7
ref	XM_001349842.1	Plasmodium falciparum 3D7 hypothetical prote...	44	1.7
gb	AC187618.3	Pan troglodytes BAC clone CH251-584I16 from chrom...	44	1.7
gb	AC192762.3	Pan troglodytes BAC clone CH251-676O11 from chrom...	44	1.7
emb	CT961058.16	M. truncatula DNA sequence from clone MTH2-80N17...	44	1.7
ref	XM_001032614.1	Tetrahymena thermophila conserved hypothetic...	44	1.7
emb	CT827810.6	Zebrafish DNA sequence from clone DKEY-120E24 in...	44	1.7
emb	AM231674.1	Prunus dulcis partial s-RNase gene for ribonucle...	44	1.7
gb	AC154194.2	Mus musculus BAC clone RP24-401L2 from chromosome...	44	1.7
gb	AC091473.2	Mus musculus chromosome X clones RP21-114F21, RP2...	44	1.7
gb	AC006353.3	Homo sapiens PAC clone RP5-1062J16 from 7, comple...	44	1.7
gb	AC132451.3	Mus musculus BAC clone RP23-194C20 from chromosom...	44	1.7
ref	XM_651154.1	Entamoeba histolytica HM-1:IMSS hypothetical pr...	44	1.7
gb	AC113349.2	Homo sapiens chromosome 5 clone CTD-2544H17, comp...	44	1.7
emb	AL353592.9	Human DNA sequence from clone RP11-569012 on chr...	44	1.7
emb	AL031297.4	Human DNA sequence from clone RP1-97P20 on chrom...	44	1.7
emb	BX571852.20	Zebrafish DNA sequence from clone DKEY-175N6 in...	44	1.7
emb	BX936441.6	Zebrafish DNA sequence from clone CH211-234M15 i...	44	1.7
emb	BX511195.5	Zebrafish DNA sequence from clone DKEYP-57D12 in...	44	1.7
emb	BX255948.4	Zebrafish DNA sequence from clone CH211-250J1, c...	44	1.7
gb	AC108005.8	Homo sapiens chromosome 11, clone CTD-2515M10, co...	44	1.7
emb	AL445564.1	Mycoplasma pulmonis (strain UAB CTIP) complete g...	44	1.7
gb	AC008436.5	AC008436 Homo sapiens chromosome 5 clone CTC-327B1...	44	1.7
gb	AC149381.2	Phakopsora pachyrhizi clone JGI AFNA-5A7, complete...	44	1.7

emb	AL928731.11	Mouse DNA sequence from clone RP23-171N20 on ch...	44	1.7
gb	AC238432.1	Mus musculus BAC clone RP24-76M8 from chromosome ...	42	6.6
gb	CP001701.1	Cyanothece sp. PCC 8802, complete genome	42	6.6
ref	NW_003033920.1	Schistosoma mansoni genome sequence supercon...	42	6.6
emb	FN409584.1	Equus caballus microsatellite DNA, locus ABGe15567	42	6.6
ref	XM_002445459.1	Sorghum bicolor hypothetical protein, mRNA	42	6.6
ref	XM_002444559.1	Sorghum bicolor hypothetical protein, mRNA	42	6.6
ref	XM_002450673.1	Sorghum bicolor hypothetical protein, mRNA	42	6.6
emb	FN357601.1	Schistosoma mansoni genome sequence supercontig ...	42	6.6
emb	FN368115.1	Schistosoma mansoni genome sequence supercontig ...	42	6.6
gb	AC202790.4	Gallus gallus BAC clone CH261-161K24 from chromos...	42	6.6
gb	AC235243.1	Glycine max strain Williams 82 clone GM_WBb0032L2...	42	6.6
gb	AC235153.1	Glycine max strain Williams 82 clone GM_WBa0085L0...	42	6.6
gb	AC235140.1	Glycine max strain Williams 82 clone GM_WBa0068I0...	42	6.6
emb	AL844502.1	Plasmodium falciparum 3D7 chromosome 3	42	6.6
gb	CP000857.1	Salmonella enterica subsp. enterica serovar Parat...	42	6.6
emb	FM992689.1	Candida dubliniensis CD36 chromosome 2, complete...	42	6.6
gb	FJ581043.1	Oryza punctata clone OP_Ba0017E18, complete sequence	42	6.6
ref	XM_002166130.1	PREDICTED: Hydra magnipapillata similar to p...	42	6.6
gb	CP001176.1	Bacillus cereus B4264, complete genome	42	6.6
emb	CU855905.8	Zebrafish DNA sequence from clone CH73-190M24 in...	42	6.6
ref	NG_008899.1	Homo sapiens sarcoglycan zeta (SGCZ) on chromos...	42	6.6
ref	NM_001135888.1	Bombyx mori osiris 9 (Osi9), mRNA >gi 207339...	42	6.6
emb	CU914133.2	Medicago truncatula chromosome 5 clone mth2-150o...	42	6.6
gb	CP001120.1	Salmonella enterica subsp. enterica serovar Heide...	42	6.6
emb	AM910991.1	Plasmodium knowlesi strain H chromosome 9, compl...	42	6.6
gb	AC198044.3	Pongo abelii BAC clone CH276-446K19 from chromoso...	42	6.6
gb	AC216598.1	Populus trichocarpa clone POP037-D13, complete se...	42	6.6
gb	AC205959.4	Canis familiaris, clone XX-180015, complete sequence	42	6.6
gb	AC213090.1	Populus trichocarpa clone POP118-019, complete se...	42	6.6
gb	AC212636.1	Solanum lycopersicum chromosome 7 clone C07HBa017...	42	6.6
gb	CP000409.1	Rickettsia canadensis str. McKiel, complete genome	42	6.6
gb	AC198093.4	Pongo abelii BAC clone CH276-31L11 from chromosom...	42	6.6
emb	CU329671.1	Schizosaccharomyces pombe chromosome II	42	6.6
ref	XM_001645942.1	Vanderwaltozyma polyspora DSM 70294 hypothet...	42	6.6
gb	AC209107.1	Populus trichocarpa clone POP088-K16, complete se...	42	6.6
ref	XM_001638933.1	Nematostella vectensis predicted protein (NE...	42	6.6
gb	AC174335.10	Medicago truncatula clone mth2-155122, complete ...	42	6.6
gb	CP000721.1	Clostridium beijerinckii NCIMB 8052, complete genome	42	6.6
gb	AC202303.8	Medicago truncatula clone mth2-155j9, complete se...	42	6.6
gb	EF533700.1	Glycine max clone BAC GM_WBb080D08, complete sequ...	42	6.6
gb	DQ914719.1	Fungal sp. EXP0495F 18S ribosomal RNA gene, parti...	42	6.6
emb	AM473707.2	Vitis vinifera contig VV78X111932.6, whole genom...	42	6.6
emb	AM483283.2	Vitis vinifera contig VV78X178586.8, whole genom...	42	6.6
emb	AM481633.2	Vitis vinifera contig VV78X190383.5, whole genom...	42	6.6
emb	AM479192.2	Vitis vinifera contig VV78X197549.13, whole geno...	42	6.6
emb	AM425055.2	Vitis vinifera contig VV78X086233.8, whole genom...	42	6.6
emb	AM463129.2	Vitis vinifera contig VV78X099343.8, whole genom...	42	6.6
emb	AM453496.2	Vitis vinifera contig VV78X099343.7, whole genom...	42	6.6

emb	AM433228.2	Vitis vinifera contig VV78X071247.4, whole genom...	42	6.6
emb	AM432606.2	Vitis vinifera contig VV78X032134.1, whole genom...	42	6.6
emb	AM436044.2	Vitis vinifera contig VV78X143044.4, whole genom...	42	6.6
gb	BC140581.1	Bos taurus cDNA clone IMAGE:8238248	42	6.6
ref	XM_001017552.2	Tetrahymena thermophila hypothetical protein...	42	6.6
emb	CU210926.7	Mouse DNA sequence from clone CH29-115D7 on chro...	42	6.6
ref	XM_001351252.1	Plasmodium falciparum 3D7 hypothetical prote...	42	6.6
gb	AC197607.1	Pongo abelii BAC clone CH276-100H12 from chromoso...	42	6.6
emb	CT583646.5	Zebrafish DNA sequence from clone DKEYP-72G6 in ...	42	6.6
emb	AM471960.1	Vitis vinifera contig VV78X029428.17, whole geno...	42	6.6
emb	AM458894.1	Vitis vinifera, whole genome shotgun sequence, c...	42	6.6
gb	AC192717.3	Gallus gallus BAC clone CH261-36N8 from chromosom...	42	6.6
dbj	AP009289.1	Solanum lycopersicum genomic DNA, chromosome 8, ...	42	6.6
emb	CT573243.6	Zebrafish DNA sequence from clone CH73-365J20 in...	42	6.6
emb	CU024879.5	M.truncatula DNA sequence from clone MTH2-70F3 o...	42	6.6
emb	CR790361.11	Zebrafish DNA sequence from clone DKEY-29N19, c...	42	6.6
gb	AE014297.2	Drosophila melanogaster chromosome 3R, complete s...	42	6.6
ref	XM_392161.3	PREDICTED: Apis mellifera similar to CG2931-PA,...	42	6.6
emb	CR627495.19	Zebrafish DNA sequence from clone DKEY-58G10 in...	42	6.6
emb	CR533579.7	Zebrafish DNA sequence from clone CH211-232J20 i...	42	6.6
emb	CT573422.5	Mouse DNA sequence from clone RP24-76M8 on chrom...	42	6.6
emb	CR848045.10	Zebrafish DNA sequence from clone DKEY-8K3 in l...	42	6.6
gb	CP000153.1	Sulfurimonas denitrificans DSM 1251, complete genome	42	6.6
gb	AC164170.7	Mus musculus 10 BAC RP24-419C12 (Roswell Park Can...	42	6.6
gb	AC102324.9	Mus musculus chromosome 1, clone RP24-476A18, com...	42	6.6
gb	AC158641.12	Mus musculus 10 BAC RP23-461E22 (Roswell Park Ca...	42	6.6
gb	AC150800.3	Medicago truncatula chromosome 7 clone mth2-77m9,...	42	6.6
gb	AY018508.1	Oryza sativa microsatellite MRG0833 containing (A...	42	6.6
gb	U23181.2	Caenorhabditis elegans cosmid ZK84, complete sequence	42	6.6
gb	AY330624.1	Galleria mellonella inducible metalloproteinase i...	42	6.6
gb	AC146790.16	Medicago truncatula clone mth2-123b21, complete ...	42	6.6
gb	AC137078.24	Medicago truncatula clone mth2-10e12, complete s...	42	6.6
gb	AC108876.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	42	6.6
gb	AC117265.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	42	6.6
gb	AC142111.3	Mus musculus BAC clone RP24-63G9 from chromosome ...	42	6.6
gb	AC139290.15	Medicago truncatula clone mth2-23f4, complete se...	42	6.6
gb	AC124558.4	Mus musculus BAC clone RP23-24808 from chromosome...	42	6.6
gb	AC123865.5	Mus musculus BAC clone RP23-365C14 from chromosom...	42	6.6
gb	AC123714.6	Mus musculus chromosome 9, clone RP23-393E20, com...	42	6.6
gb	AC110169.7	Mus musculus chromosome 9, clone RP23-233D3, comp...	42	6.6
gb	AE017245.1	Mycoplasma synoviae 53, complete genome	42	6.6
dbj	AP008983.1	Clostridium phage c-st genomic DNA, complete genome	42	6.6
gb	AC164090.3	Mus musculus BAC clone RP23-403F3 from chromosome...	42	6.6
gb	AC157542.11	Mus musculus chromosome 1, clone RP23-115I1, com...	42	6.6
emb	CR450724.10	Zebrafish DNA sequence from clone DKEY-168I4 in...	42	6.6
ref	XM_805808.1	Trypanosoma cruzi strain CL Brener hypothetical...	42	6.6
ref	XM_803717.1	Trypanosoma cruzi strain CL Brener hypothetical...	42	6.6
gb	DQ075075.1	Scirtothrips astrictus isolate PA-04-009 18S ribo...	42	6.6
gb	AC163647.3	Mus musculus BAC clone RP23-214L4 from chromosome...	42	6.6

emb	CR931715.1	Streptococcus pneumoniae strain 198/71 (serotype...	42	6.6
emb	CR931706.1	Streptococcus pneumoniae strain 7765/43 (serotyp...	42	6.6
emb	CR931704.1	Streptococcus pneumoniae strain 1936/39 (serotyp...	42	6.6
ref	NM_001021038.1	Schizosaccharomyces pombe transcription fact...	42	6.6
gb	AC157474.2	Mus musculus BAC clone RP24-565B5 from chromosome...	42	6.6
emb	CR352233.9	Zebrafish DNA sequence from clone CH211-193J5 in...	42	6.6
gb	AC143340.4	Medicago truncatula clone mth2-7f4, complete sequ...	42	6.6
dbj	AK054176.1	Mus musculus 2 days pregnant adult female oviduc...	42	6.6
dbj	AK053595.1	Mus musculus 0 day neonate eyeball cDNA, RIKEN f...	42	6.6
gb	AC044781.12	Homo sapiens chromosome 10 clone RP11-142M10, co...	42	6.6
gb	AC117398.3	Homo sapiens 3 BAC RP11-715A9 (Roswell Park Cance...	42	6.6
gb	AC002505.3	Arabidopsis thaliana chromosome 2 clone T9J22 map...	42	6.6
gb	AC096687.5	Oryza sativa chromosome 3 BAC OSJNBa0010E04 genom...	42	6.6
gb	AC020992.10	Homo sapiens chromosome 8, clone RP11-23H1, comp...	42	6.6
emb	AL365496.15	Human DNA sequence from clone RP11-449J3 on chr...	42	6.6
gb	AY060392.1	Drosophila melanogaster LD29917 full length cDNA	42	6.6
gb	AC034205.4	Homo sapiens chromosome 5 clone CTB-23I7, complet...	42	6.6
gb	AC091045.3	Homo sapiens chromosome 15 clone RP11-111A22 map ...	42	6.6
emb	AL137855.10	Human DNA sequence from clone RP5-1064J9 on chr...	42	6.6
emb	AL096771.11	Human DNA sequence from clone RP1-238D15 on chr...	42	6.6
emb	Z92813.1	Caenorhabditis elegans Cosmid T28A8, complete sequ...	42	6.6
emb	Z81139.1	Caenorhabditis elegans Cosmid W05H5, complete sequ...	42	6.6
gb	S74768.1	16S progenitor toxin: cha 33=hemagglutinin..cha-70...	42	6.6
emb	BX957329.9	Zebrafish DNA sequence from clone CH211-130P21 i...	42	6.6
dbj	AP005800.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
dbj	AP005000.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
emb	BX511180.7	Zebrafish DNA sequence from clone CH211-221H1 in...	42	6.6
dbj	AP005884.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
dbj	AP006164.2	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
emb	BX294435.5	Zebrafish DNA sequence from clone DKEYP-32G6 in ...	42	6.6
emb	BX890568.8	Zebrafish DNA sequence from clone DKEY-208J2 in ...	42	6.6
dbj	AP004462.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
dbj	AP003909.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
dbj	AP005249.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
dbj	AP004384.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
gb	AF476953.1	Vaucheria geminata ribulose-1,5-bisphosphate carb...	42	6.6
gb	AF476952.1	Vaucheria geminata ribulose-1,5-bisphosphate carb...	42	6.6
gb	AC091530.4	Papio anubis clone RP41-444A14, complete sequence	42	6.6
gb	AC098584.2	Homo sapiens BAC clone RP11-10L11 from 4, complet...	42	6.6
gb	AC091619.3	Papio anubis clone RP41-139B7, complete sequence	42	6.6
dbj	AP003209.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
emb	AL604063.4	Mouse DNA sequence from clone RP23-467J12 on chr...	42	6.6
gb	AC010884.11	Homo sapiens BAC clone RP11-350B7 from 2, comple...	42	6.6
gb	AC093759.3	Homo sapiens BAC clone RP11-67M1 from 4, complete...	42	6.6
gb	AC091247.4	Oryza sativa chromosome 3 BAC OJ1111_B11 genomic ...	42	6.6
gb	AC007755.6	AC007755 Drosophila melanogaster, chromosome 3R, r...	42	6.6
gb	AC007726.7	AC007726 Drosophila melanogaster, chromosome 3R, r...	42	6.6
gb	AC073166.7	Oryza sativa chromosome 10 BAC OSJNBb0064P21 geno...	42	6.6
gb	AC009232.3	Homo sapiens BAC clone RP11-352J11 from 2, comple...	42	6.6

gb AC019215.4 AC019215 Homo sapiens BAC clone RP11-480M18 from 8...	42	6.6
gb AC007404.4 Homo sapiens BAC clone RP11-547I5 from 2, complet...	42	6.6
emb X87946.1 O. sativa ZB8 gene	42	6.6
emb X62389.1 Botulinum bacteriophage genes for HA-17, HA-33, no...	42	6.6
emb X72793.1 Clostridium botulinum C phage BONT/C1, ANTP-139, A...	42	6.6
emb X66433.1 Clostridium botulinum phage 1C, CHn-14, CHn-33, Ch...	42	6.6
ref XM_672717.1 Plasmodium berghei strain ANKA hypothetical pro...	42	6.6
ref XM_668682.1 Plasmodium berghei strain ANKA hypothetical pro...	42	6.6
gb AE017220.1 Salmonella enterica subsp. enterica serovar Chole...	42	6.6
gb AC118672.3 Genomic sequence for Oryza sativa, Nipponbare str...	42	6.6
gb AC132258.3 Mus musculus BAC clone RP24-361F13 from 1, comple...	42	6.6
emb AL954656.9 Zebrafish DNA sequence from clone CH211-67N10 in...	42	6.6
emb BX120013.5 Zebrafish DNA sequence from clone DKEY-76H10, co...	42	6.6
emb BX005215.13 Mouse DNA sequence from clone RP23-280F9 on chr...	42	6.6
emb AL844857.5 Mouse DNA sequence from clone RP23-74L17 on chro...	42	6.6
emb BX247951.11 Zebrafish DNA sequence from clone DKEY-246A16 i...	42	6.6
gb AE016830.1 Enterococcus faecalis V583, complete genome	42	6.6
emb AL929523.5 Zebrafish DNA sequence from clone CH211-250I3, c...	42	6.6
emb AL773566.6 Mouse DNA sequence from clone RP23-181C9 on chro...	42	6.6
emb AL669898.17 Mouse DNA sequence from clone RP23-6C3 on chrom...	42	6.6
gb AE008384.1 Methanosarcina mazei strain Goel, complete genome	42	6.6
emb AL391158.5 Human chromosome 14 DNA sequence BAC R-560013 of...	42	6.6
dbj AB061780.1 Clostridium botulinum orf-22, ha-70, ha-17, ha-3...	42	6.6
emb AL132951.3 Caenorhabditis elegans YAC Y67H2A, complete sequ...	42	6.6
dbj AB012112.1 Clostridium botulinum D phage gene for ORF-22, H...	42	6.6
dbj AB012111.1 Clostridium botulinum D phage gene for ORF-22, H...	42	6.6
gb AC005548.1 AC005548 Homo sapiens chromosome 17, clone hRPK.75...	42	6.6
gb L22534.1 GALLHP82Z Galleria mellonella hexamerin (Lhp82) gene...	42	6.6

>gb|AC235472.1|Glycine max strain Williams 82 clone GM_WBc0099F23, complete sequence
Length = 134971

Score = 63.9 bits (32), Expect = 2e-06
Identities = 47/52 (90%)
Strand = Plus / Plus

Query: 212 tattcttttgtttcatttactttatgtgaggatataatagtaataaacatt 263
 ||||| ||||| ||||| ||||| ||||| ||||| ||| |||||
Sbjct: 77662 tattcttttgtatcatttgcattttaggttaggataatagttataaacatt 77713

Score = 42.1 bits (21), Expect = 6.6
Identities = 36/41 (87%)
Strand = Plus / Minus

Query: 216 ttttgtttcatttactttatgtgaggatataatagtaata 256

||||| ||||||||| || ||||| ||||||||| |||||
Sbjct: 78023 ttttatttcatttagttaatgtaggatataatagaaata 77983

>emb|AM473070.1| Vitis vinifera contig VV78X025151.6, whole genome shotgun sequence
Length = 4985

Score = 48.1 bits (24), Expect = 0.11
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 4 aacaatcaatattttaattcttaaactttatt 35
||||| ||||||||| ||||||||| |||||
Sbjct: 4576 aacaataaatattttaattgttaaactttatt 4607

>gb|AC233130.7| Solanum lycopersicum strain Heinz 1706 chromosome 10 clone hba-256116 map
10, complete sequence
Length = 159015

Score = 46.1 bits (23), Expect = 0.42
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 738 agaaattaactttttgtttttaaaaa 764
||||| ||||||||| ||||||||| |||||
Sbjct: 155094 agaaattaactttttcttttttaaaaa 155068

>gb|CP001633.1| Francisella tularensis subsp. tularensis NE061598, complete genome
Length = 1892681

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 950 tatgtctttctctaattgatgaa 972
||||| ||||||||| ||||||||| |||||
Sbjct: 971539 tatgtctttctctaattgatgaa 971561

>ref|XM_002426020.1| Pediculus humanus corporis synaptonemal complex protein ZIP1,
putative, mRNA
Length = 4083

Score = 46.1 bits (23), Expect = 0.42

Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 274 aaagaaaataaaaaagttaattt 296
|||||
Sbjct: 1237 aaagaaaataaaaaagttaattt 1259

>emb|AJ749949.2| Francisella tularensis subsp. tularensis SCHU S4 complete genome
Length = 1892775

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 950 tatgtctttctctaattgatgaa 972
|||||
Sbjct: 971474 tatgtctttctctaattgatgaa 971496

>gb|AC235129.1| Glycine max strain Williams 82 clone GM_WBa0052I05, complete sequence
Length = 119088

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 1045 ttagagaaaaataaataaattcttatattat 1075
|||||
Sbjct: 53261 ttagagaaaaataaataaattcatattttat 53291

>tpg|BK006741.1| TPA: TPA_reasm: Francisella tularensis subsp. holarctica OSU18, complete genome
Length = 1895727

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 950 tatgtctttctctaattgatgaa 972
|||||
Sbjct: 1193421 tatgtctttctctaattgatgaa 1193399

>ref|XM_001336009.2| PREDICTED: Danio rerio hypothetical LOC100000153 (LOC100000153), mRNA
Length = 2316

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 1049 agaaaaataataataattcttatattatgt 1079
 |||||
Sbjct: 1739 agaaaaataataataatcttatcttatatgt 1709

>gb|CP000915.1| Francisella tularensis subsp. mediasiatica FSC147, complete genome
Length = 1893886

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 950 tatgtctttctctaattgatgaa 972
 |||||
Sbjct: 1072991 tatgtctttctctaattgatgaa 1072969

>gb|AC206008.3| Pongo abelii BAC clone CH276-282M20 from chromosome unknown, complete
 sequence
Length = 222278

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 276 agaaaataaaaaagttaatttct 298
 |||||
Sbjct: 203364 agaaaataaaaaagttaatttct 203386

>gb|AC216474.1| Populus trichocarpa clone POP081-J22, complete sequence
Length = 126068

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 738 agaaattaactttttgttttttaaaaactaa 768

|||||
Sbjct: 76109 agaaattaattttttgtttcttaaaaactaa 76139

>ref|XM_001713455.1| Guillardia theta hypothetical protein (orf433) mRNA, complete cds
Length = 1302

Score = 46.1 bits (23), Expect = 0.42
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 271 tttaaagaaaataaaaaagttaatttc 297
|||||
Sbjct: 838 tttaaagaaaatacaaaaagttaatttc 864

>gb|CP000803.1| Francisella tularensis subsp. holarctica FTNF002-00, complete genome
Length = 1890909

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 950 tatgtctttctctaattgatgaa 972
|||||
Sbjct: 1189845 tatgtctttctctaattgatgaa 1189823

>ref|XM_001479242.1| PREDICTED: Mus musculus similar to MK-5 type 2 (LOC100047833), mRNA
Length = 4795

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaaac 765
|||||
Sbjct: 1815 ttaactttttgttttttaaaaac 1837

>emb|AM457942.2| Vitis vinifera contig VV78X124814.1, whole genome shotgun sequence
Length = 1077

Score = 46.1 bits (23), Expect = 0.42
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 734 tgagagaaattaactttttgttttta 760
 ||||| ||||| ||
Sbjct: 502 tgagagaaattaactttttgttttta 476

>emb|AM446264.2| Vitis vinifera contig VV78X146694.5, whole genome shotgun sequence
 Length = 3788

Score = 46.1 bits (23), Expect = 0.42
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 734 tgagagaaattaactttttgttttta 760
 ||||| ||||| ||
Sbjct: 353 tgagagaaattaactttttgttttta 379

>gb|CP000608.1| Francisella tularensis subsp. tularensis WY96-3418, complete genome
 Length = 1898476

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 950 tatgtctttctctaattgatgaa 972
 ||||| ||||| ||
Sbjct: 832314 tatgtctttctctaattgatgaa 832336

>ref|NM_001110031.1| Danio rerio zgc:136903 (zgc:136903), mRNA
 >gi|133777836|gb|BC115322.1| Danio rerio zgc:136903, mRNA
 (cDNA clone MGC:136903 IMAGE:7993315), complete cds
 Length = 2326

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 1049 agaaaaataaataaatcttatattatgt 1079
 ||||| ||||| ||
Sbjct: 1739 agaaaaataaataaatcttatattatgt 1709

>emb|AM485714.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X224594.16,

clone ENTAV 115
Length = 13699

Score = 46.1 bits (23), Expect = 0.42
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 734 tgagagaaattaactttttgttttta 760
|||||
Sbjct: 4853 tgagagaaattaaattttgttttta 4879

>gb|CP000439.1| Francisella tularensis subsp. novicida U112, complete genome
Length = 1910031

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 950 tatgtctttctctaattgatgaa 972
|||||
Sbjct: 894874 tatgtctttctctaattgatgaa 894896

>emb|CT027756.10| Zebrafish DNA sequence from clone DKEY-95F11 in linkage group 23,
complete sequence
Length = 112354

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 265 agtttatttaaagaaaataaaaa 287
|||||
Sbjct: 78389 agtttatttaaagaaaataaaaa 78367

>gb|CP000437.1| Francisella tularensis subsp. holarctica OSU18, complete genome
Length = 1895727

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 950 tatgtctttctctaattgatgaa 972

|||||
Sbjct: 1193421 tatgtctttctctaattgatgaa 1193399

>emb|AM286280.1| Francisella tularensis subsp. tularensis strain FSC 198 complete genome
Length = 1892616

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 950 tatgtctttctctaattgatgaa 972
|||||
Sbjct: 971427 tatgtctttctctaattgatgaa 971449

>gb|DQ681941.1| Synthetic construct Francisella tularensis clone FLH231418.01X xthA
gene, complete sequence
Length = 789

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 950 tatgtctttctctaattgatgaa 972
|||||
Sbjct: 144 tatgtctttctctaattgatgaa 122

>gb|AC151347.2| Xenopus (Silurana) tropicalis clone ISB-394A6, complete sequence
Length = 78040

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1047 agagaaaaataataaattctta 1069
|||||
Sbjct: 2861 agagaaaaataataaattctta 2839

>gb|AC125096.3| Mus musculus BAC clone RP24-181K19 from chromosome 18, complete
sequence
Length = 154941

Score = 46.1 bits (23), Expect = 0.42

Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1047 agagaaaaataataaattctta 1069
 |||||
Sbjct: 89959 agagaaaaataataaattctta 89937

>gb|AC131109.3| Mus musculus BAC clone RP23-362M7 from chromosome 18, complete
 sequence
 Length = 177690

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1047 agagaaaaataataaattctta 1069
 |||||
Sbjct: 635 agagaaaaataataaattctta 613

>dbj|AK137657.1| Mus musculus adult female vagina cDNA, RIKEN full-length enriched
 library, clone:9930013M24 product:MAP kinase-activated
 protein kinase 5, full insert sequence
 Length = 4783

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 743 ttaacttttgttttttaaaaac 765
 |||||
Sbjct: 1842 ttaacttttgttttttaaaaac 1864

>emb|CR690313.2| Tetraodon nigroviridis full-length cDNA
 Length = 1591

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaagtta 292
 |||||
Sbjct: 372 atttaaagaaaataaaaagtta 394

>gb|AC026100.19| Homo sapiens 3 BAC RP11-449F7 (Roswell Park Cancer Institute Human BAC Library) complete sequence
Length = 209521

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 276 agaaaataaaaaagttaatttct 298
|||||
Sbjct: 28950 agaaaataaaaaagttaatttct 28972

>gb|AF165818.4| Guillardia theta nucleomorph chromosome 1, complete sequence
Length = 196216

Score = 46.1 bits (23), Expect = 0.42
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 271 tttaaagaaaataaaaaagttaatttc 297
|||||
Sbjct: 23610 tttaaagaaaatacaaaaagttaatttc 23584

>emb|BX548071.7| Zebrafish DNA sequence from clone DKEY-25L23 in linkage group 9
Contains the 3' end of the gli2a gene for GLI-Kruppel family member GLI2a, the slc15a2 gene for solute carrier family 15 (H+/peptide transporter) member 2, the gene for a novel protein similar to vertebrate HSPB (heat shock 27kDa) associated protein 1 (HSPBAP1, zgc:100975) and the 5' end of the gene for a novel protein similar to vertebrate disrupted in renal carcinoma 2 (DIRC2, zgc:92095), complete sequence
Length = 223099

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 264 tagtttatttaaagaaaataaaa 286
|||||
Sbjct: 48437 tagtttatttaaagaaaataaaa 48415

>emb|BX537275.8| Zebrafish DNA sequence from clone DKEYP-120E12 in linkage group 11,
complete sequence
Length = 173631

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 1049 agaaaaataaataaattcttatattatgt 1079
|||||
Sbjct: 38891 agaaaaataaataaattcttatattatgt 38861

>emb|BX537269.8| Zebrafish DNA sequence from clone DKEY-181H1 in linkage group 11,
complete sequence
Length = 73125

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 1049 agaaaaataaataaattcttatattatgt 1079
|||||
Sbjct: 62729 agaaaaataaataaattcttatattatgt 62699

>dbj|AP005846.2| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC
clone:B1307A11
Length = 131538

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 744 taacttttgtttttaaaaact 766
|||||
Sbjct: 74560 taacttttgtttttaaaaact 74538

>emb|AM233362.1| Francisella tularensis subsp. holarctica LVS complete genome
Length = 1895994

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 950 tatgtctttctctaattgatgaa 972
 |||||
Sbjct: 1189937 tatgtctttctctaattgatgaa 1189915

>gb|AC151343.2| Xenopus (Silurana) tropicalis clone ISB-373E17, complete sequence
 Length = 88775

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1047 agagaaaaataataaattctta 1069
 |||||
Sbjct: 74842 agagaaaaataataaattctta 74820

>gb|AC155316.6| Mus musculus BAC clone RP23-181P9 from chromosome 5, complete sequence
 Length = 204809

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 743 ttaacttttgTTTTTAAAAC 765
 |||||
Sbjct: 115185 ttaacttttgTTTTTAAAAC 115163

>ref|XM_733026.1| Plasmodium chabaudi chabaudi hypothetical protein (PC102772.00.0)
 partial mRNA
 Length = 402

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 270 atttaaagaaaataaaaagtta 292
 |||||
Sbjct: 393 atttaaagaaaataaaaagtta 371

>emb|AL935040.6| Zebrafish DNA sequence from clone CH211-176L21, complete sequence
 Length = 159468

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 1049 agaaaaataaataaaattcttatattatgt 1079
|||||
Sbjct: 40419 agaaaaataaataaaattcttatattatgt 40389

>emb|FP236458.5| Zebrafish DNA sequence from clone CH73-374P12, complete sequence
Length = 95700

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 266 gtttatttaagaaaaataaaaa 287
|||||
Sbjct: 65875 gtttatttaagaaaaataaaaa 65854

>emb|AL844509.2| Plasmodium falciparum 3D7 chromosome 13
Length = 2895605

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 269 tatttaagaaaaataaaaaagt 290
|||||
Sbjct: 611898 tatttaagaaaaataaaaaagt 611919

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 263 ttagtttatttaagaaaaataaaaa 288
|||||
Sbjct: 1691677 ttagtttatttaagataataaaaa 1691652

>emb|AL844508.1| Plasmodium falciparum 3D7 chromosome 9

Length = 1541723

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 267 tttattttaagaaaataaaaa 288
|||||
Sbjct: 968625 tttattttaagaaaataaaaa 968604

>dbj|AP010895.1| Solanum lycopersicum DNA, chromosome 8, clone: C08HBa0121P10, complete
sequence
Length = 73815

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 1052 aaaataaataaattcttatattatat 1077
|||||
Sbjct: 27713 aaaataaataaattcttaaattatat 27738

>gb|CP001110.1| Pelodictyon phaeoclathratiforme BU-1, complete genome
Length = 3018238

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 934 ttcaaaaaatattttttatgtc 955
|||||
Sbjct: 437150 ttcaaaaaatattttttatgtc 437129

>ref|XM_001740672.1| Entamoeba dispar SAW760 F-box/leucine rich repeat protein, putative
EDI_037960 mRNA, complete cds
Length = 1980

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1008 acaaaagtgactgataaatcta 1029

|||||
Sbjct: 1735 acaaaagtgactgataaatcta 1756

>ref|XM_001712135.1| Hemiselmis andersenii hypothetical protein (HAN_1g14) mRNA, complete
cds
Length = 5982

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 267 tttatttaagaaaataaaaaa 288
|||||
Sbjct: 4655 tttatttaagaaaataaaaaa 4676

>gb|CP000881.1| Hemiselmis andersenii chromosome 1, complete sequence; nucleomorph
Length = 207524

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 267 tttatttaagaaaataaaaaa 288
|||||
Sbjct: 17839 tttatttaagaaaataaaaaa 17860

>dbj|AB270792.1| Malus x domestica MdSFBB9-alpha, S9-RNase, MdSFBB9-beta genes, complete
cds, Psi-SFBB9-alpha, Psi-SFBB9-beta pseudogenes
Length = 317412

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 833 tataaaaaatttctcaccatatttat 858
|||||
Sbjct: 160165 tataaaaaatttctcaccatctttat 160140

>ref|XM_001350114.1| Plasmodium falciparum 3D7 hypothetical protein (PF13_0235) partial
mRNA
Length = 11547

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 263 ttagttttatttaagaaaataaaaa 288
|||||
Sbjct: 2324 ttagttttatttaagataataaaaa 2349

>ref|XM_001349842.1| Plasmodium falciparum 3D7 hypothetical protein (PF13_0080) partial
mRNA
Length = 7557

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 269 tatttaagaaaataaaaaagt 290
|||||
Sbjct: 365 tatttaagaaaataaaaaagt 386

>gb|AC187618.3| Pan troglodytes BAC clone CH251-584I16 from chromosome 7, complete
sequence
Length = 216311

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1038 tctaccattagagaaaaataaa 1059
|||||
Sbjct: 199684 tctaccattagagaaaaataaa 199705

>gb|AC192762.3| Pan troglodytes BAC clone CH251-676011 from chromosome 7, complete
sequence
Length = 190460

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 1038 tctaccattagagaaaaataaa 1059
|||||

Sbjct: 108656 tctaccattagagaaaaataaa 108635

>emb|CT961058.16| *M. truncatula* DNA sequence from clone MTH2-80N17 on chromosome 3,
complete sequence
Length = 127385

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 263 ttagttttatTTAAAGAAAATAAAAAA 288
|||||
Sbjct: 52446 ttagttttatTTAAAGAAAATAAAAAA 52421

>ref|XM_001032614.1| *Tetrahymena thermophila* conserved hypothetical protein, mRNA
Length = 1491

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 255 tataacatttagttttatTTAAAGAAA 280
|||||
Sbjct: 829 tataacttttagttttatTTAAAGAAA 804

>emb|CT827810.6| Zebrafish DNA sequence from clone DKEY-120E24 in linkage group 21,
complete sequence
Length = 97913

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 1051 aaaaataaataaattcttatat 1072
|||||
Sbjct: 62570 aaaaataaataaattcttatat 62549

>emb|AM231674.1| *Prunus dulcis* partial s-RNase gene for ribonuclease S26 precursor,
exons 1-3, allele S26, cultivar Avellanera Gruesa
Length = 3717

Score = 44.1 bits (22), Expect = 1.7

Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagt 290
|||||
Sbjct: 3365 tatttaaagaaaataaaaaagt 3344

>gb|AC154194.2| Mus musculus BAC clone RP24-401L2 from chromosome 17, complete sequence
Length = 196871

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 276 agaaaataaaaaagttaatttc 297
|||||
Sbjct: 135298 agaaaataaaaaagttaatttc 135277

>gb|AC091473.2| Mus musculus chromosome X clones RP21-114F21, RP21-430D6 complete
sequence
Length = 221860

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1045 ttagagaaaataaataaattc 1066
|||||
Sbjct: 81683 ttagagaaaataaataaattc 81704

>gb|AC006353.3| Homo sapiens PAC clone RP5-1062J16 from 7, complete sequence
Length = 158090

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1038 tctaccattagagaaaataaa 1059
|||||
Sbjct: 103497 tctaccattagagaaaataaa 103518

>gb|AC132451.3| Mus musculus BAC clone RP23-194C20 from chromosome 8, complete sequence
Length = 188539

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 7 aatcaatattttaattccttaa 28
 |||||
Sbjct: 102628 aatcaatattttaattccttaa 102649

>ref|XM_651154.1| Entamoeba histolytica HM-1:IMSS hypothetical protein, mRNA
Length = 2685

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 279 aaataaaaaagttaatttctct 300
 |||||
Sbjct: 256 aaataaaaaagttaatttctct 235

>gb|AC113349.2| Homo sapiens chromosome 5 clone CTD-2544H17, complete sequence
Length = 163806

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 255 tataacatttagtttattttaa 276
 |||||
Sbjct: 110207 tataacatttagtttattttaa 110186

>emb|AL353592.9| Human DNA sequence from clone RP11-569012 on chromosome 13, complete
sequence
Length = 63325

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 267 tttatttaagaaaataaaaaa 288

|||||
Sbjct: 25137 tttattttaagaaaataaaaaa 25116

>emb|AL031297.4| Human DNA sequence from clone RP1-97P20 on chromosome 1q23.2-24.3
Contains the 3' end of a novel gene (FLJ45155 FLJ10706
FLJ39174) and the gene for ezrin-binding partner PACE-1
(PACE-1), complete sequence
Length = 103181

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 284 aaaaagttaatttctctttctg 305
|||||
Sbjct: 57119 aaaaagttaatttctctttctg 57140

>emb|BX571852.20| Zebrafish DNA sequence from clone DKEY-175N6 in linkage group 10,
complete sequence
Length = 178333

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 976 tatctatttaagtatatattttat 997
|||||
Sbjct: 3227 tatctatttaagtatatattttat 3206

>emb|BX936441.6| Zebrafish DNA sequence from clone CH211-234M15 in linkage group 18,
complete sequence
Length = 75388

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 1051 aaaaataaataaattctttatat 1072
|||||
Sbjct: 72839 aaaaataaataaattctttatat 72818

>emb|BX511195.5| Zebrafish DNA sequence from clone DKEYP-57D12 in linkage group 17,

complete sequence
Length = 79527

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1053 aaataaataaattcttatatta 1074
 |||||
Sbjct: 76946 aaataaataaattcttatatta 76967

>emb|BX255948.4| Zebrafish DNA sequence from clone CH211-250J1, complete sequence
 Length = 194257

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 1051 aaaataaataaattcttatat 1072
 |||||
Sbjct: 7443 aaaataaataaattcttatat 7422

>gb|AC108005.8| Homo sapiens chromosome 11, clone CTD-2515M10, complete sequence
 Length = 165443

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 266 gtttatttaagaaaaataaaaaagtt 291
 |||||
Sbjct: 16008 gtttatttaagaaaaataaaaaagtt 15983

>emb|AL445564.1| Mycoplasma pulmonis (strain UAB CTIP) complete genome; segment 2/3
 Length = 321250

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 267 tttatttaagaaaaataaaaa 288
 |||||

Sbjct: 42091 tttattttaagaaaataaaaaa 42112

>gb|AC008436.5|AC008436 Homo sapiens chromosome 5 clone CTC-327B12, complete sequence
Length = 118533

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 255 tataacatttagtttatttaa 276
|||||
Sbjct: 34013 tataacatttagtttatttaa 34034

>gb|AC149381.2| Phakopsora pachyrhizi clone JGIAFNA-5A7, complete sequence
Length = 35166

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 1050 gaaaaataataaattcctata 1071
|||||
Sbjct: 17774 gaaaaataataaattcctata 17753

>emb|AL928731.11| Mouse DNA sequence from clone RP23-171N20 on chromosome X Contains the
Opnlmw gene for opsin 1, medium-wave-sensitive, a
heterogeneous nuclear ribonucleoprotein A3 (Hnrpa3)
pseudogene, the gene for possible ortholog of human
chromosome X open reading frame 2 (CXorf2), a ribosomal
protein L3 (Rpl3) pseudogene and the Tktl1 gene for
transketolase-like 1, complete sequence
Length = 114243

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1045 ttagagaaaaataaataattc 1066
|||||
Sbjct: 55099 ttagagaaaaataaataattc 55120

>gb|AC238432.1| Mus musculus BAC clone RP24-76M8 from chromosome 9, complete sequence

Length = 193025

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 260 catttagttttatttaaagaaaataaaaa 288
|||||
Sbjct: 188172 catttagttttatttaaagaaaataaaaa 188144

>gb|CP001701.1| Cyanotheca sp. PCC 8802, complete genome
Length = 4669813

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 960 tctaattgatgaataatatct 980
|||||
Sbjct: 1091336 tctaattgatgaataatatct 1091316

>ref|NW_003033920.1| Schistosoma mansoni genome sequence supercontig Smp_scaff010824
Length = 3015

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 842 tttctcaccatatttattatt 862
|||||
Sbjct: 396 tttctcaccatatttattatt 416

>emb|FN409584.1| Equus caballus microsatellite DNA, locus ABGe15567
Length = 856

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 290 ttaatttctctttctgccact 310
|||||
Sbjct: 484 ttaatttctctttctgccact 464

>ref|XM_002445459.1| Sorghum bicolor hypothetical protein, mRNA
Length = 3087

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctatttaagtatattt 994
 |||||
Sbjct: 707 aatatctatttaagtatattt 727

>ref|XM_002444559.1| Sorghum bicolor hypothetical protein, mRNA
Length = 3558

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctatttaagtatattt 994
 |||||
Sbjct: 1484 aatatctatttaagtatattt 1504

>ref|XM_002450673.1| Sorghum bicolor hypothetical protein, mRNA
Length = 2985

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctatttaagtatattt 994
 |||||
Sbjct: 605 aatatctatttaagtatattt 625

>emb|FN357601.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000310
Length = 439186

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Plus

Query: 921 aaattattcctatttcaaaaaatattttt 949
||||| ||||||||| |||||||||
Sbjct: 244992 aaattgttctatttcaaaaaatattttt 245020

>emb|FN368115.1| Schistosoma mansoni genome sequence supercontig Smp_scaff010824
Length = 3015

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 842 tttctcaccatatttattatt 862
||||| ||||||||| |||||||||
Sbjct: 396 tttctcaccatatttattatt 416

>gb|AC202790.4| Gallus gallus BAC clone CH261-161K24 from chromosome z, complete
sequence
Length = 251539

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 926 attcctatttcaaaaaatattttt 950
|||| | ||||||||| |||||||||
Sbjct: 3071 attcgtatttcaaaaaatattttt 3047

>gb|AC235243.1| Glycine max strain Williams 82 clone GM_WBb0032L23, complete sequence
Length = 149341

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 920 aaaattattcctatttcaaaa 940
||||| ||||||||| |||||||||
Sbjct: 40182 aaaattattcctatttcaaaa 40162

>gb|AC235153.1| Glycine max strain Williams 82 clone GM_WBa0085L07, complete sequence
Length = 99314

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 60 ctaattcttaaacttcaataa 80
|||||
Sbjct: 90459 ctaattcttaaacttcaataa 90439

>gb|AC235140.1| Glycine max strain Williams 82 clone GM_WBa0068I04, complete sequence
Length = 138531

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 60 ctaattcttaaacttcaataa 80
|||||
Sbjct: 102190 ctaattcttaaacttcaataa 102210

>emb|AL844502.1| Plasmodium falciparum 3D7 chromosome 3
Length = 1060087

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 843 ttctcaccatatttattattatata 867
|||||
Sbjct: 912945 ttctcacaatatttattattatata 912921

>gb|CP000857.1| Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594,
complete genome
Length = 4833080

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 448 acgtaattgctaccgccgcaacgg 472
|||||
Sbjct: 1614993 acgtaattgctcccgccgcaacgg 1614969

>emb|FM992689.1| *Candida dubliniensis* CD36 chromosome 2, complete sequence
Length = 2289089

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 919 aaaaattattcctatttcaaa 939
|||||
Sbjct: 1754450 aaaaattattcctatttcaaa 1754470

>gb|FJ581043.1| *Oryza punctata* clone OP_Ba0017E18, complete sequence
Length = 167491

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 277 gaaaataaaaaagtaatttctctt 301
|||||
Sbjct: 62747 gaaaataaaaaagctaatttctctt 62723

>ref|XM_002166130.1| PREDICTED: *Hydra magnipapillata* similar to putative mediator of RNA
polymerase II transcription subunit 6 homolog
(LOC100200798), mRNA
Length = 942

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 146 ttcttacctatTTTTccattgaaat 170
|||||
Sbjct: 791 ttcttaactatTTTTccattgaaat 767

>gb|CP001176.1| *Bacillus cereus* B4264, complete genome
Length = 5419036

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 269 tttttaagaaaaataaaaaag 289
 ||||||||||||||||||
Sbjct: 2481986 tttttaagaaaaataaaaaag 2482006

>emb|CU855905.8| Zebrafish DNA sequence from clone CH73-190M24 in linkage group 13,
 complete sequence
 Length = 41814

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 930 ctatttcaaaaaatatttttt 950
 ||||||||||||||||||
Sbjct: 25952 ctatttcaaaaaatatttttt 25932

>ref|NG_008899.1| Homo sapiens sarcoglycan zeta (SGCZ) on chromosome 8
 Length = 1155420

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 735 gagagaaattaactttttgttttt 759
 |||||||||||||||||| |||||
Sbjct: 56971 gagagaaattaacttttttttttt 56995

>ref|NM_001135888.1| Bombyx mori osiris 9 (Osi9), mRNA >gi|207339261|gb|FJ176298.1| Bombyx
 mori osiris 9 mRNA, complete cds
 Length = 1375

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctatttaagtatattt 994
 ||||||||||||||||||
Sbjct: 1201 aatatctatttaagtatattt 1221

>emb|CU914133.2| Medicago truncatula chromosome 5 clone mth2-150o3, COMPLETE SEQUENCE
 Length = 130287

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 740 aaattaactttttgttttttaaaaa 764
||||||| ||||||||||||||||
Sbjct: 21545 aaattaactttttgttttttaaaaa 21569

>gb|CP001120.1| Salmonella enterica subsp. enterica serovar Heidelberg str. SL476, complete genome
Length = 4888768

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 738 agaaattaactttttgttttttaa 762
||||||||||||||||| |||||
Sbjct: 1916878 agaaattaactttttgttttttaa 1916902

>emb|AM910991.1| Plasmodium knowlesi strain H chromosome 9, complete genome
Length = 2147124

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaa 288
|||||||||||||||||
Sbjct: 283639 ttatttaaagaaaataaaaaa 283659

>gb|AC198044.3| Pongo abelii BAC clone CH276-446K19 from chromosome unknown, complete sequence
Length = 193379

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatattttta 951
|||||||||||||||||
Sbjct: 97735 tatttcaaaaaatattttta 97755

>gb|AC216598.1| Populus trichocarpa clone POP037-D13, complete sequence
Length = 86619

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 278 aaaataaaaaagttaatttct 298
|||||
Sbjct: 10003 aaaataaaaaagttaatttct 9983

>gb|AC205959.4| Canis familiaris, clone XX-180015, complete sequence
Length = 191292

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaagaaaaataaaaaa 288
|||||
Sbjct: 129514 ttatttaagaaaaataaaaaa 129534

>gb|AC213090.1| Populus trichocarpa clone POP118-019, complete sequence
Length = 119882

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 17 ttaattcttaactttattaatct 41
||||| |||||
Sbjct: 89074 ttaattcttaacttaattaatct 89050

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 17 ttaattcttaactttattaatct 41
||||| |||||

Sbjct: 113171 ttaattetttaaacttaattaaatct 113147

>gb|AC212636.1| Solanum lycopersicum chromosome 7 clone C07HBa0174J08, complete
sequence

Length = 36680

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 962 taattgatgaataatatctat 982

|||||

Sbjct: 26965 taattgatgaataatatctat 26945

>gb|CP000409.1| Rickettsia canadensis str. McKiel, complete genome

Length = 1159772

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 922 aattattcctatttcaaaaaa 942

|||||

Sbjct: 891128 aattattcctatttcaaaaaa 891108

>gb|AC198093.4| Pongo abelii BAC clone CH276-31L11 from chromosome unknown, complete
sequence

Length = 203750

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Plus

Query: 262 tttagtttattttaaagaaaat 282

|||||

Sbjct: 13576 tttagtttattttaaagaaaat 13596

>emb|CU329671.1| Schizosaccharomyces pombe chromosome II

Length = 4539804

Score = 42.1 bits (21), Expect = 6.6

Identities = 24/25 (96%)

Strand = Plus / Minus

Query: 928 tcctatttcaaaaaatattttttat 952
|||||
Sbjct: 318999 tcctatttcaaaaaatatttgttat 318975

>ref|XM_001645942.1| Vanderwaltozyma polyspora DSM 70294 hypothetical protein
(Kpo1_1031p38) partial mRNA
Length = 1161

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttatttaagaaaataaaaa 287
|||||
Sbjct: 756 tttatttaagaaaataaaaa 776

>gb|AC209107.1| Populus trichocarpa clone POP088-K16, complete sequence
Length = 93454

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 937 aaaaaatattttttatgtctt 957
|||||
Sbjct: 61180 aaaaaatattttttatgtctt 61200

>ref|XM_001638933.1| Nematostella vectensis predicted protein (NEMVEDRAFT_v1g199871) mRNA,
complete cds
Length = 3138

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 269 tatttaagaaaataaaaaag 289
|||||
Sbjct: 1630 tatttaagaaaataaaaaag 1610

>gb|AC174335.10| Medicago truncatula clone mth2-155122, complete sequence
Length = 87546

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Plus

Query: 261 atttagtttatttaagaaaataaaaaag 289
|||||
Sbjct: 81934 atttagtttatttcaagaaaacaaaaag 81962

>gb|CP000721.1| Clostridium beijerinckii NCIMB 8052, complete genome
Length = 6000632

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1055 ataaataaattcttatattat 1075
|||||
Sbjct: 1804335 ataaataaattcttatattat 1804315

>gb|AC202303.8| Medicago truncatula clone mth2-155j9, complete sequence
Length = 103788

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 1047 agagaaaaataaataaattcttata 1071
|||||
Sbjct: 41726 agagaaaaataaattaattcttata 41702

>gb|EF533700.1| Glycine max clone BAC GM_WBb080D08, complete sequence
Length = 154087

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 270 atttaagaaaataaaaaagttaat 294
|||||

Sbjct: 136309 atttaaaaaataaaaaagttaat 136333

>gb|DQ914719.1| Fungal sp. EXP0495F 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene,
and internal transcribed spacer 2, complete sequence; and
28S ribosomal RNA gene, partial sequence
Length = 606

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 991 attttattgtgaaatccacaa 1011
|||||
Sbjct: 207 attttattgtgaaatccacaa 227

>emb|AM473707.2| Vitis vinifera contig VV78X111932.6, whole genome shotgun sequence
Length = 4998

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1045 ttagagaaaataaataaatt 1065
|||||
Sbjct: 539 ttagagaaaataaataaatt 519

>emb|AM483283.2| Vitis vinifera contig VV78X178586.8, whole genome shotgun sequence
Length = 1891

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 740 aaattaactttttgttttttaaaaa 764
|||||
Sbjct: 968 aaattaacttttttttttaaaaa 944

>emb|AM481633.2| Vitis vinifera contig VV78X190383.5, whole genome shotgun sequence
Length = 5812

Score = 42.1 bits (21), Expect = 6.6

Identities = 22/23 (95%)
Strand = Plus / Plus

Query: 740 aaattaactttttgttttttaa 762
 ||||||| |||||||||||||
Sbjct: 1121 aaattaayttttgttttttaa 1143

>emb|AM479192.2| Vitis vinifera contig VV78X197549.13, whole genome shotgun sequence
 Length = 17080

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1044 attagagaaaaataataaat 1064
 |||||||||||||||||||
Sbjct: 11010 attagagaaaaataataaat 10990

>emb|AM425055.2| Vitis vinifera contig VV78X086233.8, whole genome shotgun sequence
 Length = 10725

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 748 tttttgttttttaaactaa 768
 |||||||||||||||||||
Sbjct: 10704 tttttgttttttaaactaa 10684

>emb|AM463129.2| Vitis vinifera contig VV78X099343.8, whole genome shotgun sequence
 Length = 3031

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 748 tttttgttttttaaactaa 768
 |||||||||||||||||||
Sbjct: 2255 tttttgttttttaaactaa 2275

>emb|AM453496.2| Vitis vinifera contig VV78X099343.7, whole genome shotgun sequence

Length = 3607

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 748 tttttgttttttaaaaactaa 768
 |||||
Sbjct: 2185 tttttgttttttaaaaactaa 2165

>emb|AM433228.2| Vitis vinifera contig VV78X071247.4, whole genome shotgun sequence
Length = 6173

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 748 tttttgttttttaaaaactaa 768
 |||||
Sbjct: 473 tttttgttttttaaaaactaa 453

>emb|AM432606.2| Vitis vinifera contig VV78X032134.1, whole genome shotgun sequence
Length = 1047

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 11 aatattttaattcttaactttatt 35
 |||||
Sbjct: 627 aatattttaattcttaactttatt 651

>emb|AM436044.2| Vitis vinifera contig VV78X143044.4, whole genome shotgun sequence
Length = 38850

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1049 agaaaaataaataattctta 1069
 |||||
Sbjct: 26978 agaaaaataaataattctta 26998

>gb|BC140581.1| Bos taurus cDNA clone IMAGE:8238248
Length = 3140

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttattttaagaaaataaaaa 287
|||||
Sbjct: 2105 tttattttaagaaaataaaaa 2125

>ref|XM_001017552.2| Tetrahymena thermophila hypothetical protein, mRNA
Length = 1332

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttta 951
|||||
Sbjct: 1276 tatttcaaaaaatatttttta 1296

>emb|CU210926.7| Mouse DNA sequence from clone CH29-115D7 on chromosome 6 Contains the
5' end of the Bicd1 gene for bicaudal D homolog 1
(Drosophila), an MRT4, mRNA turnover 4, homolog (S.
cerevisiae) (Mrto4) pseudogene, the Bicd1 gene for
bicaudal D homolog 1 (Drosophila), a DnaJ (Hsp40) homolog,
subfamily B , member 6 (Dnajb6) pseudogene, and an
adaptor-related protein complex AP-1 and sigma 3 (Apls3)
pseudogene, complete sequence
Length = 87584

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 278 aaaataaaaagttaatttct 298
|||||
Sbjct: 26238 aaaataaaaagttaatttct 26218

>ref|XM_001351252.1| Plasmodium falciparum 3D7 hypothetical protein (MAL3P7.22) partial

mRNA
Length = 8121

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 843 ttctcacatatttattattatata 867
||||||| |||||||||||||||||
Sbjct: 3359 ttctcacaatatttattattatata 3335

>gb|AC197607.1| Pongo abelii BAC clone CH276-100H12 from chromosome unknown, complete
sequence
Length = 199991

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 748 tttttgttttttaaaaactaa 768
|||||||||||||||||||||
Sbjct: 56604 tttttgttttttaaaaactaa 56584

>emb|CT583646.5| Zebrafish DNA sequence from clone DKEYP-72G6 in linkage group 1,
complete sequence
Length = 39926

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 1046 tagagaaaataaataaattcttat 1070
||||||||||||||||||| |||||
Sbjct: 5219 tagagaaaataaataaataacttat 5195

>emb|AM471960.1| Vitis vinifera contig VV78X029428.17, whole genome shotgun sequence
Length = 18189

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 931 tatttcaaaaaatatttttta 951
|||||
Sbjct: 14133 tatttcaaaaaatatttttta 14113

>emb|AM458894.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X000850.16,
clone ENTAV 115
Length = 55294

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 734 tgagagaaattaactttttgttttt 758
|||||
Sbjct: 16240 tgagagaaattaactttttgttttt 16264

>gb|AC192717.3| Gallus gallus BAC clone CH261-36N8 from chromosome z, complete sequence
Length = 217438

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 926 attcctatttcaaaaaatatttttt 950
||||
Sbjct: 112379 attcgtatttcaaaaaatatttttt 112355

>dbj|AP009289.1| Solanum lycopersicum genomic DNA, chromosome 8, clone: C08HBa0294K15,
complete sequence
Length = 72577

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttta 951
|||||
Sbjct: 52866 tatttcaaaaaatatttttta 52886

>emb|CT573243.6| Zebrafish DNA sequence from clone CH73-365J20 in linkage group 1,
complete sequence
Length = 19888

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 1046 tagagaaaataaataaattcttat 1070
|||||
Sbjct: 14596 tagagaaaataaataaataacttat 14620

>emb|CU024879.5| M. truncatula DNA sequence from clone MTH2-70F3 on chromosome 3,
complete sequence
Length = 66861

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 262 tttagtttatttaagaaaataaaa 286
|||||
Sbjct: 56908 tttagtttattcaagaaaataaaa 56932

>emb|CR790361.11| Zebrafish DNA sequence from clone DKEY-29N19, complete sequence
Length = 140025

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 847 caccatatttattattatata 867
|||||
Sbjct: 17770 caccatatttattattatata 17790

>gb|AE014297.2| Drosophila melanogaster chromosome 3R, complete sequence
Length = 27905053

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 270 atttaaagaaaataaaaagt 290
|||||
Sbjct: 11830374 atttaaagaaaataaaaagt 11830354

>ref|XM_392161.3| PREDICTED: Apis mellifera similar to CG2931-PA, transcript variant 1
(LOC408620), mRNA
Length = 1381

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1057 aaataaattcttatattatat 1077
|||||
Sbjct: 1361 aaataaattcttatattatat 1381

>emb|CR627495.19| Zebrafish DNA sequence from clone DKEY-58G10 in linkage group 14,
complete sequence
Length = 110289

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 215 cttttgtttcatttactttat 235
|||||
Sbjct: 6302 cttttgtttcatttactttat 6282

>emb|CR533579.7| Zebrafish DNA sequence from clone CH211-232J20 in linkage group 6,
complete sequence
Length = 199327

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1045 ttagagaaaataataaatt 1065
|||||
Sbjct: 154257 ttagagaaaataataaatt 154277

>emb|CT573422.5| Mouse DNA sequence from clone RP24-76M8 on chromosome 9, complete
sequence
Length = 193236

Score = 42.1 bits (21), Expect = 6.6

Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 260 catttagttttatttaaagaaaataaaaaa 288
|||||
Sbjct: 188383 catttagttttatttaaagaaaataaaaaa 188355

>emb|CR848045.10| Zebrafish DNA sequence from clone DKEY-8K3 in linkage group 16,
complete sequence
Length = 104737

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 156 tttttccattgaaatatgtta 176
|||||
Sbjct: 78404 tttttccattgaaatatgtta 78384

>gb|CP000153.1| Sulfurimonas denitrificans DSM 1251, complete genome
Length = 2201561

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 932 atttcaaaaaatattttttat 952
|||||
Sbjct: 1368329 atttcaaaaaatattttttat 1368349

>gb|AC164170.7| Mus musculus 10 BAC RP24-419C12 (Roswell Park Cancer Institute
(C57BL/6J Male) Mouse BAC Library) complete sequence
Length = 158496

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 932 atttcaaaaaatattttttat 952
|||||
Sbjct: 35072 atttcaaaaaatattttttat 35092

>gb|AC102324.9| Mus musculus chromosome 1, clone RP24-476A18, complete sequence
Length = 129634

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 957 ttctctaattgatgaataata 977
|||||
Sbjct: 105079 ttctctaattgatgaataata 105059

>gb|AC158641.12| Mus musculus 10 BAC RP23-461E22 (Roswell Park Cancer Institute
(C57BL/6J Female) Mouse BAC Library) complete sequence
Length = 186390

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 932 atttcaaaaaatattttttat 952
|||||
Sbjct: 35658 atttcaaaaaatattttttat 35638

>gb|AC150800.3| Medicago truncatula chromosome 7 clone mth2-77m9, complete sequence
Length = 116865

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 740 aaattaactttttgttttttaaaaa 764
||||| |||||
Sbjct: 11958 aaattaactttttgttttttaaaaa 11982

>gb|AY018508.1| Oryza sativa microsatellite MRG0833 containing (AT)X17, genomic
sequence
Length = 234

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
 |||||
Sbjct: 81 taactttttgttttttaaaaa 61

>gb|U23181.2| Caenorhabditis elegans cosmid ZK84, complete sequence
Length = 26759

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 277 gaaaataaaaaagttaatttc 297
 |||||
Sbjct: 12138 gaaaataaaaaagttaatttc 12158

>gb|AY330624.1| Galleria mellonella inducible metalloproteinase inhibitor (IMPI)
mRNA, complete cds
Length = 878

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 930 ctatttcaaaaaatattttt 950
 |||||
Sbjct: 755 ctatttcaaaaaatattttt 735

>gb|AC146790.16| Medicago truncatula clone mth2-123b21, complete sequence
Length = 114449

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 261 atttagtttatttaagaaaaataaaaaag 289
 ||||| ||||| |||||
Sbjct: 108866 atttagtttatttcaagaaacaaaaag 108838

>gb|AC137078.24| Medicago truncatula clone mth2-10e12, complete sequence
Length = 144306

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 1047 agagaaaaataataaattcttata 1071
|||||
Sbjct: 109171 agagaaaaataaattaattcttata 109195

>gb|AC108876.2| Oryza sativa Japonica Group chromosome 5 clone OJ1525_A02, complete
sequence
Length = 93826

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taacttttgttttttaaaaa 764
|||||
Sbjct: 37355 taacttttgttttttaaaaa 37335

>gb|AC117265.2| Oryza sativa Japonica Group chromosome 5 clone OJ1281_H05, complete
sequence
Length = 163130

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taacttttgttttttaaaaa 764
|||||
Sbjct: 131712 taacttttgttttttaaaaa 131692

>gb|AC142111.3| Mus musculus BAC clone RP24-63G9 from chromosome 9, complete sequence
Length = 185361

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 926 attcctatttcaaaaaatattttt 950
|||||
Sbjct: 61984 attcctttttcaaaaaatattttt 62008

>gb|AC139290.15| Medicago truncatula clone mth2-23f4, complete sequence
Length = 127701

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1045 ttagagaaaaataaataaatt 1065
|||||
Sbjct: 23952 ttagagaaaaataaataaatt 23972

>gb|AC124558.4| Mus musculus BAC clone RP23-24808 from chromosome 10, complete sequence
Length = 199938

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttta 951
|||||
Sbjct: 183212 tatttcaaaaaatatttttta 183232

>gb|AC123865.5| Mus musculus BAC clone RP23-365C14 from chromosome 10, complete sequence
Length = 212994

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 931 tatttcaaaaaatatttttta 951
|||||
Sbjct: 187954 tatttcaaaaaatatttttta 187934

>gb|AC123714.6| Mus musculus chromosome 9, clone RP23-393E20, complete sequence
Length = 217860

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 920 aaaattattcctatttcaaaa 940
|||||
Sbjct: 70799 aaaattattcctatttcaaaa 70819

>gb|AC110169.7| Mus musculus chromosome 9, clone RP23-233D3, complete sequence
Length = 193041

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 740 aaattaactttttgttttttaaaaa 764
|||| |
Sbjct: 158008 aaatgaactttttgttttttaaaaa 157984

>gb|AE017245.1| Mycoplasma synoviae 53, complete genome
Length = 799476

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 15 ttttaattcttaaactttattaaat 39
|||||
Sbjct: 365410 ttttaattcttaaactttattaaat 365386

>dbj|AP008983.1| Clostridium phage c-st genomic DNA, complete genome
Length = 185683

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1059 ataaattcttatattatgt 1079
|||||
Sbjct: 70595 ataaattcttatattatgt 70575

>gb|AC164090.3| Mus musculus BAC clone RP23-403F3 from chromosome 6, complete sequence
Length = 189441

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)

Strand = Plus / Plus

Query: 278 aaaataaaaaagttaatttct 298
 |||||
Sbjct: 149086 aaaataaaaaagttaatttct 149106

>gb|AC157542.11| Mus musculus chromosome 1, clone RP23-115I1, complete sequence
 Length = 211677

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 957 ttctctaattgatgaataata 977
 |||||
Sbjct: 157507 ttctctaattgatgaataata 157487

>emb|CR450724.10| Zebrafish DNA sequence from clone DKEY-168I4 in linkage group 18,
 complete sequence
 Length = 197565

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 930 ctatttcaaaaaatatTTTTT 950
 |||||
Sbjct: 68918 ctatttcaaaaaatatTTTTT 68898

>ref|XM_805808.1| Trypanosoma cruzi strain CL Brener hypothetical protein partial mRNA
 Length = 4338

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 319 atggtggagagatccgatgca 339
 |||||
Sbjct: 1283 atggtggagagatccgatgca 1263

>ref|XM_803717.1| Trypanosoma cruzi strain CL Brener hypothetical protein partial mRNA

Length = 4338

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 319 atggtggagagatccgatgca 339
 |||||
Sbjct: 1283 atggtggagagatccgatgca 1263

>gb|DQ075075.1| Scirtothrips astrictus isolate PA-04-009 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1,
complete sequence; and 5.8S ribosomal RNA gene, partial
sequence
Length = 1419

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 932 atttcaaaaaatattttttat 952
 |||||
Sbjct: 89 atttcaaaaaatattttttat 69

>gb|AC163647.3| Mus musculus BAC clone RP23-214L4 from chromosome 6, complete sequence
Length = 197408

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 278 aaaataaaaaagttaatttct 298
 |||||
Sbjct: 39336 aaaataaaaaagttaatttct 39356

>emb|CR931715.1| Streptococcus pneumoniae strain 198/71 (serotype 42)
Length = 19403

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 975 atatctatttaagtatattttattg 999
||||||| |||||||||
Sbjct: 7307 atatctattaaagtatattttattg 7331

>emb|CR931706.1| Streptococcus pneumoniae strain 7765/43 (serotype 35c)
Length = 19741

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 975 atatctatttaagtatattttattg 999
||||||| |||||||||
Sbjct: 7438 atatctattaaagtatattttattg 7462

>emb|CR931704.1| Streptococcus pneumoniae strain 1936/39 (serotype 35a)
Length = 21463

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 975 atatctatttaagtatattttattg 999
||||||| |||||||||
Sbjct: 7100 atatctattaaagtatattttattg 7124

>ref|NM_001021038.1| Schizosaccharomyces pombe transcription factor (predicted)
(SPBC1773.16c) partial mRNA
Length = 1788

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 928 tcctatttcaaaaaatatttttat 952
||||||| |||||||||
Sbjct: 1482 tcctatttcaaaaaatatttgttat 1506

>gb|AC157474.2| Mus musculus BAC clone RP24-565B5 from chromosome 9, complete sequence
Length = 192701

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 920 aaaattattcctatttcaaaa 940
|||||
Sbjct: 52223 aaaattattcctatttcaaaa 52203

>emb|CR352233.9| Zebrafish DNA sequence from clone CH211-193J5 in linkage group 13,
complete sequence
Length = 149899

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 930 ctatttcaaaaaatattttt 950
|||||
Sbjct: 91402 ctatttcaaaaaatattttt 91422

>gb|AC143340.4| Medicago truncatula clone mth2-7f4, complete sequence
Length = 114535

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1045 ttagagaaaaataataaatt 1065
|||||
Sbjct: 58432 ttagagaaaaataataaatt 58452

>dbj|AK054176.1| Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN
full-length enriched library, clone:E230025E05
product:unclassifiable, full insert sequence
Length = 3790

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 278 aaaataaaaagttaatttct 298
|||||
Sbjct: 2424 aaaataaaaagttaatttct 2404

>dbj|AK053595.1| Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:EI30112N04 product:unclassifiable, full insert sequence
Length = 3686

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 278 aaaataaaaaagttaatttct 298
|||||
Sbjct: 442 aaaataaaaaagttaatttct 422

>gb|AC044781.12| Homo sapiens chromosome 10 clone RP11-142M10, complete sequence
Length = 177448

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 736 agagaaattaactttttgttt 756
|||||
Sbjct: 144613 agagaaattaactttttgttt 144593

>gb|AC117398.3| Homo sapiens 3 BAC RP11-715A9 (Roswell Park Cancer Institute Human BAC Library) complete sequence
Length = 109182

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 740 aaattaactttttgttttttaaaaa 764
|||||
Sbjct: 60250 aaattaacttttttttttaaaaa 60226

>gb|AC002505.3| Arabidopsis thaliana chromosome 2 clone T9J22 map B68, complete sequence
Length = 115851

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1057 aaataaattccttatattatat 1077
 |||||
Sbjct: 88379 aaataaattccttatattatat 88359

>gb|AC096687.5| Oryza sativa chromosome 3 BAC OSJNBa0010E04 genomic sequence, complete
 sequence
 Length = 117505

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 744 taactttttgtttttaaaaa 764
 |||||
Sbjct: 108186 taactttttgtttttaaaaa 108206

>gb|AC020992.10| Homo sapiens chromosome 8, clone RP11-23H1, complete sequence
 Length = 129413

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 735 gagagaaattaactttttgttttt 759
 |||||
Sbjct: 26314 gagagaaattaactttttttttt 26290

>emb|AL365496.15| Human DNA sequence from clone RP11-449J3 on chromosome 10 Contains the
 3' end of the PCDH15 gene for protocadherin 15 and a novel
 gene, complete sequence
 Length = 173728

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 262 tttagtttatttaagaaaat 282
 |||||
Sbjct: 92667 tttagtttatttaagaaaat 92687

>gb|AY060392.1| Drosophila melanogaster LD29917 full length cDNA
Length = 2146

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagt 290
|||||
Sbjct: 2098 atttaaagaaaataaaaaagt 2118

>gb|AC034205.4| Homo sapiens chromosome 5 clone CTB-23I7, complete sequence
Length = 159562

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttatttaagaaaataaaaa 287
|||||
Sbjct: 49356 tttatttaagaaaataaaaa 49376

>gb|AC091045.3| Homo sapiens chromosome 15 clone RP11-111A22 map 15q14, complete
sequence
Length = 171947

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 156 tttttccattgaaatatgta 176
|||||
Sbjct: 73166 tttttccattgaaatatgta 73186

>emb|AL137855.10| Human DNA sequence from clone RP5-1064J9 on chromosome 1p32.2-33,
complete sequence
Length = 106970

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1045 ttagagaaaaataataaatt 1065
|||||
Sbjct: 89059 ttagagaaaaataataaatt 89039

>emb|AL096771.11| Human DNA sequence from clone RP1-238D15 on chromosome 6q12-14.3
Contains 3' end of COL12A1 gene for collagen, type XII,
alpha 1, complete sequence
Length = 112292

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 839 aaatttctcaccatatttattatata 867
|||||
Sbjct: 46476 aaatttctcaccatataatattatata 46448

>emb|Z92813.1| Caenorhabditis elegans Cosmid T28A8, complete sequence
Length = 34388

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 931 tatttcaaaaaatatttttta 951
|||||
Sbjct: 19536 tatttcaaaaaatatttttta 19516

>emb|Z81139.1| Caenorhabditis elegans Cosmid W05H5, complete sequence
Length = 14770

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 277 gaaaataaaaaagttaatttc 297
|||||
Sbjct: 483 gaaaataaaaaagttaatttc 463

>gb|S74768.1| 16S progenitor toxin: cha 33=hemagglutinin...cha-70=hemagglutinin 70

[Clostridium botulinum, type C, Genomic, 3 genes, 2636
nt]
Length = 2636

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1059 ataaattcttatattatgt 1079
|||||||
Sbjct: 400 ataaattcttatattatgt 420

>emb|BX957329.9| Zebrafish DNA sequence from clone CH211-130P21 in linkage group 23,
complete sequence
Length = 76351

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 259 acatttagtttatttaaagaaaataaaaa 287
||||||| ||||| |||||
Sbjct: 2458 acatttagtttctttaataaaaaataaaaa 2430

>dbj|AP005800.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC
clone:OSJNBa0016D04
Length = 147313

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 744 taactttttgttttttaaaaa 764
|||||||
Sbjct: 92509 taactttttgttttttaaaaa 92529

>dbj|AP005000.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, PAC
clone:P0042D01
Length = 148305

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taacttttggtttttaaaaa 764
|||||||
Sbjct: 41741 taacttttggtttttaaaaa 41721

>emb|BX511180.7| Zebrafish DNA sequence from clone CH211-221H1 in linkage group 3,
complete sequence
Length = 155448

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 62 aattcttaacttcaataaacaata 86
||||||| |||||
Sbjct: 153095 aattcttaaaattcaataaacaata 153119

>dbj|AP005884.3| Oryza sativa Japonica Group genomic DNA, chromosome 9, PAC clone:P0598D02
Length = 155238

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 744 taacttttggtttttaaaaa 764
|||||||
Sbjct: 138870 taacttttggtttttaaaaa 138890

>dbj|AP006164.2| Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC
clone:B1386G10
Length = 121827

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 945 tttttatgtctttctctaat 965
|||||||
Sbjct: 27229 tttttatgtctttctctaat 27249

>emb|BX294435.5| Zebrafish DNA sequence from clone DKEYP-32G6 in linkage group 25,

complete sequence
Length = 128861

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 1051 aaaaataaataaattcttatattat 1075
|||||
Sbjct: 4297 aaaaataaataaataacttatattat 4321

>emb|BX890568.8| Zebrafish DNA sequence from clone DKEY-208J2 in linkage group 20 Contains
the ches1 gene for checkpoint suppressor 1, a novel gene
(wu:fc15h02) (general transcription factor IIA, 1,
19/37kDa) and a CpG island, complete sequence
Length = 188167

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 30 tttattaaatctaacaataaactgt 54
|||||
Sbjct: 130161 tttataaaatctaacaataaactgt 130185

>dbj|AP004462.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, PAC
clone:P0450B04
Length = 153268

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
|||||
Sbjct: 19568 taactttttgttttttaaaaa 19548

>dbj|AP003909.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC
clone:OJ1300_E01
Length = 103022

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
 |||||
Sbjct: 76480 taactttttgttttttaaaaa 76460

>dbj|AP005249.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC
 clone:OSJNBa0087F21
 Length = 187401

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
 |||||
Sbjct: 168637 taactttttgttttttaaaaa 168617

>dbj|AP004384.3| Oryza sativa Japonica Group genomic DNA, chromosome 7, PAC
 clone:P0506C07
 Length = 123451

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaa 763
 |||||
Sbjct: 80250 ttaactttttgttttttaaaa 80270

>gb|AF476953.1| Vaucheria geminata ribulose-1,5-bisphosphate carboxylase/oxygenase
 large subunit (rbcL) gene, complete cds; chloroplast
 gene for chloroplast product
 Length = 1980

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 18 taattcttaactttatataa 38
 |||||
Sbjct: 110 taattcttaactttatataa 130

>gb|AF476952.1| *Vaucheria geminata* ribulose-1,5-bisphosphate carboxylase/oxygenase
large subunit (rbcL) gene, complete cds; chloroplast
gene for chloroplast product
Length = 1983

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 18 taattcttaaactttatttaa 38
|||||
Sbjct: 114 taattcttaaactttatttaa 134

>gb|AC091530.4| *Papio anubis* clone RP41-444A14, complete sequence
Length = 162413

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 264 tagtttatttaagaaaaataaaaa 288
|||||
Sbjct: 12255 tagtttatttaagaaaaataaaaa 12279

>gb|AC098584.2| *Homo sapiens* BAC clone RP11-10L11 from 4, complete sequence
Length = 159206

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 261 atttagtttatttaagaaaaataaa 285
|||||
Sbjct: 23374 atttagtttatttaagaaaaataaa 23350

>gb|AC091619.3| *Papio anubis* clone RP41-139B7, complete sequence
Length = 181302

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 264 tagttttatttaaagaaaataaaaaa 288
|||||
Sbjct: 174048 tagttttatttaaagaaaaaaaaa 174072

>dbj|AP003209.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC clone:B1189A09
Length = 167761

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 744 taactttttgtttttaaaaa 764
|||||
Sbjct: 127755 taactttttgtttttaaaaa 127775

>emb|AL604063.4| Mouse DNA sequence from clone RP23-467J12 on chromosome 11, complete
sequence
Length = 146759

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgtttttaaaaa 763
|||||
Sbjct: 46882 ttaactttttgtttttaaaaa 46902

>gb|AC010884.11| Homo sapiens BAC clone RP11-350B7 from 2, complete sequence
Length = 137172

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 934 ttcaaaaaatatttttatgtcttt 958
|||||
Sbjct: 70408 ttcaaaaaatatttttatttcttt 70384

>gb|AC093759.3| Homo sapiens BAC clone RP11-67M1 from 4, complete sequence
Length = 177807

|||||
Sbjct: 33586 atttaaagaaaataaaaaagt 33566

>gb|AC073166.7| Oryza sativa chromosome 10 BAC OSJNBb0064P21 genomic sequence, complete sequence
Length = 142114

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
|||||
Sbjct: 92239 taactttttgttttttaaaaa 92219

>gb|AC009232.3| Homo sapiens BAC clone RP11-352J11 from 2, complete sequence
Length = 139885

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 425 tgacagttgatgggtggagaagac 449
|||||
Sbjct: 103613 tgacagttgatgggtggagcagac 103589

>gb|AC019215.4|AC019215 Homo sapiens BAC clone RP11-480M18 from 8, complete sequence
Length = 192579

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 735 gagagaaattaactttttgttttt 759
|||||
Sbjct: 152163 gagagaaattaactttttttttt 152139

>gb|AC007404.4| Homo sapiens BAC clone RP11-547I5 from 2, complete sequence
Length = 168506

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)

Strand = Plus / Plus

Query: 748 tttttgttttttaaaaactaa 768
|||||||
Sbjct: 59454 tttttgttttttaaaaactaa 59474

>emb|X87946.1| O. sativa ZB8 gene
Length = 4660

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 744 taactttttgttttttaaaaa 764
|||||||
Sbjct: 1051 taactttttgttttttaaaaa 1071

>emb|X62389.1| Botulinum bacteriophage genes for HA-17, HA-33, nontoxic components
and C1 toxin
Length = 9613

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1059 ataaattcttatattatatgt 1079
|||||||
Sbjct: 272 ataaattcttatattatatgt 252

>emb|X72793.1| Clostridium botulinum C phage BONT/C1, ANTP-139, ANTP-33, ANTP-17,
ANTP-70 genes and ORF-22
Length = 12297

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1059 ataaattcttatattatatgt 1079
|||||||
Sbjct: 2962 ataaattcttatattatatgt 2942

>emb|X66433.1| Clostridium botulinum phage 1C, CHn-14, CHn-33, Chn-138 and BoNT/C1
genes
Length = 9689

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1059 ataaattcttatattatgt 1079
|||||
Sbjct: 354 ataaattcttatattatgt 334

>ref|XM_672717.1| Plasmodium berghei strain ANKA hypothetical protein (PB108599.00.0)
partial mRNA
Length = 213

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 270 atttaaagaaaataaaaaagttaat 294
|||||
Sbjct: 133 atttaaagaaaataaaaaagataat 109

>ref|XM_668682.1| Plasmodium berghei strain ANKA hypothetical protein (PB300464.00.0)
partial mRNA
Length = 579

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaa 288
|||||
Sbjct: 139 ttatttaaagaaaataaaaaa 159

>gb|AE017220.1| Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67,
complete genome
Length = 4755700

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 448 acgtaattgctaccgccgtcaacgg 472
|||||
Sbjct: 2278219 acgtaattgctcccgccgtcaacgg 2278243

>gb|AC118672.3| Genomic sequence for Oryza sativa, Nipponbare strain, clone
OSJNBb0078P24, from chromosome 3, complete sequence
Length = 146930

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 744 taactttttgttttttaaaaa 764
|||||
Sbjct: 52650 taactttttgttttttaaaaa 52670

>gb|AC132258.3| Mus musculus BAC clone RP24-361F13 from 1, complete sequence
Length = 130493

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 1008 acaaaagtgactgataaatctaatt 1032
|||||
Sbjct: 40309 acaaaagtgactgataaatgtaatt 40333

>emb|AL954656.9| Zebrafish DNA sequence from clone CH211-67N10 in linkage group 23,
complete sequence
Length = 180590

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Plus

Query: 259 acatttagttttatttaagaaaataaaaa 287
|||||
Sbjct: 122350 acatttagttttctttaataaaaataaaaa 122378

>emb|BX120013.5| Zebrafish DNA sequence from clone DKEY-76H10, complete sequence

Length = 170264

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 847 caccatatttattattatata 867
|||||
Sbjct: 29453 caccatatttattattatata 29433

>emb|BX005215.13| Mouse DNA sequence from clone RP23-280F9 on chromosome X Contains the 5' end of the Cask gene for calcium/calmodulin-dependent serine protein kinase (MAGUK family), a makorin, ring finger protein, 2 (Mkrn2) pseudogene and one CpG island, complete sequence
Length = 189900

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagttaatttct 298
|||||
Sbjct: 28440 atttaaagaaaataaaaaaacgtaatttct 28468

>emb|AL844857.5| Mouse DNA sequence from clone RP23-74L17 on chromosome X, complete sequence
Length = 209399

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1045 ttagagaaaaataaataaatt 1065
|||||
Sbjct: 42758 ttagagaaaaataaataaatt 42778

>emb|BX247951.11| Zebrafish DNA sequence from clone DKEY-246A16 in linkage group 18 Contains the 5' end of the gene for a novel protein similar to vertebrate protein inhibitor of activated STAT, 1 (PIAS1), three novel genes and two CpG islands, complete sequence
Length = 189723

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 930 ctatttcaaaaaatattttt 950
|||||
Sbjct: 101732 ctatttcaaaaaatattttt 101752

>gb|AE016830.1| Enterococcus faecalis V583, complete genome
Length = 3218031

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaagaaaataaaaa 288
|||||
Sbjct: 2933665 ttatttaagaaaataaaaa 2933685

>emb|AL929523.5| Zebrafish DNA sequence from clone CH211-250I3, complete sequence
Length = 133678

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 262 tttagtttatttaagaaaataaaa 286
|||||
Sbjct: 29372 tttagtttatttaagaaaataaaa 29396

>emb|AL773566.6| Mouse DNA sequence from clone RP23-181C9 on chromosome 2 Contains a
pseudogene similar to part of ring finger and WD repeat
domain 2 (Rfwd2) and the 5' end of a novel gene, complete
sequence
Length = 184254

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 266 gtttatttaagaaaataaaa 286

|||||
Sbjct: 56693 gtttatttaaagaaaataaaa 56713

>emb|AL669898.17| Mouse DNA sequence from clone RP23-6C3 on chromosome X Contains a novel pseudogene, the 5' end of a novel gene, a heat shock protein 9A (Hspa9a) pseudogene, a ribosomal protein L7a (Rpl7a) pseudogene, a farnesyl diphosphate synthetase (Fdps) pseudogene and one CpG island, complete sequence
Length = 220201

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 263 ttagtttatttaaagaaaataaaaagtt 291
|||||
Sbjct: 102002 ttagtttatttaaagaaaataaaaagtt 101974

>gb|AE008384.1| Methanosarcina mazei strain Goel, complete genome
Length = 4096345

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttta 951
|||||
Sbjct: 1964887 tatttcaaaaaatatttttta 1964907

>emb|AL391158.5| Human chromosome 14 DNA sequence BAC R-560013 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence
Length = 202792

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 939 aaaatattttttatgtctttc 959
|||||
Sbjct: 141390 aaaatattttttatgtctttc 141370

>dbj|AB061780.1| Clostridium botulinum orf-22, ha-70, ha-17, ha-33, ntnha, nt genes

for ORF-22, HA-70, HA-17, HA-33, NTNHA, neurotoxin,
complete cds
Length = 11747

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1059 ataaattcttatattatgt 1079
|||||||
Sbjct: 2666 ataaattcttatattatgt 2646

>emb|AL132951.3| Caenorhabditis elegans YAC Y67H2A, complete sequence
Length = 57745

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 15 ttttaattcttaaactttattaaat 39
|||||||
Sbjct: 12667 ttttaattcttaaactttattaaat 12691

>dbj|AB012112.1| Clostridium botulinum D phage gene for ORF-22, HA3, HA2, HA1, NTNH,
NTX, complete and partial sequence
Length = 11584

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1059 ataaattcttatattatgt 1079
|||||||
Sbjct: 2688 ataaattcttatattatgt 2668

>dbj|AB012111.1| Clostridium botulinum D phage gene for ORF-22, HA3, HA2, HA1, NTNH,
complete and partial sequence
Length = 4525

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1059 ataaattcttatattatatgt 1079
 |||||
Sbjct: 2791 ataaattcttatattatatgt 2771

>gb|AC005548.1|AC005548 Homo sapiens chromosome 17, clone hRPK.756_K_11, complete sequence
 Length = 156811

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 737 gagaaattaactttttgtttttaa 761
 |||||
Sbjct: 101272 gagaaaataactttttgtttttaa 101296

>gb|L22534.1|GALLHP82Z Galleria mellonella hexamerin (Lhp82) gene, exons 1-6
 Length = 9420

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 917 taaaaaattattcctatttcaaaaa 941
 |||||
Sbjct: 6455 taaaaaatattcctatttcaaaaa 6479

Database: /usr/local/blast/db/blastlibs/nt
Posted date: Feb 13, 2010 7:27 AM
Number of letters in database: 30,212,464,392
Number of sequences in database: 10,930,266

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 10930266
Number of Hits to DB: 418,746,764

Number of extensions: 32796916
Number of successful extensions: 1090417
Number of sequences better than 10.0: 251
Number of HSP's gapped: 1090417
Number of HSP's successfully gapped: 254
Length of query: 1082
Length of database: 30,212,464,392
Length adjustment: 23
Effective length of query: 1059
Effective length of database: 29,961,068,274
Effective search space: 31728771302166
Effective search space used: 31728771302166
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 50 (99.1 bits)
S1: 14 (28.2 bits)
S2: 21 (42.1 bits)

BLASTn Output of the 3' Border Sequences Flanking the Insert in Soybean Event DAS-68416-4 against GeneBank No_human and No_mouse ESTs (est_others)

BLASTN 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Query= 68416_3_border
(1082 letters)

Database: /usr/local/blast/db/blastlibs/est_others
51,680,690 sequences; 29,218,461,503 total letters

Searching..... done

		Score	E
Sequences producing significant alignments:		(bits)	Value
emb	FM898080.1 FM898080 MS (sb101) Brachionus plicatilis cDNA c...	48	0.10
emb	FM898359.1 FM898359 MS (sb101) Brachionus plicatilis cDNA c...	48	0.10
emb	FM927614.1 FM927614 REH (sb103) Brachionus plicatilis cDNA ...	48	0.10
emb	FM924849.1 FM924849 REH (sb103) Brachionus plicatilis cDNA ...	48	0.10
emb	FM913370.1 FM913370 RE (sb102) Brachionus plicatilis cDNA c...	48	0.10
gb	FD053629.1 CBPO2606.b1 CBPO: Normalized channel catfish cDNA...	46	0.40
gb	ES577805.1 FPS016.C7_I22 LSG10-01 Lymnaea stagnalis cDNA clo...	46	0.40
gb	EH469861.1 FDR103-P00035-DEPE-R_A05 FDR103 Danio rerio cDNA ...	46	0.40
gb	GW128346.1 CABF3044.b1 CABF Amphimedon queenslandica release...	44	1.6
gb	GR579840.1 CBZY2359.b1 CBZY Dictyostelium purpureum 18 hr st...	44	1.6
gb	GR571694.1 CBTG2131.g1 CBTG Dictyostelium purpureum 12 hr ve...	44	1.6
gb	GR569517.1 CBTF493.g1 CBTF Dictyostelium purpureum 12 hr veg...	44	1.6
emb	FM898411.1 FM898411 MS (sb101) Brachionus plicatilis cDNA c...	44	1.6
gb	EG296472.1 MSAM275665_3153_3889 LCM-dissected maize inbred l...	44	1.6
gb	FC660687.1 CAXW1786.fwd CAXW Lottia gigantea from female gon...	44	1.6
gb	EY322309.1 CAWX8378.fwd CAWX Helobdella robusta Primary Earl...	44	1.6
gb	EL503163.1 F09_PFLAB1-M-PLATE11B.AB1 Blood stage Plasmodium ...	44	1.6
gb	EE473560.1 BNYS2DCT_UP_002_G01_27FEB2005_003 Brassica napus ...	44	1.6
gb	DW737772.1 MSAM049071_0042_0724 LCM-dissected maize shoot ap...	44	1.6
gb	DW273902.1 UI-S-GS1-acu-g-13-0-UI.s1 UI-S-GS1 Euprymna scol...	44	1.6
gb	BE682501.1 180577 MARC 4BOV Bos taurus cDNA 5', mRNA sequence	44	1.6
gb	GW128347.1 CABF3044.g1 CABF Amphimedon queenslandica release...	42	6.2
gb	GT905149.1 CBWA5555.b1 CBWA Piromyces sp. E2 fungal mat and ...	42	6.2
gb	GT905946.1 CBWA6101.b1 CBWA Piromyces sp. E2 fungal mat and ...	42	6.2
gb	GT899067.1 CBWA1102.b1 CBWA Piromyces sp. E2 fungal mat and ...	42	6.2

gb G0898162.1	hsxao_0013_A09.ab1 cucumber stamen suppression su...	42	6.2
gb G0632170.1	EST_afim_evh_929871 afimevh mixed_tissue Anoplopo...	42	6.2
gb G0632169.1	EST_afim_evh_929103 afimevh mixed_tissue Anoplopo...	42	6.2
gb G0619033.1	EST_afim_evh_744874 afimevh mixed_tissue Anoplopo...	42	6.2
gb G0616757.1	EST_afim_evh_740424 afimevh mixed_tissue Anoplopo...	42	6.2
gb G0290381.1	CAXN8486.rev CAXN Teleopsis dalmanni Late larval ...	42	6.2
gb GE815430.1	EST_scau_evk_976152 scauevk mixed_tissue Sebastes...	42	6.2
gb FE945836.1	Sma-USC-EA-2734 S. maximus Aeromonas cDNA library...	42	6.2
emb FM141483.1	FM141483 etnokid Rattus norvegicus cDNA clone et...	42	6.2
dbj DC436761.1	DC436761 epM- Bombyx mori cDNA clone E_FL_epM-1...	42	6.2
gb FD375664.1	CBPN7243.g1 CBPN: Subtracted channel catfish cDNA...	42	6.2
dbj DC567981.1	DC567981 wd-- Bombyx mori cDNA clone E_FL_wd--1...	42	6.2
gb FK484441.1	454GmaGlobSeed219073 Soybean Seeds Containing Glo...	42	6.2
gb FG146004.1	AGN_RPC010xgl17f1.ab1 AGN_RPC Nicotiana tabacum cD...	42	6.2
dbj DK032256.1	DK032256 OLBR Oryzias latipes cDNA clone olbr29a...	42	6.2
dbj DK030432.1	DK030432 OLBR Oryzias latipes cDNA clone olbr23m...	42	6.2
gb FD480788.1	NADI-aaa35b01.g1 Rhodnius prolixus_EST_NADI_5th_i...	42	6.2
gb FC800453.1	CBGC3708.fwd CBGC Lottia gigantea 15h 18h embryos...	42	6.2
gb FC796037.1	CBGC23939.fwd CBGC Lottia gigantea 15h 18h embryo...	42	6.2
gb FC796036.1	CBGC23939.rev CBGC Lottia gigantea 15h 18h embryo...	42	6.2
gb FC782133.1	CBGC13519.rev CBGC Lottia gigantea 15h 18h embryo...	42	6.2
gb FC777700.1	CBGC10606.fwd CBGC Lottia gigantea 15h 18h embryo...	42	6.2
gb FC766135.1	CBBN2940.rev CBBN Lottia gigantea 3, 4, 5, 6. 5d Larv...	42	6.2
gb FC753028.1	CBBI6751.rev CBBI Lottia gigantea 26h, 37h, 61h Lar...	42	6.2
gb FC756058.1	CBBI9130.rev CBBI Lottia gigantea 26h, 37h, 61h Lar...	42	6.2
gb FC735597.1	CBBG9775.rev CBBG Lottia gigantea 12, 15, 18h embry...	42	6.2
gb FC731985.1	CBBG6977.rev CBBG Lottia gigantea 12, 15, 18h embry...	42	6.2
gb EY387612.1	CAXA6853.fwd CAXA Helobdella robusta Subtracted L...	42	6.2
gb EY381443.1	CAXA3466.fwd CAXA Helobdella robusta Subtracted L...	42	6.2
gb EY369837.1	CAXA12577.fwd CAXA Helobdella robusta Subtracted ...	42	6.2
gb EL503377.1	G09_PFLAB1-LARGE-PLATE11B.AB1 Blood stage Plasmod...	42	6.2
gb ES451332.1	26302 Myzus persicae 2001-12 (red), Fenton Myzus ...	42	6.2
gb ES389027.1	MUS07-B22.yld-s SHGC-MUS Mytilus californianus cD...	42	6.2
gb EB332296.1	CNSN01-F-138072-501 Normalized CNS library (juven...	42	6.2
gb EB304551.1	CNSN01-F-064136-501 Normalized CNS library (juven...	42	6.2
gb EB293882.1	CNSN01-F-043505-501 Normalized CNS library (juven...	42	6.2
gb EH367395.1	D04_j001_plate_103 j001 Nicotiana benthamiana cDN...	42	6.2
dbj DC106228.1	DC106228 Yamamoto/Hyodo-Miura NIBB/NBRP Xenopus ...	42	6.2
dbj DC006569.1	DC006569 Osada Taira anterior endomesoderm (AEM)...	42	6.2
gb DW756131.1	MSAM097773_1318_0782 LCM-dissected maize shoot ap...	42	6.2
emb CU072018.1	CU072018 AGENAE Rainbow trout multi-tissues libr...	42	6.2
dbj DB762915.1	DB762915 RIKEN full-length enriched honey bee cD...	42	6.2
dbj DB767567.1	DB767567 RIKEN full-length enriched honey bee cD...	42	6.2
dbj BB982965.1	BB982965 ovS3 Bombyx mori cDNA clone ovS3014B06r...	42	6.2
dbj BB982491.1	BB982491 ovS3 Bombyx mori cDNA clone ovS3007D09r...	42	6.2
gb EC327493.1	GUTF089549D10 POSSUM_01-POSSUM-GUT-2KB Trichosuru...	42	6.2
gb EC272309.1	TT1BV58TV Tetrahymena thermophila SB210 cDNA libr...	42	6.2
gb EC226765.1	410398 CK01 Drosophila melanogaster cDNA clone 15...	42	6.2
gb EC215214.1	410484 CK01 Drosophila melanogaster cDNA clone 15...	42	6.2

dbj DB393193.1	DB393193 APE Asterina pectinifera unfertilized e...	42	6.2
dbj BY919518.1	BY919518 fcP8 Bombyx mori cDNA clone E_EL_fcP8_1...	42	6.2
gb DY231459.1	EST02214 BmP Bombyx mori cDNA clone BmpM13_E09 3'...	42	6.2
gb DY230884.1	EST01628 BmP Bombyx mori cDNA clone BmpC_C53R_200...	42	6.2
gb DY227165.1	ID0AAK10YF21CM1 ApHL3SD Acyrthosiphon pisum cDNA ...	42	6.2
gb DV791356.1	Hw_liver_61_050822_A05 Bos taurus CF-24-HW liver ...	42	6.2
gb DV691543.1	CGN-35248 Leaf Coffea canephora cDNA clone cccl15...	42	6.2
gb DV280402.1	NAAGL61TF Aedes aegypti - Fat Bodies Normalized (...)	42	6.2
gb DT954953.1	CFW136-D04.y1d-s SHGC-CFW Gasterosteus aculeatus ...	42	6.2
gb DT280951.1	JGI_CAAV9522.rev CAAV Pimephales promelas testis ...	42	6.2
gb DR769667.1	ILLUMIGEN_MCQ_63477 Katze_MMTE Macaca mulatta cDN...	42	6.2
emb AJ926041.1	AJ926041 Theileria annulata merozoite Theileria ...	42	6.2
gb CV503593.1	70065.1 Mixed Floral Solanum tuberosum cDNA clone...	42	6.2
gb C0315764.1	EK262410.5prime Exelixis FlyTag CK01 pCDNA-SK+ Dr...	42	6.2
gb C0284895.1	EK167420.5prime Exelixis FlyTag CK01 pCDNA-SK+ Dr...	42	6.2
gb CN575474.1	rc41b03.x1 Meloidogyne hapla egg pAMP1 v1 Meloido...	42	6.2
gb CN574214.1	rc04h06.x1 Meloidogyne hapla egg pAMP1 v1 Meloido...	42	6.2
gb CN573213.1	rc15f08.x1 Meloidogyne hapla egg pAMP1 v1 Meloido...	42	6.2
gb CK550790.1	swkz0_009396.z1 swk Bombyx mori cDNA, mRNA sequence	42	6.2
dbj AU260586.1	AU260586 Paralichthys olivaceus kidney adult Par...	42	6.2
gb CK427090.1	r171c02.y1 Meloidogyne javanica J2 SL1 pGEM Meloi...	42	6.2
gb CF980407.1	re04e06.y1 Meloidogyne incognita female SL1 pGEM ...	42	6.2
gb CF803136.1	rd94e05.y1 Meloidogyne incognita female SL1 pGEM ...	42	6.2
dbj BP181391.1	BP181391 ovS3 Bombyx mori cDNA clone ovS327G04f ...	42	6.2
dbj BP180165.1	BP180165 ovS3 Bombyx mori cDNA clone ovS312A08f ...	42	6.2
gb CF522058.1	AGENCOURT_15528907 NICHD_XGC_Kid1 Xenopus laevis ...	42	6.2
gb CB196840.2	AGENCOURT_11244860 NICHD_XGC_Tad2 Xenopus laevis ...	42	6.2
dbj BJ080944.1	BJ080944 NIBB Mochii normalized Xenopus tailbud ...	42	6.2
dbj BJ079923.1	BJ079923 NIBB Mochii normalized Xenopus tailbud ...	42	6.2
gb BI974397.1	saj01b04.y1 Gm-c1065 Glycine max cDNA clone GENOM...	42	6.2
gb BI747251.1	rm37g11.y1 Meloidogyne arenaria egg pAMP1 v1 Chia...	42	6.2
gb AW942998.1	LD29917.3prime LD Drosophila melanogaster embryo ...	42	6.2
gb AW441094.1	ra06b06.y1 Bird-Rao Meloidogyne incognita J2 Melo...	42	6.2

>emb|FM898080.1| FM898080 MS (sb101) Brachionus plicatilis cDNA clone sb101P0003A04
5', mRNA sequence
Length = 496

Score = 48.1 bits (24), Expect = 0.10
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagttaattt 296
||||||| |||||||||||||||||
Sbjct: 459 tatttaaaaaaataaaaaagttaattt 432

>emb|FM898359.1| FM898359 MS (sb101) Brachionus plicatilis cDNA clone sb101P0003M07

5', mRNA sequence
Length = 521

Score = 48.1 bits (24), Expect = 0.10
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagttaattt 296
 ||||||| |
Sbjct: 460 tatttaaaaaaataaaaaagttaattt 433

>emb|FM927614.1| FM927614 REH (sb103) Brachionus plicatilis cDNA clone sb103P0027M11
5', mRNA sequence
Length = 522

Score = 48.1 bits (24), Expect = 0.10
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagttaattt 296
 ||||||| |
Sbjct: 460 tatttaaaaaaataaaaaagttaattt 433

>emb|FM924849.1| FM924849 REH (sb103) Brachionus plicatilis cDNA clone sb103P0018F21
5', mRNA sequence
Length = 418

Score = 48.1 bits (24), Expect = 0.10
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagttaattt 296
 ||||||| |
Sbjct: 368 tatttaaaaaaataaaaaagttaattt 341

>emb|FM913370.1| FM913370 RE (sb102) Brachionus plicatilis cDNA clone sb102P0013J07
5', mRNA sequence
Length = 520

Score = 48.1 bits (24), Expect = 0.10
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagttaattt 296
 ||||||| |||||||||||||||||
Sbjct: 459 tatttaaaaaataaaaaagttaattt 432

>gb|FD053629.1| CBP02606.b1 CBP0: Normalized channel catfish cDNA library from
LPS-stimulated peripheral blood leukocytes (JxLPS1)
Ictalurus punctatus cDNA 5', mRNA sequence
Length = 729

Score = 46.1 bits (23), Expect = 0.40
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagtt 291
 ||||||| |||||||||||||||||
Sbjct: 419 tatttaaagaaaataaaaaagtt 397

>gb|ES577805.1| FPS016.C7_I22 LSG10-01 Lymnaea stagnalis cDNA clone FPS016_I22 3',
mRNA sequence
Length = 870

Score = 46.1 bits (23), Expect = 0.40
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 266 gtttatttaagaaaataaaaaa 288
 ||||||| |||||||||||||||||
Sbjct: 188 gtttatttaagaaaataaaaaa 210

>gb|EH469861.1| FDR103-P00035-DEPE-R_A05 FDR103 Danio rerio cDNA clone
FDR103-P00035-BR_A05 3', mRNA sequence
Length = 740

Score = 46.1 bits (23), Expect = 0.40
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 1049 agaaaaataaataaatccttatattatgt 1079
 ||||||| ||||| |||||
Sbjct: 362 agaaaaataaataaatccttatattatgt 392

>gb|GW128346.1| CABF3044.b1 CABF Amphimedon queenslandica released competent larvae
Amphimedon queenslandica cDNA clone CABF3044 5', mRNA
sequence
Length = 389

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 931 tatttcaaaaaatattttttat 952
|||||
Sbjct: 388 tatttcaaaaaatattttttat 367

>gb|GR579840.1| CBZY2359.b1 CBZY Dictyostelium purpureum 18 hr starvation induced
multicellular development (H) Dictyostelium purpureum
cDNA clone CBZY2359 5', mRNA sequence
Length = 700

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 267 tttatttaagaaaataaaaaa 288
|||||
Sbjct: 70 tttatttaagaaaataaaaaa 49

>gb|GR571694.1| CBTG2131.g1 CBTG Dictyostelium purpureum 12 hr vegetative phase for
Dictyostelium discoideum (L) Dictyostelium purpureum
cDNA clone CBTG2131 3', mRNA sequence
Length = 625

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 267 tttatttaagaaaataaaaaa 288
|||||
Sbjct: 66 tttatttaagaaaataaaaaa 45

>gb|GR569517.1| CBTF493.g1 CBTF Dictyostelium purpureum 12 hr vegetative phase for
Dictyostelium discoideum (H) Dictyostelium purpureum
cDNA clone CBTF493 3', mRNA sequence
Length = 739

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 267 tttatttaaagaaaataaaaaa 288
 |||||
Sbjct: 59 tttatttaaagaaaataaaaaa 38

>emb|FM898411.1| FM898411 MS (sb101) Brachionus plicatilis cDNA clone sb101P0003017
 5', mRNA sequence
 Length = 517

Score = 44.1 bits (22), Expect = 1.6
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagttaat 294
 |||||
Sbjct: 459 tatttaaaaaataaaaaagttaat 434

>gb|EG296472.1| MSAM275665_3153_3889 LCM-dissected maize inbred line Mo17 shoot
 apical meristem cDNA Zea mays cDNA, mRNA sequence
 Length = 114

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 14 attttaattcttaactttatt 35
 |||||
Sbjct: 55 attttaattcttaactttatt 34

>gb|FC660687.1| CAXW1786.fwd CAXW Lottia gigantea from female gonad Lottia gigantea
 cDNA clone CAXW1786 5', mRNA sequence
 Length = 151

Score = 44.1 bits (22), Expect = 1.6
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 919 aaaaattattcctatttcaaaaaata 944

|||||
Sbjct: 6 aaaaattattcctatttttaaaaaata 31

>gb|EY322309.1| CAWX8378.fwd CAWX Helobdella robusta Primary Early Library, Embryo
st. 1-6 Helobdella robusta cDNA clone CAWX8378 5', mRNA
sequence
Length = 822

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatattttttat 952
|||||
Sbjct: 34 tatttcaaaaaatattttttat 55

>gb|EL503163.1| F09_PFLAB1-M-PLATE11B.AB1 Blood stage Plasmodium falciparum cDNA
library PfSuOrig Plasmodium falciparum 3D7 cDNA, mRNA
sequence
Length = 477

Score = 44.1 bits (22), Expect = 1.6
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 263 ttagttttatttaaagaaaataaaaaa 288
|||||
Sbjct: 30 ttagttttatttaaagataataaaaaa 55

>gb|EE473560.1| BNYS2DCT_UP_002_G01_27FEB2005_003 Brassica napus seeds BNYS2DCT
Brassica napus cDNA 5', mRNA sequence
Length = 624

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaaa 764
|||||
Sbjct: 577 ttaactttttgttttttaaaaa 598

>gb|DW737772.1| MSAM049071_0042_0724 LCM-dissected maize shoot apical meristem cDNA

Zea mays cDNA, mRNA sequence
Length = 137

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 14 attttaattcttaaactttatt 35
 |||||
Sbjct: 123 attttaattcttaaactttatt 102

>gb|DW273902.1| UI-S-GS1-acu-g-13-0-UI.s1 UI-S-GS1 Euprymna scolopes cDNA clone
 UI-S-GS1-acu-g-13-0-UI 3', mRNA sequence
 Length = 546

Score = 44.1 bits (22), Expect = 1.6
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 917 taaaaaattattcctatttcaaaaa 942
 |||||
Sbjct: 38 taaaaaattattcctatttcaaaaa 13

>gb|BE682501.1| 180577 MARC 4BOV Bos taurus cDNA 5', mRNA sequence
 Length = 307

Score = 44.1 bits (22), Expect = 1.6
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaagttaa 293
 |||||
Sbjct: 203 ttatttaaataaaaaataaaaaagttaa 228

>gb|GW128347.1| CABF3044.g1 CABF Amphimedon queenslandica released competent larvae
 Amphimedon queenslandica cDNA clone CABF3044 3', mRNA
 sequence
 Length = 389

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 932 atttcaaaaaatattttttat 952
 |||||
Sbjct: 3 atttcaaaaaatattttttat 23

>gb|GT905149.1| CBWA5555.b1 CBWA Piromyces sp. E2 fungal mat and spores Piromyces
 sp. E2 cDNA clone CBWA5555 5', mRNA sequence
 Length = 645

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaa 288
 |||||
Sbjct: 158 ttatttaaagaaaataaaaaa 178

>gb|GT905946.1| CBWA6101.b1 CBWA Piromyces sp. E2 fungal mat and spores Piromyces
 sp. E2 cDNA clone CBWA6101 5', mRNA sequence
 Length = 566

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaa 288
 |||||
Sbjct: 158 ttatttaaagaaaataaaaaa 178

>gb|GT899067.1| CBWA1102.b1 CBWA Piromyces sp. E2 fungal mat and spores Piromyces
 sp. E2 cDNA clone CBWA1102 5', mRNA sequence
 Length = 648

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaa 288
 |||||
Sbjct: 162 ttatttaaagaaaataaaaaa 182

>gb|G0898162.1| hsxao_0013_A09.ab1 cucumber stamen suppression subtractive

hybridization Cucumis sativus cDNA, mRNA sequence
Length = 538

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1047 agagaaaaataataaattct 1067
 |||||
Sbjct: 464 agagaaaaataataaattct 484

>gb|G0632170.1| EST_afim_evh_929871 afimevh mixed_tissue Anoplopoma fimbria cDNA
 Anoplopoma fimbria cDNA clone afim_evh_511_111 3', mRNA
 sequence
 Length = 630

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttatttaaagaaaataaaaa 287
 |||||
Sbjct: 26 tttatttaaagaaaataaaaa 46

>gb|G0632169.1| EST_afim_evh_929103 afimevh mixed_tissue Anoplopoma fimbria cDNA
 Anoplopoma fimbria cDNA clone afim_evh_511_111 5', mRNA
 sequence
 Length = 630

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 267 tttatttaaagaaaataaaaa 287
 |||||
Sbjct: 605 tttatttaaagaaaataaaaa 585

>gb|G0619033.1| EST_afim_evh_744874 afimevh mixed_tissue Anoplopoma fimbria cDNA
 Anoplopoma fimbria cDNA clone afim_evh_006_106 3', mRNA
 sequence
 Length = 534

Score = 42.1 bits (21), Expect = 6.2

Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttatttaaagaaaataaaaa 287
 |||||
Sbjct: 16 tttatttaaagaaaataaaaa 36

>gb|G0616757.1| EST_afim_evh_740424 afimevh mixed_tissue Anoplopoma fimbria cDNA
Anoplopoma fimbria cDNA clone afim_evh_002_264 3', mRNA
sequence
Length = 748

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttatttaaagaaaataaaaa 287
 |||||
Sbjct: 16 tttatttaaagaaaataaaaa 36

>gb|G0290381.1| CAXN8486.rev CAXN Teleopsis dalmanni Late larval eye-antennal disc
EST library Teleopsis dalmanni cDNA clone CAXN8486 3',
mRNA sequence
Length = 681

Score = 42.1 bits (21), Expect = 6.2
Identities = 33/37 (89%)
Strand = Plus / Minus

Query: 917 taaaaaattattcctatttcaaaaatattttttatg 953
 ||||| | |||| | |||||
Sbjct: 104 taaaaaattatttcaatttaacaaaatattttttatg 68

>gb|GE815430.1| EST_scau_evk_976152 scauevk mixed_tissue Sebastes caurinus cDNA
Sebastes caurinus cDNA clone scau_evk_513_312 3', mRNA
sequence
Length = 840

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttatttaaagaaaataaaaa 287
 |||||
Sbjct: 32 tttatttaaagaaaataaaaa 52

>gb|FE945836.1| Sma-USC-EA-2734 *S. maximus* Aeromonas cDNA library Psetta maxima
cDNA 3', mRNA sequence
Length = 169

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 267 tttatttaaagaaaataaaaa 287
 |||||
Sbjct: 138 tttatttaaagaaaataaaaa 118

>emb|FM141483.1| FM141483 etnokid *Rattus norvegicus* cDNA clone etnokidP0065H24 5',
mRNA sequence
Length = 693

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 917 taaaaaattattcctatttca 937
 |||||
Sbjct: 448 taaaaaattattcctatttca 428

>dbj|DC436761.1| DC436761 epM- *Bombyx mori* cDNA clone E_FL_epM-_16P19_F_0 5', mRNA
sequence
Length = 628

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctatttaagtatattt 994
 |||||
Sbjct: 516 aatatctatttaagtatattt 536

>gb|FD375664.1| CBPN7243.g1 CBPN: Subtracted channel catfish cDNA library from
liver, pituitary, ovary and testes (Mixed tissue library)

5, MTL5) Ictalurus punctatus cDNA 3', mRNA sequence
Length = 647

Score = 42.1 bits (21), Expect = 6.2
Identities = 27/29 (93%)
Strand = Plus / Plus

Query: 737 gagaaattaactttttgttttttaaaaac 765
 ||||| ||||||| |||||||
Sbjct: 157 gagaaataacttttttttttaaaaac 185

>dbj|DC567981.1| DC567981 wd-- Bombyx mori cDNA clone E_FL_wd--_13K20_R_0 3', mRNA
 sequence
 Length = 560

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 974 aatatctathtaagtatattt 994
 |||||
Sbjct: 178 aatatctathtaagtatattt 158

>gb|FK484441.1| 454GmaGlobSeed219073 Soybean Seeds Containing Globular-Stage
 Embryos Glycine max cDNA, mRNA sequence
 Length = 216

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 267 tttathtaagaaaataaaaa 287
 |||||
Sbjct: 48 tttathtaagaaaataaaaa 28

>gb|FG146004.1| AGN_RPC010xg17f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA
 sequence
 Length = 883

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 933 tttcaaaaaatattttttatg 953
 |||||
Sbjct: 41 tttcaaaaaatattttttatg 61

>dbj|DK032256.1| DK032256 OLBR Oryzias latipes cDNA clone olbr29a11 3', mRNA
 sequence
 Length = 934

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 740 aaattaactttttgtttttta 760
 |||||
Sbjct: 338 aaattaactttttgtttttta 318

>dbj|DK030432.1| DK030432 OLBR Oryzias latipes cDNA clone olbr23m13 3', mRNA
 sequence
 Length = 921

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 740 aaattaactttttgtttttta 760
 |||||
Sbjct: 338 aaattaactttttgtttttta 318

>gb|FD480788.1| NADI-aaa35b01.g1 Rhodnius prolixus_EST_NADI_5th_instar_CNS Rhodnius
 prolixus cDNA 5', mRNA sequence
 Length = 540

Score = 42.1 bits (21), Expect = 6.2
Identities = 27/29 (93%)
Strand = Plus / Plus

Query: 270 atttaaaagaaaaataaaaaagttaatttct 298
 ||||| |||| |
Sbjct: 388 atttaaaaaaaataaaaaagttaatttct 416

>gb|FC800453.1| CBGC3708.fwd CBGC Lottia gigantea 15h 18h embryos Lottia gigantea

cdna clone CBGC3708 5', mRNA sequence
Length = 842

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 935 tcaaaaaatattttttatgtctttc 959
||||| ||||||||||||||||||||
Sbjct: 618 tcaaagaatattttttatgtctttc 642

>gb|FC796037.1| CBGC23939.fwd CBGC Lottia gigantea 15h 18h embryos Lottia gigantea
cdna clone CBGC23939 5', mRNA sequence
Length = 693

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 935 tcaaaaaatattttttatgtctttc 959
||||| ||||||||||||||||||||
Sbjct: 511 tcaaagaatattttttatgtctttc 535

>gb|FC796036.1| CBGC23939.rev CBGC Lottia gigantea 15h 18h embryos Lottia gigantea
cdna clone CBGC23939 3', mRNA sequence
Length = 628

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaatattttttatgtctttc 959
||||| ||||||||||||||||||||
Sbjct: 376 tcaaagaatattttttatgtctttc 352

>gb|FC782133.1| CBGC13519.rev CBGC Lottia gigantea 15h 18h embryos Lottia gigantea
cdna clone CBGC13519 3', mRNA sequence
Length = 721

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaaatatTTTTTatgtctttc 959
||||| ||||||||||||||||||
Sbjct: 398 tcaagaatTTTTTatgtctttc 374

>gb|FC777700.1| CBGC10606.fwd CBGC Lottia gigantea 15h 18h embryos Lottia gigantea
cDNA clone CBGC10606 5', mRNA sequence
Length = 693

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 935 tcaaaaaaatatTTTTTatgtctttc 959
||||| ||||||||||||||||||
Sbjct: 293 tcaagaatTTTTTatgtctttc 317

>gb|FC766135.1| CBBN2940.rev CBBN Lottia gigantea 3, 4, 5, 6.5d Larvae (M) Lottia
gigantea cDNA clone CBBN2940 3', mRNA sequence
Length = 725

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaaatatTTTTTatgtctttc 959
||||| ||||||||||||||||||
Sbjct: 400 tcaagaatTTTTTatgtctttc 376

>gb|FC753028.1| CBBI6751.rev CBBI Lottia gigantea 26h, 37h, 61h Larvae (L) Lottia
gigantea cDNA clone CBBI6751 3', mRNA sequence
Length = 720

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaaatatTTTTTatgtctttc 959
||||| ||||||||||||||||||
Sbjct: 399 tcaagaatTTTTTatgtctttc 375

>gb|FC756058.1| CBBI9130.rev CBBI Lottia gigantea 26h, 37h, 61h Larvae (L) Lottia

gigantea cDNA clone CBBI9130 3', mRNA sequence
Length = 774

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaatattttttatgtctttc 959
||||| ||||||||||||||||||||
Sbjct: 400 tcaaagaatattttttatgtctttc 376

>gb|FC735597.1| CBBG9775.rev CBBG Lottia gigantea 12,15,18h embryos Lottia gigantea
cDNA clone CBBG9775 3', mRNA sequence
Length = 745

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaatattttttatgtctttc 959
||||| ||||||||||||||||||||
Sbjct: 398 tcaaagaatattttttatgtctttc 374

>gb|FC731985.1| CBBG6977.rev CBBG Lottia gigantea 12,15,18h embryos Lottia gigantea
cDNA clone CBBG6977 3', mRNA sequence
Length = 710

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaatattttttatgtctttc 959
||||| ||||||||||||||||||||
Sbjct: 398 tcaaagaatattttttatgtctttc 374

>gb|EY387612.1| CAXA6853.fwd CAXA Helobdella robusta Subtracted Late Library,
Embryo st. 7-11 Helobdella robusta cDNA clone CAXA6853
5', mRNA sequence
Length = 747

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 274 aaagaaaataaaaaagttaat 294
 |||||
Sbjct: 25 aaagaaaataaaaaagttaat 45

>gb|EY381443.1| CAXA3466.fwd CAXA Helobdella robusta Subtracted Late Library,
 Embryo st. 7-11 Helobdella robusta cDNA clone CAXA3466
 5', mRNA sequence
 Length = 832

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 274 aaagaaaataaaaaagttaat 294
 |||||
Sbjct: 48 aaagaaaataaaaaagttaat 68

>gb|EY369837.1| CAXA12577.fwd CAXA Helobdella robusta Subtracted Late Library,
 Embryo st. 7-11 Helobdella robusta cDNA clone CAXA12577
 5', mRNA sequence
 Length = 750

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 274 aaagaaaataaaaaagttaat 294
 |||||
Sbjct: 23 aaagaaaataaaaaagttaat 43

>gb|EL503377.1| G09_PFLAB1-LARGE-PLATE11B.AB1 Blood stage Plasmodium falciparum
 cDNA library PfSuOrig Plasmodium falciparum 3D7 cDNA,
 mRNA sequence
 Length = 468

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 843 ttctcaccatatttattattatata 867
 |||||

Sbjct: 76 ttctcacaatattttattattatata 52

>gb|ES451332.1| 26302 Myzus persicae 2001-12 (red), Fenton Myzus persicae cDNA clone
GMAWCDNA60_D10_D10_037 5', mRNA sequence
Length = 506

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1052 aaaataaataaattcttatat 1072
|||||
Sbjct: 385 aaaataaataaattcttatat 365

>gb|ES389027.1| MUS07-B22.y1d-s SHGC-MUS Mytilus californianus cDNA 3', mRNA
sequence
Length = 925

Score = 42.1 bits (21), Expect = 6.2
Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 736 agagaaattaactttttgttttttaaaaa 764
|||||
Sbjct: 557 agagaaattaactttttgttttttaaaaa 529

>gb|EB332296.1| CNSN01-F-138072-501 Normalized CNS library (juvenile 1) Aplysia
californica cDNA clone CNSN01-F-138072 5', mRNA sequence
Length = 604

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 267 tttatttaagaaaaataaaaaagtt 291
|||||
Sbjct: 318 tttatttaagaaaaataaaaaagtt 294

>gb|EB304551.1| CNSN01-F-064136-501 Normalized CNS library (juvenile 1) Aplysia
californica cDNA clone CNSN01-F-064136 5', mRNA sequence
Length = 543

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 267 tttattttaagaaaataaaaaagtt 291
 |||||
Sbjct: 284 tttattttaagaaaataagaaagtt 260

>gb|EB293882.1| CNSN01-F-043505-501 Normalized CNS library (juvenile 1) Aplysia
californica cDNA clone CNSN01-F-043505 5', mRNA sequence
Length = 608

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 267 tttattttaagaaaataaaaaagtt 291
 |||||
Sbjct: 336 tttattttaagaaaataagaaagtt 312

>gb|EH367395.1| D04_j001_plate_103 j001 Nicotiana benthamiana cDNA 5' similar to
unknown function, mRNA sequence
Length = 113

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 267 tttattttaagaaaataaaaa 287
 |||||
Sbjct: 71 tttattttaagaaaataaaaa 51

>dbj|DC106228.1| DC106228 Yamamoto/Hyodo-Miura NIBB/NBRP Xenopus DMZ pCS2p+ cDNA
library Xenopus laevis cDNA clone xl241k05 5', mRNA
sequence
Length = 740

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaa 763

|||||
Sbjct: 184 ttaactttttgttttttaaaa 204

>dbj|DC006569.1| DC006569 Osada Taira anterior endomesoderm (AEM) pCS105 cDNA
library Xenopus laevis cDNA clone rxlk112c20ex 3', mRNA
sequence
Length = 815

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 743 ttaactttttgttttttaaaa 763
|||||
Sbjct: 139 ttaactttttgttttttaaaa 119

>gb|DW756131.1| MSAM097773_1318_0782 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 109

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 264 tagtttatttaagaaaataaaaaa 288
|||||
Sbjct: 35 tagtttatttaaaaaataaaaaa 11

>emb|CU072018.1| CU072018 AGENAE Rainbow trout multi-tissues library (tcce)
Oncorhynchus mykiss cDNA clone tcba0007.e.09 3', mRNA
sequence
Length = 972

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 265 agtttatttaagaaaataaa 285
|||||
Sbjct: 800 agtttatttaagaaaataaa 820

>dbj|DB762915.1| DB762915 RIKEN full-length enriched honey bee cDNA library, head Apis

mellifera cDNA clone BH10028M11 3', mRNA sequence
Length = 519

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1057 aaataaattcttatattatat 1077
|||||
Sbjct: 498 aaataaattcttatattatat 518

>dbj|DB767567.1| DB767567 RIKEN full-length enriched honey bee cDNA library, head
Apis mellifera cDNA clone BH10045D23 3', mRNA sequence
Length = 486

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 265 agtttattttaagaaaataaa 285
|||||
Sbjct: 345 agtttattttaagaaaataaa 325

>dbj|BB982965.1| BB982965 ovS3 Bombyx mori cDNA clone ovS3014B06r 3', mRNA sequence
Length = 435

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 974 aatatctatttaagtatattt 994
|||||
Sbjct: 184 aatatctatttaagtatattt 164

>dbj|BB982491.1| BB982491 ovS3 Bombyx mori cDNA clone ovS3007D09r 3', mRNA sequence
Length = 607

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 974 aatatctatttaagtatattt 994

|||||
Sbjct: 168 aatatctatttaagtatattt 148

>gb|EC327493.1| GUTF089549D10 POSSUM_01-POSSUM-GUT-2KB Trichosurus vulpecula cDNA
clone 1061024742945, mRNA sequence
Length = 843

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 278 aaaataaaaaagttaatttctcttt 302
|||||
Sbjct: 510 aaaaaaaaaagttaatttctcttt 486

>gb|EC272309.1| TT1BV58TV Tetrahymena thermophila SB210 cDNA library (starved)
Tetrahymena thermophila cDNA clone TT1BV58, mRNA
sequence
Length = 775

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 931 tatttcaaaaaatatttttta 951
|||||
Sbjct: 57 tatttcaaaaaatatttttta 37

>gb|EC226765.1| 410398 CK01 Drosophila melanogaster cDNA clone 159188, mRNA
sequence
Length = 440

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagt 290
|||||
Sbjct: 189 atttaaagaaaataaaaaagt 209

>gb|EC215214.1| 410484 CK01 Drosophila melanogaster cDNA clone 159120, mRNA
sequence

Length = 473

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagt 290
 |||||
Sbjct: 188 atttaaagaaaataaaaaagt 208

>dbj|DB393193.1| DB393193 APE Asterina pectinifera unfertilized egg cDNA library
 Patiria pectinifera cDNA clone ape24f18 5', mRNA sequence
 Length = 703

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1045 ttagagaaaataataaatt 1065
 |||||
Sbjct: 486 ttagagaaaataataaatt 466

>dbj|BY919518.1| BY919518 fcP8 Bombyx mori cDNA clone E_EL_fcP8_11B06_F_0 5', mRNA
 sequence
 Length = 814

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 974 aatatctathtaagtatattt 994
 |||||
Sbjct: 175 aatatctathtaagtatattt 155

>gb|DY231459.1| EST02214 BmP Bombyx mori cDNA clone BmpM13_E09 3', mRNA sequence
 Length = 402

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctathtaagtatattt 994

|||||
Sbjct: 215 aatatctatttaagtatattt 235

>gb|DY230884.1| EST01628 BmP Bombyx mori cDNA clone
BmpC_C53R_2005-09-11_WDOTHERS-050911 3', mRNA sequence
Length = 376

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctatttaagtatattt 994
|||||
Sbjct: 191 aatatctatttaagtatattt 211

>gb|DY227165.1| ID0AAK10YF21CM1 ApHL3SD Acyrthosiphon pisum cDNA clone ID0AAK10YF21
5', mRNA sequence
Length = 218

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1052 aaaataaataaattcttatat 1072
|||||
Sbjct: 103 aaaataaataaattcttatat 83

>gb|DV791356.1| Hw_liver_61_050822_A05 Bos taurus CF-24-HW liver cDNA library Bos
taurus cDNA, mRNA sequence
Length = 1292

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 740 aaattaactttttgtttttcaaaa 764
|||||
Sbjct: 1081 aaattaactttttgtttttcaaaa 1105

>gb|DV691543.1| CGN-35248 Leaf Coffea canephora cDNA clone cccl15m24 5', mRNA
sequence
Length = 624

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 740 aaattaactttttgttttttaaaaa 764
 ||||| |
Sbjct: 506 aaattagctttttgttttttaaaaa 482

>gb|DV280402.1| NAAGL61TF Aedes aegypti - Fat Bodies Normalized (NAFFB2) Aedes
 aegypti cDNA clone NAAGL61, mRNA sequence
 Length = 764

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1035 ggatctaccattagagaaaa 1055
 ||||| |
Sbjct: 174 ggatctaccattagagaaaa 154

>gb|DT954953.1| CFW136-D04.y1d-s SHGC-CFW Gasterosteus aculeatus cDNA clone
 CFW136-D04 5', mRNA sequence
 Length = 1282

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatattttta 951
 ||||| |
Sbjct: 1236 tatttcaaaaaatattttta 1256

>gb|DT280951.1| JGI_CAAV9522.rev CAAV Pimephales promelas testis 7-8 month adults,
 males and females pooled (H) Pimephales promelas cDNA
 clone CAAV9522 3', mRNA sequence
 Length = 857

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaactaa 768
 |||||
Sbjct: 210 taactttttgttttttaaaaactaa 186

>gb|DR769667.1| ILLUMIGEN_MCQ_63477 Katze_MMTE Macaca mulatta cDNA clone
 IBIUW:35675 5' similar to Bases 28 to 453 highly similar
 to human TTF2 (Hs.486818), mRNA sequence
 Length = 553

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 209 tactatcttttgtttcattta 229
 |||||
Sbjct: 483 tactatcttttgtttcattta 503

>emb|AJ926041.1| AJ926041 Theileria annulata merozoite Theileria annulata cDNA clone
 tam010f09_q1k, mRNA sequence
 Length = 1076

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 273 taaagaaaataaaaaagttta 293
 |||||
Sbjct: 1056 taaagaaaataaaaaagttta 1076

>gb|CV503593.1| 70065.1 Mixed Floral Solanum tuberosum cDNA clone 70065 5', mRNA
 sequence
 Length = 672

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 887 aaaggaagttggatttcttct 907
 |||||
Sbjct: 206 aaaggaagttggatttcttct 226

>gb|C0315764.1| EK262410.5prime Exelixis FlyTag CK01 pCDNA-SK+ Drosophila

melanogaster cDNA clone EK262410 5, mRNA sequence
Length = 473

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagt 290
 |||||
Sbjct: 188 atttaaagaaaataaaaaagt 208

>gb|C0284895.1| EK167420.5prime Exelixis FlyTag CK01 pCDNA-SK+ Drosophila
 melanogaster cDNA clone EK167420 5, mRNA sequence
 Length = 440

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagt 290
 |||||
Sbjct: 354 atttaaagaaaataaaaaagt 374

>gb|CN575474.1| rc41b03.x1 Meloidogyne hapla egg pAMP1 v1 Meloidogyne hapla cDNA 3'
 similar to SW:YP87_CAEEL Q09444 HYPOTHETICAL 37.7 KD
 PROTEIN C08B11.7 IN CHROMOSOME II. [1] ;, mRNA sequence
 Length = 257

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttta 951
 |||||
Sbjct: 6 tatttcaaaaaatatttttta 26

>gb|CN574214.1| rc04h06.x1 Meloidogyne hapla egg pAMP1 v1 Meloidogyne hapla cDNA 3'
 similar to SW:YP87_CAEEL Q09444 HYPOTHETICAL 37.7 KD
 PROTEIN C08B11.7 IN CHROMOSOME II. [1] ;, mRNA sequence
 Length = 435

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)

Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttta 951
 |||||
Sbjct: 10 tatttcaaaaaatatttttta 30

>gb|CN573213.1| rc15f08.x1 Meloidogyne hapla egg pAMP1 v1 Meloidogyne hapla cDNA 3'
 similar to SW:YP87_CAEEL Q09444 HYPOTHETICAL 37.7 KD
 PROTEIN C08B11.7 IN CHROMOSOME II. [1] ;, mRNA sequence
 Length = 322

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttta 951
 |||||
Sbjct: 20 tatttcaaaaaatatttttta 40

>gb|CK550790.1| swkz0_009396.z1 swk Bombyx mori cDNA, mRNA sequence
 Length = 628

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 974 aatatctatttaagtatattt 994
 |||||
Sbjct: 135 aatatctatttaagtatattt 115

>dbj|AU260586.1| AU260586 Paralichthys olivaceus kidney adult Paralichthys olivaceus
 cDNA clone HKC173, mRNA sequence
 Length = 613

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 415 gcatggtggtgacaggttga 435
 |||||
Sbjct: 590 gcatggtggtgacaggttga 570

>gb|CK427090.1| rl71c02.y1 Meloidogyne javanica J2 SL1 pGEM Meloidogyne javanica
cDNA 5' similar to TR:Q21581 Q21581 COSMID M60. [1]
;contains element MER9 repetitive element ;, mRNA
sequence
Length = 548

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 266 gtttattttaagaaaataaaa 286
|||||
Sbjct: 539 gtttattttaagaaaataaaa 519

>gb|CF980407.1| re04e06.y1 Meloidogyne incognita female SL1 pGEM Meloidogyne
incognita cDNA 5' similar to TR:Q21581 Q21581 COSMID
M60. [1] ;, mRNA sequence
Length = 570

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 266 gtttattttaagaaaataaaa 286
|||||
Sbjct: 562 gtttattttaagaaaataaaa 542

>gb|CF803136.1| rd94e05.y1 Meloidogyne incognita female SL1 pGEM Meloidogyne
incognita cDNA 5' similar to TR:Q21581 Q21581 COSMID
M60. [1] ;, mRNA sequence
Length = 647

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 266 gtttattttaagaaaataaaa 286
|||||
Sbjct: 586 gtttattttaagaaaataaaa 566

>dbj|BP181391.1| BP181391 ovS3 Bombyx mori cDNA clone ovS327G04f 5', mRNA sequence
Length = 521

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 974 aatatctatttaagtatattt 994
 |||||
Sbjct: 175 aatatctatttaagtatattt 155

>dbj|BP180165.1| BP180165 ovS3 Bombyx mori cDNA clone ovS312A08f 5', mRNA sequence
 Length = 521

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 974 aatatctatttaagtatattt 994
 |||||
Sbjct: 138 aatatctatttaagtatattt 118

>gb|CF522058.1| AGENCOURT_15528907 NICHD_XGC_Kid1 Xenopus laevis cDNA clone
 IMAGE:7009679 5', mRNA sequence
 Length = 722

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaa 763
 |||||
Sbjct: 235 ttaactttttgttttttaaaa 255

>gb|CB196840.2| AGENCOURT_11244860 NICHD_XGC_Tad2 Xenopus laevis cDNA clone
 IMAGE:6871687 5', mRNA sequence
 Length = 834

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaa 763
 |||||

Sbjct: 343 ttaactttttgttttttaaaa 363

>dbj|BJ080944.1| BJ080944 NIBB Mochii normalized Xenopus tailbud library Xenopus
laevis cDNA clone XL069o10 3', mRNA sequence
Length = 596

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 743 ttaactttttgttttttaaaa 763
|||||
Sbjct: 132 ttaactttttgttttttaaaa 112

>dbj|BJ079923.1| BJ079923 NIBB Mochii normalized Xenopus tailbud library Xenopus
laevis cDNA clone XL073p03 3', mRNA sequence
Length = 608

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 743 ttaactttttgttttttaaaa 763
|||||
Sbjct: 155 ttaactttttgttttttaaaa 135

>gb|BI974397.1| saj01b04.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1065-8912 5', mRNA sequence
Length = 557

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaa 288
|||||
Sbjct: 325 ttatttaaagaaaataaaaaa 345

>gb|BI747251.1| rm37g11.y1 Meloidogyne arenaria egg pAMP1 v1 Chiapelli McCarter
Meloidogyne arenaria cDNA 5' similar to TR:Q21581 Q21581
COSMID M60. [1] ;contains element MER9 MER9 repetitive
element ;, mRNA sequence

Length = 421

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 266 gtttattttaagaaaataaaa 286
 |||||
Sbjct: 412 gtttattttaagaaaataaaa 392

>gb|AW942998.1| LD29917.3prime LD Drosophila melanogaster embryo pOT2 Drosophila
 melanogaster cDNA clone LD29917 3, mRNA sequence
 Length = 629

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 270 atttaaagaaaataaaaagt 290
 |||||
Sbjct: 31 atttaaagaaaataaaaagt 11

>gb|AW441094.1| ra06b06.y1 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita
 cDNA 5' similar to WP:M60.3 CE02832 ;, mRNA sequence
 Length = 542

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 266 gtttattttaagaaaataaaa 286
 |||||
Sbjct: 541 gtttattttaagaaaataaaa 521

Database: /usr/local/blast/db/blastlibs/est_others
Posted date: Feb 13, 2010 7:48 AM
Number of letters in database: 29,218,461,503
Number of sequences in database: 51,680,690

Lambda K H
 1.37 0.711 1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 51680690
Number of Hits to DB: 344,427,558
Number of extensions: 24743020
Number of successful extensions: 7648314
Number of sequences better than 10.0: 108
Number of HSP's gapped: 7648314
Number of HSP's successfully gapped: 108
Length of query: 1082
Length of database: 29,218,461,503
Length adjustment: 23
Effective length of query: 1059
Effective length of database: 28,029,805,633
Effective search space: 29683564165347
Effective search space used: 29683564165347
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 50 (99.1 bits)
S1: 12 (24.3 bits)
S2: 21 (42.1 bits)

BLASTx Output of the 3' Border Sequence Flanking the Insert in Soybean Event DAS-68416-4 against GenBank Non-redundant Protein Sequences (nr)

BLASTX 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Query= 68416_3_border
(1082 letters)

Database: /usr/local/blast/db/blastlibs/nr
10,432,217 sequences; 3,559,509,877 total letters

Searching..... done

Sequences producing significant alignments:	Score (bits)	E Value
ref NP_001037088.1 hemolin [Bombyx mori] >gi 41350234 gb AAS004...	36	6.6
gb AAS00443.1 hemolin [Bombyx mori]	36	6.6
dbj BAC79387.1 hemolin [Bombyx mori]	36	6.6
gb EFC40574.1 predicted protein [Naegleria gruberi]	36	8.7
ref XP_002011940.1 GI14470 [Drosophila mojavensis] >gi 19390919...	36	8.7

>ref|NP_001037088.1| hemolin [Bombyx mori]
gb|AAS00444.1| hemolin [Bombyx mori]
gb|AAS00445.1| hemolin [Bombyx mori]
Length = 410

Score = 36.2 bits (82), Expect = 6.6
Identities = 25/96 (26%), Positives = 46/96 (47%), Gaps = 4/96 (4%)
Frame = -1

Query: 461 GSNYVFSTHQPVNH-HALPHRRIRSLQLRRHTYVSRPGSTTASDLSTIEYQWQKEKLT 285
G+ +++T QPVN +P + + L R +R T D S +EY W+K+ + F
Sbjct: 10 GTCVIYTTGQPVNSGDKVPVLKEAPEVLFREGQATRLECATGDDSGVEYSWRKDGMMHF 69

Query: 284 LFSLNKLNVI---LLLYPSHKVNETKDSRVFCQNFF 186
L+ L I L++ K ++ + + F ++ F
Sbjct: 70 SVGLDTLTTIDAGSLVFSQTKASDEGEYQCFKASDF 105

>gb|AAS00443.1| hemolin [Bombyx mori]

Length = 410

Score = 36.2 bits (82), Expect = 6.6
Identities = 25/96 (26%), Positives = 46/96 (47%), Gaps = 4/96 (4%)
Frame = -1

Query: 461 GSNYVFSTHQPVNH-HALPHRRIRSLQQLRRHTYVSRPGSTTASDLSTIEYQWQKEKLT 285
G+ +++T QPVN +P + + L R +R T D S +EY W+K+ + F
Sbjct: 10 GTCVIYTTGQPVNSGDKVPVLKEAPAEVLFREGQATRLECATGDDSGVEYSWRKDGMMHF 69

Query: 284 LFSLNKLNVI---LLLYPSHKVNETKDSRVFCQNFF 186
L+ L I L++ K ++ + + F ++ F
Sbjct: 70 SVGLDTLTTIDAGSLVFSQTKASDEGEYQCFKASDF 105

>dbj|BAC79387.1| hemolin [Bombyx mori]
Length = 410

Score = 36.2 bits (82), Expect = 6.6
Identities = 25/96 (26%), Positives = 46/96 (47%), Gaps = 4/96 (4%)
Frame = -1

Query: 461 GSNYVFSTHQPVNH-HALPHRRIRSLQQLRRHTYVSRPGSTTASDLSTIEYQWQKEKLT 285
G+ +++T QPVN +P + + L R +R T D S +EY W+K+ + F
Sbjct: 10 GTCVIYTTGQPVNSGDKVPVLKEAPAEVLFREGQATRLECATGDDSGVEYSWRKDGMMHF 69

Query: 284 LFSLNKLNVI---LLLYPSHKVNETKDSRVFCQNFF 186
L+ L I L++ K ++ + + F ++ F
Sbjct: 70 SVGLDTLTTIDAGSLVFSQTKASDEGEYQCFKASDF 105

>gb|EFC40574.1| predicted protein [Naegleria gruberi]
Length = 716

Score = 35.8 bits (81), Expect = 8.7
Identities = 35/131 (26%), Positives = 58/131 (44%), Gaps = 13/131 (9%)
Frame = -1

Query: 593 TINXXXXXFFALQ--PSRDFFKGNETASQPHNFHIRDIFAPSSVDGG-----SN 453
T+NY ++ S++ +K N + + NF + F S VDGG SN
Sbjct: 163 TVNYRNSRDSFIKLLDSQELYKENMMSDK--NFTLGYSF-DSLVDGGWENKKPLTLVSSN 219

Query: 452 YVFSTHQPVNH-HALPHRRIRSLQQLRRHTYVSRPGSTTASDLSTIEYQWQKEKLTFLFSL 273
+ +H+ +IR+L+ LR+HTY S +TT +L+ E + L
Sbjct: 220 MEYKEAVYSIYHS---EKIRTLEALRKHTYRSTTWNTTVEELTICTEDSDMEFMLSCKKL 276

Query: 272 NKLNVILLLYP 240
KLN++ + P
Sbjct: 277 RKLNILTTVMP 287

>ref|XP_002011940.1| GI14470 [Drosophila mojavensis]
gb|EDW08061.1| GI14470 [Drosophila mojavensis]
Length = 2018

Score = 35.8 bits (81), Expect = 8.7
Identities = 22/62 (35%), Positives = 32/62 (51%), Gaps = 1/62 (1%)
Frame = -1

Query: 533 GNETASQPHNFHIRDIFAPSSVDGGSNYVFSTHQPVNHH-ALPHRRIRSLQQLRRHTYVS 357
GNETAS HN I++ + S S+ + H P +H L ++ + QQL +HT
Sbjct: 322 GNETASNSHNPFIFIKEHYWESPPTYASSLL---HSPTEYHDELQKQKQEQQLPQHTSAR 378

Query: 356 RP 351
RP
Sbjct: 379 RP 380

Database: /usr/local/blast/db/blastlibs/nr
Posted date: Feb 13, 2010 7:16 AM
Number of letters in database: 3,559,509,877
Number of sequences in database: 10,432,217

Lambda	K	H
0.318	0.134	0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 10432217
Number of Hits to DB: 5,113,556,002
Number of extensions: 90438379
Number of successful extensions: 211424
Number of sequences better than 10.0: 5
Number of HSP's gapped: 211246
Number of HSP's successfully gapped: 5
Length of query: 360
Length of database: 3,559,509,877
Length adjustment: 138
Effective length of query: 222
Effective length of database: 2,119,863,931
Effective search space: 470609792682
Effective search space used: 470609792682
Neighboring words threshold: 12

Window for multiple hits: 40

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 33 (17.3 bits)

BLASTn Output of the Sequence at the Parental Locus of Soybean Event DAS-68416-4 against GenBank Nucleotide Collection (nt/nr)

BLASTN 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Query= 68416_parent_locus
(3867 letters)

Database: /usr/local/blast/db/blastlibs/nt
10,930,266 sequences; 30,212,464,392 total letters

Searching.....done

Sequences producing significant alignments:	Score	E
	(bits)	Value
gb BT093225.1 Soybean clone JCVI-FLGm-17C9 unknown mRNA	1039	0.0
gb BT093496.1 Soybean clone JCVI-FLGm-17I24 unknown mRNA	731	0.0
gb EF456703.1 Medicago truncatula peroxidase (PRX1) mRNA, compl...	176	6e-40
gb BT098008.1 Soybean clone JCVI-FLGm-22H8 unknown mRNA	174	3e-39
emb CU137662.1 Medicago truncatula chromosome 5 clone mth2-155l...	172	1e-38
emb CR938710.1 Medicago truncatula chromosome 5 clone mth2-170k...	172	1e-38
gb AF149281.1 AF149281 Phaseolus vulgaris clone pBPERB5 peroxida...	163	1e-35
ref XM_002520789.1 Ricinus communis Peroxidase 52 precursor, pu...	129	1e-25
gb BT052838.1 Medicago truncatula clone MTYFH_FI_FJ_FK1G-0-8 un...	111	3e-20
gb AY311597.1 Gossypium hirsutum class III peroxidase (pod7) mR...	105	2e-18
emb FP100639.1 Phyllostachys edulis cDNA clone: bphyem110n02, f...	103	8e-18
emb FP099994.1 Phyllostachys edulis cDNA clone: bphyem210i11, f...	103	8e-18
dbj AB027752.1 Nicotiana tabacum mRNA for peroxidase, complete ...	96	2e-15
gb AY837788.2 Catharanthus roseus clone Prx4 putative secretory...	90	1e-13
gb FJ644943.1 Sesuvium portulacastrum peroxidase 1 (POD1) mRNA,...	88	5e-13
dbj AK242814.1 Oryza sativa Japonica Group cDNA, clone: J090061...	86	2e-12
ref NM_001072100.1 Oryza sativa (japonica cultivar-group) Os1lg...	86	2e-12
tpe BN000659.1 TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	86	2e-12
dbj AB019228.1 Arabidopsis thaliana genomic DNA, chromosome 5, ...	86	2e-12
emb BX000512.1 Oryza sativa chromosome 11, . BAC OSJNBa0025K19 ...	86	2e-12
gb EF661875.2 Catharanthus roseus putative secretory peroxidase...	84	7e-12
ref NM_125225.1 Arabidopsis thaliana peroxidase, putative (AT5G...	80	1e-10
dbj AK117722.1 Arabidopsis thaliana At5g58390 mRNA for putative...	80	1e-10
gb AY085030.1 Arabidopsis thaliana clone 124846 mRNA, complete ...	80	1e-10
gb EZ329073.1 TSA: Artemisia annua strain Madagascar Contig1561...	76	2e-09

ref XM_002450087.1	Sorghum bicolor hypothetical protein, mRNA	76	2e-09
ref XM_002269882.1	PREDICTED: Vitis vinifera hypothetical prote...	76	2e-09
emb AM447728.2	Vitis vinifera contig VV78X018697.9, whole genom...	76	2e-09
ref XM_002278960.1	PREDICTED: Vitis vinifera hypothetical prote...	72	3e-08
gb AY206413.1	Ipomoea batatas anionic peroxidase swpb2 mRNA, co...	72	3e-08
gb EZ399860.1	TSA: Artemisia annua strain Uganda Contig16355, m...	70	1e-07
gb EZ145065.1	TSA: Artemisia annua strain Artemis Contig4471, m...	70	1e-07
gb EZ141680.1	TSA: Artemisia annua strain Artemis Contig1086, m...	70	1e-07
ref XM_002489001.1	Sorghum bicolor hypothetical protein (SORBID...	70	1e-07
ref XM_002441657.1	Sorghum bicolor hypothetical protein, mRNA	70	1e-07
emb AM456467.1	Vitis vinifera, whole genome shotgun sequence, c...	70	1e-07
gb GU230149.1	Ipomoea batatas anionic peroxidase mRNA, complete...	68	4e-07
ref XM_002268223.1	PREDICTED: Vitis vinifera hypothetical prote...	68	4e-07
gb FJ099755.1	Pinus taeda isolate 1286 anonymous locus 2_6350_0...	68	4e-07
emb CU231251.1	Populus EST from mild drought-stressed leaves	68	4e-07
gb AY206412.1	Ipomoea batatas anionic peroxidase swpb1 mRNA, co...	68	4e-07
dbj AK322204.1	Solanum lycopersicum cDNA, clone: LEFL1035AA07, ...	66	2e-06
ref XM_002328955.1	Populus trichocarpa predicted protein, mRNA	66	2e-06
ref XM_002319932.1	Populus trichocarpa predicted protein, mRNA	66	2e-06
gb AC214418.1	Populus trichocarpa clone POP106-D21, complete se...	66	2e-06
gb BT096974.1	Soybean clone JCVI-FLGm-21M8 unknown mRNA	64	7e-06
gb AC235472.1	Glycine max strain Williams 82 clone GM_WBc0099F2...	64	7e-06
gb FJ596178.1	Capsicum annuum peroxidase (POD) mRNA, complete cds	64	7e-06
gb EF433455.1	Ipomoea batatas basic peroxidase swpb4 mRNA, comp...	64	7e-06
gb AC235385.1	Glycine max strain Williams 82 clone GM_WBb0113B1...	62	3e-05
gb GQ258782.1	Brassica rapa peroxidase 52 mRNA, partial cds	60	1e-04
gb FJ099770.1	Pinus taeda isolate 1299 anonymous locus 2_6350_0...	60	1e-04
gb FJ099768.1	Pinus taeda isolate 1282 anonymous locus 2_6350_0...	60	1e-04
gb FJ099767.1	Pinus taeda isolate 1292 anonymous locus 2_6350_0...	60	1e-04
gb FJ099766.1	Pinus taeda isolate 1285 anonymous locus 2_6350_0...	60	1e-04
gb FJ099765.1	Pinus taeda isolate 1288 anonymous locus 2_6350_0...	60	1e-04
gb FJ099762.1	Pinus taeda isolate 1298 anonymous locus 2_6350_0...	60	1e-04
gb FJ099761.1	Pinus taeda isolate 1289 anonymous locus 2_6350_0...	60	1e-04
gb FJ099760.1	Pinus taeda isolate 1297 anonymous locus 2_6350_0...	60	1e-04
gb FJ099759.1	Pinus taeda isolate 1283 anonymous locus 2_6350_0...	60	1e-04
gb FJ099758.1	Pinus taeda isolate 1287 anonymous locus 2_6350_0...	60	1e-04
gb FJ099757.1	Pinus taeda isolate 1291 anonymous locus 2_6350_0...	60	1e-04
gb EF433456.1	Ipomoea batatas basic peroxidase swpb5 mRNA, comp...	60	1e-04
gb AC226196.1	Musa acuminata clone BAC MA4-125A12, complete seq...	60	1e-04
ref XM_001754018.1	Physcomitrella patens subsp. patens predicte...	60	1e-04
emb AM449831.1	Vitis vinifera, whole genome shotgun sequence, c...	60	1e-04
gb AY206414.1	Ipomoea batatas anionic peroxidase swpb3 mRNA, co...	60	1e-04
gb AF485265.1	Gossypium hirsutum class III peroxidase (pod3) mR...	60	1e-04
gb EZ328614.1	TSA: Artemisia annua strain Madagascar Contig1516...	58	4e-04
gb EZ256818.1	TSA: Artemisia annua strain Artemis Contig23488, ...	58	4e-04
gb EZ397212.1	TSA: Artemisia annua strain Uganda Contig13707, m...	58	4e-04
dbj AK328734.1	Solanum lycopersicum cDNA, clone: LEFL3035G12, H...	58	4e-04
gb AC235153.1	Glycine max strain Williams 82 clone GM_WBa0085L0...	58	4e-04
gb AC235140.1	Glycine max strain Williams 82 clone GM_WBa0068I0...	58	4e-04

emb	AJ544515.1	Asparagus officinalis partial mRNA for peroxidas...	58	4e-04
ref	XM_002521820.1	Ricinus communis Lignin-forming anionic pero...	56	0.002
ref	XM_002521805.1	Ricinus communis Lignin-forming anionic pero...	56	0.002
ref	XM_002521804.1	Ricinus communis Peroxidase 30 precursor, pu...	56	0.002
gb	FJ529216.1	Cucumis sativus 1-aminocyclopropane-1-carboxylate...	56	0.002
ref	XM_002450088.1	Sorghum bicolor hypothetical protein, mRNA	56	0.002
gb	FJ050772.1	Pinus taeda isolate 4650 anonymous locus 0_13032_...	56	0.002
gb	FJ050764.1	Pinus taeda isolate 4651 anonymous locus 0_13032_...	56	0.002
gb	FJ050758.1	Pinus taeda isolate 4655 anonymous locus 0_13032_...	56	0.002
gb	FJ050757.1	Pinus taeda isolate 4653 anonymous locus 0_13032_...	56	0.002
gb	AF149278.1	AF149278 Phaseolus vulgaris peroxidase 3 precursor...	56	0.002
dbj	AK320453.1	Solanum lycopersicum cDNA, clone: LEFL1009CA06, ...	54	0.006
dbj	AK320190.1	Solanum lycopersicum cDNA, clone: LEFL1006BD07, ...	54	0.006
gb	AC235342.1	Glycine max strain Williams 82 clone GM_WBb0088H1...	54	0.006
emb	CT832689.1	Oryza sativa (indica cultivar-group) cDNA clone:...	54	0.006
emb	CT832688.1	Oryza sativa (indica cultivar-group) cDNA clone:...	54	0.006
emb	CT832687.1	Oryza sativa (indica cultivar-group) cDNA clone:...	54	0.006
ref	NM_001072503.1	Oryza sativa (japonica cultivar-group) Os12g...	54	0.006
tpe	BN000664.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	54	0.006
dbj	AK069456.1	Oryza sativa Japonica Group cDNA clone:J023019E0...	54	0.006
emb	X91172.1	R. sativus prxK1 gene	54	0.006
emb	BX000510.1	Oryza sativa chromosome 12, . BAC OJ1769_D07 of ...	54	0.006
gb	EZ315890.1	TSA: Artemisia annua strain Madagascar Contig2436...	52	0.025
gb	EZ359220.1	TSA: Artemisia annua strain Uganda Contig6381, mR...	52	0.025
gb	EZ166433.1	TSA: Artemisia annua strain Artemis Contig25839, ...	52	0.025
gb	BT106781.1	Picea glauca clone GQ03010_F17 mRNA sequence	52	0.025
ref	XM_002285606.1	PREDICTED: Vitis vinifera hypothetical prote...	52	0.025
gb	AC235417.1	Glycine max strain Williams 82 clone GM_WBb0135A0...	52	0.025
ref	XM_002334206.1	Populus trichocarpa predicted protein, mRNA	52	0.025
ref	NM_001157951.1	Zea mays peroxidase 2 (LOC100285056), mRNA >...	52	0.025
gb	BT044614.1	Arabidopsis thaliana unknown protein (At4g33420) ...	52	0.025
gb	FJ099764.1	Pinus taeda isolate 1294 anonymous locus 2_6350_0...	52	0.025
gb	FJ099763.1	Pinus taeda isolate 1290 anonymous locus 2_6350_0...	52	0.025
gb	BT042071.1	Zea mays full-length cDNA clone ZM_BFb0125B03 mRN...	52	0.025
emb	AM450885.2	Vitis vinifera contig VV78X220288.8, whole genom...	52	0.025
ref	NM_119496.3	Arabidopsis thaliana peroxidase, putative (AT4G...	52	0.025
emb	AM446475.1	Vitis vinifera, whole genome shotgun sequence, c...	52	0.025
emb	AM436560.1	Vitis vinifera, whole genome shotgun sequence, c...	52	0.025
emb	AM429435.1	Vitis vinifera, whole genome shotgun sequence, c...	52	0.025
ref	NM_101322.1	Arabidopsis thaliana anionic peroxidase, putati...	52	0.025
gb	AF453791.1	Ipomoea batatas anionic peroxidase (POD) gene, pr...	52	0.025
dbj	AB193816.1	Pisum sativum mRNA for peroxidase, complete cds,...	52	0.025
dbj	AK176812.1	Arabidopsis thaliana mRNA for peroxidase ATP17a ...	52	0.025
gb	AY089094.1	Arabidopsis thaliana clone 32346 mRNA, complete s...	52	0.025
gb	AC108072.3	Homo sapiens BAC clone RP11-704A16 from 2, comple...	52	0.025
gb	AF451951.1	Arabidopsis thaliana class III peroxidase ATP32 m...	52	0.025
emb	AL161583.2	Arabidopsis thaliana DNA chromosome 4, contig fr...	52	0.025
gb	AC010657.3	AC010657 Genomic sequence for Arabidopsis thaliana...	52	0.025
emb	AL035678.1	Arabidopsis thaliana DNA chromosome 4, BAC clone...	52	0.025

gb AC012188.2	F14L17 Sequence of BAC F14L17 from Arabidopsis tha...	52	0.025
gb EZ395724.1	TSA: Artemisia annua strain Uganda Contig12219, m...	50	0.099
gb EZ362599.1	TSA: Artemisia annua strain Uganda Contig9760, mR...	50	0.099
gb BT066765.1	Zea mays full-length cDNA clone ZM_BFb0066D03 mRN...	50	0.099
gb BT055307.1	Zea mays full-length cDNA clone ZM_BFc0167H14 mRN...	50	0.099
gb EU962146.1	Zea mays clone 240603 mRNA sequence	50	0.099
gb FJ070719.1	Pinus taeda isolate 7938 anonymous locus 0_3458_0...	50	0.099
gb FJ070718.1	Pinus taeda isolate 7947 anonymous locus 0_3458_0...	50	0.099
gb FJ070717.1	Pinus taeda isolate 7943 anonymous locus 0_3458_0...	50	0.099
gb FJ070716.1	Pinus taeda isolate 7950 anonymous locus 0_3458_0...	50	0.099
gb FJ070715.1	Pinus taeda isolate 7940 anonymous locus 0_3458_0...	50	0.099
gb FJ070714.1	Pinus taeda isolate 7948 anonymous locus 0_3458_0...	50	0.099
gb FJ070713.1	Pinus taeda isolate 7949 anonymous locus 0_3458_0...	50	0.099
gb FJ070712.1	Pinus taeda isolate 7952 anonymous locus 0_3458_0...	50	0.099
gb FJ070711.1	Pinus taeda isolate 7941 anonymous locus 0_3458_0...	50	0.099
gb FJ070710.1	Pinus taeda isolate 7951 anonymous locus 0_3458_0...	50	0.099
gb FJ070709.1	Pinus taeda isolate 7942 anonymous locus 0_3458_0...	50	0.099
gb FJ070708.1	Pinus taeda isolate 7953 anonymous locus 0_3458_0...	50	0.099
gb FJ070707.1	Pinus taeda isolate 7937 anonymous locus 0_3458_0...	50	0.099
gb FJ070706.1	Pinus taeda isolate 7946 anonymous locus 0_3458_0...	50	0.099
gb FJ070705.1	Pinus taeda isolate 7945 anonymous locus 0_3458_0...	50	0.099
gb FJ070703.1	Pinus taeda isolate 7939 anonymous locus 0_3458_0...	50	0.099
ref NM_001137528.1	Zea mays hypothetical protein LOC100192105 (...)	50	0.099
gb DQ244260.1	Zea mays clone 3973 mRNA sequence	50	0.099
tpe BN000615.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	50	0.099
dbj AP004731.3	Oryza sativa Japonica Group genomic DNA, chromos...	50	0.099
dbj AB007645.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	50	0.099
emb Y10465.1	S.oleracea mRNA for peroxidase, clone PC44	50	0.099
gb CP000102.1	Methanosphaera stadtmanae DSM 3091, complete genome	50	0.099
emb FP012230.5	Pig DNA sequence from clone CH242-162F1 on chrom...	48	0.39
gb EZ275595.1	TSA: Artemisia annua strain Madagascar Contig1982...	48	0.39
gb EZ286664.1	TSA: Artemisia annua strain Madagascar Contig1305...	48	0.39
gb EZ342046.1	TSA: Artemisia annua strain Uganda Contig9262, mR...	48	0.39
gb EZ321242.1	TSA: Artemisia annua strain Madagascar Contig7788...	48	0.39
gb EZ318330.1	TSA: Artemisia annua strain Madagascar Contig4876...	48	0.39
gb EZ247069.1	TSA: Artemisia annua strain Artemis Contig13739, ...	48	0.39
gb EZ258457.1	TSA: Artemisia annua strain Madagascar Contig1560...	48	0.39
gb EZ396283.1	TSA: Artemisia annua strain Uganda Contig12778, m...	48	0.39
gb EZ220993.1	TSA: Artemisia annua Contig18004	48	0.39
gb EZ366681.1	TSA: Artemisia annua strain Uganda Contig132, mRN...	48	0.39
gb EZ196247.1	TSA: Artemisia annua strain Artemis Contig9804, m...	48	0.39
gb EZ355157.1	TSA: Artemisia annua strain Uganda Contig2318, mR...	48	0.39
gb EZ173232.1	TSA: Artemisia annua strain Artemis Contig32638, ...	48	0.39
gb BT102799.1	Picea glauca clone GQ02016_E21 mRNA sequence	48	0.39
gb BT101612.1	Picea glauca clone GQ01308_P23 mRNA sequence	48	0.39
gb AC212861.3	Pongo abelii BAC clone CH276-236D6 from chromosom...	48	0.39
ref XM_002451803.1	Sorghum bicolor hypothetical protein, mRNA	48	0.39
gb AC235800.1	Solanum lycopersicum chromosome 3 clone C03HBa013...	48	0.39
ref XM_002285687.1	PREDICTED: Vitis vinifera hypothetical prote...	48	0.39

ref XM_002269022.1	PREDICTED: <i>Vitis vinifera</i> hypothetical prote...	48	0.39
dbj AK323976.1	<i>Solanum lycopersicum</i> cDNA, clone: LEFL1068DD08, ...	48	0.39
ref XM_002320381.1	<i>Populus trichocarpa</i> predicted protein, mRNA	48	0.39
gb CP001098.1	<i>Halothermothrix orenii</i> H 168, complete genome	48	0.39
gb EF677600.1	<i>Picea sitchensis</i> clone WS02771_I11 unknown mRNA	48	0.39
gb FJ050773.1	<i>Pinus taeda</i> isolate 4643 anonymous locus 0_13032_...	48	0.39
gb FJ050771.1	<i>Pinus taeda</i> isolate 4657 anonymous locus 0_13032_...	48	0.39
gb FJ050770.1	<i>Pinus taeda</i> isolate 4649 anonymous locus 0_13032_...	48	0.39
gb FJ050769.1	<i>Pinus taeda</i> isolate 4648 anonymous locus 0_13032_...	48	0.39
gb FJ050768.1	<i>Pinus taeda</i> isolate 4659 anonymous locus 0_13032_...	48	0.39
gb FJ050767.1	<i>Pinus taeda</i> isolate 4658 anonymous locus 0_13032_...	48	0.39
gb FJ050766.1	<i>Pinus taeda</i> isolate 4644 anonymous locus 0_13032_...	48	0.39
gb FJ050765.1	<i>Pinus taeda</i> isolate 4645 anonymous locus 0_13032_...	48	0.39
gb FJ050763.1	<i>Pinus taeda</i> isolate 4660 anonymous locus 0_13032_...	48	0.39
gb FJ050762.1	<i>Pinus taeda</i> isolate 4647 anonymous locus 0_13032_...	48	0.39
gb FJ050761.1	<i>Pinus taeda</i> isolate 4654 anonymous locus 0_13032_...	48	0.39
gb FJ050760.1	<i>Pinus taeda</i> isolate 4646 anonymous locus 0_13032_...	48	0.39
gb FJ050759.1	<i>Pinus taeda</i> isolate 4656 anonymous locus 0_13032_...	48	0.39
gb FJ050756.1	<i>Pinus taeda</i> isolate 4652 anonymous locus 0_13032_...	48	0.39
gb EF083074.1	<i>Picea sitchensis</i> clone WS02728_C07 unknown mRNA	48	0.39
gb EU024896.1	Uncultured bacterium clone tgutfos2_Contig107 gen...	48	0.39
emb BX548174.1	<i>Prochlorococcus marinus</i> MED4 complete genome	48	0.39
gb CP000647.1	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> MGH 78578...	48	0.39
emb AM454579.2	<i>Vitis vinifera</i> contig VV78X062755.15, whole geno...	48	0.39
emb AM428729.2	<i>Vitis vinifera</i> contig VV78X273545.5, whole genom...	48	0.39
emb AM462968.1	<i>Vitis vinifera</i> , whole genome shotgun sequence, c...	48	0.39
emb AM473070.1	<i>Vitis vinifera</i> contig VV78X025151.6, whole genom...	48	0.39
emb AM453059.1	<i>Vitis vinifera</i> , whole genome shotgun sequence, c...	48	0.39
emb AM481723.1	<i>Vitis vinifera</i> contig VV78X090480.3, whole genom...	48	0.39
dbj AP006865.1	<i>Lotus japonicus</i> genomic DNA, chromosome 2, clone...	48	0.39
dbj AB049589.1	<i>Avicennia marina</i> PER mRNA for secretory peroxida...	48	0.39
emb BX828399.1	<i>Arabidopsis thaliana</i> Full-length cDNA Complete s...	48	0.39
emb BX832751.1	<i>Arabidopsis thaliana</i> Full-length cDNA Complete s...	48	0.39
dbj AB010692.1	<i>Arabidopsis thaliana</i> genomic DNA, chromosome 5, ...	48	0.39
emb Y10467.1	<i>S. oleracea</i> mRNA for peroxidase, clone PC23	48	0.39
ref XM_670091.1	<i>Plasmodium berghei</i> strain ANKA hypothetical pro...	48	0.39
gb AF109124.1	AF109124 <i>Ipomoea batatas</i> anionic peroxidase swpa2 ...	48	0.39
gb EZ295716.1	TSA: <i>Artemisia annua</i> strain Madagascar Contig1601...	46	1.5
gb EZ256521.1	TSA: <i>Artemisia annua</i> strain Artemis Contig23191, ...	46	1.5
gb EZ360402.1	TSA: <i>Artemisia annua</i> strain Uganda Contig7563, mR...	46	1.5
gb EZ150610.1	TSA: <i>Artemisia annua</i> strain Artemis Contig10016, ...	46	1.5
gb AC233130.7	<i>Solanum lycopersicum</i> strain Heinz 1706 chromosome...	46	1.5
gb AC239433.3	<i>Solanum lycopersicum</i> strain Heinz 1706 chromosome...	46	1.5
gb CP001633.1	<i>Francisella tularensis</i> subsp. <i>tularensis</i> NE061598...	46	1.5
ref NW_003037936.1	<i>Schistosoma mansoni</i> genome sequence supercon...	46	1.5
gb BT095984.1	Soybean clone JCVI-FLGm-20M19 unknown mRNA	46	1.5
gb BT093602.1	Soybean clone JCVI-FLGm-17D17 unknown mRNA	46	1.5
gb AC237089.1	<i>Oryza granulata</i> clone OG_ABa0096023, complete seq...	46	1.5
ref XM_002448761.1	<i>Sorghum bicolor</i> hypothetical protein, mRNA	46	1.5

ref	XM_002426020.1	Pediculus humanus corporis synaptonemal comp...	46	1.5
emb	AJ749949.2	Francisella tularensis subsp. tularensis SCHU S4...	46	1.5
emb	FN357570.1	Schistosoma mansoni genome sequence supercontig ...	46	1.5
emb	FN357441.1	Schistosoma mansoni genome sequence supercontig ...	46	1.5
gb	BT086529.1	Zea mays full-length cDNA clone ZM_BFc0177005 mRN...	46	1.5
gb	EZ053600.1	TSA: Zea mays contig54722, mRNA sequence	46	1.5
emb	AL844509.2	Plasmodium falciparum 3D7 chromosome 13	46	1.5
gb	AC235371.1	Glycine max strain Williams 82 clone GM_WBb0104B0...	46	1.5
gb	AC235196.1	Glycine max strain Williams 82 clone GM_WBb0014G1...	46	1.5
gb	AC235187.1	Glycine max strain Williams 82 clone GM_WBb0010C0...	46	1.5
gb	AC235182.1	Glycine max strain Williams 82 clone GM_WBb0008C1...	46	1.5
gb	AC235129.1	Glycine max strain Williams 82 clone GM_WBa0052IO...	46	1.5
ref	XM_002319931.1	Populus trichocarpa predicted protein, mRNA	46	1.5
ref	NM_001158468.1	Zea mays peroxidase 52 (LOC100285577), mRNA ...	46	1.5
gb	EU954765.1	Zea mays clone 1482328 mRNA sequence	46	1.5
gb	EU951047.1	Zea mays clone 687198 mRNA sequence	46	1.5
tpg	BK006741.1	TPA: TPA_reasm: Francisella tularensis subsp. ho...	46	1.5
gb	FJ088527.1	Pinus taeda isolate 6658 anonymous locus 2_10243_...	46	1.5
gb	FJ088526.1	Pinus taeda isolate 6661 anonymous locus 2_10243_...	46	1.5
gb	FJ088525.1	Pinus taeda isolate 6650 anonymous locus 2_10243_...	46	1.5
gb	FJ088524.1	Pinus taeda isolate 6653 anonymous locus 2_10243_...	46	1.5
gb	FJ088523.1	Pinus taeda isolate 6663 anonymous locus 2_10243_...	46	1.5
gb	FJ088522.1	Pinus taeda isolate 6662 anonymous locus 2_10243_...	46	1.5
gb	FJ088521.1	Pinus taeda isolate 6654 anonymous locus 2_10243_...	46	1.5
gb	FJ088520.1	Pinus taeda isolate 6655 anonymous locus 2_10243_...	46	1.5
gb	FJ088519.1	Pinus taeda isolate 6657 anonymous locus 2_10243_...	46	1.5
gb	FJ088518.1	Pinus taeda isolate 6664 anonymous locus 2_10243_...	46	1.5
gb	FJ088517.1	Pinus taeda isolate 6651 anonymous locus 2_10243_...	46	1.5
gb	FJ088516.1	Pinus taeda isolate 6649 anonymous locus 2_10243_...	46	1.5
gb	FJ088515.1	Pinus taeda isolate 6666 anonymous locus 2_10243_...	46	1.5
gb	FJ088514.1	Pinus taeda isolate 6660 anonymous locus 2_10243_...	46	1.5
gb	FJ088513.1	Pinus taeda isolate 6665 anonymous locus 2_10243_...	46	1.5
gb	FJ088512.1	Pinus taeda isolate 6656 anonymous locus 2_10243_...	46	1.5
gb	FJ088511.1	Pinus taeda isolate 4039 anonymous locus 2_10243_...	46	1.5
gb	FJ088510.1	Pinus taeda isolate 4033 anonymous locus 2_10243_...	46	1.5
gb	FJ088509.1	Pinus taeda isolate 4024 anonymous locus 2_10243_...	46	1.5
gb	FJ088508.1	Pinus taeda isolate 4026 anonymous locus 2_10243_...	46	1.5
gb	FJ088507.1	Pinus taeda isolate 4025 anonymous locus 2_10243_...	46	1.5
gb	FJ088506.1	Pinus taeda isolate 4031 anonymous locus 2_10243_...	46	1.5
gb	FJ088505.1	Pinus taeda isolate 4032 anonymous locus 2_10243_...	46	1.5
gb	FJ088504.1	Pinus taeda isolate 4037 anonymous locus 2_10243_...	46	1.5
gb	FJ088503.1	Pinus taeda isolate 4022 anonymous locus 2_10243_...	46	1.5
gb	FJ088502.1	Pinus taeda isolate 4028 anonymous locus 2_10243_...	46	1.5
gb	FJ088501.1	Pinus taeda isolate 4034 anonymous locus 2_10243_...	46	1.5
gb	FJ088500.1	Pinus taeda isolate 4038 anonymous locus 2_10243_...	46	1.5
gb	FJ088499.1	Pinus taeda isolate 4030 anonymous locus 2_10243_...	46	1.5
gb	FJ088498.1	Pinus taeda isolate 4035 anonymous locus 2_10243_...	46	1.5
gb	FJ088497.1	Pinus taeda isolate 4036 anonymous locus 2_10243_...	46	1.5
gb	FJ088496.1	Pinus taeda isolate 4029 anonymous locus 2_10243_...	46	1.5

gb FJ088495.1	Pinus taeda isolate 4027 anonymous locus 2_10243_...	46	1.5
gb FJ088494.1	Pinus taeda isolate 4023 anonymous locus 2_10243_...	46	1.5
gb AC189631.2	Brassica rapa subsp. pekinensis clone KBrS003K07,...	46	1.5
dbj AB374543.1	Spirometra erinaceieuropaei mitochondrial DNA, c...	46	1.5
ref XM_001336009.2	PREDICTED: Danio rerio hypothetical LOC10000...	46	1.5
dbj AP010414.1	Lotus japonicus genomic DNA, chromosome 6, clone...	46	1.5
dbj AP009714.1	Lotus japonicus genomic DNA, clone: Ljt08001, TM...	46	1.5
gb CP001056.1	Clostridium botulinum B str. Eklund 17B, complete...	46	1.5
gb CP000915.1	Francisella tularensis subsp. mediasiatica FSC147...	46	1.5
ref XM_001751456.1	Physcomitrella patens subsp. patens predicte...	46	1.5
gb AC206008.3	Pongo abelii BAC clone CH276-282M20 from chromoso...	46	1.5
gb AC216474.1	Populus trichocarpa clone POP081-J22, complete se...	46	1.5
ref XM_001713455.1	Guillardia theta hypothetical protein (orf43...	46	1.5
gb EF087739.1	Picea sitchensis clone WS02740_P19 unknown mRNA	46	1.5
gb AC213540.1	Populus trichocarpa clone POP053-A08, complete se...	46	1.5
gb EU060241.1	Uncultured bacterium clone LMOABA27ZD09RM1 genomi...	46	1.5
gb CP000803.1	Francisella tularensis subsp. holarctica FTNF002-...	46	1.5
gb EF645823.1	Manihot esculenta cultivar MTA18 cationic peroxid...	46	1.5
ref XM_001479242.1	PREDICTED: Mus musculus similar to MK-5 type...	46	1.5
emb AM457942.2	Vitis vinifera contig VV78X124814.1, whole genom...	46	1.5
emb AM446264.2	Vitis vinifera contig VV78X146694.5, whole genom...	46	1.5
emb AM489166.2	Vitis vinifera contig VV78X028632.7, whole genom...	46	1.5
emb AM444565.2	Vitis vinifera contig VV78X153928.11, whole geno...	46	1.5
emb AM436965.2	Vitis vinifera contig VV78X063704.11, whole geno...	46	1.5
ref NM_117724.3	Arabidopsis thaliana peroxidase 40 (PER40) (P40...	46	1.5
gb CP000608.1	Francisella tularensis subsp. tularensis WY96-341...	46	1.5
ref NM_001110031.1	Danio rerio zgc:136903 (zgc:136903), mRNA >g...	46	1.5
emb BX293980.2	Mycoplasma mycoides subsp. mycoides SC str. PG1,...	46	1.5
emb AM485714.1	Vitis vinifera, whole genome shotgun sequence, c...	46	1.5
ref NM_001097269.1	Xenopus (Silurana) tropicalis hypothetical p...	46	1.5
gb CP000439.1	Francisella tularensis subsp. novicida U112, comp...	46	1.5
gb EF055261.1	Sesbania rostrata peroxidase 1 (prx1) mRNA, compl...	46	1.5
emb CT027756.10	Zebrafish DNA sequence from clone DKEY-95F11 in...	46	1.5
gb CP000437.1	Francisella tularensis subsp. holarctica OSU18, c...	46	1.5
ref XM_623898.2	PREDICTED: Apis mellifera similar to Muscle pro...	46	1.5
emb AM286280.1	Francisella tularensis subsp. tularensis strain ...	46	1.5
gb DQ681941.1	Synthetic construct Francisella tularensis clone ...	46	1.5
ref NM_120616.2	Arabidopsis thaliana peroxidase, putative (AT5G...	46	1.5
gb AC151347.2	Xenopus (Silurana) tropicalis clone ISB-394A6, co...	46	1.5
gb BT017949.1	Zea mays clone EL01N0522B07.c mRNA sequence	46	1.5
gb BT013033.1	Lycopersicon esculentum clone 114281R, mRNA sequence	46	1.5
gb BT011747.1	Arabidopsis thaliana At4g16270 gene, complete cds	46	1.5
gb AC125096.3	Mus musculus BAC clone RP24-181K19 from chromosom...	46	1.5
gb AC131109.3	Mus musculus BAC clone RP23-362M7 from chromosome...	46	1.5
gb AY065270.1	Arabidopsis thaliana putative peroxidase (At5g053...	46	1.5
dbj AK137657.1	Mus musculus adult female vagina cDNA, RIKEN ful...	46	1.5
emb AJ809342.1	Picea abies mRNA for peroxidase (px7 gene)	46	1.5
emb AJ809341.1	Picea abies mRNA for peroxidase (px6 gene)	46	1.5
emb CR690313.2	Tetraodon nigroviridis full-length cDNA	46	1.5

gb AC026100.19	Homo sapiens 3 BAC RP11-449F7 (Roswell Park Canc...	46	1.5
gb AC084740.5	Homo sapiens BAC clone RP11-423E20 from 4, comple...	46	1.5
gb AC099520.2	Homo sapiens chromosome 5 clone RP11-6N13, comple...	46	1.5
gb AC012602.4	Homo sapiens chromosome 5 clone CTC-328N13, compl...	46	1.5
gb AF165818.4	Guillardia theta nucleomorph chromosome 1, comple...	46	1.5
emb BX005227.12	Zebrafish DNA sequence from clone CH211-286C23 ...	46	1.5
emb BX548071.7	Zebrafish DNA sequence from clone DKEY-25L23 in ...	46	1.5
dbj AK175982.1	Arabidopsis thaliana mRNA, complete cds, clone: ...	46	1.5
dbj AK175661.1	Arabidopsis thaliana mRNA, complete cds, clone: ...	46	1.5
emb BX537275.8	Zebrafish DNA sequence from clone DKEYP-120E12 i...	46	1.5
emb BX537269.8	Zebrafish DNA sequence from clone DKEY-181H1 in ...	46	1.5
emb BX826801.1	Arabidopsis thaliana Full-length cDNA Complete s...	46	1.5
dbj AP005846.2	Oryza sativa Japonica Group genomic DNA, chromos...	46	1.5
emb BX537286.4	Zebrafish DNA sequence from clone DKEY-28J4 in l...	46	1.5
dbj AP006135.1	Lotus japonicus genomic DNA, chromosome 1, clone...	46	1.5
gb AC008970.4	AC008970 Homo sapiens chromosome 5 clone CTD-2374C...	46	1.5
emb AL161543.2	Arabidopsis thaliana DNA chromosome 4, contig fr...	46	1.5
emb AL132978.1	Arabidopsis thaliana DNA chromosome 3, BAC clone...	46	1.5
emb Z97340.2	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA ...	46	1.5
emb Z82992.1	A. thaliana FCA gene encoding FCA alpha, beta, gamm...	46	1.5
emb AM233362.1	Francisella tularensis subsp. holarctica LVS com...	46	1.5
gb AC151343.2	Xenopus (Silurana) tropicalis clone ISB-373E17, c...	46	1.5
gb AC155316.6	Mus musculus BAC clone RP23-181P9 from chromosome...	46	1.5
gb AC166091.3	Glycine max clone gmw1-11j16, complete sequence	46	1.5
ref XM_733026.1	Plasmodium chabaudi chabaudi hypothetical prote...	46	1.5
emb AL935040.6	Zebrafish DNA sequence from clone CH211-176L21, ...	46	1.5
gb AY108407.1	Zea mays PC0110242 mRNA sequence	46	1.5
emb AL157764.12	Human DNA sequence from clone RP11-562E17 on ch...	46	1.5
gb AF145349.1	AF145349 Glycine max peroxidase (Prx3) mRNA, parti...	46	1.5
gb AF078691.1	AF078691 Manihot esculenta peroxidase gene, partia...	46	1.5
gb AF067188.1	AF067188 Beta vulgaris cell wall peroxidase mRNA, ...	46	1.5
gb L36231.1	SSNPX12A Stylosanthes humilis peroxidase (px12) mRNA...	46	1.5
gb L36110.1	SSNPEROXIA Stylosanthes humilis peroxidase mRNA	46	1.5
emb FN554766.1	Escherichia coli 042 complete genome	44	6.1
emb FP236458.5	Zebrafish DNA sequence from clone CH73-374P12, c...	44	6.1
gb EZ396827.1	TSA: Artemisia annua strain Uganda Contig13322, m...	44	6.1
gb AC239575.2	Solanum lycopersicum strain Heinz 1706 clone hba-...	44	6.1
ref NG_016144.1	Homo sapiens inositol 1,4,5-triphosphate recept...	44	6.1
gb BT106566.1	Picea glauca clone GQ03005_B15 mRNA sequence	44	6.1
gb FJ415216.1	Gossypium hirsutum clone Ghpx5 class III peroxid...	44	6.1
emb CU633361.7	Pig DNA sequence from clone CH242-1G8 on chromos...	44	6.1
gb AE014187.2	Plasmodium falciparum 3D7 chromosome 14, complete...	44	6.1
gb DQ676955.1	Ipomoea batatas anionic peroxidase (swpa4) gene, ...	44	6.1
emb FP099688.1	Phyllostachys edulis cDNA clone: bphylf045i10, f...	44	6.1
emb FP094559.1	Phyllostachys edulis cDNA clone: bphylf061m22, f...	44	6.1
emb FP093329.1	Phyllostachys edulis cDNA clone: bphyst031i16, f...	44	6.1
emb FP092972.1	Phyllostachys edulis cDNA clone: bphylf025d09, f...	44	6.1
emb FP091819.1	Phyllostachys edulis cDNA clone: bphyem202n22, f...	44	6.1
emb FP101172.1	Phyllostachys edulis cDNA clone: bphyem105e15, f...	44	6.1

ref XM_002442921.1	Sorghum bicolor hypothetical protein, mRNA	44	6.1
ref XM_002455522.1	Sorghum bicolor hypothetical protein, mRNA	44	6.1
ref XM_002455521.1	Sorghum bicolor hypothetical protein, mRNA	44	6.1
ref XM_002432395.1	Pediculus humanus corporis conserved hypothe...	44	6.1
gb EU725468.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	6.1
gb EU725467.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	6.1
gb EU725466.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	6.1
gb EU725465.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	6.1
gb EU725464.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	6.1
gb EU725463.1	Triticum aestivum class III peroxidase (Prx109-A)...	44	6.1
gb AC216032.2	Oryza minuta clone OM_Ba0196N15, complete sequence	44	6.1
gb EZ063624.1	TSA: Zea mays contig64746, mRNA sequence	44	6.1
emb AL844507.2	Plasmodium falciparum 3D7 chromosome 8	44	6.1
dbj AK329676.1	Solanum lycopersicum cDNA, clone: LEFL3153D08, H...	44	6.1
gb AC235246.1	Glycine max strain Williams 82 clone GM_WBb0033G1...	44	6.1
gb AC235231.1	Glycine max strain Williams 82 clone GM_WBb0026L1...	44	6.1
gb AC235115.1	Glycine max strain Williams 82 clone GM_WBa0021N1...	44	6.1
gb AE013600.1	Mus musculus piebald deletion region complete seq...	44	6.1
emb AL844508.1	Plasmodium falciparum 3D7 chromosome 9	44	6.1
ref XM_002338588.1	Populus trichocarpa predicted protein, mRNA	44	6.1
ref XM_002336305.1	Populus trichocarpa predicted protein, mRNA	44	6.1
ref XM_002303984.1	Populus trichocarpa predicted protein, mRNA	44	6.1
gb BT061140.1	Zea mays full-length cDNA clone ZM_BFb0114015 mRN...	44	6.1
emb CU928163.2	Escherichia coli UMN026 chromosome, complete genome	44	6.1
emb CU928164.2	Escherichia coli IAI39 chromosome, complete genome	44	6.1
dbj AK245281.1	Glycine max cDNA, clone: GMFL01-25-021	44	6.1
gb EU960147.1	Zea mays clone 222156 mRNA sequence	44	6.1
gb EU945238.1	Zea mays clone 245264 mRNA sequence	44	6.1
gb AC232892.1	Oryza officinalis clone 00_Ba0082D20, complete s...	44	6.1
dbj AP010895.1	Solanum lycopersicum DNA, chromosome 8, clone: C...	44	6.1
gb FJ078274.1	Pinus taeda isolate 5928 anonymous locus 0_6659_0...	44	6.1
gb FJ078266.1	Pinus taeda isolate 5925 anonymous locus 0_6659_0...	44	6.1
gb FJ078265.1	Pinus taeda isolate 5919 anonymous locus 0_6659_0...	44	6.1
gb FJ078264.1	Pinus taeda isolate 5914 anonymous locus 0_6659_0...	44	6.1
gb FJ078263.1	Pinus taeda isolate 5916 anonymous locus 0_6659_0...	44	6.1
gb FJ078262.1	Pinus taeda isolate 5915 anonymous locus 0_6659_0...	44	6.1
gb FJ078261.1	Pinus taeda isolate 5922 anonymous locus 0_6659_0...	44	6.1
gb BT038706.1	Zea mays full-length cDNA clone ZM_BFb0310H17 mRN...	44	6.1
gb BT037971.1	Zea mays full-length cDNA clone ZM_BFb0205C16 mRN...	44	6.1
ref NM_001143045.1	Zea mays hypothetical protein LOC100216632 (...)	44	6.1
ref NM_001137329.1	Zea mays hypothetical protein LOC100191905 (...)	44	6.1
gb CP001110.1	Pelodictyon phaeoclathratiforme BU-1, complete ge...	44	6.1
gb EU795178.1	Uncultured bacterium HF0010_09016 genomic sequence	44	6.1
gb CP000970.1	Escherichia coli SMS-3-5, complete genome	44	6.1
emb CU570896.5	Zebrafish DNA sequence from clone DKEY-194E13 in...	44	6.1
gb EF444530.1	Oryza sativa Japonica Group putative peroxidase m...	44	6.1
ref XM_001740672.1	Entamoeba dispar SAW760 F-box/leucine rich r...	44	6.1
gb AC216704.1	Solanum lycopersicum chromosome 2 clone C02HBa023...	44	6.1
emb CU570678.3	M.truncatula DNA sequence from clone MTH2-16J21 ...	44	6.1

gb AC215650.1	Populus trichocarpa clone POP108-K22, complete se...	44	6.1
gb AC215390.1	Solanum lycopersicum chromosome 2 clone C02HBa012...	44	6.1
ref XM_001712135.1	Hemiselmis andersenii hypothetical protein (...)	44	6.1
gb CP000881.1	Hemiselmis andersenii chromosome 1, complete sequ...	44	6.1
gb AC210491.1	Oryza glaberrima clone OG_BBa0088K23, complete se...	44	6.1
ref XM_001553571.1	Botryotinia fuckeliana B05.10 60S ribosomal ...	44	6.1
gb EF533695.1	Glycine max clone BAC GM_WBb098N15, complete sequ...	44	6.1
emb AM483376.2	Vitis vinifera contig VV78X083975.15, whole geno...	44	6.1
emb AM466347.2	Vitis vinifera contig VV78X176098.3, whole genom...	44	6.1
emb AM464800.2	Vitis vinifera contig VV78X220659.11, whole geno...	44	6.1
emb AM445395.2	Vitis vinifera contig VV78X136138.6, whole genom...	44	6.1
emb AM434275.2	Vitis vinifera contig VV78X203901.6, whole genom...	44	6.1
emb CT025903.11	Zebrafish DNA sequence from clone DKEY-66H5 in ...	44	6.1
emb AM432525.2	Vitis vinifera contig VV78X143782.10, whole geno...	44	6.1
emb AM451582.2	Vitis vinifera contig VV78X210575.8, whole genom...	44	6.1
ref XM_001446891.1	Paramecium tetraurelia hypothetical protein ...	44	6.1
ref XM_001428564.1	Paramecium tetraurelia hypothetical protein ...	44	6.1
ref NM_129711.3	Arabidopsis thaliana electron carrier/ heme bin...	44	6.1
ref NM_126037.4	Arabidopsis thaliana peroxidase 72 (PER72) (P72...	44	6.1
dbj AB270792.1	Malus x domestica MdSFBB9-alpha, S9-RNase, MdSFB...	44	6.1
gb EF421197.1	Nelumbo nucifera cationic peroxidase (CP) mRNA, c...	44	6.1
ref XM_001350114.1	Plasmodium falciparum 3D7 hypothetical prote...	44	6.1
ref XM_001349842.1	Plasmodium falciparum 3D7 hypothetical prote...	44	6.1
gb AC187618.3	Pan troglodytes BAC clone CH251-584I16 from chrom...	44	6.1
emb AM463654.1	Vitis vinifera contig VV78X012147.8, whole genom...	44	6.1
emb AM464677.1	Vitis vinifera contig VV78X194278.8, whole genom...	44	6.1
emb AM475805.1	Vitis vinifera contig VV78X097027.7, whole genom...	44	6.1
gb AE014298.4	Drosophila melanogaster chromosome X, complete se...	44	6.1
gb CP000551.1	Prochlorococcus marinus str. AS9601, complete genome	44	6.1
gb AC192762.3	Pan troglodytes BAC clone CH251-676011 from chrom...	44	6.1
emb CT961058.16	M. truncatula DNA sequence from clone MTH2-80N17...	44	6.1
ref XM_001032614.1	Tetrahymena thermophila conserved hypothetic...	44	6.1
gb AC120193.5	Homo sapiens chromosome 8, clone RP11-10H17, comp...	44	6.1
gb AC185364.2	Populus trichocarpa clone Pop1-63B23, complete se...	44	6.1
emb CT830771.1	Oryza sativa (indica cultivar-group) cDNA clone:...	44	6.1
emb CT836342.1	Oryza sativa (indica cultivar-group) cDNA clone:...	44	6.1
emb CT828052.1	Oryza sativa (indica cultivar-group) cDNA clone:...	44	6.1
dbj AK243473.1	Oryza sativa Japonica Group cDNA, clone: J100072...	44	6.1
ref NM_001071707.1	Oryza sativa (japonica cultivar-group) Os10g...	44	6.1
ref NM_001071706.1	Oryza sativa (japonica cultivar-group) Os10g...	44	6.1
ref NM_001061107.1	Oryza sativa (japonica cultivar-group) Os05g...	44	6.1
ref NM_001055328.1	Oryza sativa (japonica cultivar-group) Os03g...	44	6.1
ref NM_001052935.1	Oryza sativa (japonica cultivar-group) Os02g...	44	6.1
ref NM_001049442.1	Oryza sativa (japonica cultivar-group) Os01g...	44	6.1
emb CT827810.6	Zebrafish DNA sequence from clone DKEY-120E24 in...	44	6.1
emb AM231674.1	Prunus dulcis partial s-RNase gene for ribonucle...	44	6.1
emb AM293547.1	Picea abies mRNA for properoxidase (px17 gene), ...	44	6.1
tpe BN000657.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1
tpe BN000656.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1

tpe BN000598.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1
tpe BN000562.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1
tpe BN000559.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1
tpe BN000544.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1
tpe BN000535.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1
dbj AK227717.1	Arabidopsis thaliana mRNA for peroxidase, comple...	44	6.1
gb AY206411.1	Ipomoea batatas anionic peroxidase swpa6 mRNA, co...	44	6.1
gb AY206409.1	Ipomoea batatas anionic peroxidase swpa4 mRNA, co...	44	6.1
gb AC154194.2	Mus musculus BAC clone RP24-401L2 from chromosome...	44	6.1
gb AC102440.12	Mus musculus chromosome 1, clone RP24-146C18, co...	44	6.1
gb AC087552.3	Oryza sativa Japonica Group chromosome 5 clone P0...	44	6.1
gb AC091473.2	Mus musculus chromosome X clones RP21-114F21, RP2...	44	6.1
gb AE017263.1	Mesoplasma florum L1 complete genome	44	6.1
gb AC006353.3	Homo sapiens PAC clone RP5-1062J16 from 7, comple...	44	6.1
gb AC132451.3	Mus musculus BAC clone RP23-194C20 from chromosom...	44	6.1
gb AC123834.4	Mus musculus BAC clone RP24-132N9 from chromosome...	44	6.1
gb AC133523.3	Mus musculus BAC clone RP23-34E20 from 19, comple...	44	6.1
gb AC126691.3	Mus musculus BAC clone RP23-221H11 from 14, compl...	44	6.1
gb AC069248.4	Homo sapiens chromosome 3 clone RP11-6I21 map 3p,...	44	6.1
gb AC113010.10	Mus musculus chromosome 18, clone RP23-172F6, co...	44	6.1
gb AC155955.2	Xenopus (Silurana) tropicalis clone CH216-151P9, ...	44	6.1
dbj AP007151.1	Aspergillus oryzae RIB40 DNA, SC005	44	6.1
gb BT008727.1	Arabidopsis thaliana At2g41480 gene, complete cds	44	6.1
gb BT008314.1	Arabidopsis thaliana At5g66390 gene, complete cds	44	6.1
emb BX546477.9	Zebrafish DNA sequence from clone DKEYP-79C5 in ...	44	6.1
emb BX842700.35	Zebrafish DNA sequence from clone DKEY-2P18 in ...	44	6.1
gb AC161005.4	Pan troglodytes BAC clone CH251-668M6 from chromo...	44	6.1
ref XM_651154.1	Entamoeba histolytica HM-1:IMSS hypothetical pr...	44	6.1
gb AC161283.2	Pan troglodytes BAC clone CH251-354N8 from chromo...	44	6.1
dbj AK081398.1	Mus musculus 16 days embryo head cDNA, RIKEN ful...	44	6.1
gb AY139994.1	Arabidopsis thaliana putative peroxidase (At2g414...	44	6.1
gb AC074196.14	Oryza sativa chromosome 10 BAC OSJNBa0040D23 gen...	44	6.1
gb AC105363.2	Oryza sativa Japonica Group chromosome 3 clone OJ...	44	6.1
gb AC113349.2	Homo sapiens chromosome 5 clone CTD-2544H17, comp...	44	6.1

>gb|BT093225.1| Soybean clone JCVI-FLGm-17C9 unknown mRNA
Length = 1274

Score = 1039 bits (524), Expect = 0.0
Identities = 539/544 (99%)
Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 639 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 580

Query: 1849 accaacatagaaccgcatattgcaaggacttaggcagcaaagctgccttagaacatcaggg 1908

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtggtttgagcaaatta 567
|||||
Sbjct: 1272 acaccctttcaatcaaacacaaacactcgaagtactaagttagtggttcgagcaaatta 1213

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
|||||
Sbjct: 1212 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 1153

Query: 628 gggagtccaatgcacaactttctacaaacttttactaccattcatgtccaacctcttc 687
|||||
Sbjct: 1152 gggagtccaatgcacaactttctacaaacttttactaccattcatgtccaacctcttc 1093

Query: 688 tcctctgtgaaatccacagtgaatctgccatatctaaggagaccgcatgggtgcttct 747
|||||
Sbjct: 1092 tcctctgtgaaatccgacagtgaatctgccatatctaaggagaccgcatgggtgcttct 1033

Query: 748 ctcttcgcttggttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 1032 ctcttcgcttggttcttccacgattgctttgtcaatg 996

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 996 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 937

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 936 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 877

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 876 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 817

Query: 1337 tctgttcagatt 1348
|||||

Sbjct: 811 tacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgttcaat 870

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccacccgggcaccttctcctct 2088
|||||

Sbjct: 871 ggtgggtccaccgactccattgtgcgtggctacagcaccacccgagctccttctcctct 930

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||

Sbjct: 931 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaacgga 990

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt--tgattcagtccttgaatattaagg 2206
|||||

Sbjct: 991 gaaatcaggaagaattgtagaaggattaactaattactaattgagctccaatattaagg 1050

Query: 2207 gtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaacatgtttt 2263
|||

Sbjct: 1051 gtctactacacatacgaagcaatttaattgtgtttaataagttgttaaacatgtttt 1110

Query: 2264 gttgtattttgattcc 2281
|||||

Sbjct: 1111 gttgtattttgattcc 1128

Score = 412 bits (208), Expect = e-111
Identities = 260/277 (93%), Gaps = 4/277 (1%)
Strand = Plus / Plus

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtggtttgagcaaatta 567
|||||

Sbjct: 2 acaccctctcaagcaaacacaaacacttgaagtactaagttagtggtttgagcaa--- 58

Query: 568 actatggcttcgttttgttctagattgacaatttggctctgtttgcctcatatgg 627
|||||

Sbjct: 59 -ctatggcttcgttttgttctagattgaccatttggctctgtttgcctcatattg 117

Query: 628 gggagtgccaatgcacaactttctacaaactttactaccattcatgtccaaacctcttc 687
|||||

Sbjct: 118 gggagtgccaatgccaaactttctacaaactttactaccattcgtgtccaaacctcttc 177

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttct 747
||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 178 tccactgtgaaatccacagtgcaatctgccatatcaaaggagaccgcatgggtgcttct 237

Query: 748 ctctctcgcttgttcttccacgattgctttgtcaatg 784
||||| ||| ||||||||||||||||||||||||||||||||
Sbjct: 238 ctctccgcccgttcttccacgattgctttgtcaatg 274

Score = 331 bits (167), Expect = 2e-86
Identities = 185/191 (96%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 274 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 333

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Sbjct: 334 aaccccaacaggaactctgctcgtggatacagggtcattgacaacattaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgttctcctgcgcagatatccttgccatcgctgccagagac 1336
||||||| |||||||||||||| |||||||||||||||||||| |||||||||
Sbjct: 394 gagaaagcatgtccaggagttgtctcctgcgcagatatccttgccatagctgccagagac 453

Query: 1337 tctgttcagat 1347
||||||||||
Sbjct: 454 tctgttcagat 464

Score = 293 bits (148), Expect = 4e-75
Identities = 163/168 (97%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 466 cttggaggccctagttggaatgttaaagtggagaagagacgctagaactgctagccaa 525

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||||||||||||||||||| |||||||||||||||||||| |||||||||

Score = 145 bits (73), Expect = 2e-30
Identities = 136/157 (86%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaacctcttc 687
|||||
Sbjct: 64 gggagtgccaatgcacaactttctacaaacttttactcaaaaacttgccccaaactctct 123

Query: 688 tectctgtgaaatccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttct 747
|||
Sbjct: 124 accacagtgaaatccacactgcaaactgccatatcaaaggaggcccgaatgggtgcctct 183

Query: 748 ctctctcgttgttcttccacgattgctttgtcaatg 784
||||
Sbjct: 184 atctctcgttgttcttccacgattgctttgtcaatg 220

Score = 123 bits (62), Expect = 8e-24
Identities = 155/186 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 220 ggatgtgatggatcaattctcttagatgacacatcaagctttaccggtgagaagaatgca 279

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaatcagccgtg 1276
|||
Sbjct: 280 aatccaatagaaactccgctcgtggatttgatgtcatcgacaacataaagacagccgta 339

Query: 1277 gaaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 340 gagaacgtatgccccggagttgtatcatgtgctgatatcctagccattgctgccgagac 399

Query: 1337 tctgtt 1342
|||||
Sbjct: 400 tctgtt 405

Score = 89.7 bits (45), Expect = 1e-13
Identities = 87/101 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||||| || || ||||| ||||||||| ||||| ||| ||||| |||
Sbjct: 412 cttggaggtccaacctggaatgtaaaacttgaagaagagatgctaaaacggctagtcaa 471

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacct 1578
|| ||||| || ||||| ||||| ||||| |||||
Sbjct: 472 tccgctgctaacaactgccatcccggcaccaacttcaaacct 512

>gb|BT098008.1| Soybean clone JCVI-FLGm-22H8 unknown mRNA
Length = 1324

Score = 174 bits (88), Expect = 3e-39
Identities = 316/392 (80%)
Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
||||| ||||||||| ||||||||| ||| ||||| ||||||||| |||
Sbjct: 678 ggtcatacaattggacaagcaaggtgcacaacctttagagcccgaatctacaacgagagc 619

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
||||||| | | ||||| | | || | | || | | ||||| ||||| |||
Sbjct: 618 aacatagatagctcttttgcccgcatgagacaatctaggtgtcccgaacctcaggatca 559

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaaactccaaccagctttgacaactactac 1971
||||||| || ||||| ||||| || ||||| || ||||| ||||| |||||
Sbjct: 558 ggggacaacaaccttgaccattgactttgccactcccactttctttgacaaccactac 499

Query: 1972 ttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacgggt 2031
||||||| ||||||||| ||||| || ||||| || ||||| ||||| |||
Sbjct: 498 ttcaagaacctcattcagaagaagggttcatccattccgaccaagaactcttcaatggt 439

Query: 2032 ggttccaccgactccattgtgctggttacagcaccaaccgggcaccttctctctgat 2091
|| ||||| ||||| | || | | ||||||||| ||||| | | |||
Sbjct: 438 ggttccactgactccttagtgggtacctacagcaccaaccggcctccttttccgcat 379

Sbjct: 915 aaagtgtgtccgggtgtggtttcttgcgctgacattcttgccatcgctgccagagactct 856

Query: 1340 gttcagat 1347

||| ||||

Sbjct: 855 gttgagat 848

Score = 121 bits (61), Expect = 3e-23
Identities = 85/93 (91%)
Strand = Plus / Minus

Query: 692 ctgtgaaatccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctcc 751

||||||| ||||||| |||| | ||||||| ||||||||| ||||||||| ||||||||| |||||||||

Sbjct: 1130 ctgtgaaacgcacagtggaatcgccatatcaaaggagaccgcatgggtgcttctctcc 1071

Query: 752 ttcgcttgttcttccacgattgctttgtcaatg 784

| || ||||||||| ||||||||| ||||

Sbjct: 1070 tacgtttgttcttccacgattgctttgttaatg 1038

>emb|CU137662.1| Medicago truncatula chromosome 5 clone mth2-15518, COMPLETE SEQUENCE
Length = 111929

Score = 172 bits (87), Expect = 1e-38
Identities = 150/171 (87%)
Strand = Plus / Plus

Query: 1476 agcttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagcc 1535

||||||||||| |||||| | ||| ||||||||| ||||||||| || ||||| |||||

Sbjct: 97958 agcttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagta 98017

Query: 1536 aatctgctgctaacaatggcatccctgacccacttcaaaccttaaccaactcatctcaa 1595

|||| | |||| | |||||| | |||| | ||||||||| || | ||||||||| |||||

Sbjct: 98018 aatcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaa 98077

Query: 1596 gatttagcgctcttggactttccaccaaggacttggctgccttgtccggta 1646

| |||| | |||||| | ||||||||| ||||||||| ||||| ||||

Sbjct: 98078 ggtttaatgctcttggctttccaccaaggatttggctgcattgtctggta 98128

Score = 157 bits (79), Expect = 6e-34

Identities = 172/203 (84%)
Strand = Plus / Plus

Query: 1152 tgcagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
|||||
Sbjct: 97540 tgcagggatgtgatggttcaattctctcgcgatgacacatcaagcttcaccggagagaaaa 97599

Query: 1212 acgcaaaccacaacaggaactctgctcgtggattcgaggttattgacaacattaaatcag 1271
|||
Sbjct: 97600 ctgccaatcccaacaaaaattcggcccgtggattcgaagtgatcgacaaaatcaaatacag 97659

Query: 1272 ccgtggagaaagtgtgtccaggagttgttctcgcgcagatatccttgccatcgctgcca 1331
|
Sbjct: 97660 cagtggagaaagtgtgtccaggatgcagtttcatgcgctgacatccttaccatcactgcta 97719

Query: 1332 gagactctgttcagattgtaagt 1354
|||
Sbjct: 97720 gagactctgttgagatcgtaagt 97742

Score = 119 bits (60), Expect = 1e-22
Identities = 288/364 (79%)
Strand = Plus / Plus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcactcacaacg 1846
|||
Sbjct: 98322 taggggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacg 98381

Query: 1847 agaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcag 1906
|
Sbjct: 98382 actccaacatagatacttctttgctcgcacaaggcaatcagggtgcccgaagacatcgg 98441

Query: 1907 ggtcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaact 1966
|||
Sbjct: 98442 gttccggggacaataatttggcacccttgatcttgcaacaccaacatcctttgacaacc 98501

Query: 1967 actacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttca 2026
|
Sbjct: 98502 attacttcaagaacctagttgacagtaagggtactcactccgaccaacaactcttta 98561

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
|||||
Sbjct: 421 tggaatgttaaacttgaagaagagatgctagaactgcaagccttctgctgccaataat 480

Query: 1553 ggcacccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggga 1612
|||||
Sbjct: 481 ggcattccagctccaacttctaacttgaaccaactcatctcaagatttagtgccttggc 540

Query: 1613 ctttc 1617
|||||
Sbjct: 541 ctttc 545

Score = 54.0 bits (27), Expect = 0.006
Identities = 33/35 (94%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatc 1191
|||||
Sbjct: 214 ggatgtgatggttcaattctacttgatgacacatc 248

Score = 50.1 bits (25), Expect = 0.099
Identities = 31/33 (93%)
Strand = Plus / Plus

Query: 752 ttcgcttggttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 182 ttcgcttggttcttccacgactgctttgttaatg 214

Score = 50.1 bits (25), Expect = 0.099
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaa 1823
|||||
Sbjct: 577 cacacaatcggacaagcaaggtgcacaaa 605

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 2103 catgatcaagatgggagacattag 2126
|||||
Sbjct: 879 catgatcaagatgggagacattag 902

>gb|BT052838.1| Medicago truncatula clone MTYFH_FI_FJ_FK1G-0-8 unknown mRNA
Length = 773

Score = 111 bits (56), Expect = 3e-20
Identities = 146/176 (82%)
Strand = Plus / Minus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| | ||||| ||| ||||| ||||| |||
Sbjct: 464 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactccc 405

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||| ||| ||||| || ||||| || | ||| |||||
Sbjct: 404 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 345

Query: 1283 gtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagactc 1338
|| || || ||||| || || || ||||| ||||| |||||
Sbjct: 344 gtatgccccggagttgtatcatgtgtgatatccttgccattgctgccacagactc 289

Score = 95.6 bits (48), Expect = 2e-15
Identities = 72/80 (90%)
Strand = Plus / Minus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
||||| ||||| ||||| | || || ||||| ||||| |||||
Sbjct: 549 agtgcaatccgccatatcaaaggaggcacgaattgggtgcttctatcctccgcttgttctt 490

Query: 765 ccacgattgctttgtcaatg 784
|||||
Sbjct: 489 ccacgattgctttgtcaatg 470

|||||||
Sbjct: 890 caagaacctcgt 901

Score = 54.0 bits (27), Expect = 0.006
Identities = 78/95 (82%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||| ||||||||||||||||||||| | | || | || |||||||||||||
Sbjct: 1005 gatttcgtggccggcatgatcaagatgggagacgtcacgccgttgacgggctccaatgga 1064

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt 2183
| ||||||||||| || ||||||| |||||||||
Sbjct: 1065 caggtcaggaagaactgcagaagggttaactaatt 1099

>emb|FP099994.1| Phyllostachys edulis cDNA clone: bphyem210i11, full insert sequence
Length = 1213

Score = 103 bits (52), Expect = 8e-18
Identities = 157/192 (81%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||||| || || ||||||| | ||||||||||||||||||| | | ||||||||| |||||||
Sbjct: 688 tcacacataggccaagcacgctgcacaaacttcagagccacgtatacaacgacaccaa 747

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || ||| ||||| ||||| ||||| | | ||||||||| ||||||||| |||||
Sbjct: 748 catcgacggcgcctttgcgaggacgaggcagtcaggttgccctaggacatcaggctcagg 807

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||| ||||| || || || || ||||||||| ||||| ||| || ||| |||||
Sbjct: 808 tgacaacaacctggcgcctctggaccttcaaaccccaaccgtcttcgagaacaactacta 867

Query: 1974 caagaacctcgt 1985
|||||||
Sbjct: 868 caagaacctcgt 879

Score = 54.0 bits (27), Expect = 0.006
Identities = 78/95 (82%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcccgatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||| ||||||||||||||||||| | | || | || |||||||||||||
Sbjct: 983 gatttcgtggccggcatgatcaagatgggagacgtcacgccgttgacgggctccaatgga 1042

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt 2183
| ||||||||||| || ||||||| |||||||||||
Sbjct: 1043 caggtcaggaagaactgcagaagggttaactaatt 1077

>dbj|AB027752.1| Nicotiana tabacum mRNA for peroxidase, complete cds, clone:tpoxC1
Length = 1356

Score = 95.6 bits (48), Expect = 2e-15
Identities = 111/132 (84%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||||| ||||| ||||||| ||||||||||||||||||| ||||||||||||||||||| |||||||||
Sbjct: 719 ctgccaagaagttcagggtcaggggacaacaatttggcaccacttgatcttcaaactcc 778

Query: 1950 aaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctctcctcactc 2009
| || ||||||||||| | || ||||||||||| || |||| | || ||||||||||| || |||||||
Sbjct: 779 taacaaattgacaacaattatttcaagaatcttgttgacaaaagggtctctcctcactc 838

Query: 2010 tgatcagcaact 2021
||||||| |||||||
Sbjct: 839 tgatcaacaact 850

Score = 54.0 bits (27), Expect = 0.006
Identities = 60/71 (84%)
Strand = Plus / Plus

Query: 1232 tctgctcgtggattcgaggttattgacaacattaatcagccgtggagaaagtgtgtcca 1291
||||||| | ||||||| || ||||||||||||||| || ||||||| || ||||||||||||||| ||
Sbjct: 333 tctgctagaggatttgaagttattgacaatatcaaatctgctgtggagaaagtgtgcctc 392

Query: 1292 ggagttgtttc 1302
|| |||||
Sbjct: 393 ggtgtgtttc 403

Score = 50.1 bits (25), Expect = 0.099
Identities = 43/49 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctctcttcgcttgttcttccacgattgctttgtcaatg 784
||||| ||||| | ||||| ||||| |||||
Sbjct: 210 atgggtgcttctctcttcgcttattcttccatgattgcttctgtcaatg 258

Score = 46.1 bits (23), Expect = 1.5
Identities = 104/131 (79%)
Strand = Plus / Plus

Query: 1493 tggaaatgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||| ||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 465 tggaaatgtaaaattggagaagagattctagaactgcaagtcaaagtgtgccaatagt 524

Query: 1553 ggcattcctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggga 1612
||||| ||| | | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 525 ggcattcctcctgctacttctaaccttaatagactcatctcaagtttcagtgtgttggc 584

Query: 1613 ctttccaccaa 1623
||||| |||||
Sbjct: 585 ctttctaccaa 595

>gb|AY837788.2| Catharanthus roseus clone Prx4 putative secretory peroxidase mRNA,
complete cds
Length = 1055

Score = 89.7 bits (45), Expect = 1e-13
Identities = 126/153 (82%)
Strand = Plus / Plus

Query: 1493 tggaaatgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 459 tggaaatgtgaaacttggagaagagatgcaacaactgcaagccaagtgtgctgctaacaat 518

>gb|FJ644943.1| Sesuvium portulacastrum peroxidase 1 (POD1) mRNA, complete cds
Length = 1293

Score = 87.7 bits (44), Expect = 5e-13
Identities = 71/80 (88%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
|||||
Sbjct: 937 atgatcaagatgggtgacatcaaaccttactggttcaatggagaaattaggaagaat 996

Query: 2164 tgtagaaggattaactaatt 2183
||
Sbjct: 997 tgcagaaggattaactaatt 1016

Score = 61.9 bits (31), Expect = 3e-05
Identities = 61/71 (85%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 457 cttggaggaccaacatgggatgtgaaactaggaagaagagatgccagaacagctaacca 516

Query: 1538 tctgctgctaa 1548
|||||
Sbjct: 517 gctgctgctaa 527

Score = 54.0 bits (27), Expect = 0.006
Identities = 51/59 (86%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacttacaacga 1847
|||||
Sbjct: 622 ggtggcactcaataggacaagcaaggtgcacaaatctcagggtcacatatacaacga 680

>dbj|AK242814.1| Oryza sativa Japonica Group cDNA, clone: J090061H15, full insert
sequence
Length = 1215

Score = 85.7 bits (43), Expect = 2e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||| ||||||||||| | ||||||||||||||| | || ||||||| |||||
Sbjct: 662 tcacaccattggacaagcagcatgcacaaacttcagagctcacatatacaacgaaaccaa 721

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaagctgccctagaacatcagggtcagg 1913
||| || | | ||||| | || ||||| | ||||||| | | ||||| |||||
Sbjct: 722 catcgacagtggctttgcatgagcaggcaatcaggctgccctcgtagctcaggctcagg 781

Query: 1914 ggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactactactt 1973
||||||||||||||||| | |||||||| | |||||| | | || || || |||||
Sbjct: 782 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 841

Query: 1974 caagaacctgcttcagaagaagggtctcctccactctgatcag 2016
||||||||||| ||||||| ||||| |||||||||||
Sbjct: 842 caagaacctgctcgaagaagggtctcctgcactctgatcag 884

>ref|NM_001072100.1| Oryza sativa (japonica cultivar-group) Os11g0112400 (Os11g0112400)
mRNA, complete cds
Length = 975

Score = 85.7 bits (43), Expect = 2e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||| ||||||||||| | ||||||||||||||| | || ||||||| |||||
Sbjct: 588 tcacaccattggacaagcagcatgcacaaacttcagagctcacatatacaacgaaaccaa 647

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaagctgccctagaacatcagggtcagg 1913
||| || | | ||||| | || ||||| | ||||||| | | ||||| |||||
Sbjct: 648 catcgacagtggctttgcatgagcaggcaatcaggctgccctcgtagctcaggctcagg 707

Query: 1914 ggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactactactt 1973
||||||||||||||||| | |||||||| | |||||| | | || || || |||||
Sbjct: 708 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 767

Query: 1974 caagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 768 caagaacctcgctgcaagaagggctcctgcactctgatcag 810

>tpe|BN000659.1| TPA: TPA_inf: Oryza sativa (japonica cultivar-group) prx130 gene for
class III peroxidase 130 precursor, exons 1-4
Length = 2195

Score = 85.7 bits (43), Expect = 2e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcactctacaacgagaccaa 1853
||||| ||||||| ||||| ||||||| ||||||| ||||| ||||| ||||| |||||
Sbjct: 1808 tcacaccattggacaagcagcatgcacaaacttcagagctcacatatacaacgaaaccaa 1867

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaagctgccctagaacatcagggtcagg 1913
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1868 catcgacagtggctttgcatgagcaggcaatcaggctgccctcgtagctcaggctcagg 1927

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactact 1973
||||||| ||||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1928 tgacaacaatctggcacctttgatcttcagacccaaccgtgttcgagaacaactacta 1987

Query: 1974 caagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1988 caagaacctcgctgcaagaagggctcctgcactctgatcag 2030

>dbj|AB019228.1| Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCK7
Length = 87090

Score = 85.7 bits (43), Expect = 2e-12
Identities = 52/55 (94%)
Strand = Plus / Minus

Query: 733 cgcattgggtgcttctctccttcgcttcttccacgattgctttgtcaatgtaa 787
||||||| ||||||| ||||| ||||| ||||| |||||
Sbjct: 74225 cgcattgggtgcttctctccttcgcttcttccatgattgtttgtcaatgtaa 74171

>emb|BX000512.1| Oryza sativa chromosome 11, . BAC OSJNBa0025K19 of library OSJNBa from

chromosome 11 of cultivar Nipponbare of ssp. japonica of
Oryza sativa (rice), complete sequence
Length = 181322

Score = 85.7 bits (43), Expect = 2e-12
Identities = 178/223 (79%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||| ||||||||| | ||||||||| ||| ||||||| |||||
Sbjct: 158955 tcacaccattggacaagcacgatgcacaaacttcagagctcacatatacaacgaaaccaa 158896

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | | ||||| || ||||| | ||||||| | | ||||| |||||
Sbjct: 158895 catcgacagtggctttgcatgagcaggcaatcaggctgccctcgtagctcaggctcagg 158836

Query: 1914 ggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactactactt 1973
||||||||||| ||| ||||||| || ||||| || || ||| |||||
Sbjct: 158835 tgacaacaatctggcaccttggatcttcagacgccaaccgtgttcgagaacaactacta 158776

Query: 1974 caagaacctcgcttcagaagaagggtctctcctcactctgatcag 2016
||||||| ||| ||||| ||||| |||||||||
Sbjct: 158775 caagaacctcgctcgaagaagggtctcctcactctgatcag 158733

>gb|EF661875.2| Catharanthus roseus putative secretory peroxidase (Prx3) mRNA,
complete cds
Length = 1233

Score = 83.8 bits (42), Expect = 7e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttgcgccgccatgatcaagatgggagacattagtcctctcactggc 2139
|||| ||||||||| || ||||||||| ||||||||| ||||||||| | |||||
Sbjct: 924 ttctactctgatttgcgccgccatgatcaagatgggagatattagtcctttgactggt 983

Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
|| ||||||| | ||||| ||||||| || |||||
Sbjct: 984 tcaaatggagaggttaggaaaaattgtagagggttaa 1021

Score = 46.1 bits (23), Expect = 1.5
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcaca 1821
 |||||
Sbjct: 639 cacacaattgggtcaagcaaggtgcaca 665

>ref|NM_125225.1| Arabidopsis thaliana peroxidase, putative (AT5G58390) mRNA,
 complete cds
 Length = 1220

Score = 79.8 bits (40), Expect = 1e-10
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
 |||||
Sbjct: 229 cgc atgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 280

>dbj|AK117722.1| Arabidopsis thaliana At5g58390 mRNA for putative peroxidase,
 complete cds, clone: RAFL17-40-J20
 Length = 656

Score = 79.8 bits (40), Expect = 1e-10
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
 |||||
Sbjct: 226 cgc atgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 277

>gb|AY085030.1| Arabidopsis thaliana clone 124846 mRNA, complete sequence
 Length = 1220

Score = 79.8 bits (40), Expect = 1e-10
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
 |||||
Sbjct: 229 cgc atgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 280

>ref|XM_002269882.1| PREDICTED: Vitis vinifera hypothetical protein LOC100257005
(LOC100257005), mRNA
Length = 1180

Score = 75.8 bits (38), Expect = 2e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 754 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 813

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 814 tactacaagaacct 827

Score = 58.0 bits (29), Expect = 4e-04
Identities = 47/53 (88%)
Strand = Plus / Plus

Query: 732 ccgcatgggcttctctccttcgcttgttcttccagattgctttgtcaatg 784
||||||||| ||||||||||| || | ||||||| |||||||||||
Sbjct: 225 ccgcatgggcttctctccttcgcttcttccatgattgctttgtcaatg 277

>emb|AM447728.2| Vitis vinifera contig VV78X018697.9, whole genome shotgun sequence
Length = 22220

Score = 75.8 bits (38), Expect = 2e-09
Identities = 65/74 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 11004 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 10945

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 10944 tactacaagaacct 10931

Score = 65.9 bits (33), Expect = 2e-06
Identities = 51/57 (89%)
Strand = Plus / Minus

Query: 732 ccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaat 788
||||||| ||||||||| || | ||||||| |||||||||
Sbjct: 12714 ccgcatgggcgcttctctcctccgtctcttccatgattgctttgtcaatgtaat 12658

>ref|XM_002278960.1| PREDICTED: Vitis vinifera hypothetical protein LOC100257059
(LOC100257059), mRNA
Length = 966

Score = 71.9 bits (36), Expect = 3e-08
Identities = 101/120 (84%), Gaps = 2/120 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagcttt-gacaacta 1967
||||||| |||| | | ||||||| || ||||| || || |
Sbjct: 694 tcaggggacaacaacttggccctctggatcttcaactcctac-agcttttgagaaca 752

Query: 1968 ctacttcaagaacctggtcagaagaagggtctcctcactctgatcagcaactgttcaa 2027
||||| ||||||| | ||||||| || | ||||||| |||||||
Sbjct: 753 ctactacaagaacctgatcaagaagaagggtctcctcactctgatcagcagctgttcaa 812

Score = 67.9 bits (34), Expect = 4e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaac 1854
||||||| ||||||||| ||||| ||||||| ||||| ||||| |||
Sbjct: 580 cacacaattgggcaagcaaggtgcacatccttcagggcccgcataataatgagacaac 639

Query: 1855 at 1856
||
Sbjct: 640 at 641

Score = 65.9 bits (33), Expect = 2e-06
Identities = 129/161 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| |||| | |||| | || ||||| | ||||| | | || || |||||
Sbjct: 409 cttggaggccctagctggaacgtaaaacttggcgaagagacgcccgaccgcaagccag 468

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
||||||| |||| | ||||| | || ||||| ||||| ||||| ||||| |||||
Sbjct: 469 gctgctgcaacaacagcatccctcctccaacttcaaactgaaccaactaatctctaga 528

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgcctt 1638
|| | ||||| || || || || || ||||| |||||
Sbjct: 529 ttccaagctcttggcctctcaaccaggacttggttgcctt 569

Score = 58.0 bits (29), Expect = 4e-04
Identities = 59/69 (85%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||||| ||||| || || || || ||||| || ||||| || ||||| || |||||
Sbjct: 889 atgatcaagatgggagatatcagccactcactggatcaaatggagagattaggaagaac 948

Query: 2164 tgtagaagg 2172
|| |||||
Sbjct: 949 tgcagaagg 957

>gb|AY206413.1| Ipomoea batatas anionic peroxidase swpb2 mRNA, complete cds
Length = 1263

Score = 71.9 bits (36), Expect = 3e-08
Identities = 57/64 (89%)
Strand = Plus / Plus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaaga 2161
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 989 ccatgatcaagatggccaacatttcgctctcactggctccaaggagaaatcaggaaga 1048

Query: 2162 attg 2165
|||
Sbjct: 1049 attg 1052

>gb|EZ399860.1| TSA: Artemisia annua strain Uganda Contig16355, mRNA sequence
Length = 1170

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||||||||| ||||||||||| |||||||| | ||||| |||||||
Sbjct: 518 ctgccaagaacctcagggtcaggagacaacaatttggcaccgctagatctcaaactcc 459

Query: 1950 aac 1952
|||
Sbjct: 458 aac 456

>gb|EZ145065.1| TSA: Artemisia annua strain Artemis Contig4471, mRNA sequence
Length = 1332

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||||||||| ||||||||||| |||||||| | ||||| |||||||
Sbjct: 713 ctgccaagaacctcagggtcaggagacaacaatttggcaccgctagatctcaaactcc 772

Query: 1950 aac 1952
|||
Sbjct: 773 aac 775

Score = 58.0 bits (29), Expect = 4e-04
Identities = 44/49 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgcttcttccacgattgctttgtcaatg 784
||||| ||||||||||||||| ||| ||||||| |||||||||||||||
Sbjct: 207 atgggcgcttctctccttcgcttgcttccatgattgctttgtcaatg 255

Score = 48.1 bits (24), Expect = 0.39
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgggaaga 1513
||||||| ||||||||||||| ||||| |||||
Sbjct: 447 cttggaggacctacatggaatgtgaaactgggaaga 482

>gb|EZ141680.1| TSA: Artemisia annua strain Artemis Contig1086, mRNA sequence
Length = 456

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||||||||| ||||||||| ||||||| || ||||| |||||||
Sbjct: 224 ctgccaagaacctcagggtcagggagacaacaatttggcaccgctagatctcaaactcc 283

Query: 1950 aac 1952
|||
Sbjct: 284 aac 286

>ref|XM_002489001.1| Sorghum bicolor hypothetical protein (SORBIDRAFT_0246s002010) mRNA,
complete cds
Length = 1045

Score = 69.9 bits (35), Expect = 1e-07
Identities = 200/255 (78%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||| ||||||| || || ||||||| | ||||| ||||||||| || |||||||||
Sbjct: 653 ggtgctcacacataggccaagcagctgcaccaacttcagagaccacatctacaacgac 712

Query: 1849 accaacatagaaacgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
||||||| | || || ||||||||| ||||| | | || ||||| || |||||
Sbjct: 713 accaacgtcgacggagcctttgaaggacaaggcaatcaggttgctcctagcacctcagga 772

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

Query: 1596 gatttagcgtcttggactttccaccaaggacttggtcgcctt 1638
||||| ||||||| || || ||||| ||||||| |||||
Sbjct: 15048 gattccaagctcttggcctctcaaccaggacttggttgcctt 15090

Score = 67.9 bits (34), Expect = 4e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcctctacaacgagaccaac 1854
||||||||| ||||||||||||| ||||| ||||||| ||||| ||||| |||
Sbjct: 15195 cacacaattgggcaagcaaggtgcacatccttcagggcccgcatatacaatgagacaaac 15254

Query: 1855 at 1856
||
Sbjct: 15255 at 15256

Score = 67.9 bits (34), Expect = 4e-07
Identities = 100/120 (83%), Gaps = 2/120 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaactctggcaccacttgatcttcaaactccaaccagcttt-gacaacta 1967
||| ||||||||| |||| || || ||||||||||||| || ||||||| || ||| |
Sbjct: 15309 tcargggacaacaacttggccctctggatcttcaaactcctac-agcttttgagaacaa 15367

Query: 1968 ctacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaa 2027
||||| ||||||||| | ||||||| || || ||||||||||||| |||||||
Sbjct: 15368 ctactacaagaacctgatcaagaagaagggtctcctccactctgatcagcagctgttcaa 15427

Score = 58.0 bits (29), Expect = 4e-04
Identities = 59/69 (85%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||||||||||||| || || || ||||||| || ||||||| || |||||||
Sbjct: 15504 atgatcaagatgggagatatcagcccactcactggatcaaatggagagattaggaagaac 15563

Query: 2164 tgtagaagg 2172

|| |||||
Sbjct: 15564 tgcagaagg 15572

>gb|GU230149.1| Ipomoea batatas anionic peroxidase mRNA, complete cds
Length = 1125

Score = 67.9 bits (34), Expect = 4e-07
Identities = 46/50 (92%)
Strand = Plus / Plus

Query: 730 acccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgt 779
|||||
Sbjct: 289 acccgcatgggtgcttccctcattcgcttgttcttccatgactgctttgt 338

>ref|XM_002268223.1| PREDICTED: Vitis vinifera hypothetical protein LOC100263665
(LOC100263665), mRNA
Length = 1002

Score = 67.9 bits (34), Expect = 4e-07
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttc 1827
|||||
Sbjct: 516 tcacacaattggacaagcaaggtgcacaaacttc 549

>gb|FJ099755.1| Pinus taeda isolate 1286 anonymous locus 2_6350_01 genomic sequence
Length = 410

Score = 67.9 bits (34), Expect = 4e-07
Identities = 61/70 (87%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacg 1846
||||| ||| ||||| ||||| ||||| | |||||
Sbjct: 308 tagtggtcacaattggccaagcaggtgcaccacattcagagcccgcattctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>emb|CU231251.1| Populus EST from mild drought-stressed leaves
Length = 584

Score = 67.9 bits (34), Expect = 4e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| || ||||||||||||||||| ||| ||||| ||||| ||||| |||||||||
Sbjct: 138 cacacaatcgggcaagcaaggtgcacaagctttagagctcgcataatacaatgagaccaac 197

Query: 1855 at 1856
||
Sbjct: 198 at 199

>gb|AY206412.1| Ipomoea batatas anionic peroxidase swpb1 mRNA, complete cds
Length = 1257

Score = 67.9 bits (34), Expect = 4e-07
Identities = 37/38 (97%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaagaattg 2165
||||||||| |||||||||||||||||||||
Sbjct: 1002 cctctcactggtccaatggagaaatcaggaagaattg 1039

Score = 44.1 bits (22), Expect = 6.1
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 1217 aacccaacaggaactctgctcgtgg 1242
||||||||| |||||||||||||
Sbjct: 348 aacccaacagaaactctgctcgtgg 373

>dbj|AK322204.1| Solanum lycopersicum cDNA, clone: LEFL1035AA07, HTC in leaf
Length = 1170

Score = 65.9 bits (33), Expect = 2e-06
Identities = 48/53 (90%)
Strand = Plus / Plus

Query: 2023 ttcaa 2027
|||||
Sbjct: 867 ttcaa 871

>ref|XM_002328955.1| Populus trichocarpa predicted protein, mRNA
Length = 1047

Score = 65.9 bits (33), Expect = 2e-06
Identities = 57/65 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
|||||
Sbjct: 633 cacacaattggacaagcaagatgcacaaactttagggcacgcatatataatgagaccacc 692

Query: 1855 ataga 1859
|||||
Sbjct: 693 ataga 697

Score = 54.0 bits (27), Expect = 0.006
Identities = 66/79 (83%)
Strand = Plus / Plus

Query: 2103 catgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
|||||
Sbjct: 941 catgatcaagatgggagatatcaggcctctcactggatccagaggagagattagaaataa 1000

Query: 2163 ttgtagaaggattaactaa 2181
||| || ||||| |||||
Sbjct: 1001 ttgcaggaggatcaactaa 1019

Score = 44.1 bits (22), Expect = 6.1
Identities = 34/38 (89%)
Strand = Plus / Plus

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactcc 1949
|||||
Sbjct: 750 ggggacaacaacttggcaccacttgattgcaaactcc 787

>ref|XM_002319932.1| Populus trichocarpa predicted protein, mRNA
Length = 1220

Score = 65.9 bits (33), Expect = 2e-06
Identities = 57/65 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| || ||||||||||| |||| ||| ||||| ||||| ||||| |||||||||
Sbjct: 592 cacacaatcgggcaagcaaggtgtacaagctttagagctcgcatatacaatgagaccaac 651

Query: 1855 ataga 1859
|||||
Sbjct: 652 ataga 656

Score = 48.1 bits (24), Expect = 0.39
Identities = 39/44 (88%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgcttcttccacgattgctttgt 779
||||||||||||| ||||||||||| || ||||| |||||
Sbjct: 178 atgggtgcttctcttgttcgcttgcttcttccatgattgctttgt 221

>gb|AC214418.1| Populus trichocarpa clone POP106-D21, complete sequence
Length = 88637

Score = 65.9 bits (33), Expect = 2e-06
Identities = 57/65 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| || ||||||||||| |||| ||| ||||| ||||| ||||| |||||||||
Sbjct: 88236 cacacaatcgggcaagcaaggtgtacaagctttagagctcgcatatacaatgagaccaac 88295

Query: 1855 ataga 1859
|||||
Sbjct: 88296 ataga 88300

Score = 52.0 bits (26), Expect = 0.025
Identities = 41/46 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtca 781
|||||
Sbjct: 86397 atgggtgcttctcttgttcgcttggttcttccatgattgtttgtca 86442

>gb|BT096974.1| Soybean clone JCVI-FLGm-21M8 unknown mRNA
Length = 1201

Score = 63.9 bits (32), Expect = 7e-06
Identities = 44/48 (91%)
Strand = Plus / Plus

Query: 1810 gcaaggtgcacaaacttcagagcccgcatctacaacgagaccaacata 1857
|||||
Sbjct: 639 gcaaggtgcactaccttcagagaccgcatctacaacgacaccaacata 686

>gb|AC235472.1| Glycine max strain Williams 82 clone GM_WBc0099F23, complete sequence
Length = 134971

Score = 63.9 bits (32), Expect = 7e-06
Identities = 47/52 (90%)
Strand = Plus / Plus

Query: 2997 tatcttttgtttcatttactttatgtgaggatataatagtaataataacatt 3048
|||||
Sbjct: 77662 tatcttttgtatcatttgcattatgttaggatataatagttataaaacatt 77713

>gb|FJ596178.1| Capsicum annuum peroxidase (POD) mRNA, complete cds
Length = 1353

Score = 63.9 bits (32), Expect = 7e-06
Identities = 59/68 (86%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
|||||
Sbjct: 646 agtgctcacacaattggacaagcaaggtgcacatcattcagggcacgtatatacaatga 705

Query: 1848 gaccaaca 1855
 |||||||
Sbjct: 706 gaccaaca 713

Score = 61.9 bits (31), Expect = 3e-05
Identities = 55/63 (87%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
 ||||||| ||| | ||| | | ||||| | | ||||| |||||||
Sbjct: 965 atgatcaagatgggtgacaatcgccacttactggatctaatggagaaattaggaagaat 1024

Query: 2164 tgt 2166
 |||
Sbjct: 1025 tgt 1027

Score = 54.0 bits (27), Expect = 0.006
Identities = 48/55 (87%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
 ||||||| ||| | || | ||||| |||||||
Sbjct: 290 ggatgtgatggatcactgctccttgatgacacatcaagcttcactggagagaaga 344

Score = 44.1 bits (22), Expect = 6.1
Identities = 43/50 (86%)
Strand = Plus / Plus

Query: 1568 acttcaaaccttaaccaactcatctcaagatttagcgctcttggactttc 1617
 ||||| ||||| ||||| || ||||| || ||||| |||||
Sbjct: 572 acttctaaccttaactcaactcatctctagtttagtgctgttggcctttc 621

>gb|EF433455.1| Ipomoea batatas basic peroxidase swpb4 mRNA, complete cds
Length = 1369

Score = 63.9 bits (32), Expect = 7e-06
Identities = 47/52 (90%)
Strand = Plus / Plus

Query: 733 cgc atgggtcttctctctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||||| || ||||||||||||| | ||||||||||| |||||||||||
Sbjct: 180 cgc atgggcctctctctctccttcgcctcttcttccacgactgctttgtcaatg 231

Score = 60.0 bits (30), Expect = 1e-04
Identities = 63/74 (85%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcccgatgatcaagatgggagacattagtcctctcactggetccaatgga 2148
||||||| ||||||||||||||||||||| || || | || ||||||| |||||||
Sbjct: 888 gatttcgcagcccgatgatcaagatgggtgatatcaagcccctcactgggaacaatgga 947

Query: 2149 gaaatcaggaagaa 2162
|| |||||||||
Sbjct: 948 gagatcaggaagaa 961

Score = 44.1 bits (22), Expect = 6.1
Identities = 43/50 (86%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaa 1209
||||||| ||||||| ||||| || ||||| |||||||||||||
Sbjct: 234 tgtgatggatcaattctcttggacgatacatcttccttcaccggagagaa 283

>gb|AC235385.1| Glycine max strain Williams 82 clone GM_WBb0113B18, complete sequence
Length = 137121

Score = 61.9 bits (31), Expect = 3e-05
Identities = 37/39 (94%)
Strand = Plus / Minus

Query: 277 aaattatTTTTCTTTAATTCTTAATTAATATCCTAA 315
|||| ||||||||||||||||| |||||||||||||
Sbjct: 62660 aaataatTTTTCTTTAATTTTTAATTAATATCCTAA 62622

>gb|GQ258782.1| Brassica rapa peroxidase 52 mRNA, partial cds
Length = 1113

Score = 60.0 bits (30), Expect = 1e-04
Identities = 147/186 (79%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| || ||||| ||||| | ||||||||||||||||| || ||||| | |||||
Sbjct: 172 ggatgcgacggttctattctactagatgacacatcaagctttacgggagaacaaaacgcg 231

Query: 1217 aaccccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276
||||| ||| | || ||||| ||||| || | || || || ||||| ||||| ||| ||
Sbjct: 232 aaccccaaccgcaattctgctcgtgggtttaatgtgatagacaacattaaaacagcggtt 291

Query: 1277 gaaaagtgtgtccaggagttgtttcctgcgcatatccttgccatcgctgccagagac 1336
|| || ||||| || ||||| || || || ||||| || ||||| || |||||
Sbjct: 292 gaagcagcatgtcccgggttggtgtcttgtgctgatatcttagccatcgagctagagac 351

Query: 1337 tctgtt 1342
|||||
Sbjct: 352 tctgtt 357

>gb|FJ099770.1| Pinus taeda isolate 1299 anonymous locus 2_6350_01 genomic sequence
Length = 439

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||| ||||| ||||| | ||||| ||||| ||||| |||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099768.1| Pinus taeda isolate 1282 anonymous locus 2_6350_01 genomic sequence
Length = 448

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)

>gb|FJ099765.1| Pinus taeda isolate 1288 anonymous locus 2_6350_01 genomic sequence
Length = 438

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099762.1| Pinus taeda isolate 1298 anonymous locus 2_6350_01 genomic sequence
Length = 357

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||
Sbjct: 307 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 248

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 247 aatccaacat 238

>gb|FJ099761.1| Pinus taeda isolate 1289 anonymous locus 2_6350_01 genomic sequence
Length = 360

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099760.1| Pinus taeda isolate 1297 anonymous locus 2_6350_01 genomic sequence
Length = 357

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099759.1| Pinus taeda isolate 1283 anonymous locus 2_6350_01 genomic sequence
Length = 357

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099758.1| Pinus taeda isolate 1287 anonymous locus 2_6350_01 genomic sequence
Length = 449

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099757.1| Pinus taeda isolate 1291 anonymous locus 2_6350_01 genomic sequence
Length = 358

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcacatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|EF433456.1| Ipomoea batatas basic peroxidase swpb5 mRNA, complete cds
Length = 1331

Score = 60.0 bits (30), Expect = 1e-04
Identities = 36/38 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaagaattg 2165
||||||||||| ||| |||||||||||||||||||
Sbjct: 1038 cctctcactggttcccatggagaaatcaggaagaattg 1075

>gb|AC226196.1| Musa acuminata clone BAC MA4-125A12, complete sequence
Length = 110853

Score = 60.0 bits (30), Expect = 1e-04
Identities = 51/58 (87%)
Strand = Plus / Plus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||| ||||| ||| |||| | ||||| || | ||||| ||||| |||||
Sbjct: 32082 cagggctgtgatggatcagttctgctggatgacacgtccagcttcaccggagagaaga 32139

Score = 46.1 bits (23), Expect = 1.5
Identities = 71/87 (81%)
Strand = Plus / Plus

Query: 1960 gacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaa 2019
||||| ||||| |||| | || | ||||| || | |||| | |||||
Sbjct: 32773 gacaacttctacttcaggaacttggtgaagaagaaggcctgctgcactcggaccagcag 32832

Query: 2020 ctgttcaacgggtgggtccaccgactcc 2046
||||| || || ||||| |||||
Sbjct: 32833 ctgttcagtggaggatccaccgactcc 32859

>ref|XM_001754018.1| Physcomitrella patens subsp. patens predicted protein
(PHYPADRAFT_115024) mRNA, complete cds
Length = 1095

Score = 60.0 bits (30), Expect = 1e-04
Identities = 36/38 (94%)
Strand = Plus / Plus

Query: 741 tgcttctctccttcgcttggttcttccacgattgctttg 778
|||| |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 273 tgctgctctgcttcgcttggttcttccacgattgctttg 310

>emb|AM449831.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X191828.16,
clone ENTAV 115
Length = 47040

Score = 60.0 bits (30), Expect = 1e-04
Identities = 33/34 (97%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttc 1827
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 34025 tcacacaattggacaagcaaggtgcacaagcttc 33992

>gb|AY206414.1| Ipomoea batatas anionic peroxidase swpb3 mRNA, complete cds
Length = 1290

Score = 60.0 bits (30), Expect = 1e-04
Identities = 63/74 (85%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcccgatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||||||||||||||||| || || | || ||||||| |||||
Sbjct: 918 gatttcgcagcccgatgatcaagatgggtgatatcaagccactcactgggaacaatgga 977

Query: 2149 gaaatcaggaagaa 2162
|| |||||||||
Sbjct: 978 gagatcaggaagaa 991

Score = 56.0 bits (28), Expect = 0.002
Identities = 46/52 (88%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||||| || ||||||||||||| | ||||||| || |||||||||
Sbjct: 210 cgcatgggcgctctctccttcgcttcttcttccatgactgctttgtcaatg 261

>gb|AF485265.1| Gossypium hirsutum class III peroxidase (pod3) mRNA, complete cds
Length = 1336

Score = 60.0 bits (30), Expect = 1e-04
Identities = 42/46 (91%)
Strand = Plus / Plus

Query: 737 tgggtgcttctctccttcgcttgttcttccacgattgctttgtcaa 782
||||||||||||||| ||||||||||||| || || |||||
Sbjct: 257 tgggtgcttctctcctccgcttgttcttccatgactgttttgtcaa 302

Score = 52.0 bits (26), Expect = 0.025
Identities = 53/62 (85%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163

||||| ||||||||||||| |||| | || ||||| || | ||||| |||||||||||||||||
Sbjct: 979 atgataaagatgggagatattaagccactcaccgatcaaattggtgaaatcaggaagaat 1038

Query: 2164 tg 2165

||
Sbjct: 1039 tg 1040

>gb|EZ328614.1| TSA: Artemisia annua strain Madagascar Contig15160, mRNA sequence
Length = 324

Score = 58.0 bits (29), Expect = 4e-04
Identities = 44/49 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgcttcttccacgattgctttgtcaatg 784

||||| ||||||||||||||||| ||| ||||||| |||||||||||||||||
Sbjct: 202 atgggcgcttctctccttcgcttgcacttccatgattgctttgtcaatg 250

>gb|EZ256818.1| TSA: Artemisia annua strain Artemis Contig23488, mRNA sequence
Length = 426

Score = 58.0 bits (29), Expect = 4e-04
Identities = 44/49 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgcttcttccacgattgctttgtcaatg 784

||||| ||||||||||||||||| ||| ||||||| |||||||||||||||||
Sbjct: 204 atgggcgcttctctccttcgcttgcacttccatgattgctttgtcaatg 252

>gb|EZ397212.1| TSA: Artemisia annua strain Uganda Contig13707, mRNA sequence
Length = 491

Score = 58.0 bits (29), Expect = 4e-04
Identities = 44/49 (89%)
Strand = Plus / Minus

Query: 736 atgggtgcttctctccttcgcttgcttcttccacgattgctttgtcaatg 784

||||| ||||||||||||||||| ||| ||||||| |||||||||||||||||
Sbjct: 167 atgggcgcttctctccttcgcttgcacttccatgattgctttgtcaatg 119

>dbj|AK328734.1| Solanum lycopersicum cDNA, clone: LEFL3035G12, HTC in root

Length = 1222

Score = 58.0 bits (29), Expect = 4e-04
Identities = 59/69 (85%)
Strand = Plus / Plus

Query: 1215 caaaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccg 1274
|||||
Sbjct: 354 caaaccccaacaggaactcggtcgtggatttgatgtcattgatgatattaaatctgcac 413

Query: 1275 tggagaaag 1283
|||||
Sbjct: 414 tggagaaag 422

>gb|AC235153.1| Glycine max strain Williams 82 clone GM_WBa0085L07, complete sequence
Length = 99314

Score = 58.0 bits (29), Expect = 4e-04
Identities = 68/81 (83%)
Strand = Plus / Minus

Query: 2736 ttaaatcattcgaacgtaaataaactaaacattagaacataatcatccttaacaatc 2795
|||||
Sbjct: 90525 ttaaatcattcaacaacatcataattaacattcgaacataaccatttttaatgatc 90466

Query: 2796 aatattttaattcttaaactt 2816
|||||
Sbjct: 90465 aatattctaattcttaaactt 90445

>gb|AC235140.1| Glycine max strain Williams 82 clone GM_WBa0068I04, complete sequence
Length = 138531

Score = 58.0 bits (29), Expect = 4e-04
Identities = 68/81 (83%)
Strand = Plus / Plus

Query: 2736 ttaaatcattcgaacgtaaataaactaaacattagaacataatcatccttaacaatc 2795
|||||
Sbjct: 102124 ttaaatcattcaacaacatcataattaacattcgaacataaccatttttaatgatc 102183

Query: 2796 aatattttaattcttaaactt 2816

||||| |||||||||
Sbjct: 102184 aatattctaattcttaaactt 102204

>emb|AJ544515.1| Asparagus officinalis partial mRNA for peroxidase (prx2 gene)
Length = 1041

Score = 58.0 bits (29), Expect = 4e-04
Identities = 53/61 (86%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
||||| ||||||||| ||||| || ||||||| || || ||||| || |||||
Sbjct: 826 gccatgatcaagatgggagatattagccccctcactgggtctaaaggagagattaggaag 885

Query: 2161 a 2161
|
Sbjct: 886 a 886

>ref|XM_002521820.1| Ricinus communis Lignin-forming anionic peroxidase precursor,
putative, mRNA
Length = 978

Score = 56.0 bits (28), Expect = 0.002
Identities = 49/56 (87%)
Strand = Plus / Plus

Query: 1265 aaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcatatccttgc 1320
||||| || ||||||||| | ||||| ||||||||| ||||||||| |||||||||
Sbjct: 343 aaatctgcagtgagaaagatatgtcctggagttgtttcctgcgctgatatccttgc 398

>ref|XM_002521805.1| Ricinus communis Lignin-forming anionic peroxidase precursor,
putative, mRNA
Length = 978

Score = 56.0 bits (28), Expect = 0.002
Identities = 49/56 (87%)
Strand = Plus / Plus

Query: 1265 aaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcatatccttgc 1320
||||| || ||||||||| | ||||| ||||||||| ||||||||| |||||||||
Sbjct: 343 aaatctgcagtgagaaagatatgtcctggagttgtttcctgcgctgatatccttgc 398

>ref|XM_002521804.1| Ricinus communis Peroxidase 30 precursor, putative, mRNA
Length = 891

Score = 56.0 bits (28), Expect = 0.002
Identities = 49/56 (87%)
Strand = Plus / Plus

Query: 1265 aaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagatataccttgc 1320
||||| || |||||||| | ||||| ||||||||||||||||| |||||||||
Sbjct: 343 aaatctgcagtgagagaagatatgtcctggagttgtttcctgcgctgatataccttgc 398

>gb|FJ529216.1| Cucumis sativus 1-aminocyclopropane-1-carboxylate synthase (ACS2) gene,
ACS2-M allele and putative peroxidase gene, complete cds
Length = 52751

Score = 56.0 bits (28), Expect = 0.002
Identities = 34/36 (94%)
Strand = Plus / Minus

Query: 751 cttcgcttgttcttccacgattgctttgtcaatgta 786
||||| ||||||||||||||||||| |||||
Sbjct: 50350 cttcgcatgttcttccacgattgctttgtaaagta 50315

>ref|XM_002450088.1| Sorghum bicolor hypothetical protein, mRNA
Length = 1265

Score = 56.0 bits (28), Expect = 0.002
Identities = 58/68 (85%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||| ||||| ||||| ||||| | ||||| ||||||||||||| ||| |||||||
Sbjct: 686 ggtgctcacaccattgggcaagcacggtgcacaaacttcagagcccacatatacaacgac 745

Query: 1849 accaacat 1856
||| ||||
Sbjct: 746 accgacat 753

>gb|FJ050772.1| Pinus taeda isolate 4650 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.002
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcaggcccgcattctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||
Sbjct: 442 cgaatccaacat 431

>gb|FJ050764.1| Pinus taeda isolate 4651 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.002
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcaggcccgcattctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||
Sbjct: 442 cgaatccaacat 431

>gb|FJ050758.1| Pinus taeda isolate 4655 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.002
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtgcgcacacgataggccaagcgcggtgcacaagcttcaggcccgcattctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||
Sbjct: 442 cgaatccaacat 431

>gb|FJ050757.1| Pinus taeda isolate 4653 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.002
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtggtcacacacataggccaagcgcggtgcacaagcttcaggcccgcacatctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||
Sbjct: 442 cgaatccaacat 431

>gb|AF149278.1|AF149278 Phaseolus vulgaris peroxidase 3 precursor (FBP3) mRNA, complete cds
Length = 1850

Score = 56.0 bits (28), Expect = 0.002
Identities = 46/52 (88%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||||| ||||||||| ||||| || || |||||||||
Sbjct: 981 cgcatgggagcttctctccttcgcctcttcttcatgactgctttgtcaatg 1032

>dbj|AK320453.1| Solanum lycopersicum cDNA, clone: LEFL1009CA06, HTC in leaf
Length = 1260

Score = 54.0 bits (27), Expect = 0.006
Identities = 57/67 (85%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
||| ||||||||| ||||| || || || || || || |||||
Sbjct: 649 ggtggtcacacaattggacaagcaagatgcacaacatttagggcacgtatatacaatgag 708

Query: 1849 accaaca 1855
|||||
Sbjct: 709 accaaca 715

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
|||||
Sbjct: 967 atgatcaagatgggagatattcgtccacttactggatcgaatggtgaaattaggaagaa 1025

>dbj|AK320190.1| Solanum lycopersicum cDNA, clone: LEFL1006BD07, HTC in leaf
Length = 1236

Score = 54.0 bits (27), Expect = 0.006
Identities = 48/55 (87%)
Strand = Plus / Plus

Query: 1215 caaaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatc 1269
|||||
Sbjct: 354 caaaccccaacaggaattcagctcgtggattcgaagtccttgacgagattaaatc 408

>gb|AC235342.1| Glycine max strain Williams 82 clone GM_WBb0088H14, complete sequence
Length = 183165

Score = 54.0 bits (27), Expect = 0.006
Identities = 33/35 (94%)
Strand = Plus / Plus

Query: 281 tattttttcttttaatttcttaattaatcctaa 315
|||||
Sbjct: 50421 tattttttcttttaatttctcaattaatgtcctaa 50455

>emb|CT832689.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCRN133B17, full
insert sequence
Length = 1270

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853

||||| ||||| ||||| | ||||| ||||| ||||| | ||||| ||||| |||||
Sbjct: 717 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 776

Query: 1854 cat 1856

|||
Sbjct: 777 cat 779

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 826 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 885

Query: 1963 aactactacttcaagaacctgctcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 886 aacaactactacaagaacctgctcagaagaagggtctcctgcattctgatcag 939

>emb|CT832688.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCFA237B02, full
insert sequence
Length = 2326

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||| ||||| | ||||| ||||| ||||| | || ||||| |||||
Sbjct: 1773 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 1832

Query: 1854 cat 1856

|||
Sbjct: 1833 cat 1835

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 1882 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 1941

Query: 1963 aactactacttcaagaacctcgttcagaagaagggctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1942 aacaactactacaagaacctcgtcgtcaagaagggctcctgcattctgatcag 1995

>emb|CT832687.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCFA219E15, full
insert sequence
Length = 1331

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||| ||||| | ||||| ||||| ||||| || ||||| ||||| |||||
Sbjct: 783 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaccaa 842

Query: 1854 cat 1856
|||
Sbjct: 843 cat 845

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 892 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 951

Query: 1963 aactactacttcaagaacctcgttcagaagaagggctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 952 aacaactactacaagaacctcgtcgtcaagaagggctcctgcattctgatcag 1005

>ref|NM_001072503.1| Oryza sativa (japonica cultivar-group) Os12g0112000 (Os12g0112000)
mRNA, complete cds
Length = 1318

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||| ||||| ||||| | ||||||||||||||||| | || ||||||| |||||
Sbjct: 719 tcacaccattgggcaagcagcatgcacaaacttcagagctcatatatacaacgaaaccaa 778

Query: 1854 cat 1856
|||
Sbjct: 779 cat 781

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||||||| || ||||||||| || ||||| || ||
Sbjct: 828 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 887

Query: 1963 aactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||||||| || ||||||||| ||||| || |||||||||
Sbjct: 888 aacaactactacaagaacctcgtcgtcaagaagggctcctgcattctgatcag 941

>tpe|BN000664.1| TPA: TPA_inf: Oryza sativa (japonica cultivar-group) prx135 gene for
class III peroxidase 135 precursor, exons 1-4
Length = 2198

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||| ||||| ||||| | ||||||||||||||||| | || ||||||| |||||
Sbjct: 1811 tcacaccattgggcaagcagcatgcacaaacttcagagctcatatatacaacgaaaccaa 1870

Query: 1854 cat 1856
|||
Sbjct: 1871 cat 1873

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 1920 tcaggatcaggtgacaataacctggcacctctggatcttcagacccaaccgtgttcgag 1979

Query: 1963 aactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| || ||||| |||||
Sbjct: 1980 acaactactacaagaacctcgtcgtcaagaagggtccttcattctgatcag 2033

>dbj|AK069456.1| Oryza sativa Japonica Group cDNA clone:J023019E08, full insert
sequence
Length = 1319

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||| ||||| | ||||| ||||| ||||| || ||||| |||||
Sbjct: 720 tcacaccattgggcaagcagatgcacaaacttcagagctcatatatacaacgaaaccaa 779

Query: 1854 cat 1856
|||
Sbjct: 780 cat 782

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 829 tcaggatcaggtgacaataacctggcacctctggatcttcagacccaaccgtgttcgag 888

Query: 1963 aactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcag 2016

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Minus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||||||| || ||||||||| || ||||| || ||
Sbjct: 24220 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 24161

Query: 1963 aactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||||||| ||||||| ||||| || |||||||||
Sbjct: 24160 aacaactactacaagaacctcgtcgtcaagaagggtcctgcattctgatcag 24107

>gb|EZ315890.1| TSA: Artemisia annua strain Madagascar Contig2436, mRNA sequence
Length = 309

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Minus

Query: 2089 gatttcgccgcccgatgatcaagatgggagacattagtcctctcactgg 2138
||||||| || ||||||||| ||||| || ||||||| || |||||
Sbjct: 265 gatttcgcgctgccatgatcaagatgggtgatattagtcacttactgg 216

>gb|EZ359220.1| TSA: Artemisia annua strain Uganda Contig6381, mRNA sequence
Length = 492

Score = 52.0 bits (26), Expect = 0.025
Identities = 41/46 (89%)
Strand = Plus / Plus

Query: 1907 ggtcaggggacaacaatctggcaccacttgatcttcaaactccaac 1952
||||||| ||||||||| ||||| || ||||| |||||||||
Sbjct: 11 ggtcaggagacaacaatttggcacccgctagatctccaactccaac 56

>gb|EZ166433.1| TSA: Artemisia annua strain Artemis Contig25839, mRNA sequence
Length = 448

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 2089 gatttcgcccgcgccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| || ||||||||||||||||||| || ||||||||| || |||||
Sbjct: 164 gatttcgcgctgccatgatcaagatgggtgatattagtcacttactgg 213

>gb|BT106781.1| Picea glauca clone GQ03010_F17 mRNA sequence
Length = 722

Score = 52.0 bits (26), Expect = 0.025
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 1957 ttgacaactactacttcaagaacct 1982
|||||||||||||||||||||||||||
Sbjct: 192 ttgacaactactacttcaagaacct 217

>ref|XM_002285606.1| PREDICTED: Vitis vinifera hypothetical protein LOC100253646
(LOC100253646), mRNA
Length = 1032

Score = 52.0 bits (26), Expect = 0.025
Identities = 50/58 (86%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatataccttgccatcgtgccagagactctgttc 1343
||||||||||||||||||||||| || || || ||||| || || ||||| |||||
Sbjct: 382 tgtccaggagttgtttcctgcgctgacatactagccatagccgccgagactccgttc 439

>gb|AC235417.1| Glycine max strain Williams 82 clone GM_WBb0135A07, complete sequence
Length = 184957

Score = 52.0 bits (26), Expect = 0.025
Identities = 35/38 (92%)
Strand = Plus / Plus

Query: 279 attatTTTTtctTTtaatttcttaattaatatacctaag 316
||||||||| ||||||||| ||||||||||| |||||
Sbjct: 56366 attatTTTTtatttTaatttattaattaatattctaag 56403

>ref|XM_002334206.1| Populus trichocarpa predicted protein, mRNA
Length = 954

Score = 52.0 bits (26), Expect = 0.025

Identities = 35/38 (92%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactgg 2138
|||||
Sbjct: 874 gccatgatcaaaatgggagacatcagtcctcactgg 911

>ref|NM_001157951.1| Zea mays peroxidase 2 (LOC100285056), mRNA
>gi|195646697|gb|EU970699.1| Zea mays clone 349100
peroxidase 2 precursor, mRNA, complete cds
Length = 1360

Score = 52.0 bits (26), Expect = 0.025
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 2092 ttcgccgcccatgatcaagatggg 2117
|||||
Sbjct: 956 ttcgccgcccatgatcaagatggg 981

>gb|BT044614.1| Arabidopsis thaliana unknown protein (At4g33420) mRNA, complete cds
Length = 978

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 373 tgtccaggagttgtatcatgcgcagatatagttgccatggctgctagaga 422

>gb|FJ099764.1| Pinus taeda isolate 1294 anonymous locus 2_6350_01 genomic sequence
Length = 414

Score = 52.0 bits (26), Expect = 0.025
Identities = 59/70 (84%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
|||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagtcgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099763.1| Pinus taeda isolate 1290 anonymous locus 2_6350_01 genomic sequence
Length = 448

Score = 52.0 bits (26), Expect = 0.025
Identities = 59/70 (84%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | ||||||||| |||||||
Sbjct: 307 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 248

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 247 aatccaacat 238

>gb|BT042071.1| Zea mays full-length cDNA clone ZM_BFb0125B03 mRNA, complete cds
Length = 1342

Score = 52.0 bits (26), Expect = 0.025
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 2092 ttcgccgcccgatgatcaagatggg 2117
||||||||||||||||||||||||||
Sbjct: 1003 ttcgccgcccgatgatcaagatggg 1028

>emb|AM450885.2| Vitis vinifera contig VV78X220288.8, whole genome shotgun sequence
Length = 12944

Score = 52.0 bits (26), Expect = 0.025
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 1797 cacaattggacaagcaaggtgcacaa 1822
||||||||||||||||||||||||||
Sbjct: 1055 cacaattggacaagcaaggtgcacaa 1080

>ref|NM_119496.3| Arabidopsis thaliana peroxidase, putative (AT4G33420) mRNA, complete
cds
Length = 1197

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatataccttgccatcgctgccagaga 1335
|||||
Sbjct: 401 tgtccaggagttgtatcatgcgagatatagttgccatggctgctagaga 450

>emb|AM446475.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X020658.13,
clone ENTAV 115
Length = 18355

Score = 52.0 bits (26), Expect = 0.025
Identities = 50/58 (86%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagactctgttc 1343
|||||
Sbjct: 15894 tgtccaggagttgtttcctgcgctgacatactagccatagccgcccagactccgttc 15951

>emb|AM436560.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X083975.17,
clone ENTAV 115
Length = 6769

Score = 52.0 bits (26), Expect = 0.025
Identities = 50/58 (86%)
Strand = Plus / Minus

Query: 1154 cagggatgtagtggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
|||||
Sbjct: 5849 cagggatgtagtgcttctatattattggacgacactgcaagctttaccggagagaaga 5792

Score = 44.1 bits (22), Expect = 6.1
Identities = 49/58 (84%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
|||||
Sbjct: 1513 cagggatgtgatgcttctatattattggatgacactgcaaactttactggagagaaga 1456

>emb|AM429435.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X154826.4,
clone ENTAV 115
Length = 7609

Score = 52.0 bits (26), Expect = 0.025
Identities = 50/58 (86%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
|||||
Sbjct: 2278 cagggatgtgatgcttctatattattggacgacactgcaagctttaccggagagaaga 2221

>ref|NM_101322.1| Arabidopsis thaliana anionic peroxidase, putative (AT1G14550) mRNA,
complete cds
Length = 966

Score = 52.0 bits (26), Expect = 0.025
Identities = 32/34 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaaga 2161
|||||
Sbjct: 913 cctctcactggctctaattggagaaatcaggaaga 946

>gb|AF453791.1| Ipomoea batatas anionic peroxidase (POD) gene, promoter region and
partial cds
Length = 3741

Score = 52.0 bits (26), Expect = 0.025
Identities = 47/54 (87%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttcttccacgattgctttgtcaatgta 786
|||||
Sbjct: 2101 cgcattggggcttccctcattcgtctcttcttccacgattgctttgtcgatgta 2154

>dbj|AB193816.1| Pisum sativum mRNA for peroxidase, complete cds, clone:PsPOX11
Length = 1217

Query: 1286 tgtccaggagttgtttcctgcgagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 395 tgtccaggagttgtatcatgcgagatatagttgccatggctgctagaga 444

>gb|AC108072.3| Homo sapiens BAC clone RP11-704A16 from 2, complete sequence
Length = 36787

Score = 52.0 bits (26), Expect = 0.025
Identities = 29/30 (96%)
Strand = Plus / Minus

Query: 1045 atatatttaagataataaatatttctgct 1074
|||||
Sbjct: 31744 atatatttaagttaataaatatttctgct 31715

>gb|AF451951.1| Arabidopsis thaliana class III peroxidase ATP32 mRNA, complete cds
Length = 1082

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 373 tgtccaggagttgtatcatgcgagatatagttgccatggctgctagaga 422

>emb|AL161583.2| Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
Length = 199536

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 113403 tgtccaggagttgtatcatgcgagatatagttgccatggctgctagaga 113452

>gb|AC010657.3|AC010657 Genomic sequence for Arabidopsis thaliana BAC T5E21 from chromosome I,
complete sequence
Length = 83351

Score = 52.0 bits (26), Expect = 0.025

Identities = 32/34 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaaga 2161
|||||
Sbjct: 17743 cctctcactggctcctaattggagaaatcagaaaga 17776

>emb|AL035678.1| Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)
Length = 96475

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 48624 tgtccaggagttgtatcatgcgcagatatagttgccatggctgctagaga 48673

>gb|AC012188.2|F14L17 Sequence of BAC F14L17 from Arabidopsis thaliana chromosome 1, complete
sequence
Length = 111686

Score = 52.0 bits (26), Expect = 0.025
Identities = 32/34 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaaga 2161
|||||
Sbjct: 111350 cctctcactggctcctaattggagaaatcagaaaga 111383

>gb|EZ395724.1| TSA: Artemisia annua strain Uganda Contig12219, mRNA sequence
Length = 273

Score = 50.1 bits (25), Expect = 0.099
Identities = 55/65 (84%)
Strand = Plus / Minus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggetccaatggagaaatcaggaag 2160
|||||
Sbjct: 221 gccatgatcaagatgggtgatattagtcacttactggacgtaatggtgagatcaggaag 162

Query: 2161 aattg 2165
 |||||
Sbjct: 161 aattg 157

>gb|EZ362599.1| TSA: Artemisia annua strain Uganda Contig9760, mRNA sequence
 Length = 346

Score = 50.1 bits (25), Expect = 0.099
Identities = 55/65 (84%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
 ||||||| ||||||||||||||| ||||| ||||| | ||| | || ||||| |||||
Sbjct: 216 cttggaggacctacatggaatgtgaaactgggaagacgtgactcaaggactgcgagccaa 275

Query: 1538 tctgc 1542
 |||||
Sbjct: 276 gctgc 280

>gb|BT066765.1| Zea mays full-length cDNA clone ZM_BFb0066D03 mRNA, complete cds
 Length = 1217

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcacatctacaacgagaccaacat 1856
 ||||| ||||||||||||||| ||||||||||||| ||| |||||
Sbjct: 665 tgcaccaacttcagagcccacacatctacaacgacaccgacat 705

>gb|BT055307.1| Zea mays full-length cDNA clone ZM_BFc0167H14 mRNA, complete cds
 Length = 1194

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcacatctacaacgagaccaacat 1856
 ||||| ||||||||||||||| ||||||||||||| ||| |||||
Sbjct: 640 tgcaccaacttcagagcccacacatctacaacgacaccgacat 680

>gb|EU962146.1| Zea mays clone 240603 mRNA sequence
Length = 1299

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856
||||| ||||||||||||||| ||||||||||||||| ||| |||||
Sbjct: 737 tgcaccaacttcagagcccacatctacaacgacaccgacat 777

>gb|FJ070719.1| Pinus taeda isolate 7938 anonymous locus 0_3458_02 genomic sequence
Length = 364

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||||| ||||||||| |||||||||||||
Sbjct: 269 ccatgataaagatgggaaacattagccctctcactgg 233

>gb|FJ070718.1| Pinus taeda isolate 7947 anonymous locus 0_3458_02 genomic sequence
Length = 440

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||||| ||||||||| |||||||||||||
Sbjct: 295 ccatgataaagatgggaaacattagccctctcactgg 259

>gb|FJ070717.1| Pinus taeda isolate 7943 anonymous locus 0_3458_02 genomic sequence
Length = 359

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||||| ||||||||| |||||||||||||

Sbjct: 263 ccatgataaagatgggaaacattagccctctcactgg 227

>gb|FJ070716.1| Pinus taeda isolate 7950 anonymous locus 0_3458_02 genomic sequence
Length = 350

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 254 ccatgataaagatgggaaacattagccctctcactgg 218

>gb|FJ070715.1| Pinus taeda isolate 7940 anonymous locus 0_3458_02 genomic sequence
Length = 366

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 270 ccatgataaagatgggaaacattagccctctcactgg 234

>gb|FJ070714.1| Pinus taeda isolate 7948 anonymous locus 0_3458_02 genomic sequence
Length = 440

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 295 ccatgataaagatgggaaacattagccctctcactgg 259

>gb|FJ070713.1| Pinus taeda isolate 7949 anonymous locus 0_3458_02 genomic sequence
Length = 438

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 293 ccatgataaagatgggaaacattagccctctcactgg 257

>gb|FJ070712.1| Pinus taeda isolate 7952 anonymous locus 0_3458_02 genomic sequence
Length = 349

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 253 ccatgataaagatgggaaacattagccctctcactgg 217

>gb|FJ070711.1| Pinus taeda isolate 7941 anonymous locus 0_3458_02 genomic sequence
Length = 350

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 254 ccatgataaagatgggaaacattagccctctcactgg 218

>gb|FJ070710.1| Pinus taeda isolate 7951 anonymous locus 0_3458_02 genomic sequence
Length = 360

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 264 ccatgataaagatgggaaacattagccctctcactgg 228

>gb|FJ070709.1| Pinus taeda isolate 7942 anonymous locus 0_3458_02 genomic sequence
Length = 440

Score = 50.1 bits (25), Expect = 0.099

Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcaactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 295 ccatgataaagatgggaaacattagccctctcaactgg 259

>gb|FJ070708.1| Pinus taeda isolate 7953 anonymous locus 0_3458_02 genomic sequence
Length = 349

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcaactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 254 ccatgataaagatgggaaacattagccctctcaactgg 218

>gb|FJ070707.1| Pinus taeda isolate 7937 anonymous locus 0_3458_02 genomic sequence
Length = 420

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcaactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 275 ccatgataaagatgggaaacattagccctctcaactgg 239

>gb|FJ070706.1| Pinus taeda isolate 7946 anonymous locus 0_3458_02 genomic sequence
Length = 297

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcaactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 191 ccatgataaagatgggaaacattagccctctcaactgg 155

>gb|FJ070705.1| Pinus taeda isolate 7945 anonymous locus 0_3458_02 genomic sequence

Length = 350

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 255 ccatgataaagatgggaaacattagccctctcactgg 219

>gb|FJ070703.1| Pinus taeda isolate 7939 anonymous locus 0_3458_02 genomic sequence
Length = 355

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 259 ccatgataaagatgggaaacattagccctctcactgg 223

>ref|NM_001137528.1| Zea mays hypothetical protein LOC100192105 (LOC100192105), mRNA
>gi|194690673|gb|BT034416.1| Zea mays full-length cDNA
clone ZM_BFc0170D07 mRNA, complete cds
Length = 1217

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856
||||| ||||||||| ||||||||| ||| |||||
Sbjct: 665 tgcaccaacttcagagcccacatctacaacgacaccgacat 705

>gb|DQ244260.1| Zea mays clone 3973 mRNA sequence
Length = 1224

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856

||||| ||||||||||||||| |||||||||||| | ||| |||||
Sbjct: 672 tgcaccaacttcagagcccacatctacaacgacaccgacat 712

>tpe|BN000615.1| TPA: TPA_inf: Oryza sativa (japonica cultivar-group) prx86 gene for
class III peroxidase 86 precursor, exons 1-3
Length = 1188

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 749 tccttcgcttggttcttccacgattgctttgtcaatgtaatt 789
||||||| | ||||||||| ||||||||| ||||||||| |||||
Sbjct: 197 tccttcgcctcttcttccatgattgcttcgtcaatgtaatt 237

>dbj|AP004731.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC
clone:OSJNBa0016D02
Length = 157822

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Minus

Query: 749 tccttcgcttggttcttccacgattgctttgtcaatgtaatt 789
||||||| | ||||||||| ||||||||| ||||||||| |||||
Sbjct: 82216 tccttcgcctcttcttccatgattgcttcgtcaatgtaatt 82176

>dbj|AB007645.1| Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K8K14
Length = 72698

Score = 50.1 bits (25), Expect = 0.099
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 760 ttcttccacgattgctttgtcaatgtaatt 788
||||||||||||||||| |||||||||||
Sbjct: 46952 ttcttccacgattgcttcgtcaatgtaatt 46980

>emb|Y10465.1| S. oleracea mRNA for peroxidase, clone PC44
Length = 1176

Score = 50.1 bits (25), Expect = 0.099

Identities = 43/49 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||||| | ||||| ||||||||| ||||||| ||||
Sbjct: 209 atgggtgcttccatacttcgtttgttcttccacgactgctttgtaaag 257

Score = 46.1 bits (23), Expect = 1.5
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 1481 ggaggccctacatggaatgttaaacttgaagaagagacgctagaac 1527
||||||| ||||||||| ||||| || ||||||| || |||||
Sbjct: 455 ggaggccccacatggaatgtaaaactaggtagaagagatgcaagaac 501

>gb|CP000102.1| Methanosphaera stadtmanae DSM 3091, complete genome
Length = 1767403

Score = 50.1 bits (25), Expect = 0.099
Identities = 25/25 (100%)
Strand = Plus / Plus

Query: 285 ttttcttttaatttcttaattaata 309
||||||| ||||||||| ||||||||| |||||
Sbjct: 31679 ttttcttttaatttcttaattaata 31703

>emb|FP012230.5| Pig DNA sequence from clone CH242-162F1 on chromosome X, complete
sequence
Length = 116800

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 268 atttctataaaattatTTTTTTTtttaa 295
||||||| ||||||||| |||||
Sbjct: 24562 atttctataaaattatTTTTTTTtttaa 24589

>gb|EZ275595.1| TSA: Artemisia annua strain Madagascar Contig1982, mRNA sequence
Length = 688

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 |||||
Sbjct: 69 cacacaattggacaagcaagatgcacaa 96

>gb|EZ286664.1| TSA: Artemisia annua strain Madagascar Contig13051, mRNA sequence
 Length = 813

Score = 48.1 bits (24), Expect = 0.39
Identities = 33/36 (91%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttgaaga 1513
 |||||
Sbjct: 789 cttggaggacctacatggaatgtgaaactggaaga 754

Score = 46.1 bits (23), Expect = 1.5
Identities = 38/43 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaa 1951
 |||||
Sbjct: 501 tcaggggacaacaatttggcaccactagactccaaactccaa 459

>gb|EZ342046.1| TSA: Artemisia annua strain Uganda Contig9262, mRNA sequence
 Length = 588

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 |||||
Sbjct: 493 cacacaattggacaagcaagatgcacaa 466

>gb|EZ321242.1| TSA: Artemisia annua strain Madagascar Contig7788, mRNA sequence

Length = 1218

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 |||||
Sbjct: 599 cacacaattggacaagcaagatgcacaa 626

>gb|EZ318330.1| TSA: Artemisia annua strain Madagascar Contig4876, mRNA sequence
Length = 457

Score = 48.1 bits (24), Expect = 0.39
Identities = 33/36 (91%)
Strand = Plus / Minus

Query: 1478 cttgaggccctacatggaatgttaaacttgaaga 1513
 |||||
Sbjct: 236 cttgaggacctacatggaatgtgaaactggaaga 201

>gb|EZ247069.1| TSA: Artemisia annua strain Artemis Contig13739, mRNA sequence
Length = 438

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 |||||
Sbjct: 104 cacacaattggacaagcaagatgcacaa 131

>gb|EZ258457.1| TSA: Artemisia annua strain Madagascar Contig1560, mRNA sequence
Length = 246

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 |||||
Sbjct: 68 cacacaattggacaagcaagatgcacaa 95

>gb|EZ396283.1| TSA: Artemisia annua strain Uganda Contig12778, mRNA sequence
Length = 352

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||
Sbjct: 119 cacacaattggacaagcaagatgcacaa 146

>gb|EZ220993.1| TSA: Artemisia annua Contig18004
Length = 707

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||
Sbjct: 649 cacacaattggacaagcaagatgcacaa 622

>gb|EZ366681.1| TSA: Artemisia annua strain Uganda Contig132, mRNA sequence
Length = 790

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||
Sbjct: 723 cacacaattggacaagcaagatgcacaa 696

>gb|EZ196247.1| TSA: Artemisia annua strain Artemis Contig9804, mRNA sequence
Length = 252

Score = 48.1 bits (24), Expect = 0.39
Identities = 33/36 (91%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttgaaga 1513
||||||| ||||||||||||| ||||| |||||
Sbjct: 223 cttggaggacctacatggaatgtgaaactgggaaga 188

>gb|EZ355157.1| TSA: Artemisia annua strain Uganda Contig2318, mRNA sequence
Length = 246

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
||||||||||||||||||| |||||
Sbjct: 67 cacacaattggacaagcaagatgcacaa 94

>gb|EZ173232.1| TSA: Artemisia annua strain Artemis Contig32638, mRNA sequence
Length = 709

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
||||||||||||||||||| |||||
Sbjct: 622 cacacaattggacaagcaagatgcacaa 595

>gb|BT102799.1| Picea glauca clone GQ02016_E21 mRNA sequence
Length = 953

Score = 48.1 bits (24), Expect = 0.39
Identities = 42/48 (87%)
Strand = Plus / Plus

Query: 2110 aagatgggagacattagtccctcactggctccaatggagaaatcagg 2157
||||||| ||||| ||||||||| || ||||||||| |||||||||
Sbjct: 768 aagatggggaacatcagtcctcttacaggctccaaggagaaatcagg 815

>gb|BT101612.1| Picea glauca clone GQ01308_P23 mRNA sequence
Length = 919

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)

Strand = Plus / Plus

Query: 1957 ttgacaactactacttcaagaac 1980
 |||||
Sbjct: 605 ttgacaactactacttcaagaac 628

>gb|AC212861.3| Pongo abelii BAC clone CH276-236D6 from chromosome 1, complete sequence
 Length = 192235

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 268 atttctataaaattatTTTTtctt 291
 |||||
Sbjct: 126165 atttctataaaattatTTTTtctt 126188

>ref|XM_002451803.1| Sorghum bicolor hypothetical protein, mRNA
 Length = 837

Score = 48.1 bits (24), Expect = 0.39
Identities = 53/60 (88%), Gaps = 2/60 (3%)
Strand = Plus / Plus

Query: 2059 tacagcacaacccgggcac-cttctcctctgatttcgcccgcccatgatcaagatggg 2117
 ||||| ||||| ||| |||| ||| || ||||| ||||| |||||
Sbjct: 709 tacagctcaacccgg-cactcttcgctcagaacttcgcccgcccatgataaagatggg 767

>gb|AC235800.1| Solanum lycopersicum chromosome 3 clone C03HBa0137K15, complete
 sequence
 Length = 110892

Score = 48.1 bits (24), Expect = 0.39
Identities = 45/52 (86%)
Strand = Plus / Minus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaa 787
 ||||| || ||||| ||||| | ||||| ||||| |||||
Sbjct: 31655 atgggagcgtctctcattcgcctcttcttccacgactgctttgtcgatgtaa 31604

>ref|XM_002285687.1| PREDICTED: Vitis vinifera hypothetical protein LOC100257440

(LOC100257440), mRNA
Length = 1215

Score = 48.1 bits (24), Expect = 0.39
Identities = 48/56 (85%)
Strand = Plus / Plus

Query: 1156 gggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||||| ||| || ||||| |||| | ||||| ||||| |||||
Sbjct: 307 gggatgtgatgcttctatattattggacgacactgcaagctttaccggagagaaga 362

>ref|XM_002269022.1| PREDICTED: Vitis vinifera hypothetical protein LOC100263220
(LOC100263220), mRNA
Length = 960

Score = 48.1 bits (24), Expect = 0.39
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcgttcagaagaagggtct 2000
||||||| ||| ||||| ||||| |||||
Sbjct: 748 tacttcaagaatctcattcagaagaagggtct 779

>dbj|AK323976.1| Solanum lycopersicum cDNA, clone: LEFL1068DD08, HTC in leaf
Length = 1123

Score = 48.1 bits (24), Expect = 0.39
Identities = 45/52 (86%)
Strand = Plus / Plus

Query: 2087 ctgatttgcgccgcccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| || || ||||| || ||||| ||||| ||||| |||||
Sbjct: 924 ctgattttgctgcagccatgattaaatgggagatattagtcctetaactgg 975

>ref|XM_002320381.1| Populus trichocarpa predicted protein, mRNA
Length = 951

Score = 48.1 bits (24), Expect = 0.39
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 749 tccttcgcttgttcttccacgattgctttgtcaatg 784

||||| ||||||||||||||||||| ||||||||| |||||
Sbjct: 176 tcctccgcttgttcttccacgaactgctttgtgaatg 211

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1298 gtttctgctgcagatataccttgc 1320
|||||||||||||||||||||
Sbjct: 352 gtttctgctgcagatataccttgc 374

>gb|CP001098.1| Halothermothrix orenii H 168, complete genome
Length = 2578146

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 188 aaactaattaagaaattaataaaaaat 215
||||||||||||| |||||||||||
Sbjct: 1223172 aaactaattaagagattaataaaaaat 1223199

>gb|EF677600.1| Picea sitchensis clone WS02771_I11 unknown mRNA
Length = 1895

Score = 48.1 bits (24), Expect = 0.39
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1999 ctctccactctgatcagcaactgttcaacgg 2030
||||||||||||||||| ||||| |||||||
Sbjct: 1536 ctctccactctgatcaggaactattcaacgg 1567

>gb|FJ050773.1| Pinus taeda isolate 4643 anonymous locus 0_13032_02 genomic sequence
Length = 640

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| ||||||||| |||||
Sbjct: 485 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggccgcattctacaa 426

>gb|FJ050767.1| Pinus taeda isolate 4658 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| ||||||||| |||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggccgcattctacaa 443

>gb|FJ050766.1| Pinus taeda isolate 4644 anonymous locus 0_13032_02 genomic sequence
Length = 640

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| ||||||||| |||||
Sbjct: 503 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggccgcattctacaa 444

>gb|FJ050765.1| Pinus taeda isolate 4645 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| ||||||||| |||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggccgcattctacaa 443

>gb|FJ050763.1| Pinus taeda isolate 4660 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtggtcacaccataggccaagcgcggtgcacaagcttcagggcccgcattctacaa 443

>gb|FJ050762.1| Pinus taeda isolate 4647 anonymous locus 0_13032_02 genomic sequence
Length = 623

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 486 attaggtggtcacaccataggccaagcgcggtgcacaagcttcagggcccgcattctacaa 427

>gb|FJ050761.1| Pinus taeda isolate 4654 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtggtcacaccataggccaagcgcggtgcacaagcttcagggcccgcattctacaa 443

>gb|FJ050760.1| Pinus taeda isolate 4646 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtggtcacaccataggccaagcgcggtgcacaagcttcagggcccgcattctacaa 443

|||||
Sbjct: 2185 aaaattattttttttataattacttaattaatatc 2220

>emb|BX548174.1| Prochlorococcus marinus MED4 complete genome
Length = 1657990

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 279 attattttttcttttaatttctta 302
|||||
Sbjct: 602985 attattttttcttttaatttctta 602962

>gb|CP000647.1| Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete sequence
Length = 5315120

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 881 gaaacaacacttgttccttttatt 904
|||||
Sbjct: 3390746 gaaacaacacttgttccttttatt 3390723

>emb|AM454579.2| Vitis vinifera contig VV78X062755.15, whole genome shotgun sequence
Length = 6610

Score = 48.1 bits (24), Expect = 0.39
Identities = 30/32 (93%)
Strand = Plus / Minus

Query: 192 taattaagaaattaaataaaaaatatttatca 223
|||||
Sbjct: 2152 taattaagaaattaaataaaaaatatttatca 2121

>emb|AM428729.2| Vitis vinifera contig VV78X273545.5, whole genome shotgun sequence
Length = 39883

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 284 tttttcttttaatttcttaattaa 307
|||||
Sbjct: 39856 tttttcttttaatttcttaattaa 39879

>emb|AM462968.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X116164.8,
clone ENTAV 115
Length = 13500

Score = 48.1 bits (24), Expect = 0.39
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcgttcagaagaagggtct 2000
||||| |||
Sbjct: 6764 tacttcaagaatctcattcagaagaagggtct 6795

>emb|AM473070.1| Vitis vinifera contig VV78X025151.6, whole genome shotgun sequence
Length = 4985

Score = 48.1 bits (24), Expect = 0.39
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 2789 aacaatcaatattttaattcttaactttatt 2820
||||| |||
Sbjct: 4576 aacaataaatattttaattgtaactttatt 4607

>emb|AM453059.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X216487.15,
clone ENTAV 115
Length = 18125

Score = 48.1 bits (24), Expect = 0.39
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcgttcagaagaagggtct 2000
||||| |||
Sbjct: 4424 tacttcaagaatctcattcagaagaagggtct 4455

>emb|AM481723.1| Vitis vinifera contig VV78X090480.3, whole genome shotgun sequence

Length = 13986

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 1747 ttttgttgaggaatattgcatggt 1770
|||||
Sbjct: 3837 ttttgttgaggaatattgcatggt 3860

>dbj|AP006865.1| Lotus japonicus genomic DNA, chromosome 2, clone: LjT37H21, TM1032,
complete sequence
Length = 95067

Score = 48.1 bits (24), Expect = 0.39
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 1154 cagggatgtgatggttcaattctattggatgacaca 1189
|||||
Sbjct: 32185 cagggatgtgatgcatcaataactattggatgacaca 32220

>dbj|AB049589.1| Avicennia marina PER mRNA for secretory peroxidase, complete cds
Length = 1345

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1292 ggagttgtttctgctgcagatattcttg 1319
|||||
Sbjct: 412 ggagttgtttctgctgcagatattcttg 439

>emb|BX828399.1| Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTPGH84ZE10 of Hormone Treated Callus of strain col-0
of Arabidopsis thaliana (thale cress)
Length = 1002

Score = 48.1 bits (24), Expect = 0.39
Identities = 39/44 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatatccttgccatcgctgc 1329
|||||
Sbjct: 380 tgtccaggagttgtatcatgcgagatatagttgccatggctgc 423

>emb|BX832751.1| Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTPGH95ZG01 of Hormone Treated Callus of strain col-0
of Arabidopsis thaliana (thale cress)
Length = 1192

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1956 cttgacaactactacttcaagaacctc 1983
||||
Sbjct: 820 cttcacaactactacttcaagaacctc 847

>dbj|AB010692.1| Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18I23
Length = 72691

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 760 ttcttccacgattgctttgtcaatgtaa 787
|||||
Sbjct: 31924 ttcttccacgattgctttgtcaacgtaa 31897

>emb|Y10467.1| S.oleracea mRNA for peroxidase, clone PC23
Length = 1091

Score = 48.1 bits (24), Expect = 0.39
Identities = 45/52 (86%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 127 cgc atgggcgttcaataacttcgcttgttcttcatgactgctttgtcaatg 178

>ref|XM_670091.1| Plasmodium berghei strain ANKA hypothetical protein (PB301568.00.0)
partial mRNA
Length = 2721

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 275 taaaattatTTTTCTTTAATT 298
|||||
Sbjct: 2667 taaaattatTTTTCTTTAATT 2644

>gb|AF109124.1|AF109124 Ipomoea batatas anionic peroxidase swpa2 (swpa2) mRNA, complete cds
Length = 1291

Score = 48.1 bits (24), Expect = 0.39
Identities = 42/48 (87%)
Strand = Plus / Plus

Query: 733 cgcattgggtctctctccttcgcttgttcttccacgattgctttgtc 780
||||| ||||| ||| |||| | |||||
Sbjct: 322 cgcattggggcttcctcattcgtctcttcttccacgattgctttgtc 369

>gb|EZ295716.1| TSA: Artemisia annua strain Madagascar Contig1601, mRNA sequence
Length = 540

Score = 46.1 bits (23), Expect = 1.5
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1796 acacaattggacaagcaaggtgcacaa 1822
|||||
Sbjct: 72 acacaattggacaagcaagatgcacaa 98

>gb|EZ256521.1| TSA: Artemisia annua strain Artemis Contig23191, mRNA sequence
Length = 253

Score = 46.1 bits (23), Expect = 1.5
Identities = 43/50 (86%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactgg 2138
||||| || ||||| || ||||| || |||||
Sbjct: 165 gatttcggcctgccatgatcaagatggntgatattagtcgcttactgg 214

>gb|EZ360402.1| TSA: Artemisia annua strain Uganda Contig7563, mRNA sequence
Length = 276

Score = 46.1 bits (23), Expect = 1.5
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaa 1951
|||||
Sbjct: 208 tcaggggacaacaatttggcaccactagacgtccaaactccaa 250

>gb|EZ150610.1| TSA: Artemisia annua strain Artemis Contig10016, mRNA sequence
Length = 265

Score = 46.1 bits (23), Expect = 1.5
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaa 1951
|||||
Sbjct: 176 tcaggggacaacaatttggcaccactagacgtccaaactccaa 218

>gb|AC233130.7| Solanum lycopersicum strain Heinz 1706 chromosome 10 clone hba-256116 map
10, complete sequence
Length = 159015

Score = 46.1 bits (23), Expect = 1.5
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 3523 agaaattaactttttgtttttaaaaa 3549
|||||
Sbjct: 155094 agaaattaactttttcttttttaaaaa 155068

>gb|AC239433.3| Solanum lycopersicum strain Heinz 1706 chromosome 1 clone hba-208m24
map 1, complete sequence
Length = 154446

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 274 ataaaattatTTTTtctTTtaT 296
|||||
Sbjct: 83633 ataaaattatTTTTtctTTtaT 83655

>gb|CP001633.1| Francisella tularensis subsp. tularensis NE061598, complete genome
Length = 1892681

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 3735 tatgtctttctctaattgatgaa 3757
|||||
Sbjct: 971539 tatgtctttctctaattgatgaa 971561

>ref|NW_003037936.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000150
Length = 760080

Score = 46.1 bits (23), Expect = 1.5
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 172 aatcagtatctttgaaaactaattaagaaattaa 206
|||||
Sbjct: 116245 aatcagtatctttgaaaactaattaagaaattaa 116279

>gb|BT095984.1| Soybean clone JCVI-FLGm-20M19 unknown mRNA
Length = 1268

Score = 46.1 bits (23), Expect = 1.5
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1810 gcaaggtgcacaaacttcagagcccgcactctacaacgagacca 1852
|||||
Sbjct: 643 gcaaggtgcactaccttcaggaccgcactctacaacgacacca 685

>gb|BT093602.1| Soybean clone JCVI-FLGm-17D17 unknown mRNA
Length = 1079

Score = 46.1 bits (23), Expect = 1.5

Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattct 1176
 |||||
Sbjct: 850 cagggatgtgatggttcaattct 828

>gb|AC237089.1| Oryza granulata clone OG_ABa0096023, complete sequence
 Length = 145921

Score = 46.1 bits (23), Expect = 1.5
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 762 cttccacgattgctttgtcaatgtaat 788
 |||||
Sbjct: 78176 cttccacgattgctttgtaaataatgtaat 78150

>ref|XM_002448761.1| Sorghum bicolor hypothetical protein, mRNA
 Length = 2469

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483
 |||||
Sbjct: 1616 gttttgcttttgcttctaaatta 1594

>ref|XM_002426020.1| Pediculus humanus corporis synaptonemal complex protein ZIP1,
 putative, mRNA
 Length = 4083

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 3059 aaagaaaataaaaaagttaattt 3081
 |||||
Sbjct: 1237 aaagaaaataaaaaagttaattt 1259

>emb|AJ749949.2| Francisella tularensis subsp. tularensis SCHU S4 complete genome
Length = 1892775

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 3735 tatgtctttctctaattgatgaa 3757
 |||||
Sbjct: 971474 tatgtctttctctaattgatgaa 971496

>emb|FN357570.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000279
Length = 107846

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 2232 attgtgtttaataagttgtaaa 2254
 |||||
Sbjct: 30598 attgtgtttaataagttgtaaa 30620

>emb|FN357441.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000150
Length = 760080

Score = 46.1 bits (23), Expect = 1.5
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 172 aatcagtatcttttagaaaactaattaagaaattaa 206
 ||||| ||||| ||||| |||||
Sbjct: 116245 aatcagtatcttttagaaaactaattaagaaattaa 116279

>gb|BT086529.1| Zea mays full-length cDNA clone ZM_BFc0177005 mRNA, complete cds
Length = 2218

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gtttgcttttgcttctaaatta 2483
 |||||

Sbjct: 1467 gttttgcttttgcttctaaatta 1445

>gb|EZ053600.1| TSA: Zea mays contig54722, mRNA sequence
Length = 1441

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483

|||||

Sbjct: 688 gttttgcttttgcttctaaatta 666

>emb|AL844509.2| Plasmodium falciparum 3D7 chromosome 13
Length = 2895605

Score = 46.1 bits (23), Expect = 1.5
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 193 aattaagaaattaataaaaaatattt 219

|||||

Sbjct: 2326925 aattaagaaattaataaaaaatattt 2326951

Score = 44.1 bits (22), Expect = 6.1
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 3054 tatttaaagaaaataaaaaagt 3075

|||||

Sbjct: 611898 tatttaaagaaaataaaaaagt 611919

Score = 44.1 bits (22), Expect = 6.1
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 3048 ttagtttatttaaagaaaataaaaa 3073

|||||

Sbjct: 1691677 ttagtttatttaaagataataaaaa 1691652

>gb|AC235371.1| Glycine max strain Williams 82 clone GM_WBb0104B04, complete sequence
Length = 191941

Score = 46.1 bits (23), Expect = 1.5
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 269 tttctataaaattatTTTTCTTTAATTTCTTAATTAATATCCTAA 315
||||| ||||||| ||||||| ||| ||||||| ||||||| |||||||
Sbjct: 155381 tttcaataaaaaatTTTTATTTAAATTTTAAATTAATATCCTAA 155427

>gb|AC235196.1| Glycine max strain Williams 82 clone GM_WBb0014G10, complete sequence
Length = 114082

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1154 cagggatgtgatggttcaattct 1176
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 65728 cagggatgtgatggttcaattct 65750

>gb|AC235187.1| Glycine max strain Williams 82 clone GM_WBb0010C08, complete sequence
Length = 184070

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 281 tattttttctTTTAATTTCTTAA 303
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 7796 tattttttctTTTAATTTCTTAA 7774

>gb|AC235182.1| Glycine max strain Williams 82 clone GM_WBb0008C11, complete sequence
Length = 100806

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 293 taatttcttaattaatcctaa 315
|||||
Sbjct: 22206 taatttcttaattaatcctaa 22184

>gb|AC235129.1| Glycine max strain Williams 82 clone GM_WBa0052I05, complete sequence
Length = 119088

Score = 46.1 bits (23), Expect = 1.5
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 3830 ttagagaaaaataaataaattcttatattat 3860
|||||
Sbjct: 53261 ttagagaaaaataaataaattcatattttat 53291

>ref|XM_002319931.1| Populus trichocarpa predicted protein, mRNA
Length = 939

Score = 46.1 bits (23), Expect = 1.5
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgcttctccacgattgctttgtcaa 782
|||||
Sbjct: 148 atgggtgcttctcttgcttgcttctccacgattgctttgtcaa 194

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1993 aagggtctcctcactctgatca 2015
|||||
Sbjct: 751 aagggtctcctcactctgatca 773

>ref|NM_001158468.1| Zea mays peroxidase 52 (LOC100285577), mRNA
>gi|195651250|gb|EU972975.1| Zea mays clone 391021
peroxidase 52 precursor, mRNA, complete cds
Length = 1358

Score = 46.1 bits (23), Expect = 1.5
Identities = 53/63 (84%)

Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||||| || || ||||||| | ||||||| ||||||||| || || ||||||| |||||
Sbjct: 670 tcacaccatcgccaagcacgctgcaccaacttcagagcccacgtgtacaacgacaccaa 729

Query: 1854 cat 1856
|||
Sbjct: 730 cat 732

>gb|EU954765.1| Zea mays clone 1482328 mRNA sequence
Length = 1445

Score = 46.1 bits (23), Expect = 1.5
Identities = 47/55 (85%)
Strand = Plus / Plus

Query: 733 cgcattgggtcttctctcttcgcttgttcttccacgattgctttgtcaatgtaa 787
||||||| || || ||||| ||| | ||||||||| ||||| |||||||||
Sbjct: 241 cgcattggggcgtcctctctcgcctcttcttccacgactgcttcgtcaatgtaa 295

>gb|EU951047.1| Zea mays clone 687198 mRNA sequence
Length = 845

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgctttgcttctaaatta 2483
|||||||||||||||||||||||
Sbjct: 231 gttttgctttgcttctaaatta 209

>tpg|BK006741.1| TPA: TPA_reasm: Francisella tularensis subsp. holarctica OSU18, complete
genome
Length = 1895727

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 3735 tatgtctttctctaattgatgaa 3757

|||||
Sbjct: 1193421 tatgtctttctctaattgatgaa 1193399

>gb|FJ088527.1| Pinus taeda isolate 6658 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088526.1| Pinus taeda isolate 6661 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088525.1| Pinus taeda isolate 6650 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088524.1| Pinus taeda isolate 6653 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088523.1| Pinus taeda isolate 6663 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088522.1| Pinus taeda isolate 6662 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088521.1| Pinus taeda isolate 6654 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088520.1| Pinus taeda isolate 6655 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088519.1| Pinus taeda isolate 6657 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088518.1| Pinus taeda isolate 6664 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088517.1| Pinus taeda isolate 6651 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088516.1| Pinus taeda isolate 6649 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| ||| | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

Database: /usr/local/blast/db/blastlibs/nt
Posted date: Feb 13, 2010 7:27 AM
Number of letters in database: 30,212,464,392
Number of sequences in database: 10,930,266

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 10930266
Number of Hits to DB: 1,401,816,410
Number of extensions: 94213288
Number of successful extensions: 2655515
Number of sequences better than 10.0: 586
Number of HSP's gapped: 2655491
Number of HSP's successfully gapped: 696
Length of query: 3867
Length of database: 30,212,464,392
Length adjustment: 24
Effective length of query: 3843
Effective length of database: 29,950,138,008
Effective search space: 115098380364744
Effective search space used: 115098380364744
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 50 (99.1 bits)
S1: 14 (28.2 bits)
S2: 22 (44.1 bits)

BLASTn Output of the Sequence at the Parental Locus of Soybean Event DAS-68416-4 against GenBank No-human and No_mouse ESTs (est_others)

BLASTN 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Query= 68416_parent_locus
(3867 letters)

Database: /usr/local/blast/db/blastlibs/est_others
51,680,690 sequences; 29,218,461,503 total letters

Searching..... done

Sequences producing significant alignments:			Score	E
			(bits)	Value
gb CX703225.1	gmrtDrNS01_14-B_M13R_D10_074.s2	Water stressed 5h...	1070	0.0
gb CX709633.1	gmrtDrNS01_10-D_M13R_A04_032.s2	Water stressed 5h...	1063	0.0
gb CF807990.1	psHB031xA07f	USDA-IFAFS:Expression of Phytophthor...	1059	0.0
gb BG509781.1	sad25h05.y1	Gm-c1074 Glycine max cDNA clone GENOM...	924	0.0
gb BM731124.1	sal68a04.y1	Gm-c1061 Glycine max cDNA clone SOYBE...	894	0.0
gb BG882707.1	sae51e08.y2	Gm-c1051 Glycine max cDNA clone GENOM...	880	0.0
gb EV267121.1	GLLBF04TF	JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	731	0.0
gb CF806428.1	psHB011xIO5f	USDA-IFAFS:Expression of Phytophthor...	646	0.0
gb AW349107.1	GM210004A21E9	Gm-r1021 Glycine max cDNA clone Gm-...	626	e-175
gb BG156628.1	sab31a07.y1	Gm-c1026 Glycine max cDNA clone GENOM...	618	e-173
gb FK018609.1	GLND133TF	JCVI-SOY3 Glycine max cDNA 5', mRNA seq...	557	e-154
gb BU577048.1	sar71e12.y1	Gm-c1074 Glycine max cDNA clone SOYBE...	545	e-151
gb BM093025.1	saj04a09.y1	Gm-c1065 Glycine max cDNA clone GENOM...	527	e-145
gb BE210375.1	so42h10.y1	Gm-c1039 Glycine max cDNA clone GENOME...	527	e-145
gb EV263181.1	GLLA357TF	JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	525	e-145
gb CF806168.1	psHB004x020f	USDA-IFAFS:Expression of Phytophthor...	523	e-144
gb BI972311.1	sag89h02.y1	Gm-c1084 Glycine max cDNA clone GENOM...	502	e-138
gb BE209964.1	so37a08.y1	Gm-c1039 Glycine max cDNA clone GENOME...	490	e-134
gb BG725689.1	sae39d12.y1	Gm-c1051 Glycine max cDNA clone GENOM...	464	e-126
gb FG889629.1	UCRVU08_CCNS10828_g1	Cowpea IT97K-461-4 Mixed Tis...	444	e-120
gb BE022389.1	sm85b11.y1	Gm-c1015 Glycine max cDNA clone GENOME...	438	e-118
gb BG359695.1	sac27d09.y1	Gm-c1051 Glycine max cDNA clone GENOM...	436	e-118
gb EV265313.1	GLLAS95TF	JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	412	e-111
gb AW132280.1	se02a03.y1	Gm-c1013 Glycine max cDNA clone GENOME...	381	e-101
gb CF809087.1	psHB042xH14f	USDA-IFAFS:Expression of Phytophthor...	373	5e-99

gb	BU577870.1	sar93g05.y1 Gm-c1074 Glycine max cDNA clone SOYBE...	373	5e-99
gb	AW432575.1	sh76b11.y1 Gm-c1015 Glycine max cDNA clone GENOME...	361	2e-95
gb	FG825601.1	UCRVU04_CCNI8859_g1 Cowpea 524B Mixed Tissue and ...	343	4e-90
gb	FF387035.1	MOOBI56TF MOO Vigna unguiculata cDNA 5', mRNA seq...	335	1e-87
gb	BE807926.1	ss31h12.y1 Gm-c1061 Glycine max cDNA clone GENOME...	331	2e-86
gb	FF386168.1	MOOBI56TRB MOO Vigna unguiculata cDNA, mRNA sequence	321	2e-83
gb	AI441922.1	sa51f09.y1 Gm-c1004 Glycine max cDNA clone GENOME...	291	1e-74
gb	G0029196.1	LJMAW92T0 JCVI-LJ2 Lotus japonicus cDNA 3', mRNA ...	289	6e-74
dbj	BP048143.1	BP048143 Lotus corniculatus var. japonicus pods ...	289	6e-74
dbj	BP048038.1	BP048038 Lotus corniculatus var. japonicus pods ...	289	6e-74
dbj	AV768169.1	AV768169 Lotus japonicus Young plants (two-weeks...	289	6e-74
dbj	BP048158.1	BP048158 Lotus corniculatus var. japonicus pods ...	274	3e-69
gb	G0017605.1	LJGBF85T0 JCVI-LJ1 Lotus japonicus cDNA 3', mRNA ...	266	8e-67
gb	G0023584.1	LJMCD71TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA ...	262	1e-65
gb	FG825600.1	UCRVU04_CCNI8859_b1 Cowpea 524B Mixed Tissue and ...	246	8e-61
gb	FF394030.1	MOODS81TF MOO Vigna unguiculata cDNA 5', mRNA seq...	246	8e-61
gb	FF387818.1	MOOC268TF MOO Vigna unguiculata cDNA 5', mRNA seq...	246	8e-61
gb	FF383796.1	MOOB233TF MOO Vigna unguiculata cDNA 5', mRNA seq...	246	8e-61
dbj	FS240762.1	FS240762 RPSC Glycyrrhiza uralensis cDNA clone K...	244	3e-60
gb	FG889628.1	UCRVU08_CCNS10828_b1 Cowpea IT97K-461-4 Mixed Tis...	238	2e-58
gb	FF403045.1	MOOF734TF MOO Vigna unguiculata cDNA 5', mRNA seq...	238	2e-58
gb	FF392448.1	MOOCV65TF MOO Vigna unguiculata cDNA 5', mRNA seq...	238	2e-58
gb	FF399144.1	MOOEV84TF MOO Vigna unguiculata cDNA 5', mRNA seq...	234	3e-57
gb	G0019707.1	LJMAW92TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA ...	208	2e-49
dbj	AV412875.1	AV412875 Lotus japonicus young plants (two-week ...	208	2e-49
dbj	AV771838.1	AV771838 Lotus japonicus Pods (20-30 mm in lengt...	202	1e-47
dbj	BW620524.1	BW620524 Lotus japonicus protoplasts from suspen...	196	6e-46
dbj	BW630489.1	BW630489 Lotus japonicus salicylic acid and meth...	196	6e-46
dbj	BW629863.1	BW629863 Lotus japonicus salicylic acid and meth...	196	6e-46
dbj	BW628107.1	BW628107 Lotus japonicus salicylic acid and meth...	196	6e-46
dbj	BW627140.1	BW627140 Lotus japonicus salicylic acid and meth...	196	6e-46
dbj	BW624354.1	BW624354 Lotus japonicus salicylic acid and meth...	196	6e-46
dbj	BW595840.1	BW595840 Lotus japonicus suspension-cultured cel...	196	6e-46
gb	EY976963.1	EST 83 Alfalfa aluminum suppression subtractive l...	190	4e-44
gb	EH613355.1	EST 02 Alfalfa aluminum suppression subtractive l...	190	4e-44
dbj	BB913062.1	BB913062 Trifolium pratense three week-old plant...	190	4e-44
gb	BI969832.1	GM830009A23A12 Gm-r1083 Glycine max cDNA clone Gm...	180	4e-41
gb	BI700509.1	sag61f05.y1 Gm-c1082 Glycine max cDNA clone GENOM...	180	4e-41
gb	BU578183.1	sar49a02.y1 Gm-c1074 Glycine max cDNA clone SOYBE...	176	6e-40
gb	G0258927.1	VBL1_16_M09_E001.g1 Normalized cDNA library from ...	174	2e-39
gb	CA852976.1	E14E06_J06_09.ab1 cDNA Peking library 6, 8 day SC...	174	2e-39
gb	CA852554.1	E09B05_C17_03.ab1 cDNA Peking library 6, 8 day SC...	174	2e-39
gb	AW350788.1	GM210009A20D5 Gm-r1021 Glycine max cDNA clone Gm...	174	2e-39
gb	FF401698.1	MOOE192TF MOO Vigna unguiculata cDNA 5', mRNA seq...	168	1e-37
gb	EY476317.1	METAQ01TF JCVI-MT3 Medicago truncatula cDNA 5', m...	167	6e-37
gb	EX530374.1	MTGland_A066_2007-06-28/MTGlandA066_C04_014_1 Med...	167	6e-37
gb	CX528854.1	s13dNF01B01MJ009_243775 Methyl Jasmonate-Elicited...	167	6e-37
gb	CF068375.1	EST669096 MTUS Medicago truncatula cDNA clone MTU...	167	6e-37
gb	AW268020.1	EST306242 DSIR Medicago truncatula cDNA clone pDS...	167	6e-37

gb	BI969294.1	GM830007B20G07 Gm-r1083 Glycine max cDNA clone Gm...	165	2e-36
gb	FG998035.1	GLPA295TF JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	163	9e-36
gb	EY477044.1	METAY48TF JCVI-MT3 Medicago truncatula cDNA 5', m...	163	9e-36
gb	BG448404.1	NF024B09EC1F1074 Elicited cell culture Medicago t...	155	2e-33
gb	BF644619.1	NF017G06EC1F1051 Elicited cell culture Medicago t...	155	2e-33
gb	CA919059.1	EST636777 MTUS Medicago truncatula cDNA clone MTU...	151	3e-32
gb	AW830120.1	sm23a02.y1 Gm-c1028 Glycine max cDNA clone GENOME...	151	3e-32
gb	CO513054.1	s13dSG89B0900073_122034 Glandular trichomes Medic...	149	1e-31
gb	FG998036.1	GLPA295TR JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	147	5e-31
gb	CO516034.1	s13dSG64B1200101_445396 Glandular trichomes Medic...	147	5e-31
gb	CO514259.1	s13dSG76D0500042_157180 Glandular trichomes Medic...	147	5e-31
gb	AW686470.2	NF041G08NR1F1000 Nodulated root Medicago truncatu...	145	2e-30
gb	BF639633.1	NF015A12IN1F1097 Insect herbivory Medicago trunca...	145	2e-30
gb	CX530413.1	s13dNF99F02MJ016_246858 Methyl Jasmonate-Elicited...	141	3e-29
gb	CX529528.1	s13dNF97C05MJ034_245107 Methyl Jasmonate-Elicited...	141	3e-29
gb	BF647501.1	NF068D03EC1F1029 Elicited cell culture Medicago t...	141	3e-29
gb	BF645317.1	NF030B11EC1F1092 Elicited cell culture Medicago t...	141	3e-29
gb	CO515766.1	s13dSG77F0400043_419681 Glandular trichomes Medic...	139	1e-28
gb	AW830346.1	sm33e02.y1 Gm-c1028 Glycine max cDNA clone GENOME...	139	1e-28
gb	AW703873.1	sk25b09.y1 Gm-c1028 Glycine max cDNA clone GENOME...	139	1e-28
gb	AI495213.1	sb02b01.y1 Gm-c1004 Glycine max cDNA clone GENOME...	139	1e-28
gb	AW830098.1	sm22c01.y1 Gm-c1028 Glycine max cDNA clone GENOME...	137	5e-28
gb	AW704238.1	sk18d12.y1 Gm-c1028 Glycine max cDNA clone GENOME...	135	2e-27
emb	CU524253.1	CU524253 STSSHWB2Sb_KZOACB Theobroma cacao cDNA ...	133	8e-27
dbj	AV771209.1	AV771209 Lotus japonicus Pods (20-30 mm in lengt...	133	8e-27
gb	CO516246.1	s13dSG69B0900075_445820 Glandular trichomes Medic...	131	3e-26
gb	BF071209.1	st04h08.y1 Gm-c1065 Glycine max cDNA clone GENOME...	131	3e-26
gb	EX660929.1	JS1BF51JG Salt stressed Fragaria vesca (strain Ha...	129	1e-25
gb	DN950706.1	Ost2T_331 Oak tissue culture growing 2 days in hy...	129	1e-25
gb	CO511866.1	s13dSG02H0700064_103632 Glandular trichomes Medic...	129	1e-25
gb	BF650349.1	NF096E02EC1F1017 Elicited cell culture Medicago t...	129	1e-25
gb	BE022178.1	sm68f01.y1 Gm-c1028 Glycine max cDNA clone GENOME...	129	1e-25
gb	AW666186.1	sk33d05.y1 Gm-c1028 Glycine max cDNA clone GENOME...	125	2e-24
gb	AW685593.1	NF029D05NR1F1000 Nodulated root Medicago truncatu...	117	5e-22
dbj	FS263447.1	FS263447 RPSC Glycyrrhiza uralensis cDNA clone S...	113	7e-21
gb	BF650698.1	NF099E07EC1F1053 Elicited cell culture Medicago t...	113	7e-21
gb	EV262518.1	MTYEW71TF JCVI-MT1 Medicago truncatula cDNA 5', m...	111	3e-20
gb	EV260463.1	MTYE803TF JCVI-MT1 Medicago truncatula cDNA 5', m...	111	3e-20
gb	EV258111.1	MTYDG59TF JCVI-MT1 Medicago truncatula cDNA 5', m...	111	3e-20
gb	DW017370.1	EST1226331 MTY Medicago truncatula cDNA clone MTY...	111	3e-20
gb	DW015340.1	EST1224301 MTY Medicago truncatula cDNA clone MTY...	111	3e-20
gb	CO513179.1	s13dSG23G0900068_129522 Glandular trichomes Medic...	111	3e-20
gb	CO512465.1	s13dSG100C120008_114444 Glandular trichomes Medic...	111	3e-20
gb	BG456493.1	NF082E02PL1F1017 Phosphate starved leaf Medicago ...	111	3e-20
gb	BG456057.1	NF073F02PL1F1025 Phosphate starved leaf Medicago ...	111	3e-20
gb	DW481567.1	GH_RMIRS_031_E08_R Cotton Normalized Library rand...	109	1e-19
gb	DW481566.1	GH_RMIRS_031_E08_056_F Cotton Normalized Library ...	109	1e-19
gb	DV443257.1	CV01009B1D06.f1 CV01-normalized library Manihot e...	107	5e-19
gb	DY633234.1	Medicago--03-I06.g1 Subtracted medicago cDNA libr...	105	2e-18

gb DY633115.1	Medicago--03-I06.b1 Subtracted medicago cDNA libr...	105	2e-18
gb BG359643.1	sac26g07.y1 Gm-c1051 Glycine max cDNA clone GENOM...	105	2e-18
gb GT138697.1	METCC85TF JCVI-MT3 Medicago truncatula cDNA 5', m...	103	7e-18
gb AW235016.1	sf21h05.y1 Gm-c1028 Glycine max cDNA clone GENOME...	103	7e-18
emb CU485516.1	CU485516 CUSHIONC_KZOACAC Theobroma cacao cDNA c...	101	3e-17
gb BG454205.1	NF108A01LF1F1001 Developing leaf Medicago truncat...	101	3e-17
gb BE943474.1	EST423053 MGHG Medicago truncatula cDNA clone pMG...	101	3e-17
gb ES840062.1	UFL_061_05 Cotton fiber 0-10 day post anthesis Go...	100	1e-16
gb BI262826.1	NF091E03EC1F1023 Elicited cell culture Medicago t...	100	1e-16
gb AW666202.1	sk33f05.y1 Gm-c1028 Glycine max cDNA clone GENOME...	100	1e-16
gb G0006531.1	LJGBF85TF JCVI-LJ1 Lotus japonicus cDNA 5', mRNA ...	98	4e-16
gb C0511819.1	s13dSG02D0500046_103538 Glandular trichomes Medic...	98	4e-16
gb BF648119.1	NF027G10EC1F1083 Elicited cell culture Medicago t...	98	4e-16
gb AW309606.1	sf21h05.x1 Gm-c1028 Glycine max cDNA clone GENOME...	98	4e-16
gb C0513848.1	s13dSG73C1100082_156358 Glandular trichomes Medic...	96	2e-15
gb AW691930.2	NF050G04ST1F1000 Developing stem Medicago truncat...	96	2e-15
emb AJ548283.1	AJ548283 MTAPHEU Medicago truncatula cDNA clone ...	88	4e-13
gb BF520761.1	EST458234 DSIL Medicago truncatula cDNA clone pDS...	88	4e-13
emb FN039861.1	FN039861 Petunia axillaris subsp. axillaris pool...	86	2e-12
emb FN039860.1	FN039860 Petunia axillaris subsp. axillaris pool...	86	2e-12
gb EG559283.1	CR03032H04 Root CR03 cDNA library Catharanthus ro...	86	2e-12
gb DW500373.1	GH_TMIRS_045_H05_F Cotton Normalized Library dT p...	86	2e-12
dbj CI189311.1	CI189311 Oryza sativa (japonica cultivar-group) ...	86	2e-12
dbj CI256090.1	CI256090 Oryza sativa (japonica cultivar-group) ...	86	2e-12
gb C0498078.1	G.h.fbr-sw07468 G.h.fbr-sw Gossypium hirsutum cDN...	86	2e-12
gb EY707107.1	CS00-C3-701-064-H11-CT.F Sweet orange fruit, deve...	84	7e-12
gb FD423297.1	RT00024R_T3_024_F11_31MAY2004_085_ab1 CrUniGene r...	84	7e-12
gb FD422675.1	RT00017R_T3_017_E10_31MAY2004_072_ab1 CrUniGene r...	84	7e-12
gb FD422951.1	RT00020R_T3_020_G01_31MAY2004_003_ab1 CrUniGene r...	84	7e-12
gb FD420140.1	1_SM-JB_R10-G12_T3_G12_3100394_14_ab1 CrUniGene ...	84	7e-12
gb DW508346.1	GH_TMIRS_123_D07_F Cotton Normalized Library dT p...	82	3e-11
gb GT143205.1	METCC85TR JCVI-MT3 Medicago truncatula cDNA 3', m...	80	1e-10
gb DR280730.1	157654 CERES-148 Arabidopsis thaliana cDNA clone ...	80	1e-10
gb CN910539.1	030128ABLC005555HT (ABLC) Braeburn cell culture t...	80	1e-10
gb CN908859.1	030122ABLC003031HT (ABLC) Braeburn cell culture t...	80	1e-10
gb CN908310.1	030109ABLC001919HT (ABLC) Braeburn cell culture t...	80	1e-10
dbj AU238571.1	AU238571 RAFL17 Arabidopsis thaliana cDNA clone ...	80	1e-10
emb FN019009.1	FN019009 Petunia axillaris subsp. axillaris pool...	78	4e-10
emb FN019008.1	FN019008 Petunia axillaris subsp. axillaris pool...	78	4e-10
emb FN021689.1	FN021689 Petunia axillaris subsp. axillaris pool...	78	4e-10
emb FN021688.1	FN021688 Petunia axillaris subsp. axillaris pool...	78	4e-10
emb FN034858.1	FN034858 Petunia axillaris subsp. axillaris pool...	78	4e-10
emb FN019751.1	FN019751 Petunia axillaris subsp. axillaris pool...	78	4e-10
gb FC869557.1	C31102G05EF AbioticR1 Citrus reshni cDNA clone C3...	78	4e-10
gb FC870159.1	C31109C09EF AbioticR1 Citrus reshni cDNA clone C3...	78	4e-10
gb FC924498.1	C31806G11EF StrCleopN Citrus reshni cDNA clone C3...	78	4e-10
gb FC875256.1	C31505H10EF CEVdCidro1 Citrus medica cDNA clone C...	78	4e-10
gb FC921479.1	C32105D10EF RVDevelopN Citrus clementina cDNA clo...	78	4e-10
gb FC875071.1	C31503H10EF CEVdCidro1 Citrus medica cDNA clone C...	78	4e-10

gb EY867689.1	CL06-C4-500-007-B02-CT.F Rangpur lime root, green...	78	4e-10
gb FC325468.1	P00462_C7-H9_M13-F_A09_079.ab1 Onu-Ua-pathc Ulmus...	78	4e-10
gb EG985866.1	GLE049_D04_013 Cyamopsis tetragonoloba (L.) Taub ...	78	4e-10
gb EG356679.1	P00462_C7-H9_M13-F_A09_079 Onu-Ua-pathc Ulmus ame...	78	4e-10
emb FN034857.1	FN034857 Petunia axillaris subsp. axillaris pool...	76	2e-09
emb FN045147.1	FN045147 Petunia axillaris subsp. axillaris pool...	76	2e-09
emb FN019752.1	FN019752 Petunia axillaris subsp. axillaris pool...	76	2e-09
gb G0517646.1	Mdfbg8014P16.g1 Apple_EST_Mdfbg Malus hybrid root...	76	2e-09
gb EV227910.1	VV_PeA016c06.b1 Vitis vinifera cv. perlette LibA ...	76	2e-09
gb EH047301.1	AS2RM4P1E10.ab1 Roots inoculated with Meloidogyne...	76	2e-09
gb EC991497.1	WIN1142.C21_L14 Muscat Hamburg pre-veraison berry...	76	2e-09
gb EC987303.1	WIN1130.C21_E15 Muscat Hamburg pre-veraison berry...	76	2e-09
gb EC985323.1	WIN1124.C21_I01 Muscat Hamburg pre-veraison berry...	76	2e-09
gb CV861937.1	gonad_EST09518 Embryonic gonad cDNA Library Gallu...	76	2e-09
gb CX309187.1	C18022D10Rv Drought2 Citrus reshni cDNA clone C18...	76	2e-09
gb CA105303.1	SCJFHR1C05E10.g HR1 Saccharum officinarum cDNA cl...	76	2e-09
gb CA102350.1	SCBGHR1058E08.g HR1 Saccharum officinarum cDNA cl...	76	2e-09
gb CF205258.1	RR890915I0004_IVa_Ra_B09 Vitis sp. RR890915I Viti...	76	2e-09
dbj FS421608.1	FS421608 normalized full-length tobacco cDNA lib...	74	6e-09
dbj FS420315.1	FS420315 normalized full-length tobacco cDNA lib...	74	6e-09
gb ES441310.1	TSH_EST01528 Theobroma cacao-Moniliophthora perni...	74	6e-09
emb CU488677.1	CU488677 DROUGHTLS_KZOACAF Theobroma cacao cDNA ...	74	6e-09
gb FG154278.1	AGN_RNC104xj04f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	6e-09
gb FG173223.1	AGN_RNC126xi04f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	6e-09
gb FG156951.1	AGN_RNC026xe21f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	6e-09
gb FG157638.1	AGN_RNC025xk16f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	6e-09
dbj DB920515.1	DB920515 full-length enriched cassava cDNA libra...	74	6e-09
gb EB450877.1	KT7C.108P16F.051219T7 KT7 Nicotiana tabacum cDNA ...	74	6e-09
gb DY356036.1	ZO_Ec0009K09.f ZO_Ec Zingiber officinale cDNA c...	74	6e-09
gb CV005110.1	atr02-9ms3-h07 Atr02 Amborella trichopoda cDNA cl...	74	6e-09
gb CN782128.1	EST00224 cqseed Chenopodium quinoa cDNA clone S02...	74	6e-09
gb FC869818.1	C31105F02EF AbioticR1 Citrus reshni cDNA clone C3...	72	3e-08
gb FC874065.1	C31202A05EF BiotPhyR1 Citrus aurantium cDNA clone...	72	3e-08
gb GD471713.1	454PCS0099417 Scarlet Runner Bean globular-stage ...	72	3e-08
gb GD391465.1	454PCS0019156 Scarlet Runner Bean globular-stage ...	72	3e-08
gb FG480776.1	020324KANA001021HT (KANA) Actinidia setosa stem A...	72	3e-08
gb EY845171.1	CA26-C1-002-040-C02-CT.F Sour orange leaf, field ...	72	3e-08
gb EY794850.1	CR05-C3-701-027-F03-CT.F Mandarin fruit, developm...	72	3e-08
gb EY776217.1	CR05-C1-103-015-D05-CT.F Mandarin leaf, infected ...	72	3e-08
gb EY725128.1	CS00-C3-703-086-B09-CT.F Sweet orange fruit, deve...	72	3e-08
gb C0500329.1	KH01008A04 KH01 Ipomoea batatas cDNA, mRNA sequence	72	3e-08
gb DW500299.1	GH_TMIRS_045_B08_F Cotton Normalized Library dT p...	72	3e-08
gb CX670039.1	UCRCP01_048_E06_T7 Swingle citrumelo nematode-cha...	72	3e-08
gb CX050341.1	UCRCS09_31H06_b Ruby Orange Developing Seed cDNA ...	72	3e-08
gb CV717574.1	UCRCS08_0009D08_f Parent Washington Navel Orange ...	72	3e-08
gb CV093292.1	FAMU_USDA_FP_1315 Vitis shuttleworthii L., grape ...	72	3e-08
gb C0866271.1	Mdfrt3046b02.y1 Mdfrt Malus x domestica cDNA clon...	72	3e-08
gb C0417575.1	Mdfrt3031k23.y1 Mdfrt Malus x domestica cDNA clon...	72	3e-08
gb C0070833.1	GR_Ea28B05.r GR_Ea Gossypium raimondii cDNA clo...	72	3e-08

gb	G0566201.1	Mddb5025B21_e2932.g1 Mddb Malus x domestica cDNA ...	70	1e-07
emb	CU537036.1	CU537036 TISCIVS_KZOAAQ Theobroma cacao cDNA clo...	70	1e-07
emb	CU505430.1	CU505430 PODMEUPA_KZOACAB Theobroma cacao cDNA c...	70	1e-07
emb	CU478688.1	CU478688 COPHAS_KZOAAAL Theobroma cacao cDNA clon...	70	1e-07
emb	CU478933.1	CU478933 COPHAS_KZOAAAL Theobroma cacao cDNA clon...	70	1e-07
emb	CU480774.1	CU480774 CORTEXS_KZOAAT Theobroma cacao cDNA clo...	70	1e-07
dbj	DC895850.1	DC895850 PCC Citrus unshiu cDNA clone PCC0206 5'...	70	1e-07
gb	EX266960.1	1447232_5_A14_063 PY06 Carica papaya cDNA, mRNA s...	70	1e-07
gb	EX289762.1	1577761_5_L07_022 PY06 Carica papaya cDNA, mRNA s...	70	1e-07
gb	EX272151.1	1452845_5_K11_038 PY06 Carica papaya cDNA, mRNA s...	70	1e-07
gb	EB110403.1	000430AFBC008068HT (AFBC) Royal Gala pre-opened f...	70	1e-07
gb	DW157696.1	CLVX9795.b1_E02.ab1 CLV(XYZ) lettuce virosa Lactu...	70	1e-07
gb	DW145800.1	CLVX10900.b1_H13.ab1 CLV(XYZ) lettuce virosa Lactu...	70	1e-07
gb	CO900249.1	Mddb5025b21.y1 Mddb Malus x domestica cDNA clone ...	70	1e-07
gb	CO051719.1	Mdfw2055d05.y1 Mdfw Malus x domestica cDNA clone ...	70	1e-07
gb	CN880015.1	010418AASA009843HT (AASA) Royal Gala 10 DAFB frui...	70	1e-07
gb	GR871114.1	Pq_F_00457 American ginseng Flower cDNA Library P...	68	4e-07
gb	GR875194.1	Pq_R_02677 American ginseng Root cDNA Library Pan...	68	4e-07
gb	GR873483.1	Pq_R_00966 American ginseng Root cDNA Library Pan...	68	4e-07
gb	GR873276.1	Pq_R_00759 American ginseng Root cDNA Library Pan...	68	4e-07
gb	GR871777.1	Pq_F_01120 American ginseng Flower cDNA Library P...	68	4e-07
gb	GR874357.1	Pq_R_01840 American ginseng Root cDNA Library Pan...	68	4e-07
gb	GR874227.1	Pq_R_01710 American ginseng Root cDNA Library Pan...	68	4e-07
emb	CU507988.1	CU507988 PODSSHWB1Sb_KZOACD Theobroma cacao cDNA...	68	4e-07
gb	EY664481.1	CS00-C1-101-067-A09-CT.F Sweet orange leaf, infec...	68	4e-07
gb	EW712042.1	Ginseng-Feq Contig4 Ginseng F. equiseti subtracti...	68	4e-07
gb	EL366609.1	CCES2712.b1_005.ab1 CCE(LMS) endive Cichorium end...	68	4e-07
gb	EH664510.1	11.2E05 Transformed tobacco Lambda Zap II library...	68	4e-07
gb	EC600006.1	PNSSH3G-1469 panax notoginseng subtracted cDNA li...	68	4e-07
dbj	CI205074.1	CI205074 Oryza sativa (japonica cultivar-group) ...	68	4e-07
gb	CO898341.1	Mdfrt3034e04.y3 Mdfrt Malus x domestica cDNA clon...	68	4e-07
gb	CN848323.1	PG07017B01 Ginseng cDNA library from MeJA treated...	68	4e-07
gb	CN847185.1	PG07026G09 Ginseng cDNA library from MeJA treated...	68	4e-07
gb	CN846818.1	PG07018H01 Ginseng cDNA library from MeJA treated...	68	4e-07
gb	CN846698.1	PG07019B09 Ginseng cDNA library from MeJA treated...	68	4e-07
gb	CN846059.1	PG07005D12 Ginseng cDNA library from MeJA treated...	68	4e-07
gb	CN845966.1	PG07006B07 Ginseng cDNA library from MeJA treated...	68	4e-07
gb	CK265901.1	EST711979 potato abiotic stress cDNA library Sola...	68	4e-07
gb	CK259240.1	EST742877 potato callus cDNA library, normalized ...	68	4e-07
gb	CK257963.1	EST741600 potato callus cDNA library, normalized ...	68	4e-07
gb	CK257684.1	EST741321 potato callus cDNA library, normalized ...	68	4e-07
gb	CK256437.1	EST740074 potato callus cDNA library, normalized ...	68	4e-07
gb	CK256141.1	EST739778 potato callus cDNA library, normalized ...	68	4e-07
gb	CK254968.1	EST738605 potato callus cDNA library, normalized ...	68	4e-07
gb	CK254173.1	EST737810 potato callus cDNA library, normalized ...	68	4e-07
gb	CK253943.1	EST737580 potato callus cDNA library, normalized ...	68	4e-07
gb	CK252132.1	EST735769 potato callus cDNA library, normalized ...	68	4e-07
gb	CK250936.1	EST734573 potato callus cDNA library, normalized ...	68	4e-07
gb	CK250929.1	EST734566 potato callus cDNA library, normalized ...	68	4e-07

gb	CK249912.1	EST733549 potato callus cDNA library, normalized ...	68	4e-07
gb	CK249875.1	EST733512 potato callus cDNA library, normalized ...	68	4e-07
gb	CK249724.1	EST733361 potato callus cDNA library, normalized ...	68	4e-07
gb	CK249638.1	EST733275 potato callus cDNA library, normalized ...	68	4e-07
gb	CK248882.1	EST732519 potato callus cDNA library, normalized ...	68	4e-07
gb	CK248392.1	EST732029 potato callus cDNA library, normalized ...	68	4e-07
gb	CK247774.1	EST731411 potato callus cDNA library, normalized ...	68	4e-07
gb	CK247097.1	EST730734 potato callus cDNA library, normalized ...	68	4e-07
gb	CK246328.1	EST729965 potato callus cDNA library, normalized ...	68	4e-07
gb	CK246259.1	EST729896 potato callus cDNA library, normalized ...	68	4e-07
gb	CK246252.1	EST729889 potato callus cDNA library, normalized ...	68	4e-07
gb	CK245537.1	EST729174 potato callus cDNA library, normalized ...	68	4e-07
gb	CK245042.1	EST728679 potato callus cDNA library, normalized ...	68	4e-07
gb	CK243469.1	EST727106 potato callus cDNA library, normalized ...	68	4e-07
gb	CK243468.1	EST727105 potato callus cDNA library, normalized ...	68	4e-07
dbj	AU229763.1	AU229763 RAFL17 Arabidopsis thaliana cDNA clone ...	68	4e-07
gb	BF273768.1	GA_Eb0018024f Gossypium arboreum 7-10 dpa fiber ...	68	4e-07
dbj	FS194878.1	FS194878 Solanum lycopersicum cv Micro-Tom root ...	66	2e-06
dbj	FS205634.1	FS205634 Solanum lycopersicum cv Micro-Tom root ...	66	2e-06
dbj	FS197980.1	FS197980 Solanum lycopersicum cv Micro-Tom root ...	66	2e-06
gb	GE650850.1	EST1177 Tender roots cDNA library of tea plant Ca...	66	2e-06
gb	EY412917.1	pOP-E008268_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	66	2e-06
gb	FG526917.1	030704KAYC002574HT (KAYC) Actinidia chinensis you...	66	2e-06
gb	FG525755.1	030628KAYC001240HT (KAYC) Actinidia chinensis you...	66	2e-06
gb	FE966530.1	PLATE_T3_028_D07_01DEC2004_057 Opium poppy elicite...	66	2e-06
gb	FE968334.1	PLATE_T3_047_H06_03DEC2004_034 Opium poppy elicite...	66	2e-06
gb	FE966485.1	PLATE_T3_027_H10_01DEC2004_066 Opium poppy elicite...	66	2e-06
gb	FE967467.1	PLATE_T3_038_E11_01DEC2004_087 Opium poppy elicite...	66	2e-06
gb	FE966062.1	PLATE_T3_023_D04_02DEC2004_026 Opium poppy elicite...	66	2e-06
gb	EX165442.1	A05_P-14_034 Cotton 1-14 day post anthesis Lambda...	66	2e-06
gb	EH665793.1	26.2D06 Transformed tobacco Lambda Zap II library...	66	2e-06
dbj	DB685271.1	DB685271 Solanum lycopersicum cv. Micro-Tom leaf...	66	2e-06
dbj	DB689063.1	DB689063 Solanum lycopersicum cv. Micro-Tom leaf...	66	2e-06
dbj	DB699350.1	DB699350 Solanum lycopersicum cv. Micro-Tom leaf...	66	2e-06
dbj	DB692736.1	DB692736 Solanum lycopersicum cv. Micro-Tom leaf...	66	2e-06
gb	DW080731.1	CLPX3640.b1_P21.ab1 CLP (XYZ) lettuce perennis Lac...	66	2e-06
gb	DT523193.1	WS02039.B21_A17 PTxN-IB-N-A-11 Populus trichocarp...	66	2e-06
gb	DT517809.1	WS02435.B21_F23 PTxD-ICC-N-A-14 Populus trichocar...	66	2e-06
gb	DT516973.1	WS02432.B21_P02 PTxD-ICC-N-A-14 Populus trichocar...	66	2e-06
gb	DT515726.1	WS02429.B21.1_F18 PTxD-ICC-N-A-14 Populus trichoc...	66	2e-06
gb	DT511026.1	WS02429.BR_F18 PTxD-ICC-N-A-14 Populus trichocarp...	66	2e-06
gb	DT507952.1	WS02419.BR_K15 PTxD-ICC-N-A-14 Populus trichocarp...	66	2e-06
gb	DN586754.1	46565.1 Late Blight-Challenged Tubers Solanum tub...	66	2e-06
gb	DN485372.1	M129C08.3pR Populus female catkins cDNA library P...	66	2e-06
gb	CV475162.1	23658.1 Developing Tubers Solanum tuberosum cDNA ...	66	2e-06
gb	CV269494.1	WS0208.B21_G14 PTxN-IB-N-A-11 Populus trichocarpa...	66	2e-06
gb	CV269008.1	WS0207.B21_B07 PTxN-IB-N-A-11 Populus trichocarpa...	66	2e-06
gb	CV256197.1	WS0243.B21_D05 PTxD-ICC-N-A-14 Populus trichocarp...	66	2e-06
gb	CK298355.1	EST761069 Nicotiana benthamiana mixed tissue cDNA...	66	2e-06

gb CK296485.1	EST759199	Nicotiana benthamiana mixed tissue cDNA...	66	2e-06
gb CK295751.1	EST758465	Nicotiana benthamiana mixed tissue cDNA...	66	2e-06
gb CK293902.1	EST756616	Nicotiana benthamiana mixed tissue cDNA...	66	2e-06
gb CK283472.1	EST746194	Nicotiana benthamiana mixed tissue cDNA...	66	2e-06
gb CK277562.1	EST723640	potato abiotic stress cDNA library Sola...	66	2e-06
gb CK268372.1	EST714450	potato abiotic stress cDNA library Sola...	66	2e-06
gb CK260187.1	EST706265	potato abiotic stress cDNA library Sola...	66	2e-06
gb CK245041.1	EST728678	potato callus cDNA library, normalized ...	66	2e-06
gb CA927256.1	MTU6CR.P6.H02	Aspen root cDNA Library Populus tre...	66	2e-06
gb BG597610.1	EST496288	cSTS Solanum tuberosum cDNA clone cSTS1...	66	2e-06
gb BG594826.1	EST493516	cSTS Solanum tuberosum cDNA clone cSTS8...	66	2e-06
gb AW429264.1	EST306720	tomato flower buds 0-3 mm, Cornell Univ...	66	2e-06
gb AW035301.1	EST280664	tomato callus, TAMU Solanum lycopersicu...	66	2e-06
gb G0345282.1	CS01010G03	Hotpepper under oxidative stress Capsi...	64	6e-06
dbj FS200575.1	FS200575	Solanum lycopersicum cv Micro-Tom root ...	64	6e-06
gb GD103440.1	KS21047N18	KS21 Capsicum annuum cDNA, mRNA sequence	64	6e-06
gb FG173286.1	AGN_RNC126xi04r1.ab1	AGN_RNC Nicotiana tabacum cD...	64	6e-06
gb FG157705.1	AGN_RNC025xk16r1.ab1	AGN_RNC Nicotiana tabacum cD...	64	6e-06
gb FG157012.1	AGN_RNC026xe21r1.ab1	AGN_RNC Nicotiana tabacum cD...	64	6e-06
gb EY868947.1	CL06-C4-500-024-E11-CT.F	Rangpur lime root, green...	64	6e-06
gb FE964503.1	PLATE_T3_006_A01_18NOV2004_015	Opium poppy elicite...	64	6e-06
gb EL689149.1	OPSC00922	Elaeis guineensis Suspension cell cultu...	64	6e-06
gb EL688532.1	OPSC00287	Elaeis guineensis Suspension cell cultu...	64	6e-06
gb EL689060.1	OPSC00829	Elaeis guineensis Suspension cell cultu...	64	6e-06
gb EW741112.1	10	Capsicum annuum with binucleate Rhizoctonia Li...	64	6e-06
emb AM806126.1	AM806126	seedling library, SL Nicotiana tabacum ...	64	6e-06
gb EV281455.1	GLNB506TF	JCVI-SOY3 Glycine max cDNA 5', mRNA seq...	64	6e-06
gb EB125073.1	010417AASA002377HT	(AASA) Royal Gala 10 DAFB frui...	64	6e-06
gb DY357012.1	ZO_Ed0001B05.r	ZO_Ed Zingiber officinale cDNA c...	64	6e-06
gb CN910664.1	030221ABLC006597HT	(ABLC) Braeburn cell culture t...	64	6e-06
gb CN909288.1	030123ABLC003427HT	(ABLC) Braeburn cell culture t...	64	6e-06
gb CN908413.1	030121ABLC002155HT	(ABLC) Braeburn cell culture t...	64	6e-06
gb CN908053.1	030109ABLC001478HT	(ABLC) Braeburn cell culture t...	64	6e-06
gb CF446769.1	EST683114	normalized cDNA library of onion Allium...	64	6e-06
gb CF445486.1	EST681831	normalized cDNA library of onion Allium...	64	6e-06
gb CF437063.1	EST673408	normalized cDNA library of onion Allium...	64	6e-06
gb BM878736.1	P12-A07	Sweetpotato Ipomoea batatas cDNA similar ...	64	6e-06
dbj FS124984.1	FS124984	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS024422.1	FS024422	library MLF Solanum melongena cDNA clon...	62	2e-05
dbj FS121328.1	FS121328	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS117052.1	FS117052	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS105158.1	FS105158	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS107745.1	FS107745	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS109925.1	FS109925	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS110172.1	FS110172	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS119211.1	FS119211	library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj FS049153.1	FS049153	library PST Solanum melongena cDNA clon...	62	2e-05
dbj FS021644.1	FS021644	library LS5 Solanum melongena cDNA clon...	62	2e-05
dbj FS020310.1	FS020310	library LS5 Solanum melongena cDNA clon...	62	2e-05

gb	GR347634.1	CCOX3299.g1 CCOX Avena barbata root, pooled from ...	62	2e-05
gb	GE299450.1	P006002D02 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299223.1	P005007B06 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299125.1	P005005G03 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299103.1	P005005D09 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299068.1	P005004H11 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299038.1	P005004D05 Subtractive cDNA library from laminari...	62	2e-05
gb	EY410241.1	pOP-E007772_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	62	2e-05
gb	EY410393.1	pOP-E004088_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	62	2e-05
gb	EY412233.1	pOP-E002255_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	62	2e-05
gb	DW248736.1	pOP-EON01090_EST_C_1_pSK_SK EON (Oil Palm Embryoi...	62	2e-05
gb	EY032292.1	CAIT669.fwd CAIT Artemisia annua leaf Artemisia a...	62	2e-05
gb	DY980921.1	CLSS2910.b1_K08.ab1 CLS(LMS) lettuce sativa Lactu...	62	2e-05
gb	DY963072.1	CLSM13334.b1_K22.ab1 CLS(LMS) lettuce sativa Lactu...	62	2e-05
gb	DW141853.1	CLSY9921.b1_B10.ab1 CLS(XYZ) lettuce sativa Lactu...	62	2e-05
gb	DW118586.1	CLRY7219.b1_F06.ab1 CLR(XYZ) lettuce serriola Lac...	62	2e-05
gb	DN494839.1	M129C08.5pR Populus female catkins cDNA library P...	62	2e-05
gb	CX658639.1	P001020D11 Poplar SC cDNA library Populus alba x ...	62	2e-05
gb	CX658354.1	P001034B06 Poplar SC cDNA library Populus alba x ...	62	2e-05
gb	CX656775.1	P002024B08 Poplar SC cDNA library Populus alba x ...	62	2e-05
gb	CO754834.1	Mdfrt3051n10.y1 Mdfrt Malus x domestica cDNA clon...	62	2e-05
gb	GR182521.1	CBPG8855.g1 CBPG Mimulus guttatus IM62 roots, see...	60	1e-04
gb	GR182520.1	CBPG8855.b1 CBPG Mimulus guttatus IM62 roots, see...	60	1e-04
gb	GR101494.1	CCIF25878.b1 CCIF Mimulus guttatus IM62 leaves (H...	60	1e-04
gb	GR030153.1	CCIC14356.g1 CCIC Mimulus guttatus IM62 roots (H)...	60	1e-04
gb	GR010964.1	CCIC3934.g1 CCIC Mimulus guttatus IM62 roots (H) ...	60	1e-04
gb	GR010963.1	CCIC3934.b1 CCIC Mimulus guttatus IM62 roots (H) ...	60	1e-04
gb	GE591881.1	CCPW15817.b1_A19.ab1 CCP(UWX) Globe Artichoke Cyn...	60	1e-04
gb	GE347117.1	MEUB360TF JCVI-MT2 Medicago truncatula cDNA 5', m...	60	1e-04
gb	GE299609.1	P006004H07 Subtractive cDNA library from laminari...	60	1e-04
dbj	BY912248.1	BY912248 Cryptomeria japonica male strobilus Cry...	60	1e-04
gb	FG610783.1	stem_S064_F03.SEQ Opium poppy stem cDNA library P...	60	1e-04
gb	FG230888.1	pvreacc010002_J13_M13rev_phred13_vc root hairs of...	60	1e-04
gb	FD792211.1	08VNAA8_T7_003_G04_17FEB2006_020 08VNAA8 Phaseolu...	60	1e-04
gb	FD793984.1	08VNAA8_T7_031_G10_16MAR2006_068 08VNAA8 Phaseolu...	60	1e-04
gb	EX135466.1	BR119296 root cDNA library KHRT Brassica rapa sub...	60	1e-04
gb	EX114527.1	BR100817 whole plant cDNA library KFYP Brassica r...	60	1e-04
gb	EX032022.1	BR016666 callus cDNA library KBCG Brassica rapa s...	60	1e-04
gb	EL424106.1	CHCM3704.b1_014.ab1 CHC(LMS) Texas blueweed Helia...	60	1e-04
gb	EL362738.1	CCEM7256.b1_P14.ab1 CCE(LMS) endive Cichorium end...	60	1e-04
gb	EL022129.1	EBENXNS02I7QWK 8-day Arabidopsis seedlings, aeria...	60	1e-04
gb	EH665640.1	24E09 Transformed tobacco Lambda Zap II library N...	60	1e-04
gb	EC927161.1	WIN0214.TB24_N12 Cab Sauv flower, leaf and root n...	60	1e-04
gb	DW520518.1	GH_TMIRS_241_D04_F Cotton Normalized Library dT p...	60	1e-04
dbj	BW994485.1	BW994485 Cryptomeria japonica male cone Cryptome...	60	1e-04
dbj	BW990328.1	BW990328 Chamaecyparis obtusa cambium and surrou...	60	1e-04
gb	DV857611.1	col4871 Colonial bentgrass EST Agrostis capillari...	60	1e-04
gb	DV127237.1	CV03047B1C06.f1 CV03-normalized library Euphorbia...	60	1e-04
gb	DV126025.1	CV03044A1B02.f1 CV03-normalized library Euphorbia...	60	1e-04

gb	DT512242.1	WS02418.B21_L24 PTxD-ICC-N-A-14 Populus trichocar...	60	1e-04
gb	DT507614.1	WS02418.BR_L24 PTxD-ICC-N-A-14 Populus trichocarp...	60	1e-04
gb	DT492311.1	WS02550.C21_F01 PT-MB-N-A-15 Populus trichocarpa ...	60	1e-04
gb	DT487692.1	WS02534.B21_G10 PT-MB-N-A-15 Populus trichocarpa ...	60	1e-04
gb	DT487423.1	WS02533.B21_K13 PT-MB-N-A-15 Populus trichocarpa ...	60	1e-04
gb	DT483262.1	WS02522.B21_B19 PT-MB-N-A-15 Populus trichocarpa ...	60	1e-04
gb	DT482024.1	WS02533.BR_K13 PT-MB-N-A-15 Populus trichocarpa c...	60	1e-04
gb	DT478196.1	WS02522.BR_B19 PT-MB-N-A-15 Populus trichocarpa c...	60	1e-04
gb	CX169952.1	B06_69-16_04.ab1 leaf inoculated with Marssonia p...	60	1e-04
gb	CV278268.1	WS0145.B21_021 PTxD-IL-A-5 Populus trichocarpa x ...	60	1e-04
gb	CV277650.1	WS0144.B21_C22 PTxD-IL-A-5 Populus trichocarpa x ...	60	1e-04
gb	CV131018.1	L1P03d05 Populus stem seasonal library Populus de...	60	1e-04
gb	CN848150.1	PG07006D08 Ginseng cDNA library from MeJA treated...	60	1e-04
gb	CK288635.1	EST751357 Nicotiana benthamiana mixed tissue cDNA...	60	1e-04
gb	CK258594.1	EST742231 potato callus cDNA library, normalized ...	60	1e-04
gb	CK255769.1	EST739406 potato callus cDNA library, normalized ...	60	1e-04
gb	CK255201.1	EST738838 potato callus cDNA library, normalized ...	60	1e-04
gb	CK244542.1	EST728179 potato callus cDNA library, normalized ...	60	1e-04
gb	CK244541.1	EST728178 potato callus cDNA library, normalized ...	60	1e-04
gb	CA992234.1	HC0822 GIBCOBRL CAT. NO. 19643-014 Brassica rapa ...	60	1e-04
gb	CA296237.1	SCAGLV1043F09.g LV1 Saccharum officinarum cDNA cl...	60	1e-04
dbj	BP175580.1	BP175580 Cryptomeria japonica inner bark Cryptom...	60	1e-04
gb	AI054926.1	coau0002I16 Cotton Boll Abscission Zone cDNA Libr...	60	1e-04
dbj	FS184353.1	FS184353 Solanum lycopersicum cv Micro-Tom root ...	58	4e-04
dbj	FS185438.1	FS185438 Solanum lycopersicum cv Micro-Tom root ...	58	4e-04
gb	GD111776.1	KS23009A10 KS23 Capsicum annum cDNA, mRNA sequence	58	4e-04
gb	GE508830.1	CCFT6761.b1_A12.ab1 CCF(STU) sunflower Helianthus...	58	4e-04
gb	GE507030.1	CCFT5541.g1_J17.ab1 CCF(STU) sunflower Helianthus...	58	4e-04
gb	GE507029.1	CCFT5541.b1_J17.ab1 CCF(STU) sunflower Helianthus...	58	4e-04
gb	ES294238.1	_08Y_C12 Bermudagrass Normalized cDNA Library Cyn...	58	4e-04
gb	GD594567.1	454PCS0222258 Scarlet Runner Bean globular-stage ...	58	4e-04
gb	FG509216.1	030312KAPC001477HT (KAPC) Actinidia eriantha peta...	58	4e-04
gb	FG486094.1	021104KAUB001004HT (KAUB) Actinidia chinensis CK5...	58	4e-04
gb	FG486083.1	021015KAUB999084HT (KAUB) Actinidia chinensis CK5...	58	4e-04
gb	ES595125.1	000001603252_M19.ab1 Eucalyptus globulus under lo...	58	4e-04
gb	EY948213.1	RS3DN57TF RS3(RT) Raphanus sativus cDNA 5', mRNA ...	58	4e-04
gb	EY063068.1	CATF7534.fwd CATF Artemisia annua, Tanzanian, fro...	58	4e-04
gb	EY063067.1	CATF7534.rev CATF Artemisia annua, Tanzanian, fro...	58	4e-04
gb	EY091175.1	CAZI19752.rev CAZI Artemisia annua normalized lea...	58	4e-04
gb	EX515663.1	Hops-Column-29R_2007-06-04/Hops-Column-29R_F02_00...	58	4e-04
gb	DN965021.1	218e04 longbai no.2 one month old leaves Brassica...	58	4e-04
gb	EL434417.1	CHTL1481.b2_B12.ab1 CHT (LMS) Jerusalem artichoke ...	58	4e-04
gb	EL425067.1	CHCM4607.b1_N24.ab1 CHC (LMS) Texas blueweed Helia...	58	4e-04
gb	EL424239.1	CHCM3838.b1_L24.ab1 CHC (LMS) Texas blueweed Helia...	58	4e-04
gb	DY012178.1	40JKME7D_UP_003_D09_25MAR2004_073 40JKME7D Brassi...	58	4e-04
gb	DT212598.1	E002_B10 Embryogenic SSH library Cichorium intybu...	58	4e-04
gb	DT014039.1	VVH007H01_739521 CabSau Flower Nectary Stage 25 (...	58	4e-04
gb	DT010226.1	VVH055D09_748099 CabSau Flower Nectary Stage 25 (...	58	4e-04
gb	DR929061.1	EST1120600 Aquilegia cDNA library Aquilegia formo...	58	4e-04

gb DR742871.1	RTCU1_7_C01.g2_A029	Roots plus added copper Pinus...	58	4e-04
gb DR742794.1	RTCU1_7_C01.b2_A029	Roots plus added copper Pinus...	58	4e-04
gb DR094964.1	STRR1_17_H08.g1_A033	Stem Response Resistant Pinu...	58	4e-04
gb DR094953.1	STRR1_17_G08.g1_A033	Stem Response Resistant Pinu...	58	4e-04
gb DR094872.1	STRR1_17_G08.b1_A033	Stem Response Resistant Pinu...	58	4e-04
gb DR090538.1	RTAL1_15_F06.g1_A029	Roots plus added aluminum Pi...	58	4e-04
gb DR090469.1	RTAL1_15_F06.b1_A029	Roots plus added aluminum Pi...	58	4e-04
gb DR089595.1	RTAL1_9_E05.g1_A029	Roots plus added aluminum Pin...	58	4e-04
gb DR088958.1	RTAL1_5_E09.g1_A029	Roots plus added aluminum Pin...	58	4e-04
gb DR023270.1	STRS1_56_B11.g1_A034	Shoot tip pitch canker susce...	58	4e-04
gb DR021354.1	STRS1_44_C09.b1_A034	Shoot tip pitch canker susce...	58	4e-04
gb CX658976.1	P001024H07	Poplar SC cDNA library Populus alba x ...	58	4e-04
gb C0499512.1	G.h.fbr-sw08902	G.h.fbr-sw Gossypium hirsutum cDN...	58	4e-04
gb C0498821.1	G.h.fbr-sw08211	G.h.fbr-sw Gossypium hirsutum cDN...	58	4e-04
gb C0498720.1	G.h.fbr-sw08110	G.h.fbr-sw Gossypium hirsutum cDN...	58	4e-04
gb C0496527.1	G.h.fbr-sw05917	G.h.fbr-sw Gossypium hirsutum cDN...	58	4e-04
gb C0494300.1	G.h.fbr-sw03690	G.h.fbr-sw Gossypium hirsutum cDN...	58	4e-04
gb C0491848.1	G.h.fbr-sw01238	G.h.fbr-sw Gossypium hirsutum cDN...	58	4e-04
gb CV094175.1	FAMU_USDA_FP_2198	Vitis shuttleworthii L., grape ...	58	4e-04
emb AJ805072.1	AJ805072	Antirrhinum majus whole plant Antirrhin...	58	4e-04
emb AJ795563.1	AJ795563	Antirrhinum majus whole plant Antirrhin...	58	4e-04
emb AJ795101.1	AJ795101	Antirrhinum majus whole plant Antirrhin...	58	4e-04
emb AJ793569.1	AJ793569	Antirrhinum majus whole plant Antirrhin...	58	4e-04
gb C0200887.1	RTCNT2_2_F01.b1_A029	Root control 2 (late) Pinus ...	58	4e-04
gb CN604982.1	USDA_FP_132082	Vitis shuttleworthii L., grape Vit...	58	4e-04
gb CN604205.1	USDA_FP_131305	Vitis shuttleworthii L., grape Vit...	58	4e-04
gb CF476953.1	RTWW3_4_G10.g1_A022	Well-watered loblolly pine ro...	58	4e-04
gb CF401192.1	RTWW1_10_H07.g1_A015	Well-watered loblolly pine r...	58	4e-04
gb CF401118.1	RTWW1_10_H07.b1_A015	Well-watered loblolly pine r...	58	4e-04
gb CF400173.1	RTWW1_3_F07.g1_A015	Well-watered loblolly pine ro...	58	4e-04
gb CF400086.1	RTWW1_3_F07.b1_A015	Well-watered loblolly pine ro...	58	4e-04
gb CF387460.1	RTDR1_20_H12.b1_A015	Loblolly pine roots recoveri...	58	4e-04
gb CF387171.1	RTDR1_11_H09.b1_A015	Loblolly pine roots recoveri...	58	4e-04
gb CF387078.1	RTDR1_10_H09.g1_A015	Loblolly pine roots recoveri...	58	4e-04

>gb|CX703225.1| gmrtDrNS01_14-B_M13R_D10_074.s2 Water stressed 5h segment 2
gmrtDrNS01 Glycine max cDNA 3', mRNA sequence
Length = 743

Score = 1070 bits (540), Expect = 0.0
Identities = 543/544 (99%)
Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 640 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 581

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 580 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 521

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 520 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 461

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 460 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 401

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctct 2088
|||||
Sbjct: 400 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctct 341

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||
Sbjct: 340 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 281

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||
Sbjct: 280 gaaatcaggaagaattgtagaaggattaactaatttattcagtccttgaatattaagggt 221

Query: 2209 cctacacatacgaagcaatttaattgtgttaataagttgttaaacatgttttggttg 2268
|||||
Sbjct: 220 cctacacatacgaagcaatttaattgtgttaataagttgttaaacatgttttggttg 161

Query: 2269 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 2328
|||||
Sbjct: 160 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 101

Query: 2329 tccc 2332
|||
Sbjct: 100 tccc 97

Score = 210 bits (106), Expect = 4e-50
Identities = 106/106 (100%)
Strand = Plus / Minus

Query: 1540 tgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatt 1599
|||||
Sbjct: 743 tgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatt 684

Query: 1600 tagcgctcttggactttccaccaaggacttggtcgccttgtccggt 1645
|||||
Sbjct: 683 tagcgctcttggactttccaccaaggacttggtcgccttgtccggt 638

Score = 79.8 bits (40), Expect = 1e-10
Identities = 40/40 (100%)
Strand = Plus / Minus

Query: 2388 tcctttatcaagcatttatcaagaacggagtttgcttttt 2427
|||||
Sbjct: 40 tcctttatcaagcatttatcaagaacggagtttgcttttt 1

>gb|CX709633.1| gmrtDrNS01_10-D_M13R_A04_032.s2 Water stressed 5h segment 2
gmrtDrNS01 Glycine max cDNA 3', mRNA sequence
Length = 791

Score = 1063 bits (536), Expect = 0.0
Identities = 542/544 (99%)
Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 640 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 581

Query: 1849 accaacaatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 580 accaacaatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 521

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 520 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 461

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 460 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 401

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagaccaacccgggcaccttctcctct 2088
|||||

Sbjct: 400 ggtgggtccaccgactccattgtgcgtggctacagaccaacccgggcaccttttctct 341

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||

Sbjct: 340 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 281

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagcttgaatattaagggt 2208
|||||

Sbjct: 280 gaaatcaggaagaattgtagaaggattaactaatttaattcagcttgaatattaagggt 221

Query: 2209 cctacacatacgaagcaatttaattgtgttaataagttgttaaacatgttttggttg 2268
|||||

Sbjct: 220 cctacacatacgaagcaatttaattgtgttaataagttgttaaacatgttttggttg 161

Query: 2269 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtggttctact 2328
|||||

Sbjct: 160 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtggttctact 101

Query: 2329 tccc 2332
||||

Sbjct: 100 tccc 97

Score = 297 bits (150), Expect = 2e-76
Identities = 153/154 (99%)
Strand = Plus / Minus

Query: 1492 atggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaaca 1551
|||||

Sbjct: 791 atggaatgttaaacttgaagaagagacgctagaattgctagccaatctgctgctaaca 732

Query: 1552 tggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttgg 1611
|||||

Sbjct: 731 tggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttgg 672

Query: 1612 actttccaccaaggacttggtcgccttgtccggt 1645
|||||
Sbjct: 671 actttccaccaaggacttggtcgccttgtccggt 638

Score = 79.8 bits (40), Expect = 1e-10
Identities = 40/40 (100%)
Strand = Plus / Minus

Query: 2388 tcctttatcaagcatttatcaagaacggagtttgcttttt 2427
|||||
Sbjct: 40 tcctttatcaagcatttatcaagaacggagtttgcttttt 1

>gb|CF807990.1| psHB031xA07f USDA-IFAFS:Expression of Phytophthora sojae genes during
infection and propagation Glycine max cDNA clone
sHB031A07 5, mRNA sequence
Length = 708

Score = 1059 bits (534), Expect = 0.0
Identities = 543/545 (99%), Gaps = 1/545 (0%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 149 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 208

Query: 1849 accaakatagaaaccgcatttgaaggactaggcagcaaagctgcccctagaacatcaggg 1908
|||||
Sbjct: 209 accaakatagaaaccgcatttgaaggactaggcagcaaagctgcccctagaacatcaggg 268

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
|||||
Sbjct: 269 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 328

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 329 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 388

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccacccgggcaccttctcctct 2088
|||||
Sbjct: 389 ggtgggtccaccgactccattgtgcgtggctacagcaccacccgggcaccttctcctct 448

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||

Sbjct: 449 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 508

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||

Sbjct: 509 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 568

Query: 2209 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaaacat-gttttgggt 2267
|||||

Sbjct: 569 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaaacatggttttgggt 628

Query: 2268 gtatnttgattcctagtgtagtttcgggatcaatgccgtctactttagtggttctac 2327
|||||

Sbjct: 629 gtatnttgattcctagtgtagnttcgggatcaatgccgtctactttagtggttctac 688

Query: 2328 ttccc 2332
|||||

Sbjct: 689 ttccc 693

Score = 299 bits (151), Expect = 6e-77

Identities = 151/151 (100%)

Strand = Plus / Plus

Query: 1495 gaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaatgg 1554
|||||

Sbjct: 1 gaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaatgg 60

Query: 1555 catccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgact 1614
|||||

Sbjct: 61 catccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgact 120

Query: 1615 ttccaccaaggacttggcgccttgtccgggt 1645
|||||

Sbjct: 121 ttccaccaaggacttggcgccttgtccgggt 151

>gb|BG509781.1| sad25h05.y1 Gm-c1074 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1074-1498 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
; , mRNA sequence
Length = 493

Score = 924 bits (466), Expect = 0.0
Identities = 472/474 (99%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||||
Sbjct: 20 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 79

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 80 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagatcatcaggg 139

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 140 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 199

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactggttcaac 2028
|||||
Sbjct: 200 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactggttcaac 259

Query: 2029 ggtgggtccaccgactccattgtgctgggtacagcaccacccgggcacettctcctct 2088
|||||
Sbjct: 260 ggtgggtccaccgactccattgtgctgggtacagcaccacccgggcacettctcctct 319

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||
Sbjct: 320 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 379

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagcttgaatattaagggt 2208
|||||
Sbjct: 380 gaaatcaggaagaattgtagaaggattaactaatttaattcagcttgaatattaagggt 439

Query: 2209 cctacacatacgaagcaatttaattgtgtttaataagttgttaaacaatggtt 2262
|||||
Sbjct: 440 cctacacatacgaagcaatttaattgtgtttaataagttgttaaacaatggtt 493

Score = 44.1 bits (22), Expect = 5.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1624 ggacttggtcgccttgtccggt 1645
|||||
Sbjct: 1 ggacttggtcgccttgtccggt 22

>gb|BM731124.1| sal68a04.y1 Gm-c1061 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1061-4231 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 506

Score = 894 bits (451), Expect = 0.0
Identities = 454/455 (99%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 52 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 111

Query: 1849 accaacatagaaacgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 112 accaacatagaaacgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 171

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
|||||
Sbjct: 172 tcagaggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 231

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctcactctgatcagcaactgttcaac 2028
|||||
Sbjct: 232 tacttcaagaacctcgttcagaagaagggtctcctcactctgatcagcaactgttcaac 291

Query: 2029 ggtgggtccaccgactccattgtgctgggtacagcaccacccgggcacettctcctct 2088
|||||
Sbjct: 292 ggtgggtccaccgactccattgtgctgggtacagcaccacccgggcacettctcctct 351

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||
Sbjct: 352 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 411

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||
Sbjct: 412 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 471

Query: 2209 cctacacatacgcaagcaatttaattgtgtttaat 2243
|||||
Sbjct: 472 cctacacatacgcaagcaatttaattgtgtttaat 506

Score = 107 bits (54), Expect = 5e-19
Identities = 54/54 (100%)
Strand = Plus / Plus

Query: 1592 tcaagatntagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
|||||
Sbjct: 1 tcaagatntagcgctcttggactttccaccaaggacttggcgccttgtccggt 54

>gb|BG882707.1| sae51e08.y2 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1051-8679 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 483

Score = 880 bits (444), Expect = 0.0
Identities = 444/444 (100%)
Strand = Plus / Plus

Query: 1889 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948
|||||
Sbjct: 1 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 60

Query: 1949 caaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccact 2008
|||||
Sbjct: 61 caaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccact 120

Query: 2009 ctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcacca 2068
|||||
Sbjct: 121 ctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcacca 180

Query: 2069 acccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtc 2128

Sbjct: 181 |||
acccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtc 240

Query: 2129 ctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaatttgatt 2188
|||

Sbjct: 241 ctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaatttgatt 300

Query: 2189 cagtcttgaatattaagggtcctacacatacgcaagcaatttaattgtgtttaataagtt 2248
|||

Sbjct: 301 cagtcttgaatattaagggtcctacacatacgcaagcaatttaattgtgtttaataagtt 360

Query: 2249 gttaaaacatgttttggttgattttggattcctagtgtagtttcggtgatcaatgccgt 2308
|||

Sbjct: 361 gttaaaacatgttttggttgattttggattcctagtgtagtttcggtgatcaatgccgt 420

Query: 2309 ctactttagtggttctacttccc 2332
|||

Sbjct: 421 ctactttagtggttctacttccc 444

>gb|EV267121.1| GLLBF04TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 719

Score = 731 bits (369), Expect = 0.0
Identities = 467/498 (93%), Gaps = 5/498 (1%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||

Sbjct: 113 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 172

Query: 1849 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
| |||

Sbjct: 173 agcaacatagacaccgcatttgaaggacaaggcaaaaagctgccaagaacatcaggg 232

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||

Sbjct: 233 tcaggggacaataatcttgacgacttgatcttcaaactccaaccgaattcgacaactac 292

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||

Sbjct: 293 tacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgttcaat 352

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagaccaacccggcaccttctcctct 2088
|||||

Sbjct: 353 ggtgggtccaccgactccattgtgcgtggctacagaccaacccgagctccttctcctct 412

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||

Sbjct: 413 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaacgga 472

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt--tgattcagcttgaatattaagg 2206
|||||

Sbjct: 473 gaaatcaggaagaattgtagaaggattaactaattactaattgagctccaatattaagg 532

Query: 2207 gtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaacaatgtttt 2263
|||

Sbjct: 533 gtctactacacatacgaagcaatttaattgtgtttaataagttgttaaacaatgtttt 592

Query: 2264 gttgtatgttgattcc 2281

|||||

Sbjct: 593 gttgtatgttgattcc 610

Score = 210 bits (106), Expect = 4e-50

Identities = 112/114 (98%)

Strand = Plus / Plus

Query: 1532 agccaatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatc 1591
|||||

Sbjct: 2 agccaatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatc 61

Query: 1592 tcaagatttagcgctcttgactttccaccaaggacttggcgccttgtccgg 1645
|||||

Sbjct: 62 tcaagatttagcgctcttgactttccaccaaggacttggcgccttgtccgg 115

>gb|CF806428.1| psHB011xI05f USDA-IFAFS:Expression of Phytophthora sojae genes during
infection and propagation Glycine max cDNA clone
sHB011I05 5, mRNA sequence
Length = 606

Score = 646 bits (326), Expect = 0.0
Identities = 415/443 (93%), Gaps = 5/443 (1%)
Strand = Plus / Minus

Query: 1844 acgagaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgcccctagaacat 1903
||||| ||||||| ||||||| ||||||| ||||| ||||||| |||||||
Sbjct: 606 acgagagcaacatagacaccgcatttgcaaggacaaggcaacaaagctgcccagaacat 547

Query: 1904 cagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgaca 1963
||||| ||||||| ||||| ||||| ||||||| ||||||| ||||||| |||||
Sbjct: 546 cagggtcaggggacaataatcttgcaccgcttgatcttcaaactccaaccgaattcgaca 487

Query: 1964 actactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgt 2023
||||| ||||||| ||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 486 actactacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgt 427

Query: 2024 tcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttct 2083
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Sbjct: 426 tcaatgggtgggtccaccgactccattgtgcgtggctacagcaccaaccgagctccttct 367

Query: 2084 cctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctcca 2143
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 366 cctctgacttcgccgcccatgatcaagatgggagacattagtcctctcactggctcca 307

Query: 2144 atggagaaatcaggaagaattgtagaaggattaactaatt--tgattcagctttgaatat 2201
| ||||||| ||||||| ||||||| ||||||| ||||||| ||||| ||||| |||||||
Sbjct: 306 acggagaaatcaggaagaattgtagaaggattaactaattactaattgagctcgaatat 247

Query: 2202 taagggtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaaacat 2258
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 246 taagggtcctactacacatacgaagcaatttaattgtgtttaataagttgttaaaacat 187

Query: 2259 gttttggttgatattttggattcc 2281
||||| |||||||
Sbjct: 186 gttttggttgatattttggattcc 164

Score = 63.9 bits (32), Expect = 6e-06
Identities = 38/40 (95%)
Strand = Plus / Minus

Query: 2388 tcctttatcaagcatttatcaagaacggagtttgcttttt 2427
|||||
Sbjct: 41 tcctttatcaagaatttatcaagaacagagtttgcttttt 2

>gb|AW349107.1| GM210004A21E9 Gm-r1021 Glycine max cDNA clone Gm-r1021-1362 3', mRNA
sequence
Length = 609

Score = 626 bits (316), Expect = e-175
Identities = 449/498 (90%), Gaps = 5/498 (1%)
Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcactacaacgag 1848
|||||
Sbjct: 604 ggtggtcacacaannnnacaagcaaggtgcacnannnnngagcccgcactacaacgag 545

Query: 1849 accaacatagaaaccgcatattgcaaggactaggcagcaagctgccttagaacatcaggg 1908
| |||||
Sbjct: 544 agcaacatagannncgcatattgcaaggacaaggcaacaaagctgccaagaacatcaggg 485

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
|||||
Sbjct: 484 tcaggggacaataatcttgcaacgcttgatcttcaactccaaccgaattcgacnntac 425

Query: 1969 tacttcaagaacctcggtcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 424 tacttcaagaatcttgttcaaaagaagggtctcctccactctgatcagcnnctgttcaat 365

Query: 2029 ggtgggtccaccgactccattgtgctggttacagcaccaaccgggacattctcctct 2088
|||||
Sbjct: 364 ggtgggtccaccgactccattgtgctggttacagcaccaaccggagctccttctcctct 305

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtctctcactggctccaatgga 2148
|| |||||
Sbjct: 304 gacttcgccgcccatgatcaagatgggagacattagtctctcactggctccaacgga 245

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt--tgattcagcttgaatattaagg 2206
|||||
Sbjct: 244 gaaatcaggaagaattgtagaaggattaactaattactaattgagctccaatattaagg 185

Query: 2207 gtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaacatgtttt 2263
||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 184 gtcctactacacatacgaagcaatttaattgtgtttaataagttgttaaacatgtttt 125

Query: 2264 ggttgatattttggattcc 2281
||||| ||||||||||||
Sbjct: 124 ggttgatattttggattcc 107

>gb|BG156628.1| sab31a07.y1 Gm-c1026 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1026-3086 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 425

Score = 618 bits (312), Expect = e-173
Identities = 325/328 (99%), Gaps = 1/328 (0%)
Strand = Plus / Plus

Query: 2005 cactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagc 2064
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3 cactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagc 62

Query: 2065 accaaccggggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacatt 2124
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 63 accaaccggggcaccttctcctctgatttcgccgccgc-atgatcaagatgggagacatt 121

Query: 2125 agtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaattt 2184
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 122 agtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaattt 181

Query: 2185 gattcagcttgaatattaagggtcctacacatacgaagcaatttaattgtgtttaata 2244
|||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct: 182 aattcagcttgaatattaagggtcctacacatacgcagcaatttaattgtgtttaata 241

Query: 2245 agttgttaaacatgttttggttgatattttggattcctagtgtagtttcggtgatcaatg 2304
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 242 agttgttaaacatgttttggttgatattttggattcctagtgtagtttcggtgatcaatg 301

Query: 2305 ccgtctacttttagtgtgttctacttccc 2332
||||||||||||||||||||||||||||||

Sbjct: 302 cegtctacttttagtgtgttctacttccc 329

>gb|FK018609.1| GLND133TF JCVI-SOY3 Glycine max cDNA 5', mRNA sequence
Length = 464

Score = 557 bits (281), Expect = e-154
Identities = 291/293 (99%), Gaps = 1/293 (0%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||||
Sbjct: 172 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 231

Query: 1849 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 232 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 291

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
|||||
Sbjct: 292 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 351

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactggtcaac 2028
|||||
Sbjct: 352 tacttcaaggacctcgttcagaagaagggtctcctccactctgatcagcaactggtcaac 411

Query: 2029 ggtgggtccaccgactcca-ttgtgcgtggctacagcaccaaccgggcacct 2080
|||||
Sbjct: 412 ggtgggtccaccgactccatttgtgcgtggctacagcaccaaccgggcacct 464

Score = 333 bits (168), Expect = 4e-87
Identities = 168/168 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 7 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 66

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||

Sbjct: 67 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 126

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 1645

|||||

Sbjct: 127 tttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 174

>gb|BU577048.1| sar71e12.y1 Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1074-7896 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
; , mRNA sequence
Length = 432

Score = 545 bits (275), Expect = e-151
Identities = 376/408 (92%), Gaps = 5/408 (1%)
Strand = Plus / Plus

Query: 1879 aggcagcaaagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgat 1938

|||||

Sbjct: 1 aggcacaacaagctgcccaagaacatcagggtcaggggacaataatcttgcaacgcttgat 60

Query: 1939 cttcaactccaaccagctttgacaactactacttcaagaacctcgttcagaagaagggt 1998

|||||

Sbjct: 61 cttcaactccaaccgaattcgacaactactacttcaagaatcttgttcagaagaagggt 120

Query: 1999 ctctccactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggc 2058

|||||

Sbjct: 121 ctctccactctgatcagcaactgttcaatgggtgggtccaccgactccattgtgcgtggc 180

Query: 2059 tacagcaccaaccgggcaccttctcctctgatttcgccgccgcatgatcaagatggga 2118

|||||

Sbjct: 181 tacagcaccaacttttttcttctcctctgacttcgccgccgcatgatcaagatggga 240

Query: 2119 gacattagtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaac 2178

|||||

Sbjct: 241 gacattagtcctctcactggctccaacggagaaatcaggaagaattgtagaaggattaac 300

Query: 2179 taatt--tgattcagcttgaatattaagggtc---ctacacatacgcaagcaatttaac 2233

|||||

Sbjct: 301 taattactaattgagctctccaatattaagggtcctactacacatacgcaagcaatttaac 360

Query: 2234 tgtgtttaataagttgttaaacatgttttggttgtattttgattcc 2281

|||||
Sbjct: 361 tgtgtttaataagttgttaaacatgttttggtgtgttttgattcc 408

>gb|BM093025.1| saj04a09.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1065-9257 5' similar to TR:Q9XIV9 Q9XIV9
PEROXIDASE ;, mRNA sequence
Length = 568

Score = 527 bits (266), Expect = e-145
Identities = 266/266 (100%)
Strand = Plus / Plus

Query: 519 atcaaacacaaacacttgaagtactaagttagtggtttgagcaaattaactatggcttc 578
|||||
Sbjct: 1 atcaaacacaaacacttgaagtactaagttagtggtttgagcaaattaactatggcttc 60

Query: 579 gttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaa 638
|||||
Sbjct: 61 gttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaa 120

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaaccttctcctctgtgaa 698
|||||
Sbjct: 121 tgcacaactttctacaaacttttactaccattcatgtccaaaccttctcctctgtgaa 180

Query: 699 atccacagtgcaatctgccatatctaaggagaccgcatgggtgcttctccttcgctt 758
|||||
Sbjct: 181 atccacagtgcaatctgccatatctaaggagaccgcatgggtgcttctccttcgctt 240

Query: 759 gttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 241 gttcttccacgattgctttgtcaatg 266

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 266 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 325

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 326 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 385

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 1336
|||||
Sbjct: 386 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 445

Query: 1337 tctgttcagatt 1348
|||||
Sbjct: 446 tctgttcagatt 457

Score = 218 bits (110), Expect = 2e-52
Identities = 110/110 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 458 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 517

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaact 1587
|||||
Sbjct: 518 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaact 567

>gb|BE210375.1| so42h10.y1 Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1039-668 5' similar to TR:024336 024336
KOREAN-RADISH ISOPEROXIDASE ;, mRNA sequence
Length = 520

Score = 527 bits (266), Expect = e-145
Identities = 266/266 (100%)
Strand = Plus / Plus

Query: 519 atcaaacacaacacttgaagtactaagttagtggtttgagcaaattaactatggcttc 578
|||||
Sbjct: 7 atcaaacacaacacttgaagtactaagttagtggtttgagcaaattaactatggcttc 66

Query: 579 gttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaa 638
|||||

Sbjct: 67 gttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaa 126

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaacaccttctcctctgtgaa 698
|||||

Sbjct: 127 tgcacaactttctacaaacttttactaccattcatgtccaacaccttctcctctgtgaa 186

Query: 699 atccacagtgaatctgccatatctaaggagaccgcatgggtgcttctccttcgctt 758
|||||

Sbjct: 187 atccacagtgaatctgccatatctaaggagaccgcatgggtgcttctccttcgctt 246

Query: 759 gttcttccacgattgctttgtcaatg 784
|||||

Sbjct: 247 gttcttccacgattgctttgtcaatg 272

Score = 373 bits (188), Expect = 5e-99
Identities = 191/192 (99%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||

Sbjct: 272 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 331

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||

Sbjct: 332 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 391

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 1336
|||||

Sbjct: 392 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcactgccagagac 451

Query: 1337 tctgttcagatt 1348
|||||

Sbjct: 452 tctgttcagatt 463

Score = 97.6 bits (49), Expect = 4e-16
Identities = 55/57 (96%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagc 1534
||||| ||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct: 464 cttggaagccctacatggaatgttaaacttgaagaagagacgctagaactgctagc 520

>gb|EV263181.1| GLLA357TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 813

Score = 525 bits (265), Expect = e-145
Identities = 274/277 (98%)
Strand = Plus / Plus

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtggtttgagcaaatta 567
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 3 acaccctttcaatcaaacacaaacactcgaagtactaagttagtggttcgagcaaatta 62

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 63 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 122

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 123 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 182

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttct 747
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 183 tcctctgtgaaatccgcagtgcaatctgccatatctaaggagaccgcgatgggtgcttct 242

Query: 748 ctcttcgcttgcttcttccacgattgctttgtcaatg 784
||||| ||||||||||||||||||||||| |||||||
Sbjct: 243 ctcttcgcttgcttcttccacgattgctttgtcaatg 279

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 279 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 338

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 339 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 398

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 1336
|||||
Sbjct: 399 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 458

Query: 1337 tctgttcagatt 1348
|||||
Sbjct: 459 tctgttcagatt 470

Score = 333 bits (168), Expect = 4e-87
Identities = 168/168 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 471 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 530

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 531 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 590

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtccgg 1645
|||||
Sbjct: 591 tttagcgctcttggactttccaccaaggacttggctgccttgtccgg 638

Score = 270 bits (136), Expect = 5e-68
Identities = 178/184 (96%), Gaps = 6/184 (3%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacgag 1848
|||||
Sbjct: 636 ggtggtcacacaattggacaagcaag-tgcacaaacttcagagcccgcattacaacgag 694

Query: 1849 accaacaatagaaccgatttgaaggacttaggcagcaaagctgccctagaacatcagg 1908

Score = 250 bits (126), Expect = 5e-62
Identities = 126/126 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 272 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 331

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 332 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 391

Query: 1277 gagaaa 1282
|||||
Sbjct: 392 gagaaa 397

>gb|BI972311.1| sag89h02.y1 Gm-c1084 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1084-1515 5' similar to TR:Q9XIV9 Q9XIV9
PEROXIDASE ;, mRNA sequence
Length = 573

Score = 502 bits (253), Expect = e-138
Identities = 253/253 (100%)
Strand = Plus / Plus

Query: 532 acttgaagtactaagttagtggtttgagcaaattaactatggcttcgttttgttctaga 591
|||||
Sbjct: 1 acttgaagtactaagttagtggtttgagcaaattaactatggcttcgttttgttctaga 60

Query: 592 ttgacaatttgtttggctctgtttgtcctcatatgggggagtgccaatgcacaactttct 651
|||||
Sbjct: 61 ttgacaatttgtttggctctgtttgtcctcatatgggggagtgccaatgcacaactttct 120

Query: 652 acaaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaa 711
|||||
Sbjct: 121 acaaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaa 180

Query: 712 tctgcatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccacgat 771
|||||
Sbjct: 181 tctgcatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccacgat 240

Query: 772 tgctttgtcaatg 784
 |||||||
Sbjct: 241 tgctttgtcaatg 253

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 |||||||
Sbjct: 253 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 312

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 |||||||
Sbjct: 313 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 372

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcatatccttgccatcgctgccagagac 1336
 |||||||
Sbjct: 373 gagaaagtgtgtccaggagttgtttcctgcgcatatccttgccatcgctgccagagac 432

Query: 1337 tctgttcagatt 1348
 |||||||
Sbjct: 433 tctgttcagatt 444

Score = 240 bits (121), Expect = 5e-59
Identities = 127/129 (98%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
 |||||||
Sbjct: 445 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 504

Query: 1538 tctgctgctaacaatggcatcctgcacccacttcaaaccttaaccaactcatctcaaga 1597
 |||||||
Sbjct: 505 tctgctgctaacaatggcatcctgcacccacttcaaaccttaaccaactcatctcaaga 564

Query: 1598 tttagcgct 1606
|||||||
Sbjct: 565 tttagcgct 573

>gb|BE209964.1| so37a08.y1 Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1039-111 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 391

Score = 490 bits (247), Expect = e-134
Identities = 247/247 (100%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 114 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 173

Query: 1849 accaacatagaaacgcatttgaaggactaggcagcaaagctgcacctagaacatcaggg 1908
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 174 accaacatagaaacgcatttgaaggactaggcagcaaagctgcacctagaacatcaggg 233

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 234 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 293

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 294 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 353

Query: 2029 ggtgggt 2035
|||||||
Sbjct: 354 ggtgggt 360

Score = 230 bits (116), Expect = 5e-56
Identities = 116/116 (100%)
Strand = Plus / Plus

Query: 1530 ctagccaatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactca 1589
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1 ctagccaatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactca 60

Query: 1590 tctcaagatttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 1645
|||||
Sbjct: 61 tctcaagatttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 116

>gb|BG725689.1| sae39d12.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1051-7487 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 499

Score = 464 bits (234), Expect = e-126
Identities = 285/302 (94%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacgag 1848
|||||
Sbjct: 197 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacgag 256

Query: 1849 accaacatagaaacgcatttgaaggacttaggcagcaaaagctgccctagaacatcaggg 1908
| |||||
Sbjct: 257 agcaacatagacaccgcatttgaaggacaaggcaacaaagctgcccaagaacatcaggg 316

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 317 tcaggggacaataatctggcaccgcttgatcttcaaactccaaccgaattcgacaactac 376

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 377 tacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgttcaat 436

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggacettctctct 2088
|||||
Sbjct: 437 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccggagctccttctctct 496

Query: 2089 ga 2090
||
Sbjct: 497 ga 498

Score = 293 bits (148), Expect = 4e-75

Identities = 163/168 (97%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 32 cttggaggccctagttggaatgttaaagtgaagaagagacgctagaactgctagccaa 91

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 92 tctgctgctaacaatggcatccctccaccacttcaaaccttaaccaactcatctcaaga 151

Query: 1598 tttagcgccttggactttccaccaaggacttggcgccttgtccggt 1645
||
Sbjct: 152 ttcagcgccttggactttccaccaaggacttggcgccttgtccggt 199

Score = 50.1 bits (25), Expect = 0.092
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 1319 gccatcgctgccagagactctgttcagat 1347
|||||
Sbjct: 2 gccatagctgccagagactctgttcagat 30

>gb|FG889629.1| UCRVU08_CCNS10828_g1 Cowpea IT97K-461-4 Mixed Tissue and Conditions
cDNA Library UCRVU08-1-2 Vigna unguiculata cDNA clone
CCNS10828.g1, mRNA sequence
Length = 670

Score = 444 bits (224), Expect = e-120
Identities = 341/380 (89%)
Strand = Plus / Minus

Query: 1800 aattggacaagcaaggtgcacaaacttcagagcccgcctctacaacgagaccaacataga 1859
|||||
Sbjct: 670 aattggacaagcaaggtgcacaaatttcagagcccgcctctacaacgagaccaacattga 611

Query: 1860 aaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcaggggacaa 1919
|||
Sbjct: 610 tacctcatttgccaggacaagacaatcaagctgccccagaacatcagggtcaggggacaa 551

Query: 1920 caatctggcaccacttgatcttcaaactccaaccagctttgacaactactacttcaagaa 1979
|||||
Sbjct: 550 caatctggcaccgcttgatcttcagactccgaccacattcgacaactactacttcaggaa 491

Query: 1980 cctcgttcagaagaagggtctctccactctgatcagcaactggtcaacgggtgggtccac 2039
|||
Sbjct: 490 cctggttcagaagaagggtctctccactctgaccagcaactcttcaatgggtggctccac 431

Query: 2040 cgactccattgtgcgtggctacagcaccaaccgggcaccttctcctctgatttcgccgc 2099
|||||
Sbjct: 430 tgactccatagtgcgtggctacagcaccaaccggagctccttttctctgattttgtctc 371

Query: 2100 cgccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaa 2159
|||||
Sbjct: 370 cgccattatcaagatgggagacattagtcctcctcactggctccaaggagaaatcagaaa 311

Query: 2160 gaattgtagaaggattaact 2179
|||
Sbjct: 310 gaactgcagaaggattaact 291

>gb|BE022389.1| sm85b11.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1015-6838 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 571

Score = 438 bits (221), Expect = e-118
Identities = 278/297 (93%)
Strand = Plus / Plus

Query: 1834 cgcactctacaacgagaccaacatagaaaccgcatcttgcaaggactaggcagcaaagctgc 1893
|||||
Sbjct: 6 cgcactctacaacgagagcaacatagacaccgcatcttgcaaggacaaggcaacaaagctgc 65

Query: 1894 cctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaacc 1953
||
Sbjct: 66 ccaagaacatcagggtcaggggacaataatcttgcaacgcttgatcttcaaactccaacc 125

Query: 1954 agctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgat 2013
||
Sbjct: 126 gaattcgacaactactacttcaagaatcttggtcagaagaagggtctcctccactctgat 185

Query: 2014 cagcaactgttcaacgggtgggtccaccgactccattgtgctggctacagcaccaaccg 2073
|||||
Sbjct: 186 cagcaactgttcaatgggtgggtccaccgactccattgtgctggctacagcaccaaccg 245

Query: 2074 ggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtcct 2130
||
Sbjct: 246 agtccttctcctctgacttcgccgcccatgatcaagatgggagacattagtcct 302

>gb|BG359695.1| sac27d09.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1051-3617 5' similar to TR:Q9XIV9 Q9XIV9
PEROXIDASE :, mRNA sequence
Length = 233

Score = 436 bits (220), Expect = e-118
Identities = 230/232 (99%), Gaps = 1/232 (0%)
Strand = Plus / Plus

Query: 533 cttgaagtactaagttagtggtttgagcaaattaactatggcttcgttttgttctagat 592
|||||
Sbjct: 2 cttgaagtactaagttagtggtttgagcaaattaactatggcttc-ttttgttctagat 60

Query: 593 tgacaattttgtttggctctgtttgcctcatatgggggagtccaatgcacaactttcta 652
|||||
Sbjct: 61 tgacaattttttggctctgtttgcctcatatgggggagtccaatgcacaactttcta 120

Query: 653 caaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaat 712
|||||
Sbjct: 121 caaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaat 180

Query: 713 ctgccatatctaaggagaccgcatgggtgcttctccttcgcttgttctt 764
|||||
Sbjct: 181 ctgccatatctaaggagaccgcatgggtgcttctccttcgcttgttctt 232

>gb|EV265313.1| GLLAS95TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 652

Score = 412 bits (208), Expect = e-111
Identities = 260/277 (93%), Gaps = 4/277 (1%)
Strand = Plus / Plus

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaatta 567
||||||| ||||| ||||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 2 acaccctctcaagcaaacacaaacacttgaagtactaagttagtgtttttgagcaaa--- 58

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||| |
Sbjct: 59 -ctatggcttcgttttgttctagattgaccatttgtttggctctgtttgtcctcatattg 117

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||||||||||||| ||||||||||||||||| ||||||||||||| |||||||||||||
Sbjct: 118 gggagtgccaatgccaaactttctacaaacttttactaccattcgtgtccaaacctcttc 177

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttct 747
||| ||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct: 178 tccactgtgaaatccacagtgcaatctgccatatcaaaggagaccgcatgggtgcttct 237

Query: 748 ctctctcgcttgttcttccacgattgctttgtcaatg 784
||||| ||| |||||||||||||||||||||||||
Sbjct: 238 ctctccgccgcttcttccacgattgctttgtcaatg 274

Score = 331 bits (167), Expect = 2e-86
Identities = 185/191 (96%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct: 274 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 333

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||||||||||||||||||||||||| ||||| |||||||||||||||||||||
Sbjct: 334 aacccaacaggaactctgctcgtggatacagagtcattgacaacattaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgttctctgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||||||||||||| ||||||||||||||||||||| |||||||||
Sbjct: 394 gagaaagcatgtccaggagttgtctctctgcgcagatatccttgccatagctgccagagac 453

Query: 1337 tctgttcagat 1347
|||||||

Sbjct: 454 tctgttcagat 464

Score = 293 bits (148), Expect = 4e-75
Identities = 163/168 (97%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 466 cttggaggccctagtgtgaatgttaaagtggagaagagacgctagaactgctagccaa 525

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 526 tctgctgctaacaatggcatccctccaccacttcaaacttaaccaactcatctcaaga 585

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtccggt 1645
||
Sbjct: 586 ttcagcgctcttggactttccaccaaggacttggctgccttgtccggt 633

Score = 44.1 bits (22), Expect = 5.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaag 1810
|||||
Sbjct: 631 ggtggtcacacaattggacaag 652

>gb|AW132280.1| se02a03.y1 Gm-c1013 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1013-2309 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 552

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 151 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 210

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 211 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 270

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 1336
|||||
Sbjct: 271 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 330

Query: 1337 tctgttcagatt 1348
|||||
Sbjct: 331 tctgttcagatt 342

Score = 325 bits (164), Expect = 1e-84
Identities = 167/168 (99%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 343 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 402

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 403 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 462

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtccgg 1645
| |||||
Sbjct: 463 ttagcgctcttggactttccaccaaggacttggctgccttgtccgg 510

Score = 299 bits (151), Expect = 6e-77
Identities = 151/151 (100%)
Strand = Plus / Plus

Query: 634 gccaatgcacaactttctacaaacttttactaccattcatgtccaaaccttctctctct 693
|||||
Sbjct: 1 gccaatgcacaactttctacaaacttttactaccattcatgtccaaaccttctctctct 60

Query: 694 gtgaaatccacagtgaatctgccatataagagaccgcatgggtgcttctctctct 753

|||||
Sbjct: 61 gtgaaatccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctcctt 120

Query: 754 cgcttggttcttccacgattgctttgtcaatg 784

|||||
Sbjct: 121 cgcttggttcttccacgattgctttgtcaatg 151

Score = 83.8 bits (42), Expect = 7e-12
Identities = 44/45 (97%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcc 1833

|||||
Sbjct: 508 ggtggtcacacaattggacaagcaaggtgcacanaacttcagagcc 552

>gb|CF809087.1| psHB042xH14f USDA-IFAFS:Expression of Phytophthora sojae genes during
infection and propagation Glycine max cDNA clone
SHB042H14 5, mRNA sequence
Length = 364

Score = 373 bits (188), Expect = 5e-99
Identities = 188/188 (100%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848

|||||
Sbjct: 177 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 236

Query: 1849 accaacatagaaaccgcatTTGCAAGGACTAGGCAGCAAAGCTGCCCTAGAACATCAGGG 1908

|||||
Sbjct: 237 accaacatagaaaccgcatTTGCAAGGACTAGGCAGCAAAGCTGCCCTAGAACATCAGGG 296

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

|||||
Sbjct: 297 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 356

Query: 1969 tacttcaa 1976

|||||
Sbjct: 357 tacttcaa 364

Score = 333 bits (168), Expect = 4e-87
Identities = 168/168 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 12 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 71

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 72 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 131

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
|||||
Sbjct: 132 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 179

>gb|BU577870.1| sar93g05.y1 Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1074-9922 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 426

Score = 373 bits (188), Expect = 5e-99
Identities = 231/245 (94%), Gaps = 4/245 (1%)
Strand = Plus / Plus

Query: 540 tactaagttagtgtgtttgagcaaatctatggcttcgttttgttctagattgacaat 599
|||||
Sbjct: 1 tactaagttagtgttttggagcaaa----ctatggcttcgttttgttctagattgacat 56

Query: 600 ttgtttggctctgtttgtcctcatatggggagtgccaatgcacaactttctacaaactt 659
|||||
Sbjct: 57 ttgtttggctctgtttgtcctcatattggggagtgccaatgccaactttctacaaactt 116

Query: 660 ttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaatctgcat 719
|||||
Sbjct: 117 ctactaccattcgtgtccaaacctcttctcctctgtgaaatccacagtgcaatctgcat 176

Query: 720 atctaaggagaccgcatgggtgcttctctccttcgcttgttcttccacagattgctttgt 779
|||

Sbjct: 177 atcaaaggagaccgcatgggtgcttctctcctccgctgttcttccacgattgctttgt 236

Query: 780 caatg 784

|||||

Sbjct: 237 caatg 241

Score = 321 bits (162), Expect = 2e-83

Identities = 180/186 (96%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct: 241 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 300

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||

Sbjct: 301 aaccccaacaggaactctgctcgtggatacgaggtcattgacaacattaaatcagccgtg 360

Query: 1277 gagaaagtgtgtccaggagttgtttctcgtcgcagatatccttgccatcgtgccagagac 1336

||||||| ||||||||||||||| ||||||||||||||||||||||| |||||||||||

Sbjct: 361 gagaaagcatgtccaggagttgtctcgtcgcagatatccttgccatagctgccagagac 420

Query: 1337 tctgtt 1342

|||||

Sbjct: 421 tctgtt 426

>gb|AW432575.1| sh76b11.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1015-5686 5' similar to SW:PERX_BRARA P00434

PEROXIDASE P7 ;, mRNA sequence

Length = 313

Score = 361 bits (182), Expect = 2e-95

Identities = 263/290 (90%)

Strand = Plus / Plus

Query: 1791 tggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagac 1850

||||| ||||||||||||||| ||||||||||||||||||||||| |||||||||||

Sbjct: 1 tggtcgcacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagac 60

Query: 1851 caacatagaaacgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtc 1910
||||| ||||| ||||||||| ||| ||||||||| ||||| ||||||||| ||||||||| |||||||||
Sbjct: 61 caacgtagagaccgcattggcatggactaggcggcaaaactgccctagaacatcagggtc 120

Query: 1911 aggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactacta 1970
||||||| ||||||||| ||||||||| || ||||||| || || ||||||| ||
Sbjct: 121 aggggacagcaatctggcaccacttgataacttaactccgacatagtagacaactagta 180

Query: 1971 ctcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacgg 2030
||| ||||||||| ||||||||| ||||| ||||||||| ||||||||| |||||||||
Sbjct: 181 cttgtagaacctcgttcataagaagggtctcctcactgtgatcagcaactgttcaacgg 240

Query: 2031 tgggtccaccgactccattgtgcgtggctacagcaccaaccgggacact 2080
||||||| ||||||||| ||||||||| || || ||||||||| ||
Sbjct: 241 tgggtccaccgactccgttgcgtggctacagcagcagcccgggacact 290

>gb|FG825601.1| UCRVU04_CCNI8859_g1 Cowpea 524B Mixed Tissue and Conditions cDNA
Library UCRVU04-1-2 Vigna unguiculata cDNA clone
CCNI8859.g1, mRNA sequence
Length = 604

Score = 343 bits (173), Expect = 4e-90
Identities = 263/293 (89%)
Strand = Plus / Minus

Query: 1887 aagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaac 1946
||||||| ||||||||| ||||||||| ||||||||| || || ||||||||| ||
Sbjct: 589 aagctgcccagaacatcagggtcaggggacaacaatctggccccgcttgatcttcagac 530

Query: 1947 tccaaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctcca 2006
||| |||| | ||||||||| ||||||| ||||||||| ||||||||| |||||
Sbjct: 529 tccgaccacattcgacaactactacttcaggaacctggttcagaagaagggtcttctcca 470

Query: 2007 ctctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcac 2066
||||||| ||||||||| ||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 469 ctctgaccagcaactcttcaatggtggctccactgactccatagtgctggctacagcac 410

Query: 2067 caaccgggacacttctcctctgatttcgccgcccgatgatcaagatgggagacattag 2126
|||||| | |||| | ||||||||| | | ||||||| ||||||||| |||||||||
Sbjct: 409 caaccgaagctcctttcctctgattttgtctccgattatcaagatgggagacattag 350

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 122 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 181

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 182 aaccccaacaggaactctgctcgtggatacagaggtcattgacaacattaaatcagccgtg 241

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 242 gagaaagcatgtccaggagttgtctcctgcgcatatccttgccatagctgccagagac 301

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 302 tctgttcagat 312

Score = 281 bits (142), Expect = 1e-71
Identities = 159/165 (96%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 314 cttggaggccctagttggaatgttaaagttggaagaagagacgctagaactgctagccaa 373

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 374 tctgctgctaacaatggcatccctccaccacttcaaaccttaaccaactcatctcaaga 433

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgctc 1642
||
Sbjct: 434 ttcagcgtcttggactntccaccaaggacttggctgccttgctc 478

Score = 202 bits (102), Expect = 1e-47
Identities = 117/122 (95%)
Strand = Plus / Plus

Query: 663 ctaccattcatgtccaaaccttctctctctgtgaaatccacagtgaatctgcatatc 722
|||||

Sbjct: 91 tccgaccacattcgacaactactacttccaggaacctgggttcagaagaagggtcttctcca 150

Query: 2007 ctctgatcagcaactgttcaa-cggtgggtccaccgactccattgtgcgtggctacagca 2065
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 151 ctctgaccagcaactcttcaataggtgggtccactgactccatagtgcgtggctacagca 210

Query: 2066 ccaacccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacatta 2125
||||| || |||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||

Sbjct: 211 ccaaccaagctccttttctcctctgattttgtctccgcatatcaagatgggagacatta 270

Query: 2126 gtcctctcaactggctccaatggagaaatcaggaagaattgtagaaggattaact 2179
|||| ||||| ||||| ||||| ||||| ||||| || ||||| ||||| |||||

Sbjct: 271 gtcccctcaccggctccaagagaaatcagaagaactgcagaaggattaact 324

>gb|AI441922.1| sa51f09.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1004-2850 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 480

Score = 291 bits (147), Expect = 1e-74
Identities = 165/171 (96%)
Strand = Plus / Plus

Query: 1177 attg gatgacacatcaagcttcaccggagagaagaacgcaaaccaccaaggaactctgc 1236
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 6 attg gatgacacatcaagcttcaccggagagaagaacgcaaaccaccaaggaactctgc 65

Query: 1237 tcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtccaggagt 1296
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 66 tcgtggatacaggctcattgacaacattaaatcagccgtggagaaagcatgtccaggagt 125

Query: 1297 tgtttcctgcgcagatataccttgccatcgctgccagagactctgttcagat 1347
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 126 tgtctcctgcgcagatataccttgccatagctgccagagactctgttcagat 176

Score = 287 bits (145), Expect = 2e-73
Identities = 160/165 (96%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 178 cttggaggccctagttggaatgttaaagttggagaagagacgctagaactgctagccaa 237

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 238 tctgctgctaacaatggcatccctccacccacttcaaacttaaccaactcatctcaaga 297

Query: 1598 tttagcgccttggactttccaccaaggacttggcgccttgtcc 1642
||
Sbjct: 298 ttcagcgccttggactttccaccaaggacttggcgccttgtcc 342

Score = 206 bits (104), Expect = 7e-49
Identities = 129/136 (94%), Gaps = 1/136 (0%)
Strand = Plus / Plus

Query: 1790 gtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacgaga 1849
|||||
Sbjct: 344 gtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacgaga 403

Query: 1850 ccaacatagaaaccgatttgaaggactaggcagcaaagctgccctagaacatcagggt 1909
|||||
Sbjct: 404 gcaacatagacaccgatttgaaggacaaggcaacaaagctgccaagaacatca-ggt 462

Query: 1910 caggggacaacaatct 1925
|||||
Sbjct: 463 caggggacaataatct 478

>gb|G0029196.1| LJMAW92TO JCVI-LJ2 Lotus japonicus cDNA 3', mRNA sequence
Length = 887

Score = 289 bits (146), Expect = 6e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 388 tcaggggacaacaatttggcaccacttgacctcagactccaacctcctttgacaacaac 329

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactggttcaac 2028
|||||
Sbjct: 328 tacttcaagaacctcggttcagaacaaggcctctactccgaccagcaactcttcaac 269

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
|||||
Sbjct: 268 ggtggctccaccgactccaccgtgcgtggctacagcaccaacccgagctcatttctcctct 209

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||
Sbjct: 208 gatttcgcccagcgccatggtcaagatgggagatatcagtcctctcactggatccaacggt 149

Query: 2149 gaaatcaggaagaattgtagaa 2170
|||||
Sbjct: 148 gaaatcaggaagaattgcagaa 127

Score = 180 bits (91), Expect = 4e-41
Identities = 160/183 (87%)
Strand = Plus / Minus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 865 tgtgatggttcagttctacttgatgacacatcaagcttcaccgggagaagaatgcaaac 806

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 805 cccaacagaaactctgctcgcggatttgatgattattgacaacatcaagtcagcagtagag 746

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
||
Sbjct: 745 gcagcatgccaggagttgtatcctgcgctgatatcctcgccatctctgctagagactct 686

Query: 1340 gtt 1342
|||
Sbjct: 685 gtt 683

Score = 123 bits (62), Expect = 8e-24
Identities = 134/158 (84%)

Strand = Plus / Minus

Query: 1484 ggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaatctgct 1543
||||| ||||||| ||| | ||||||| ||||||| ||||||| ||| ||

Sbjct: 670 ggccccacatggaatgtgaaagtaggaagaagagacgctaaaactgctagccagtcgcc 611

Query: 1544 gctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| |||| | ||||||| ||||||| | | | ||||||| ||||||| || ||

Sbjct: 610 gccaacacagggcatccctgcaccacttctagcttgagccaactcacctcaagttcagt 551

Query: 1604 gctcttggactttccaccaaggacttggcgccttgctc 1641
||||| ||||||| ||| ||||||| || |||||

Sbjct: 550 gctcttggactttccagcaaagacttggttgcattgctc 513

>dbj|BP048143.1| BP048143 Lotus corniculatus var. japonicus pods (less than 20 mm in length) Lotus japonicus cDNA clone SPD052d03_f 3', mRNA sequence
Length = 472

Score = 289 bits (146), Expect = 6e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||| ||

Sbjct: 418 tcaggggacaacaatttggcaccacttgaccttcagactccaacctcctttgacaacaac 359

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactggtcaac 2028
||||| ||||||| ||||||| ||||| ||||| ||||| || ||||||| |||||||

Sbjct: 358 tacttcaagaacctgggttcagaacaaggcctctactccgaccagcaactcttcaac 299

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
||||| ||||||| ||||||| ||||||| ||||||| ||| | || |||||||

Sbjct: 298 ggtgggtccaccgactccaccgtgcgtggctacagcaccaacccgagctcattttcctct 239

Query: 2089 gatttcgccgcgcatgatcaagatgggagacattagtctctcactggctccaatgga 2148
||||| ||||||| ||||||| ||||||| || ||||||| ||||||| ||| ||

Sbjct: 238 gatttcgccagcgcatgggtcaagatgggagatatcagtcctctcactggatccaacggt 179

Query: 2149 gaaatcaggaagaattgtagaa 2170

|||||
Sbjct: 178 gaaatcaggaagaattgcagaa 157

>dbj|BP048038.1| BP048038 Lotus corniculatus var. japonicus pods (less than 20 mm in length) Lotus japonicus cDNA clone SPD051a08_f 3', mRNA sequence
Length = 513

Score = 289 bits (146), Expect = 6e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 453 tcaggggacaacaattggcaccacttgaccttcagactccaacctcctttgacaacaac 394

Query: 1969 tacttcaagaacctcggttcagaagaagggtctctcctcactctgatcagcaactggttcaac 2028
|||||
Sbjct: 393 tacttcaagaacctgggttcagaacaaggcctctacactccgaccagcaactcttcaac 334

Query: 2029 ggtgggtccaccgactccattgtgctggctacagcaccaaccgggacettctctctct 2088
|||||
Sbjct: 333 ggtgggtccaccgactccaccgtgctggctacagcaccaaccgagctcattttctctct 274

Query: 2089 gatttcgccgcgccatgatcaagatgggagacattagtctctcactggctccaatgga 2148
|||||
Sbjct: 273 gatttcgccagcgccatggtcaagatgggagatatcagtctctcactggatccaacggt 214

Query: 2149 gaaatcaggaagaattgtagaa 2170
|||||
Sbjct: 213 gaaatcaggaagaattgcagaa 192

>dbj|AV768169.1| AV768169 Lotus japonicus Young plants (two-weeks old) Lotus japonicus cDNA clone MWM225a08_f 3', mRNA sequence
Length = 587

Score = 289 bits (146), Expect = 6e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

Query: 2089 gatttcgccgcccgcattgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||| ||||||||| || ||||||||| ||||| ||
Sbjct: 262 gatttcgccagcgcattggtaagatgggagatatcagtcctctcactggatccaacggt 203

Query: 2149 gaaatcaggaagaattgtagaa 2170
||||||| |||||
Sbjct: 202 gaaatcaggaagaattgcagaa 181

>gb|G0017605.1| LJGBF85T0 JCVI-LJ1 Lotus japonicus cDNA 3', mRNA sequence
Length = 420

Score = 266 bits (134), Expect = 8e-67
Identities = 230/262 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||||| ||||| ||||| || ||||| || ||||| || ||||| ||
Sbjct: 265 tcaggggacaacaatttggcaccacttgaccttcagacaccaacctccttcgacaacaac 206

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctcactctgatcagcaactgttcaac 2028
||||| ||||| ||||| || ||||| ||||| ||||||||| |||||
Sbjct: 205 tacttcaagaacctggttcaaaacaaggcctctacactctgatcagcaacttttcaac 146

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccacccggcactttctcctct 2088
||||| || ||||| || ||||| ||||| ||||| || || |||||
Sbjct: 145 ggtggctccgccgactccaccgtgcgtggctacagcaccacccgagctcattttctct 86

Query: 2089 gatttcgccgcccgcattgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||| ||||||||| || ||||||||| ||||| ||
Sbjct: 85 gatttcgccagcgcattggtaagatgggagatatcagtcctctcactggatccaacggt 26

Query: 2149 gaaatcaggaagaattgtagaa 2170
||||||| |||||
Sbjct: 25 gaaatcaggaagaattgcagaa 4

>gb|G0023584.1| LJMCD71TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA sequence
Length = 630

Score = 262 bits (132), Expect = 1e-65
Identities = 210/236 (88%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 387 tcaggggacaacaatttggcaccacttgaccttcagactccaacctcctttgacaacaac 446

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 447 tacttcaagaacctggttcagaacaaggcctctacactccgaccagcaactcttcaac 506

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
|||||
Sbjct: 507 ggtggctccaccgactccaccgtgcgtggctacagcaccaacccgagctcattttctcct 566

Query: 2089 gatttcgccgcccgatgatcaagatgggagacattagtctctcactggctcaa 2144
|||||
Sbjct: 567 gatttcgccagcggcatggtcaagatgggagatatcagtcctctcactggatcaa 622

Score = 123 bits (62), Expect = 8e-24
Identities = 134/158 (84%)
Strand = Plus / Plus

Query: 1484 ggcctacatggaatgttaaacttgaagaagagacgctagaactgctagccaatctgct 1543
|||||
Sbjct: 105 ggccccacatggaatgtgaaagtaggaagaagagacgctaaaactgctagccagtcgcc 164

Query: 1544 gtaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| ||||
Sbjct: 165 gccaacacaggcatccctgcaccacttctagcttgagccaactcacctcaagttcagt 224

Query: 1604 gctcttggactttccaccaaggacttggctgccttgtc 1641
|||||
Sbjct: 225 gctcttggactttccagcaaagacttggttgattgtc 262

Score = 69.9 bits (35), Expect = 1e-07
Identities = 77/91 (84%)
Strand = Plus / Plus

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||||||| ||||||| ||||||||| ||||||||| |||||
Sbjct: 510 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 569

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgct 1641
|| || ||||| ||||||||| ||||||||| ||||||||| |||||
Sbjct: 570 ttcagtgccttaggactttccaccaaggacttggctgccttgct 613

Score = 234 bits (118), Expect = 3e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgtttgttctagattgacaatttgtttggctctgtttgtcctcatatggggg 630
||||||| ||||||||| || || ||||| ||||||||| || |||||
Sbjct: 45 atggcttcgtttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 104

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaaccttcttcc 690
||| ||||||||| ||||| ||||| ||| || ||||| ||| |||||
Sbjct: 105 tgtgtcaatgcacaactttctactgacttctactacagttcttgcceaaaactcctctcc 164

Query: 691 tctgtgaaatccacagtgcfaatctgccatatctaaggagaccgcatgggtgcttctctc 750
||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||
Sbjct: 165 actgtgagatccacagtgcfaatctgccatatcaaaggagaccgcatgggtgcttctctc 224

Query: 751 cttcgcttgttcttccacgattgctttgtcaatg 784
|| ||||||||| ||||||||| ||||||||| |||||
Sbjct: 225 ctccgcttgttcttccacgattgctttgtcaatg 258

Score = 83.8 bits (42), Expect = 7e-12
Identities = 48/50 (96%)
Strand = Plus / Plus

Query: 1789 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcat 1838
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||
Sbjct: 615 ggtgggcacacaattggacaagcaaggtgcacaaatttcagagcccgcat 664

>gb|FF394030.1| MOODS81TF MOO Vigna unguiculata cDNA 5', mRNA sequence
Length = 786

Score = 246 bits (124), Expect = 8e-61
Identities = 172/188 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 274 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccgggagaagaacgca 333

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||||||| ||||||||||||| || || ||||| ||| |||||||||
Sbjct: 334 aacccaacagaaactctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgttctctgctgagatccttgccatcgctgccagagac 1336
||||||||| ||||||||||||| || ||||| || |||||||||
Sbjct: 394 gagaaagtgtgtccaggagttgttctctgctgagatccttgctattgctgccagagac 453

Query: 1337 tctgttca 1344
|||||||
Sbjct: 454 tctgttca 461

Score = 238 bits (120), Expect = 2e-58
Identities = 153/164 (93%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaacttggagaagagacgctagaactgctagccaa 1537
||||||||| ||||||||||||| ||||||||||| |||||||||||
Sbjct: 466 cttggaggccctagtgtgaatgttaacttggagaagagatgctagaactgctagccaa 525

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||||||| ||||| ||||||||||| ||||||||| |||
Sbjct: 526 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 585

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgtc 1641
|| || ||||| ||||||||||||| |||||||||
Sbjct: 586 ttcagtgtcttaggactttccaccaaggacttggctgccttgtc 629

Score = 234 bits (118), Expect = 3e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttgtttggtctctgtttgtcctcatatggggg 630
|||||
Sbjct: 61 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgactgggt 120

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctttctcc 690
|||
Sbjct: 121 tgtgtcaatgcacaactttctactgacttctactacagttcttgccaaaactcctctcc 180

Query: 691 tctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttctctc 750
|||||
Sbjct: 181 actgtgagatccacagtgcaatctgccatatcaaaggagaccgcatgggtgcttctctc 240

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784
||
Sbjct: 241 ctccgcttggttcttccacgattgctttgtcaatg 274

Score = 180 bits (91), Expect = 4e-41
Identities = 140/155 (90%), Gaps = 1/155 (0%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||||
Sbjct: 631 ggtggccacacaattggacaagcaaggtgcacaaatttcagagcccgcacatctacaacgag 690

Query: 1849 accaacatagaaaccgcatTTGcaaggactaggcagcaaagctgccctagaacatcaggg 1908
|
Sbjct: 691 agcaacatagatacctcattagccaggacaagacaatcaagctgccccagaacatcaggg 750

Query: 1909 tcaggggacaacaatctggcaccacttgatcttca 1943
|||
Sbjct: 751 tca-gggacaacaatctggcaccgcttgatcttca 784

>gb|FF387818.1| M00C268TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 625

Score = 246 bits (124), Expect = 8e-61
Identities = 172/188 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 226 ggatgtgacggttcgattcctttggatgacacgtcaagcttcaccgggagaagaacgca 285

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276
||||||| || ||||||||| || || ||||||| ||| |||||||||
Sbjct: 286 aacccaacagaaattctgctcgtggatgatgaagtcattgacagcataaaatcagccgtg 345

Query: 1277 gagaaagtgtgtccaggagttgtttcctgctgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||||| ||||||||| || ||||||||| ||||||||| |||||||||
Sbjct: 346 gagaaagtgtgtccaggagttgtttcctgctgcggatatccttgccattgctgccagagac 405

Query: 1337 tctgttca 1344
|||||||
Sbjct: 406 tctgttca 413

Score = 226 bits (114), Expect = 7e-55
Identities = 189/214 (88%)
Strand = Plus / Plus

Query: 571 atggettcgttttgttctagattgacaatttgtttggctctgtttgcctcatatggggg 630
||||||| || || ||||| ||||||||| || |||
Sbjct: 13 atggettcgttttgttctagattaactatcagtttgggtgctgtttgcctctactgggt 72

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
||| ||||||||| ||||| ||||| ||| ||||| ||| |||||
Sbjct: 73 tgtgtcaatgcacaactttctactgacttctactacagttcttgccaaaactcctctcc 132

Query: 691 tctgtgaaatccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctc 750
||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 133 actgtgagatccacagtgaatctgccatatcaaaggagaccgcgatgggtgcttctctc 192

Query: 751 cttcgttgttcttccacgattgctttgtcaatg 784
|| ||||||||| ||||||||| ||||||||| |||||||||

|||||
Sbjct: 206 aacccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 265

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagac 1336

|||||
Sbjct: 266 gagaaagtgtgtccaggagttgtttcctggtgagatatccttgccatcgctgccagagac 325

Query: 1337 tctgttca 1344

|||||
Sbjct: 326 tctgttca 333

Score = 216 bits (109), Expect = 7e-52
Identities = 148/161 (91%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537

|||||
Sbjct: 338 cttggaggccctagtgtgaatgttaaacttggagaagagatgctagaactgctagccga 397

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 1597

|||||
Sbjct: 398 tctgctgccaacaatggcattcctgcaccttctcaaacttaaccaactcatctctaga 457

Query: 1598 tttagcgctcttggactttccaccaaggacttgggtgcctt 1638

|| ||
Sbjct: 458 ttcagtgtctaggactttccaccaaagacttgggtgcctt 498

Score = 178 bits (90), Expect = 1e-40
Identities = 132/146 (90%)
Strand = Plus / Plus

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaaccttctcctctgtgaa 698

|||||
Sbjct: 1 tgcacaactttctactgacttctactacagttcttgccaaaactcctctccactgtgag 60

Query: 699 atccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctctcctcgctt 758

|||||
Sbjct: 61 atccacagtgaatctgccatatcaaaggagaccgcatgggtgcttctctccccgctt 120

Query: 759 gttcttcacgattgctttgtcaatg 784
 |||||
Sbjct: 121 gttcttcacgattgctttgtcaatg 146

>dbj|FS240762.1| FS240762 RPSC Glycyrrhiza uralensis cDNA clone KAN050-D13.F 5', mRNA
 sequence
 Length = 554

Score = 244 bits (123), Expect = 3e-60
Identities = 174/191 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 |||||
Sbjct: 246 ggatgtgatggttcaattctactggatgacacatcaagctttacaggggagaagaacgca 305

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 |||||
Sbjct: 306 aaccgaaacaggaactcagctcgtgggttcgaagtcacgacaacatcaagtcagccgta 365

Query: 1277 gagaaagtgtgtccaggagttgttctcctgcgcagatatccttgccatcgctgccagagac 1336
 |||||
Sbjct: 366 gagaaagtgtgccctggagttgttctcctgcgcctgatataccttgccatcgctgccagagac 425

Query: 1337 tctgttcagat 1347
 ||
Sbjct: 426 tccgttcagat 436

Score = 178 bits (90), Expect = 1e-40
Identities = 159/182 (87%)
Strand = Plus / Plus

Query: 603 tttggctctgtttgtcctcatatgggggagtgccaatgcacaactttctacaaactttta 662
 |||||
Sbjct: 65 tttggctctctgtttctcataatgggggagtgccaatgcacaactctctacaaactteta 124

Query: 663 ctaccattcatgtccaacctcttctcctctgtgaaatccacagtgcaatctgccatatac 722
 |||

Sbjct: 125 ctccagttcttgtccaaaactggtttccactgtaaaatccacagtacaatccgcatatc 184

Query: 723 taaggagaccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaa 782

|||||

Sbjct: 185 aaaggagaccgcatgggtgcttccctcctccgcttgttcttccatgattgctttgtcaa 244

Query: 783 tg 784

||

Sbjct: 245 tg 246

Score = 137 bits (69), Expect = 5e-28

Identities = 105/117 (89%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537

|||||

Sbjct: 438 cttggaggacctacttggaaatgttaaacttggagaagagacgctaagacggctagccag 497

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctca 1594

|||||

Sbjct: 498 tctgctgccaacaacggcatccctcctcccacttctaacctcaaccaactcatctca 554

>gb|FG889628.1| UCRVU08_CCNS10828_b1 Cowpea IT97K-461-4 Mixed Tissue and Conditions
cDNA Library UCRVU08-1-2 Vigna unguiculata cDNA clone
CCNS10828.b1, mRNA sequence
Length = 692

Score = 238 bits (120), Expect = 2e-58

Identities = 171/188 (90%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

|||||

Sbjct: 257 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccggggagaagaacgca 316

Query: 1217 aacccaacaggaactctgctcgtggattcgaggtattgacaacattaaatcagccgtg 1276

|||||

Sbjct: 317 aacccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 376

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 1336
|||||
Sbjct: 377 gagaaagtgtgtccaggagttgtttcctgtgcgatataccttgctattgctgccagagac 436

Query: 1337 tctgttca 1344
|||||
Sbjct: 437 tctgttca 444

Score = 238 bits (120), Expect = 2e-58
Identities = 153/164 (93%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 449 cttggaggccctagtgtgaatgttaaacttgaagaagagatgctagaactgctagccaa 508

Query: 1538 tctgctgtaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 509 tctgctgccaacaatggcattcctgcaccttctcaaacttaaccaactcatctctaga 568

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgtc 1641
|||
Sbjct: 569 ttcagtgtcttagactttccaccaaggacttggctgccttgtc 612

Score = 226 bits (114), Expect = 7e-55
Identities = 189/214 (88%)
Strand = Plus / Plus

Query: 571 atggettctgtttgttctagattgacaatttgtttggctctgtttgtcctcatatggggg 630
|||||
Sbjct: 44 atggettctgtttgttctagattaactttcagtttggttctgtttgtcctctactgggt 103

Query: 631 agtgccaatgcacaactttctacaaactttactaccattcatgtccaaacctttctcc 690
|||
Sbjct: 104 tgtgtcaatgcacaactttctactgacttctactacagttcttggccaaaactcctctcc 163

Query: 691 tctgtgaaatccacagtgcaatctgccatataagagaccgcatgggtgcttctctc 750
|||||

Sbjct: 164 actgtgagatccacagtgcaatctgccatatcaaaggagaccgcatgggtgcttctctc 223

Query: 751 cttcgcttggtcttccacgattgctttgtcaatg 784

|| ||||||||||||||||||||||||||||||||||

Sbjct: 224 ctccgcttggtcttccacgattgctttgtcaatg 257

Score = 111 bits (56), Expect = 3e-20
Identities = 65/68 (95%)
Strand = Plus / Plus

Query: 1789 ggtggcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848

||||| ||||||||||||||||||||||||||||||| ||||||||||||||||||||||

Sbjct: 614 ggtggccacacaattggacaagcaaggtgcacaaatttcagagcccgcacatctacaacgag 673

Query: 1849 accaacat 1856

| |||||

Sbjct: 674 agcaacat 681

>gb|FF403045.1| M00F734TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 745

Score = 238 bits (120), Expect = 2e-58
Identities = 153/164 (93%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537

||||||||||| ||||||||||||||||||||||||| |||||||||||||||||||||

Sbjct: 465 cttggaggccctagttggaatgttaaacttggagaagagatgctagaactgctagccaa 524

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597

||||||| ||||||||| ||||||| ||||||||||||||||||||||||| |||

Sbjct: 525 tctgctgccaacaatggcattcctgcaccttctcaaaccttaaccaactcatctctaga 584

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgtc 1641

|| || ||||| |||||||||||||||||||||||||

Sbjct: 585 ttcagtgtctaggaactttccaccaaggacttggctgccttgtc 628

Score = 234 bits (118), Expect = 3e-57

Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggettcgttttgttctagattgacaatttgtttggctctgtttgcctcatatggggg 630
|||||
Sbjct: 61 atggettcgttttgttctagattaactatcagtttggttctgtttgcctcgtactgggt 120

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 121 tgtgtcaatgcacaactttctactgacttctactacagtcttgcccaaaactcctctcc 180

Query: 691 tctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttctctc 750
|||||
Sbjct: 181 actgtgagatccacagtgcaatctgccatatcaaaggagaccgcatgggtgcttctctc 240

Query: 751 cttegcttgttcttccacgattgctttgtcaatg 784
||
Sbjct: 241 ctccgcttgttcttccacgattgctttgtcaatg 274

Score = 222 bits (112), Expect = 1e-53
Identities = 170/188 (90%), Gaps = 1/188 (0%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 274 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccggggagaagaacgca 333

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 334 aacccaacagaaattctgctcgtggatgatgaagtcattgacagcataaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgttctcgtcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 394 gagaaagtgtgt-caggggtgttctcgtcggatataccttgccattgctgccagagac 452

Query: 1337 tctgttca 1344
|||||
Sbjct: 453 tctgttca 460

Query: 571 atggcttcgttttgttctagattgacaatttgttggctctgtttgtcctcatatggggg 630
|||||
Sbjct: 59 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 118

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 119 tgtgtcaatgcacaactttctactgacttctactacagttcttgccaaaactcctctcc 178

Query: 691 tctgtgaaatccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctc 750
|||||
Sbjct: 179 actgtgagatccacagtgaatctgccatatcaaaggagaccgcgatgggtgcttctctc 238

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784
||
Sbjct: 239 ctccgcttggttcttccacgattgctttgtcaatg 272

Score = 198 bits (100), Expect = 2e-46
Identities = 133/144 (92%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 464 cttggaggccctagtgtgaatgttaaacttgaagaagagatgctagaactgctagccaa 523

Query: 1538 tctgctgtaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 524 tctgctgcaacaatggcattcctgcaccttctcaaaccttaaccaactcatctctaga 583

Query: 1598 tttagcgctcttggaactttccacc 1621
||
Sbjct: 584 ttcagtgctctaggactttccacc 607

>gb|FF399144.1| M00EV84TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 345

Score = 234 bits (118), Expect = 3e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttgtttgctctgtttgtcctcatatggggg 630
|||||
Sbjct: 64 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 123

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 124 tgtgtcaatgcacaactttctactgacttctactacagttcttgcccaaaactcctctcc 183

Query: 691 tctgtgaaatccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctc 750
|||||
Sbjct: 184 actgtgagatccacagtgaatctgccatatcaaaggagaccgcgatgggtgcttctctc 243

Query: 751 cttcgcttggttcttccacagattgctttgtcaatg 784
||
Sbjct: 244 ctccgcttggttcttccacagattgctttgtcaatg 277

Score = 89.7 bits (45), Expect = 1e-13
Identities = 63/69 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 277 ggatgtgacggttcgattctttggatgacacgtcaagcttccccgggagaagaacgca 336

Query: 1217 aacccaac 1225
|||||
Sbjct: 337 aacccaac 345

>gb|G0019707.1| LJMAW92TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA sequence
Length = 663

Score = 208 bits (105), Expect = 2e-49
Identities = 180/205 (87%)
Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttgctctgtttgtcctcatatgggggagtgccaat 639
|||||
Sbjct: 71 ttttgttctagattaactatctgttttgcctctttgtcctcatattgggggagtgccaat 130

Identities = 208/242 (85%), Gaps = 1/242 (0%)
Strand = Plus / Minus

Query: 1925 tggcaccacttgatcttcaaactccaaccagctttgacaactactacttcaagaacctcg 1984
|||||
Sbjct: 428 tggcaccacttgaccttcagactccaacctctttgactaccactacttcaagtacctgg 369

Query: 1985 ttcagaagaagggtctcctccactctgatcagcaactgttcaacgggtgggtccaccgact 2044
|||||
Sbjct: 368 ttcagaaccagggcctccgacactccgaccagcaactcttcaacgggtgggtccaccgact 309

Query: 2045 ccattgtgctgggtacagcaccaaccgggacaccttctcctctgatttcgccgccgcca 2104
|||
Sbjct: 308 ccaccgtgctgggtacagcaccaaccggagctcatttctcctctgatttcgccgagcca 249

Query: 2105 -tgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||
Sbjct: 248 ctggtccagatgggagatatcagtcctctcactggatccaacgggtgaaatcaggaagaat 189

Query: 2164 tg 2165
||
Sbjct: 188 tg 187

>dbj|BW620524.1| BW620524 Lotus japonicus protoplasts from suspension-cultured cells
Lotus japonicus cDNA clone LjFL1-sab-002-BB11 5', mRNA
sequence
Length = 480

Score = 196 bits (99), Expect = 6e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 211 tgtgatggttcaattctacttggatgacacatcaagcttcaccgggagagaagaatgcaaac 270

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 271 cccaacagaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 330

sequence
Length = 482

Score = 196 bits (99), Expect = 6e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 145 tgtgatggttcaattctacttggatgacacatcaagcttcaccgggagaagaatgcaaac 204

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 205 cccaacagaaactctgctcggattcgatgttattgacaacatcaagtcagcagtagag 264

Query: 1280 aaagtgtgtccaggagttgtttctgctgcagatataccttgccatcgtgccagagactct 1339
||
Sbjct: 265 gcagcatgccaggagttgtatcctgctgatataccttgccatcctctgctagagactct 324

Query: 1340 gtt 1342
|||
Sbjct: 325 gtt 327

Score = 127 bits (64), Expect = 5e-25
Identities = 100/112 (89%)
Strand = Plus / Plus

Query: 673 tgtccaaacctcttctcctctgtgaaatccacagtgcaatctgccatatctaaggagacc 732
|||||
Sbjct: 31 tgtccaaaccttttccactgtgaaatcctccgtgcaatccgccatatcaaaggagct 90

Query: 733 cgcgatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 91 cgcgatgggtgcttctctcctccgcttgttcttccatgattgcttcgtcaatg 142

Score = 119 bits (60), Expect = 1e-22
Identities = 117/136 (86%)
Strand = Plus / Plus

Query: 1484 ggcctacatggaatgttaaacttgaagaagagacgctagaactgctagccaatctgct 1543
||||| ||||||||||||| || ||||||||||||||||||| ||||||||||| || ||
Sbjct: 340 gccccacatggaatgtgaaagttgaagaagagacgctaaaactgctagccagtccgcc 399

Query: 1544 gctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| ||||| ||||||||||||||||||| | | | ||||||| ||||||| || ||
Sbjct: 400 gccaacacagggcatccctgcaccacttctagcttgagccaactcacctcaagttcagt 459

Query: 1604 gctcttggactttcca 1619
|||||||||||||||
Sbjct: 460 gctcttggactttcca 475

>dbj|BW629863.1| BW629863 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-024-BE11 5', mRNA
sequence
Length = 471

Score = 196 bits (99), Expect = 6e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
||||||||||||||||| | ||||||||||||||||||| ||||||| |||||
Sbjct: 276 tgtgatggttcaattctacttgatgacacatcaagcttcaccgggagaagaatgcaaac 335

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
||||||| ||||||||||| ||||||| ||||||||||||||| || ||||| || |||
Sbjct: 336 cccaacagaaactctgctcgcggattcgatgattattgacaacatcaagtcagcagtagag 395

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
|| || ||||||||||| ||||||| ||||||| ||||| ||||| |||||
Sbjct: 396 gcagcatgccaggagttgtatcctgcgctgatatcctcgccatctctgctagagactct 455

Query: 1340 gtt 1342
|||
Sbjct: 456 gtt 458

Score = 192 bits (97), Expect = 1e-44
Identities = 178/205 (86%)

Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaat 639
|||||

Sbjct: 69 ttttgttctagattaactatctgttttgcctctttgtcctcatatgggggagtgcta 128

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaccttctcctctgtgaaa 699
|||

Sbjct: 129 gctcaactttctacaaacttctattctagttcttgcctcaaaactctttccactgtgaaa 188

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttg 759
|||

Sbjct: 189 tcctccgtgcaatccgccatatcaaaggaggctcgcgatgggtgcttctctcctccgcttg 248

Query: 760 ttcttccacgattgctttgtcaatg 784
|||

Sbjct: 249 ttcttccatgattgcttctgcaatg 273

>dbj|BW628107.1| BW628107 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-019-CE07 5', mRNA
sequence
Length = 471

Score = 196 bits (99), Expect = 6e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||

Sbjct: 278 tgtgatggttcaattctacttgatgacacatcaagcttcaccggggagaagaatgcaaac 337

Query: 1220 cccaacaggaactctgctcgtggattcagggttattgacaacattaaatcagccgtggag 1279
|||||

Sbjct: 338 cccaacagaaactctgctcggattcaggttattgacaacatcaagtcagcagtagag 397

Query: 1280 aaagtgtgtccaggagtgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
|||

Sbjct: 398 gcagcatgccaggagtgtatcctgcgctgatatccttgccatcctctgctagagactct 457

Query: 1340 gtt 1342

|||
Sbjct: 458 gtt 460

Score = 192 bits (97), Expect = 1e-44
Identities = 178/205 (86%)
Strand = Plus / Plus

Query: 580 tttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaat 639
|||||
Sbjct: 71 tttgttctagattaactatctgttttgcctctttgtcctcatattggggagtgctaata 130

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaacctcttctcctctgtgaaa 699
||
Sbjct: 131 gctcaactttctacaaacttctattctagttcttgcctcaaaactcttttccactgtgaaa 190

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttg 759
|||
Sbjct: 191 tctcctgcaatccgcatatcaaaggaggctcgcctgggtgcttctctcctccgcttg 250

Query: 760 ttcttccacgattgctttgtcaatg 784
|||
Sbjct: 251 ttcttccatgattgcttctgcaatg 275

>dbj|BW627140.1| BW627140 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-017-AA04 5', mRNA
sequence
Length = 480

Score = 196 bits (99), Expect = 6e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||
Sbjct: 286 tgtgatggttcaattctacttggatgacacatcaagcttcaccggggagaagaatgcaaac 345

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||
Sbjct: 346 cccaacagaaactctgctcgggattcgatgttattgacaacatcaagtcagcagtagag 405

Identities = 177/203 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 283 tcaggggacaacaatttggcaccacttgaccttcagacaccaacctccttcgacaacaac 342

Query: 1969 tacttcaagaacctcgttcagaagaagggtctctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 343 tactttaagaacctggttcaaacaaggcctcctacactctgatcagcaacttttcaac 402

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggaccttctctct 2088
|||||
Sbjct: 403 ggtggctccgccgactccaccgtgcgtggctacagcaccaacccgagctcattttctct 462

Query: 2089 gatttcgccgcccgatgata 2111
|||||
Sbjct: 463 gatttcgccgcccgatgata 485

Score = 127 bits (64), Expect = 5e-25
Identities = 130/152 (85%)
Strand = Plus / Plus

Query: 1490 acatggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgtaac 1549
|||||
Sbjct: 7 acatggaatgtgaaagtgaagaagagacgctaaaactgctagccagtcgccgccaac 66

Query: 1550 aatggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgtctt 1609
|
Sbjct: 67 acaggcatccctgcaccacttctagcttgagccaactcacctcaaggttcagtgctctt 126

Query: 1610 ggactttccaccaaggacttggcgccttgtc 1641
|||||
Sbjct: 127 ggactttccagcaaagacttgggttcattgtc 158

>gb|EY976963.1| EST 83 Alfalfa aluminum suppression subtractive library Medicago
sativa cDNA clone E2B11, mRNA sequence
Length = 971

Score = 190 bits (96), Expect = 4e-44
Identities = 147/164 (89%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 437 cttggaggcccaacatgggatgtgaaacttgaagaagagatgctagaacagctagtaaa 496

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||
Sbjct: 497 tcagctgcaacaatggcatcccagcaccacttcaagcctcaaccaactcatctcaagg 556

Query: 1598 tttagcgtcttggactttccaccaaggacttggcgccttgtc 1641
||||
Sbjct: 557 tttaatgctcttggactttccaccaaggatttggcgcattgtc 600

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 245 ggatgtgatggttcaattcttctcggatgacacatcaagcttcaccggagagaaaactgcc 304

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 305 aatccaacagaaattcggcccgatgattcgaagtgatcgacaaaatcaaatcagcagtg 364

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatccttgccatcgctgccagagac 1336
|||||
Sbjct: 365 gagaaagtatgtccagggtgcagtttcatgtgctgatcctcgccatcactgctagagac 424

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 425 tctgttgagat 435

Score = 111 bits (56), Expect = 3e-20
Identities = 71/76 (93%)

Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 170 caatctgccatatcaaaggagaccgcatgggtgcttctcttctacgtttgttcttccac 229

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 230 gattgctttgttaatg 245

Score = 63.9 bits (32), Expect = 6e-06
Identities = 32/32 (100%)
Strand = Plus / Plus

Query: 1789 gttggtcacacaattggacaagcaaggtgcac 1820
|||||
Sbjct: 602 gttggtcacacaattggacaagcaaggtgcac 633

>gb|EH613355.1| EST 02 Alfalfa aluminum suppression subtractive library Medicago
sativa cDNA clone A4 5', mRNA sequence
Length = 748

Score = 190 bits (96), Expect = 4e-44
Identities = 147/164 (89%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 545 cttggaggcccaacatgggatgtgaaacttgaagaagagatgctagaacagctagtaaa 486

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|| |||||
Sbjct: 485 tcagctgcaacaatggcatccagcaccacttcaagcctcaaccaactcatctcaagg 426

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgtc 1641
|||||
Sbjct: 425 tttaatgctcttggactttccaccaaggatttggctgcattgtc 382

Score = 149 bits (75), Expect = 1e-31
Identities = 162/191 (84%)
Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 737 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 678

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276
||
Sbjct: 677 aatccaacagaaattcggcccggtgattcgaagtgatcgacaaaatcaaatcagcagtg 618

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 617 gagaaagtatgtccagggtgcagtttcatgtgctgatatcctcgccatcactgctagagac 558

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 557 tctgttgagat 547

Score = 99.6 bits (50), Expect = 1e-16
Identities = 212/266 (79%)
Strand = Plus / Minus

Query: 1900 acatcagggtcaggggacaacaatctggcaccacttgatcttcaactccaaccagcttt 1959
|||||
Sbjct: 269 acatcagggtccggggacaataatttggcacctcttgatcttgcaacaccaacatccttt 210

Query: 1960 gacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaa 2019
|||||
Sbjct: 209 gacaatcactatttcaagaacctagttgacagtaagggactactccactccgaccaacia 150

Query: 2020 ctgttcaacgggtgggtccaccgactccattgtgcgtggctacagaccaaccgggcacc 2079
||
Sbjct: 149 ctcttcaatgggtggatccactgattccatagtgcatgaatatggettgtatccaagctct 90

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
||
Sbjct: 89 ttttctcctgatttcgtcaccgcccatgatcaagatgggagacattagtcctcaccggt 30

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
||||| ||||||||||||||||||||||||| ||| ||||||| ||||| |||||
Sbjct: 585 ggtcatacaattggacaagcaaggtgcacaacctttagagcccgaatctacnngagagc 526

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
||||||| | | | ||||| | | | || | | | | ||| ||||| |||
Sbjct: 525 aacatagatagctcttttgcccgcatgagacaatctaggtgtccccgaacctcaggatca 466

Query: 1912 ggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactactac 1971
||||||| || | ||||| ||||| || | ||||| || | ||||||||| |||||
Sbjct: 465 ggggacaacaaccttgacccattgactttgccactcccacttttctttgacaacctactac 406

Query: 1972 ttcaagaacctcgttcagaagaaggtctcctccactctgatcagcaactgttcaacggt 2031
||||||| ||||| ||||||||||||||||||| ||| ||| ||| ||||| |||
Sbjct: 405 ttcaagaacctcattcagaagaaggtctcatccattccgaccaagaactcttcaatggt 346

Query: 2032 ggttccaccgactccattgtgctgtgctacagcaccaaccgggcaccttctcctctgat 2091
|| ||||| ||||| | ||||| ||||||||||||||||||| | ||||| | | |||
Sbjct: 345 ggttccactgactccttggctgtgctacactacagcaccaaccggcctcctttttcgccgat 286

Query: 2092 ttgccgccccatgatcaagatgggagacattagtcctctcactggctccaatggagaa 2151
||| ||||||||||||||||| ||||||||||||||||||| ||||||||||||| |||||
Sbjct: 285 ttgccgccccatgatcaggatgggagacattagtcctctcactggctcccgcggagaa 226

Query: 2152 atcaggaagaattgtagaaggattaactaatt 2183
|| ||| |||| | | || | | |||||
Sbjct: 225 ataagggagaactgcaggagggtcaactaatt 194

Score = 50.1 bits (25), Expect = 0.092
Identities = 25/25 (100%)
Strand = Plus / Minus

Query: 1611 gactttccaccaaggacttggtcgc 1635
|||||||||||||||||||||||
Sbjct: 620 gactttccaccaaggacttggtcgc 596

>gb|BI700509.1| sag61f05.y1 Gm-c1082 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1082-1041 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE

;, mRNA sequence
Length = 472

Score = 180 bits (91), Expect = 4e-41
Identities = 282/343 (82%), Gaps = 2/343 (0%)
Strand = Plus / Plus

Query: 1801 attggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaacatagaa 1860
|||||
Sbjct: 1 attggacaagcaaggtgcacaacctttagagcccgaatctacaacgagaccaacatagat 60

Query: 1861 accgcatttgaaggactagcagcaaaagctgccctagaacatcagggtcaggggacaac 1920
|||
Sbjct: 61 agctcttttctcgcacatgagacaatctaggtgtccccgaacctcagggtcaggggacaac 120

Query: 1921 aatctggcaccacttgatcttcaa-actccaaccagctttgacaactactacttcaagaa 1979
|||
Sbjct: 121aacctagcaccattga-cttcgcccactcccaggttctttgacaaccactacttcaagaa 179

Query: 1980 cctcgttcagaagaagggtctcctcactctgatcagcaactgttcaacgggtgggtccac 2039
|||||
Sbjct: 180 cctcattcagaagaagggectcatcattccgaccaacaactcttcaatgggtgggtccac 239

Query: 2040 cgactccattgtgcgtggctacagcaccaaccgggcaccttctcctctgatttcgccgc 2099
|||||
Sbjct: 240 tgactccatagtgctacactacagcaccaaccgggcctcctttttcgccgatttctccgc 299

Query: 2100 cgccatgatcaagatgggagacattagtcctctcactggctcc 2142
|||||
Sbjct: 300 cgccatgatccgatgggagacattagtcctcaccgctcc 342

>gb|BU578183.1| sar49a02.y1 Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1074-5404 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 271

Score = 176 bits (89), Expect = 6e-40
Identities = 134/149 (89%)
Strand = Plus / Plus

Query: 630 gaggccaatgcacaactttctacaaacttttactaccattcatgtccaacctcttctc 689

Query: 2030 gtgggtccaccgactccattgtgcgtggctacagcaccacccgggcaccttctctctg 2089
||||| ||||||||||||| || || | ||||||| | ||||||||| | | |||||||||||
Sbjct: 123 gtggctccaccgactctatagtcagaggctacgcctccaacccgacctcattctctctg 182

Query: 2090 atttcgccgcccatgatcaagatgggagacattagtcctctcaactggctccaatggag 2149
| ||| | ||||||||||||||||||||||||||||||||||| ||||||| ||||| || |
Sbjct: 183 acttcatcagcgccatgatcaagatgggagacattagtcctctcaactggatccaacggg 242

Query: 2150 aatcaggaagaattgtagaaggattaactaa 2181
||||||| || || ||||| |||||
Sbjct: 243 aatcaggaagaactgcaggaggatcaactaa 274

>gb|CA852976.1| E14E06_J06_09.ab1 cDNA Peking library 6, 8 day SCN3 Glycine max cDNA
clone E14E06 5', mRNA sequence
Length = 556

Score = 174 bits (88), Expect = 2e-39
Identities = 193/228 (84%)
Strand = Plus / Plus

Query: 1956 ctttgacaactactacttcaagaacctcgttcagaagaagggtctctcactctgatca 2015
||||||| ||||||||||||||||||| ||||||||||||||||||| ||||| || || ||
Sbjct: 89 ctttgacaaccactacttcaagaacctcattcagaagaagggtctcatccattccgacca 148

Query: 2016 gcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccacccggg 2075
||||| ||||| ||||| ||||| ||||| | ||||| |||||||||||||||||
Sbjct: 149 agaactcttcaatgggtgggtccactgactccttgggtgcgtacctacagcaccacccggc 208

Query: 2076 caccttctctctgatttcgccgccgccatgatcaagatgggagacattagtcctctcac 2135
| ||||| | | | ||||||| ||||||||||||||||| ||||||||||||||||| |||||
Sbjct: 209 ctcttttttcgccgatttctccgccgccatgatcaggatgggagacattagtcctctcac 268

Query: 2136 tggtccaatggagaaatcaggaagaattgtagaaggattaactaatt 2183
||||||| ||||||||| ||| ||||| || || ||| | |||||||||
Sbjct: 269 tggtcccgcggagaataaggagaactgcaggagggtcaactaatt 316

>gb|CA852554.1| E09B05_C17_03.ab1 cDNA Peking library 6, 8 day SCN3 Glycine max cDNA
clone E09B05 5', mRNA sequence
Length = 539

Score = 174 bits (88), Expect = 2e-39

Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacga 1847
|||||
Sbjct: 660 ggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacga 715

>gb|EX530374.1| MTGland_A066_2007-06-28/MTGlandA066_C04_014_1 Medicago truncatula A17
glandular trichome Medicago truncatula cDNA, mRNA
sequence
Length = 1023

Score = 167 bits (84), Expect = 6e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 487 cttggaggcccaacatgggatgtgaaacttggagaagagatgcaagaacagctagtaaa 546

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 1597
||
Sbjct: 547 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 606

Query: 1598 tttagcgtcttggactttccaccaaggacttggtcgccttgtc 1641
|||||
Sbjct: 607 tttaatgctcttggctttccaccaaggatttggtcgcattgtc 650

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 295 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 354

Query: 1217 aacccaacaggaactctgctcgatggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 355 aatccaacaaaaattcggcccgtggattcgaagtgatcgacaaaatcaaatcagcagtg 414

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 269 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 328

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276
||
Sbjct: 329 aatccaacaaaaattcggcccgaggattcgaagtgatcgacaaaatcaaatcagcagtg 388

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 389 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcaactgctagagac 448

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 449 tctgttgagat 459

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctccac 768
|||||
Sbjct: 194 caatctgccatatcaaaagagactcgcatgggtgcttctctccttcgcttgttctccac 253

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 254 gattgctttgttaatg 269

Score = 71.9 bits (36), Expect = 3e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851

Sbjct: 629 ggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacgactcc 688

Query: 1852 aacataga 1859

Sbjct: 689 aacataga 696

>gb|AW268020.1| EST306242 DSIR Medicago truncatula cDNA clone pDSIR-8B8, mRNA
sequence
Length = 702

Score = 167 bits (84), Expect = 6e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

Sbjct: 447 cttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagtaaa 506

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597

Sbjct: 507 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 566

Query: 1598 tttagcgtcttggactttccaccaaggacttggtcgccttgtc 1641

Sbjct: 567 tttaatgctcttggctttccaccaaggatttggtcgcattgtc 610

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

Sbjct: 255 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 314

Query: 1217 aacccaacaggaactctgctcgatggattcgaggttattgacaacattaaatcagccgtg 1276

Sbjct: 315 aatccaacaaaaattcggcccgtggattcgaagtgatcgacaaaatcaaatcagcagtg 374

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 302 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 361

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 362 aatccaacaaaaattcgcccggtggattcgaagtgatcgacaaaatcaaatcagcagtg 421

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 422 gagaaagtatgtccagggtgcagtttctgctgacatccttaccatcactgctagagac 481

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 482 tctgttgagat 492

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 227 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcttgttcttccac 286

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 287 gattgctttgttaatg 302

Score = 63.9 bits (32), Expect = 6e-06
Identities = 50/56 (89%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
|||||
Sbjct: 662 ggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacga 717

>gb|BG448404.1| NF024B09EC1F1074 Elicited cell culture Medicago truncatula cDNA clone

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 214 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 273

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 274 gattgctttgttaatg 289

Score = 48.1 bits (24), Expect = 0.36
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaagg 1815
|||||
Sbjct: 649 ggtcacacaattggacaagcaagg 672

>gb|BF644619.1| NF017G06EC1F1051 Elicited cell culture Medicago truncatula cDNA clone
NF017G06EC 5', mRNA sequence
Length = 684

Score = 155 bits (78), Expect = 2e-33
Identities = 142/164 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 479 cttggaggcccaacatgggatgtgaaacttggagaagagatgcaagaacagctagtaaa 538

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 1597
|||
Sbjct: 539 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaang 598

Query: 1598 tttagcgctcttggactttccaccaaggacttggctcgccttgtc 1641
|||
Sbjct: 599 tttaatgctcttggcttttccaccaangatttggctcgcattgtc 642

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 287 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 346

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 347 aatccaacaaaaattcgcccgtggattcgaagtgatcgacaaaatcaaatcagcagtg 406

Query: 1277 gagaaagtgtgtccaggagttgttctcctgcgagatccttgccatcgctgccagagac 1336
|||||
Sbjct: 407 gagaaagtgtgtccagggtgcagtttcatgctgacatccttaccatcactgctagagac 466

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 467 tctgttgagat 477

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatataaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 212 caatctgccatataaaagagactcgcatgggtgcttctctctcgtttgttcttccac 271

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 272 gattgctttgttaatg 287

Score = 58.0 bits (29), Expect = 4e-04
Identities = 29/29 (100%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcac 1820
|||||
Sbjct: 647 ggtcacacaattggacaagcaaggtgcac 675

>gb|CA919059.1| EST636777 MTUS Medicago truncatula cDNA clone MTUS-7C2, mRNA sequence
Length = 802

Score = 151 bits (76), Expect = 3e-32
Identities = 143/164 (87%), Gaps = 1/164 (0%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 754 cttggaggcccaacatgggatgtgaaact-ggaagaagagatgcaagaacagctagtaa 696

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||
Sbjct: 695 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 636

Query: 1598 tttagcgtcttggactttccaccaaggacttggctgccttgtc 1641
||||
Sbjct: 635 tttaatgctcttggctttccaccaaggatttggctgcattgtc 592

Score = 117 bits (59), Expect = 5e-22
Identities = 284/359 (79%)
Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
|||||
Sbjct: 587 ggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacgactcc 528

Query: 1852 aacatagaacccgcatcttgaaggactaggcagcaaagctgccctagaacatcagggtca 1911
|||||
Sbjct: 527 aacatagataacttcttggctgcacaaggcaatcagggtgccccagacatcgggttcc 468

Query: 1912 ggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactactac 1971
|||||
Sbjct: 467 ggggacaataatttggcacccttgatcttgaacaccaacatcctttgacaaccattac 408

Sbjct: 178 accacagtgaatccacactgcaaactgccatatcaaaggaggccccgaatgggtgctct 237

Query: 748 ctcttcgcttgttcttccacgattgctttgtcaatg 784

||||| |||||||||||||||||||||||||||||||||||

Sbjct: 238 atctccgcttgttcttccacgattgctttgtcaatg 274

Score = 123 bits (62), Expect = 8e-24
Identities = 155/186 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||||||| ||||||||| || ||||||||||||||||||| ||||| ||||||||| |||

Sbjct: 274 ggatgtgatggatcaattctcttagatgacacatcaagctttaccggtgagaagaatgca 333

Query: 1217 aacccaacaggaactctgctcgtggattcgaggtattgacaacattaaatcagccgtg 1276

|| || || || ||||| ||||||||||||| || || || || ||||||||| || |||||||||

Sbjct: 334 aatccaaatagaaactccgctcgtggatttgatgtcatcgacaacataaagacagccgta 393

Query: 1277 gagaaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336

||||||| || || || || ||||||||| || || || || ||||||||| ||||| ||||||||| |||||

Sbjct: 394 gagaacgtatgccccggagttgtatcatgtgctgatatcctagccattgctgccgagac 453

Query: 1337 tctgtt 1342

|||||||

Sbjct: 454 tctgtt 459

>gb|BF639633.1| NF015A12IN1F1097 Insect herbivory Medicago truncatula cDNA clone
NF015A12IN 5', mRNA sequence
Length = 516

Score = 145 bits (73), Expect = 2e-30
Identities = 136/157 (86%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687

||||||||||||||||||||||||||||||||||||| | ||||||| || |||||

Sbjct: 61 gggagtgccaatgcacaactttctacaaacttttactcaaaaacttgtccaaacctctct 120

Query: 688 tcctctgtgaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttct 747

|| | ||||||||||| ||||| ||||||||||| ||||||| ||||| ||||||||||| ||||
Sbjct: 121 accacagtgaatccacactgcaaactgccatatcaaaggaggcccgaatgggtgcctct 180

Query: 748 ctccttcgcttgcttcttccacgattgctttgtcaatg 784

|||| | ||||||||||||||||||||||||||||||||
Sbjct: 181 atcctccgcttgcttcttccacgattgctttgtcaatg 217

Score = 123 bits (62), Expect = 8e-24
Identities = 155/186 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||| ||||||||||| ||||||||| || ||||||||||||||| ||||| ||||||||| ||||
Sbjct: 217 ggatgtgatggatcaattctcttagatgacacatcaagctttaccggtgagaagaatgca 276

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|| || || || ||||| ||||||||||| || || || || ||||||||| || |||||||||
Sbjct: 277 aatccaaatagaaactccgctcgtggatttgatgtcatcgacaacataaagacagccgta 336

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336

||||| || || || || ||||||||| || || || || ||||||||| ||||| ||||||| ||||
Sbjct: 337 gagaacgtatgccccggagttgtatcatgtgctgatatcctagccattgctgccgagac 396

Query: 1337 tctggt 1342

|||||
Sbjct: 397 tctggt 402

Score = 81.8 bits (41), Expect = 3e-11
Identities = 86/101 (85%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

||||||| || || || ||||||||| ||||||||||||| ||||| ||||| ||||| ||||
Sbjct: 409 cttggaggtccaacctggaatgtaaaacttggaagaacagatgctaaaacggctagtcaa 468

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaact 1578

|| ||||||||||| || ||||||| ||||| ||||| |||||
Sbjct: 469 tccgctgctaacaactgccatcccgccaccaacttcaaact 509

>gb|CX530413.1| s13dNF99F02MJ016_246858 Methyl Jasmonate-Elicited Root Cell
Suspension Culture Medicago truncatula cDNA, mRNA
sequence
Length = 585

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 281 ggatgtgatggttcaattcttctc gatgacacatcaagcttcaccggagagaaaactgcc 340

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 341 aatccaacaaaaattcggcccgtggattcgaagtgatcgacaaaatcaaatcagcagtg 400

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 401 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcaactgctagagac 460

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 461 tctgttgagat 471

Score = 113 bits (57), Expect = 7e-21
Identities = 99/113 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 473 cttggaggccaacatgggatgtgaaacttggagaagagatgcaagaacagctagtaaa 532

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcat 1590
||
Sbjct: 533 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcat 585

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 206 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 265

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 266 gattgctttgttaatg 281

>gb|CX529528.1| s13dNF97C05MJ034_245107 Methyl Jasmonate-Elicited Root Cell
Suspension Culture Medicago truncatula cDNA, mRNA
sequence
Length = 545

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 290 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 349

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 350 aatcccaacaaaaattcggcccggtggattcgaagtgatcgacaaaatcaaatcagcagtg 409

Query: 1277 gagaaagtgtgtccaggagttgtttctcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 410 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 469

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 470 tctgttgagat 480

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 215 caatctgccatatcaaagagactcgcatgggtgcttctctctgcgttgttcttccac 274

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 275 gattgctttgttaatg 290

Score = 63.9 bits (32), Expect = 6e-06
Identities = 50/56 (89%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctag 1533
|||||
Sbjct: 482 cttggaggcccaacatgggatgtgaaacttggagaagagatgcaagaacagctag 537

>gb|BF647501.1| NF068D03EC1F1029 Elicited cell culture Medicago truncatula cDNA clone
NF068D03EC 5', mRNA sequence
Length = 658

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 288 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 347

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 348 aatccaacaaaaattcgcccggtgattcgaagtgatcgacaaaatcaaatcagcagtg 407

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 408 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 467

Query: 1337 tctgttcagat 1347
|||||

Sbjct: 468 tctgttgagat 478

Score = 141 bits (71), Expect = 3e-29
Identities = 142/165 (86%), Gaps = 1/165 (0%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 480 cttggaggcccaacatgggatgtgaaacttggagaagagatgcaagaacagctagtaaa 539

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||
Sbjct: 540 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctnaagg 599

Query: 1598 tttagcgct-cttggactttccaccaaggacttggtegccttgte 1641
||||
Sbjct: 600 tttaatgctccttggctctttncaccaaggatttggtegcattgte 644

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 213 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgcttgttcttccac 272

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 273 gattgctttgttaatg 288

>gb|BF645317.1| NF030B11EC1F1092 Elicited cell culture Medicago truncatula cDNA clone
NF030B11EC 5', mRNA sequence
Length = 603

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 281 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 340

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 341 aatccaacaaaaattcggcccggtggattcgaagtgatcgacaaaatcaaatcagcagtg 400

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagac 1336
||
Sbjct: 401 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcaactgctagagac 460

Query: 1337 tctgttcagat 1347
||
Sbjct: 461 tctgttgagat 471

Score = 107 bits (54), Expect = 5e-19
Identities = 108/125 (86%), Gaps = 1/125 (0%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||
Sbjct: 473 cttggaggcccaacatgggatgtgaaactnggaagaagagatgcaagaacagctagtaa 532

Query: 1538 tctgctgctaacaatggcat-ccctgcacccaacttcaaaccttaaccaactcatctcaag 1596
||
Sbjct: 533 tcagctgcaacaatgacatccccagcaccacttcaagcctcaaccaactcatctcaag 592

Query: 1597 attta 1601
||
Sbjct: 593 gttta 597

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttctccac 768
||

Sbjct: 206 caatctgccatatcaaaagagaactcgcgatgggtgcttctcttctgcgtttgttcttccac 265

Query: 769 gattgctttgtcaatg 784

|||||

Sbjct: 266 gattgctttgttaatg 281

>gb|C0515766.1| s13dSG77F0400043_419681 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 572

Score = 139 bits (70), Expect = 1e-28

Identities = 157/186 (84%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

|||||

Sbjct: 299 ggatgtgatgatcaattctcttggatgacacatcaagctttaccggtgagaagaatgca 358

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276

|||||

Sbjct: 359 aacccaatagaaactctgctcgtggatttgggtgtcatcgacaacataaagacagccgta 418

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgcagatatccttgccatcgctgccagagac 1336

|||||

Sbjct: 419 gagaacgtatgccccggagttgtctcatgtgccgatatccttgctattgctgccgagac 478

Query: 1337 tctgtt 1342

|||||

Sbjct: 479 tctgtt 484

Score = 137 bits (69), Expect = 5e-28

Identities = 135/157 (85%)

Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687

|||||

Sbjct: 143 gggagtaccaatgcacaactttctacaagtttttactccaaaacttgcctccaaactctct 202

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttct 747

|| | ||||||| | ||| ||||||| ||||| ||||| |||||||
Sbjct: 203 accacagtgaatccacactacaaactgccatatcaaaggaggcccgaatgggtgcttct 262

Query: 748 ctccttcgcttggttctccacgattgctttgtcaatg 784

||||||||||||||||||||||||||||||||||||
Sbjct: 263 atccttcgcttggttctccacgattgctttgtcaatg 299

Score = 75.8 bits (38), Expect = 2e-09
Identities = 71/82 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

||||||| || | ||||||| ||||||||||||||||||| ||||| ||| ||||| |||||
Sbjct: 491 cttggaggtccaacctggaatgtaaaacttgaagaagagatgctaaaacggctagtcaa 550

Query: 1538 tctgctgctaacaatggcatcc 1559

|| ||||||||| || |||||
Sbjct: 551 tccgctgctaacaactgccatcc 572

>gb|AW830346.1| sm33e02.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-5715 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 459

Score = 139 bits (70), Expect = 1e-28
Identities = 136/158 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

||||||||||| || ||| ||||| ||||||||||||||||||| || ||| || |||||
Sbjct: 160 cttggaggcccaacttgggatgtgaaacttgaagaagagactccaggacggcaagccaa 219

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597

||||||| ||||||| ||||||| ||||||||||||||||||| ||||||| || ||| |||||
Sbjct: 220 tctgctgccaacaatgacatccaagaccacttcaaacttaaccaacttatttccaga 279

Query: 1598 tttagcgcctcttgactttccaccaaggacttggtcgc 1635

|||| | ||||| ||||||||||||||| |||||||||
Sbjct: 280 tttaatgctctcggactttccacaaagacttggtcgc 317

Score = 111 bits (56), Expect = 3e-20
Identities = 65/68 (95%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||
Sbjct: 328 ggtcacacaattggacaagcaaggtgcacaacctttagagcccgcaatctacaacgagacc 387

Query: 1852 aacataga 1859
|||||
Sbjct: 388 aacataga 395

Score = 93.7 bits (47), Expect = 7e-15
Identities = 128/155 (82%)
Strand = Plus / Plus

Query: 1193 agcttcaccggagagaagaacgcaaaccacaacaggaactctgctcgtggattcgaggtt 1252
|||||
Sbjct: 4 agcttcaccggagagaaaaacgcaggacctaacaggaactctgcccggtgtttgaagtg 63

Query: 1253 attgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagat 1312
|||
Sbjct: 64 atcgatcaaattaagtcagctgtggaaaaagtgtgtccgggtgtggtctcttgcgctgac 123

Query: 1313 atccttgccatcgctgccagagactctgttcagat 1347
|||||
Sbjct: 124 atccttgccatcgctgcaagagactccggttgagat 158

>gb|AW703873.1| sk25b09.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-3186 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 397

Score = 139 bits (70), Expect = 1e-28
Identities = 136/158 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

Sbjct: 136 cttggaggcccaacttgggatgtgaaacttggagaagagactccaggacggcaagccaa 195
|||||

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||

Sbjct: 196 tctgctgccaacaatgacatcccaagaccacttcaaacctcaaccaacttatttccaga 255
|||||

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgc 1635
|||||

Sbjct: 256 tttaatgctctcggactttccaccaaagacttggtcgc 293
|||||

Score = 111 bits (56), Expect = 3e-20
Identities = 65/68 (95%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
|||||

Sbjct: 304 ggtcacacaattggacaagcaaggtgcacaaacttttagagcccgaatctacaacgagacc 363
|||||

Query: 1852 aacataga 1859
|||||

Sbjct: 364 aacataga 371
|||||

Score = 73.8 bits (37), Expect = 6e-09
Identities = 103/125 (82%)
Strand = Plus / Plus

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|||||

Sbjct: 10 aacaggaactctgcccgtggttttgaagtgatcgatcaaattaagtcagctgtggaaaaa 69
|||||

Query: 1283 gtgtgtccaggagtgttttctgcgcagatatccttgccatcgctgccagagactctgtt 1342
|||||

Sbjct: 70 gtgtgtccgggtgtggtctcttgcgctgacatccttgccatcgctgcaagagactccgtt 129
|||||

Query: 1343 cagat 1347
|||||

Sbjct: 130 gagat 134
|||||

Sbjct: 318 cctaacaggaattctgcccgatgtgaagtgatcgaccaaatacaatcagctgtggag 377

Query: 1280 aaagtgtgtccaggagtgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||

Sbjct: 378 aaagtgtgtccgggtgtggtttcctgcgcagatatccttgccatcgctgccagagac 434

Score = 121 bits (61), Expect = 3e-23
Identities = 85/93 (91%)
Strand = Plus / Plus

Query: 692 ctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttctctcc 751
|||||

Sbjct: 163 ctgtgaaacgcacagtggaatcgccatatcaaaggagaccgcatgggtgcttctctcc 222

Query: 752 ttcgcttggttcttccacgattgctttgtcaatg 784
|||

Sbjct: 223 tacgtttggttcttccacgattgctttgttaatg 255

>gb|AW704238.1| sk18d12.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-2544 5' similar to TR:024336 024336
KOREAN-RADISH ISOPEROXIDASE ;, mRNA sequence
Length = 566

Score = 135 bits (68), Expect = 2e-27
Identities = 158/188 (84%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||

Sbjct: 243 tgtgatgggtcaattctacttggatgacacatcaagcttcaccggagagaaaaacgcagga 302

Query: 1220 cccaacaggaactctgctcgatggattcagggttattgacaacattaaatcagccgtggag 1279
|||

Sbjct: 303 cctaacaggaactctgcccggttttgaagtgatcgatcaaattaagtcagctgtggaa 362

Query: 1280 aaagtgtgtccaggagtgtttcctgcgcagatatccttgccatcgctgccagagactct 1339
|||||

Sbjct: 363 aaagtgtgtccgggtgtggtctcttgcgcagatatccttgccatcgctgcaagagactcc 422

Sbjct: 342 tctggt 347

Score = 121 bits (61), Expect = 3e-23
Identities = 133/157 (84%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| |||||||||||||||||||| ||||||| | | |||||| || ||||
Sbjct: 6 gggagtaccaatgcacaactttctacaagtttttactccaaaacttgccccaaactctct 65

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttct 747
|| | |||||||||||| | ||| || ||||||| |||||| |||| ||||||||||||
Sbjct: 66 accacagtgaaatccacactacaaactaccatatcaaaggaggcccgaatgggtgcttct 125

Query: 748 ctctctgcttgttcttccacgattgctttgtcaatg 784
|||| ||||||||||||||||||||||||||||
Sbjct: 126 atcctccgcttgttcttccacgattgctttgtcaatg 162

Score = 103 bits (52), Expect = 7e-18
Identities = 130/156 (83%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||||| || || |||||||| |||||||||||||||| |||| ||| ||||| |||
Sbjct: 354 cttggaggctccaaactggaatgtaaaacttggagaagagatgctaaaacggctagtcaa 413

Query: 1538 tctgctgtaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
|| |||||||||| || |||||| |||| |||| |||| |||| || |||| ||||
Sbjct: 414 tccgctgtaaacactgccatcccagcaccacttcaaactcaatacactcacctcaatg 473

Query: 1598 tttagcgctcttggactttccaccaaggacttggtc 1633
|||||||| |||| |||||| |||||| ||||||
Sbjct: 474 tttagcgcggttggtctttccagcaaggatttggtc 509

>gb|BF071209.1| st04h08.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1065-376 5' similar to TR:Q9XFL7 Q9XFL7 PEROXIDASE 6
;, mRNA sequence
Length = 319

Score = 131 bits (66), Expect = 3e-26
Identities = 114/130 (87%)
Strand = Plus / Plus

Query: 1218 accccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtgg 1277
||||||| ||||| ||||||||||||||| ||||||| ||||||| ||||||| ||||| |||||
Sbjct: 81 accccaataggatctctgctcgtggatacagaggtcattgactacattagatcatccgtgt 140

Query: 1278 agaaagtgtgtccaggagttgtttcctgcgagatatccttgccatgctgccagagact 1337
||||| | ||||||||| | ||||| ||||||||||||||| ||||||||| ||||||||| |||||
Sbjct: 141 agaatgcgtgtccagtatttgtctctgcgagatatgcttgccatagctgccagatact 200

Query: 1338 ctgttcagat 1347
|||||||||||
Sbjct: 201 ctgttcagat 210

Score = 58.0 bits (29), Expect = 4e-04
Identities = 66/77 (85%), Gaps = 1/77 (1%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||||||||||| | | ||||||||| ||||||||| ||||||||| ||||||| |||||
Sbjct: 212 cttggaggccctagtttgtatgttaaagttggaagatgagacgctagatctgcttgcccta 271

Query: 1538 tctgctgctaacaatgg 1554
||||| || |||||||||
Sbjct: 272 tctggtg-taacaatgg 287

>gb|EX660929.1| JS1BF51JG Salt stressed *Fragaria vesca* (strain Hawaii-4) cDNA library
Fragaria vesca cDNA clone JS1BF51, mRNA sequence
Length = 758

Score = 129 bits (65), Expect = 1e-25
Identities = 214/263 (81%), Gaps = 3/263 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
||||||||||||||| ||||| ||||||||||||||| ||||||||| ||||| ||||||| |||||
Sbjct: 238 tcaggggacaacaacttggctccacttgatcttcaatctccaacagccttcgacaacaac 297

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttc--- 2025
||||| ||| || || | |||| | ||||||||||||||| ||||||| |||||
Sbjct: 298 tactacaataatcttatcaagaacagagggtctcctccactccgatcagcagttgttcttg 357

Query: 2026 aacgggtgggtccaccgactccattgtgctggctacagcaccaacccgggcaccttctcc 2085
|| ||||| ||||||| ||||| ||||||||||||||| || || | ||||| ||| |
Sbjct: 358 aatggtggctccaccgattccatagtgctggctacagcagcagccagagcacattcaca 417

Query: 2086 tctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaat 2145
||||| || || ||||| ||||||||||||||| |||| | || ||||||| |||||||
Sbjct: 418 tctgactttgctgcccaatgatcaagatgggaaacatcaacccgctcactggatccaat 477

Query: 2146 ggagaaatcaggaagaattgtag 2168
||||| || ||||||| |||||
Sbjct: 478 ggagagattaggaagaactgtag 500

Score = 61.9 bits (31), Expect = 2e-05
Identities = 52/59 (88%)
Strand = Plus / Plus

Query: 1574 aacctaaccaactcatctcaagatttagcgtcttggactttccaccaaggacttgg 1632
||||| ||||| ||||||| ||||| | ||||||| ||||||| ||||||| |||||
Sbjct: 46 aacctaaccagctcatctccagattcaacgctcttggcctttccaccaaggacatgg 104

>gb|DN950706.1| Ost2T_331 Oak tissue culture growing 2 days in hypertonic medium
Quercus robur cDNA 5', mRNA sequence
Length = 852

Score = 129 bits (65), Expect = 1e-25
Identities = 98/109 (89%)
Strand = Plus / Plus

Query: 676 ccaaacctcttctcctctgtgaaatccacagtgcaatctgcatatctaaggagaccgc 735
||||| ||||| ||| ||||||||||| ||||||||||||||| ||||| |||||
Sbjct: 151 ccaaaactctttccactgtgaaatccaccgtgcaatctgcatatcaaaggaagccga 210

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgcttgtcaatg 784
||||||| ||||||| ||||||||||| |||||||||||

Sbjct: 211 atgggtgectctctcctgcgcttgttcttccatgattgctttgtcaatg 259

Score = 101 bits (51), Expect = 3e-17
Identities = 120/143 (83%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
|||||
Sbjct: 466 tggaatgttaaacttgaagaagagatgctaggactgagccaggctgctgctaataat 525

Query: 1553 ggcattccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttggga 1612
||||
Sbjct: 526 agcattcctcctccaacttctaacctaaaccaactcatttctagatttaacaatttggga 585

Query: 1613 ctttccaccaaggacttgggtcgc 1635
|||||
Sbjct: 586 ctttccactaggacatgggtcgc 608

Score = 81.8 bits (41), Expect = 3e-11
Identities = 59/65 (90%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcctctacaacgagaccaac 1854
|||||
Sbjct: 622 cacacaattgggcaagcaaggtgtacatccttcagagctcgcatatatacagagaccaac 681

Query: 1855 ataga 1859
||||
Sbjct: 682 ataga 686

>gb|C0511866.1| s13dSG02H0700064_103632 Glandular trichomes *Medicago sativa* cDNA,
mRNA sequence
Length = 483

Score = 129 bits (65), Expect = 1e-25
Identities = 149/177 (84%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| ||| | ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 307 gatgggtcaatcctactagatgacacatcaaattttaccggagagaagaacgactcccc 366

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| ||||| ||||| || ||||| || ||||| || ||||| ||||| |||||
Sbjct: 367 aataggaactctgttcgaggattcgatgtcattgacaacataaagacagccgtagagaac 426

Query: 1283 gtgtgtccaggagttgtttcctgcgagatatccttgccatcgtgccagagactct 1339
| ||||| ||||| || || || ||||| ||||| ||||| ||||| |||||
Sbjct: 427 atatgtccaggagttgtatcatgtgctgatatcctagccattgctgccacagactct 483

Score = 87.7 bits (44), Expect = 4e-13
Identities = 166/206 (80%), Gaps = 3/206 (1%)
Strand = Plus / Plus

Query: 582 ttgttctagattgacaattt---gtttggctctgtttgtcctcatatgggggagtgcaa 638
||||| ||||| ||||| | ||||| ||| ||| ||||| ||||| ||||| |||||
Sbjct: 96 ttgttctagattaacaatgttcagtttggttctattttctcataataggagagtgcaa 155

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaaccttctcctctgtgaa 698
||||| ||||| ||||| ||||| || ||||| || ||||| ||| ||| |
Sbjct: 156 tgcacaactctctacaaacttttactcaaaaactgtccaaactctctccattgtcca 215

Query: 699 atccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctctccttge 758
| | ||||| || ||||| ||||| | || ||||| ||||| || || |||
Sbjct: 216 acgccaagtgaatccgctatatcaaaggaggcagaatgggtgcttctattctccgatt 275

Query: 759 gttcttccacgattgctttgtcaatg 784
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 276 gttcttccacgattgctttgtcaatg 301

>gb|BF650349.1| NF096E02EC1F1017 Elicited cell culture Medicago truncatula cDNA clone
NF096E02EC 5', mRNA sequence
Length = 474

Score = 129 bits (65), Expect = 1e-25
Identities = 154/184 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 291 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 350

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 351 aatccaacaaaaattcggcccgaggattcgaagtgatcnacaaatcaaatcagcagtg 410

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatataccttgccatcgctgccagagac 1336
|||||
Sbjct: 411 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 470

Query: 1337 tctg 1340
|||
Sbjct: 471 tctg 474

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctctccttcgcttgttcttccac 768
|||||
Sbjct: 216 caatctgccatatcaaaagagactcgcatgggtgcttctctctctgcttgttcttccac 275

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 276 gattgctttgttaatg 291

>gb|BE022178.1| sm68f01.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-9074 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 352

Score = 129 bits (65), Expect = 1e-25
Identities = 86/93 (92%)
Strand = Plus / Plus

Query: 692 ctgtgaaatccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctcc 751
|||||

Score = 111 bits (56), Expect = 3e-20
Identities = 65/68 (95%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
|||||
Sbjct: 157 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 216

Query: 1852 aacataga 1859
|||||
Sbjct: 217 aacataga 224

>gb|AW685593.1| NF029D05NR1F1000 Nodulated root Medicago truncatula cDNA clone
NF029D05NR 5', mRNA sequence
Length = 677

Score = 117 bits (59), Expect = 5e-22
Identities = 284/359 (79%)
Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
|||||
Sbjct: 592 ggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacgactcc 533

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
|||||
Sbjct: 532 aacatagataacttcctttgctcgcacaaggcaatcagggtgccccaaagacatcgggttcc 473

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaaactccaaccagctttgacaactactac 1971
|||||
Sbjct: 472 ggggacaataatttggcacccttgatcttgaacaccaacatcctttgacaaccattac 413

Query: 1972 ttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacggt 2031
|||||
Sbjct: 412 ttcaagaacctagttgacagtaagggtactcactccgaccaacaactctttaatggt 353

Query: 2032 ggtccaccgactccattgtgctggctacagcaccaaccgggcaccttctcctctgat 2091
|||
Sbjct: 352 ggatccaccgattccatagtgacgaatatagcttgtatccaagctcttttctcctctgat 293

Query: 2092 ttgcccgcgcatgatcaagatgggagacattagtcctctcactggctccaatggaga 2150
|||| | |||||||||||||||||||||||||||||||||| |||| | | ||||||||
Sbjct: 292 ttgctcaccgcatgatcaagatgggagacattagtcctcaccggttcaaatggaga 234

Score = 81.8 bits (41), Expect = 3e-11
Identities = 72/81 (88%), Gaps = 1/81 (1%)
Strand = Plus / Minus

Query: 1562 gcaccacttcaaaccttaaccaactcatctcaagatttagcgctc-ttggactttccac 1620
||||||| ||| |||||||||||||||||| |||| |||| |||| ||||||||
Sbjct: 677 gcaccacttcaagcctcaaccaactcatctcaaggttaatgctctttggtctttccac 618

Query: 1621 caaggacttggtcgcttggc 1641
|||||| |||||||| |||||
Sbjct: 617 caaggatttggtcgcttggc 597

>dbj|FS263447.1| FS263447 RPSC Glycyrrhiza uralensis cDNA clone S02198-34-013 5', mRNA
sequence
Length = 146

Score = 113 bits (57), Expect = 7e-21
Identities = 72/77 (93%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||||||||||| |||||||||||||| || | | ||||||||||||
Sbjct: 70 ggatgtgatggttcaattctactggatgacacatcaagctttacaggggagaagaacgca 129

Query: 1217 aacccaacaggaactc 1233
|||| | ||||||||
Sbjct: 130 aaccgaacaggaactc 146

Score = 107 bits (54), Expect = 5e-19
Identities = 66/70 (94%)
Strand = Plus / Plus

Query: 715 gccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccacgattgc 774
||||||| |||||||||||||||||| |||| | |||||||||||| |||||

Sbjct: 1 gccatatcaaaggagaccgcgatgggtgcttccctcctccgcttgttcttccatgattgc 60

Query: 775 tttgtcaatg 784

|||||||

Sbjct: 61 tttgtcaatg 70

>gb|BF650698.1| NF099E07EC1F1053 Elicited cell culture Medicago truncatula cDNA clone
NF099E07EC 5', mRNA sequence
Length = 501

Score = 113 bits (57), Expect = 7e-21

Identities = 157/191 (82%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||| | ||||||| | ||

Sbjct: 283 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 342

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276

|| ||||| || || || ||||| | || || ||||| || ||||| | |

Sbjct: 343 aatccaacaaaaattcggcccgtggattccaagtgatcgacaaaatcaaatcancagng 402

Query: 1277 gagaaagtgtgtccaggagttgttctcgcgagatatccttgccatcgctgccagagac 1336

||||||| ||||| | ||||| || | || ||||| ||||| ||||| |||||

Sbjct: 403 gagaaagtatgtccagggtgcagtttcatgcctgacatccttaccatcactgctagagac 462

Query: 1337 tctgttcagat 1347

||||| |||

Sbjct: 463 tctgttgagat 473

Score = 95.6 bits (48), Expect = 2e-15

Identities = 69/76 (90%)

Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttccac 768

||||||| || ||||| ||||| || || ||||| |||||

Sbjct: 208 caatctgccatatcaaaagagactcgcatgggtgcttctctccttcgcttgttcttccac 267

Query: 769 gattgctttgtcaatg 784

|||||
Sbjct: 268 gattgctttgttaatg 283

>gb|EV262518.1| MTYEW71TF JCVI-MT1 Medicago truncatula cDNA 5', mRNA sequence
Length = 742

Score = 111 bits (56), Expect = 3e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacc 1222
|||||
Sbjct: 287 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactccc 346

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|||
Sbjct: 347 aataagaactctgttcgaggattcgatgctcattgacaacataaagacggcggtagagaac 406

Query: 1283 gtgtgtccaggagttgtttctgcgagatatccttgccatcgctgccagagactc 1338
|||
Sbjct: 407 gtatgccccggagttgtatcatgtgctgatataccttgccattgctgccacagactc 462

Score = 95.6 bits (48), Expect = 2e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttctt 764
|||||
Sbjct: 202 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttggttctt 261

Query: 765 ccacgattgctttgtcaatg 784
|||||
Sbjct: 262 ccacgattgctttgtcaatg 281

Score = 71.9 bits (36), Expect = 3e-08
Identities = 132/164 (80%)
Strand = Plus / Plus

Sbjct: 660 ||||| ||||||||||||||||||| ||||||| || || | || ||||||| ||
agtgctcacacaattggacaagcaaagtgcacaacatttaggtacgaatctacaatga 719

Query: 1848 gaccaacataga 1859

|||||||||||
Sbjct: 720 gaccaacataga 731

>gb|EV258111.1| MTYDG59TF JCVI-MT1 Medicago truncatula cDNA 5', mRNA sequence
Length = 677

Score = 111 bits (56), Expect = 3e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||||||| | ||||||||||||| ||| ||||||||||||||||| |||
Sbjct: 305 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactccc 364

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||||||| ||| ||||||||| || ||||||||||||| || | || || |||||
Sbjct: 365 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 424

Query: 1283 gtgtgtccaggagttgtttctgcgagatatccttgccatcgctgccagagactc 1338
|| || || ||||||||| || || || ||||||||||||| ||||||| |||||
Sbjct: 425 gtatccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 480

Score = 95.6 bits (48), Expect = 2e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgcatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
||||||||| ||||||||| ||||| | || || ||||||||| |||| | |||||||||
Sbjct: 220 agtgcaatccgcatatcaaaggaggcacgaattggtgcttctatctccgcttgttctt 279

Query: 765 ccacgattgctttgtcaatg 784
|||||||||||
Sbjct: 280 ccacgattgctttgtcaatg 299

Score = 79.8 bits (40), Expect = 1e-10
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| ||||||||||||||||||| || | ||||||| |||
Sbjct: 491 cttggtggcccaacctggaatgtaaaacttggagaagagatgccacaactgctagtcaa 550

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||| ||| |||| || ||||||| ||| ||||| ||||||| ||||| |||||
Sbjct: 551 tctgatgcgaacaactgccatcccaagaccgacttccaaccttaataactcacctcaatg 610

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtc 1641
|||| | |||| ||||||||||||||||||| ||||| |||||
Sbjct: 611 ttaagaatgttggctttccaccaaggacttagtgcattgtc 654

>gb|DW017370.1| EST1226331 MTY Medicago truncatula cDNA clone MTYAS77, mRNA sequence
Length = 793

Score = 111 bits (56), Expect = 3e-20
Identities = 203/252 (80%)
Strand = Plus / Plus

Query: 1788 agtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcctctacaacga 1847
||||| ||||||||||||||||||||||||||| || || | ||||||| |||
Sbjct: 307 agtgctcacacaattggacaagcaaggtgcacaacatttagggtacgaatctacaatga 366

Query: 1848 gaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagg 1907
||||||||||| || | ||||| || || ||||| | ||||| | |||||||
Sbjct: 367 gaccaacatagatacttcttttgctagcacaaggcaatctaattgcccaagacatcagg 426

Query: 1908 gtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaacta 1967
||||||||||||||| ||||||| ||||||| || ||||| || |||||||
Sbjct: 427 atcaggggacaacaatttggcacctcttgatctccatactcccacttctttgacaactg 486

Query: 1968 ctacttcaagaacctcggtcagaagaaggtctctcactctgatcagcaactgttcaa 2027
||||| || ||||||| ||||| || ||||||| || || || || || ||||| |||||
Sbjct: 487 ctactacaggaacctgttcaaaacaaggtctcttcttattcagaccaacaacttttcaa 546

Query: 2028 cgggtgggtccac 2039

Sbjct: 617 ttttaagaatgttggtctttccaccaaggacttagtgcattgtc 660

Score = 71.9 bits (36), Expect = 3e-08
Identities = 63/72 (87%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaagggtgcacaaacttcagagcccgcattacaacga 1847
||||| |||||||||||||||||||||||||||| || || | || |||||||| ||
Sbjct: 661 agtgctcacacaattggacaagcaagggtgcacaacatttaggtacgaatctacaatga 720

Query: 1848 gaccaacataga 1859
|||||||||||
Sbjct: 721 gaccaacataga 732

>gb|C0513179.1| s13dSG23G0900068_129522 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 561

Score = 111 bits (56), Expect = 3e-20
Identities = 169/206 (82%), Gaps = 3/206 (1%)
Strand = Plus / Plus

Query: 582 ttgttctagattgacaat---gtttggctctgtttgtcctcatatgggggagtgcca 638
||||||||||| ||||| | |||||| || || || ||||||||| |||||||||
Sbjct: 102 ttgttctagattaacaatgttcagtttggttctatttctcctcataatagggagtgcca 161

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaaccttctcctctgtgaa 698
||||||||| ||||| ||||||||| | | | ||||| || |||| | || |||| |
Sbjct: 162 tgcacaactctctacgaacttttactccaaaacttgcccaactctcttccactgtcca 221

Query: 699 atccacagtgcaatctgccatatctaaggagaccogcatgggtgcttctctccttcgctt 758
| | ||||||||| || ||||| |||||| | || ||||||||| ||||| |||||
Sbjct: 222 acgccaagtgcaatccgctatatcgaaggaggcagaatgggtgcttctctcctccgctt 281

Query: 759 gttcttccacgattgctttgtcaatg 784
|||||||||||
Sbjct: 282 gttcttccacgattgctttgtcaatg 307

Score = 111 bits (56), Expect = 3e-20
Identities = 149/180 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| ||| | ||||| ||||| || || ||||| ||||| ||||| |||
Sbjct: 313 gatgggtcaatcctactagatgacacatcaaattttaccggagagaagaacgcactcccg 372

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| ||||| ||||| ||| ||||| || || ||||| ||||| || ||||| |||||
Sbjct: 373 aataggaactctgttcgaggatttgatgtcattgacaacataaagacagccgtagagaac 432

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactctgtt 1342
| ||||| ||||| || || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 433 atatgtccaggagttgtatcatgtgctgatatcctagccattgctgccacatactctgtt 492

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| | ||||| ||||| ||||| ||||| || || ||||| ||||| |||
Sbjct: 499 cttggaggcccaaactggaatgttaaacttggagaagagatgccacgactgctagtcaa 558

Query: 1538 tct 1540
|||
Sbjct: 559 tct 561

>gb|C0512465.1| s13dSG100C120008_114444 Glandular trichomes *Medicago sativa* cDNA,
mRNA sequence
Length = 614

Score = 111 bits (56), Expect = 3e-20
Identities = 149/180 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| ||| | ||||| ||||| || || ||||| ||||| ||||| |||
Sbjct: 77 gatgggtcaatcctactagatgacacatcaaattttactggagagaagaacgcactcccg 136

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| ||||| ||| ||||| || ||||| || ||||| || ||||| || ||||| |||||
Sbjct: 137 aataggaactctgttcgaggattcgatgtcattgacaacataaagacagtctagagAAC 196

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgtgccagagactctgtt 1342
| ||||| ||||| || || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 197 atatgtccaggagttgtatcatgtgctgatatcctagccattgctgccacagactctgtt 256

Score = 87.7 bits (44), Expect = 4e-13
Identities = 134/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||| ||||| ||||| ||||| || || ||||| |||||
Sbjct: 263 cttggtggcccaacctggaatgtaaaacttgggagaagagatgccacgactgctagtcaa 322

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
||||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 323 tctgctgcgaacctgccatcccagcaccacttccaaccttaatggactcacctcaatg 382

Query: 1598 tttagcgtcttggactttccaccaaggacttggtcgccttgtc 1641
|||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 383 tttagaatgttggctttccaccaaggacttagtcgcattgtc 426

Score = 71.9 bits (36), Expect = 3e-08
Identities = 63/72 (87%)
Strand = Plus / Plus

Query: 1788 agtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcctctacaacga 1847
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 427 agtgctcacacaattggacaagcaaggtgcacaacatttagggctcgaatctacaatga 486

Query: 1848 gaccaacataga 1859
|| ||||| |||||
Sbjct: 487 gaacaacataga 498

Score = 69.9 bits (35), Expect = 1e-07
Identities = 59/67 (88%)
Strand = Plus / Plus

Query: 718 atatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccacgattgcttt 777
||||| ||||||| | || ||||||||||||||| | || || ||||||||||||||||||||
Sbjct: 5 atatcaaaggaggcacgaatgggtgcttctattctccgattgttcttccacgattgcttt 64

Query: 778 gtcaatg 784
|||||||
Sbjct: 65 gtcaatg 71

>gb|BG456493.1| NF082E02PL1F1017 Phosphate starved leaf Medicago truncatula cDNA
clone NF082E02PL 5', mRNA sequence
Length = 675

Score = 111 bits (56), Expect = 3e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacc 1222
||||| ||||||||||| | ||||||||||||||| ||| ||||||||||||||||||| |||
Sbjct: 280 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactccc 339

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||||||| ||| ||||||||| || ||||||||||| || | || || |||||
Sbjct: 340 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 399

Query: 1283 gtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagactc 1338
|| || | ||||||||| || || || ||||||||||||||| ||||||| |||||
Sbjct: 400 gtatccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 455

Score = 95.6 bits (48), Expect = 2e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttctt 764
||||||||| ||||||||| ||||| | || || ||||||||||| |||| | |||||||||
Sbjct: 195 agtgcaatccgccatatcaaaggaggcacgaattgggtgcttctatcctccgcttgttctt 254

Score = 109 bits (55), Expect = 1e-19
Identities = 112/131 (85%)
Strand = Plus / Minus

Query: 1502 aaacttggagaagagacgctagaactgctagccaatctgctgctaacaatggcatccct 1561
|||||
Sbjct: 230 aaacttggagaagagatgcaagaagtgctagccagtctgctgctaataatggcattcct 171

Query: 1562 gcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccacc 1621
|||||
Sbjct: 170 gcaccaacttcgaacttgaaccaactcattccaggttcaatgctcttggactttccacc 111

Query: 1622 aaggacttggt 1632
|
Sbjct: 110 aaggacttggt 100

Score = 75.8 bits (38), Expect = 2e-09
Identities = 50/54 (92%)
Strand = Plus / Minus

Query: 731 cccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 499 cccgaatgggtgcttctctccttcgattgttcttccacgactgctttgtcaatg 446

Score = 56.0 bits (28), Expect = 0.001
Identities = 118/148 (79%)
Strand = Plus / Minus

Query: 1195 cttcaccggagagaagaacgcaaaccacaggaactctgctcgtggattcgaggttat 1254
|||||
Sbjct: 408 cttcaccggagagaaaaatgctatcccgaatcggaaactcagctcgcgattcgatgtgt 349

Query: 1255 tgacaacattaaatcagccgtggagaaagtgtgtccaggagttgttctcgcgagatat 1314
|||
Sbjct: 348 tgataacatcaagttagctgttgagaatgtttgccctggtgtagtttcttctgtctgatat 289

Query: 1315 ccttgccatcgctgccagagactctgtt 1342
|

Sbjct: 288 cttggccattactgctagagaactctgtt 261

>gb|DW481566.1| GH_RMIRS_031_E08_056_F Cotton Normalized Library random primed
Gossypium hirsutum cDNA, mRNA sequence
Length = 716

Score = 109 bits (55), Expect = 1e-19
Identities = 112/131 (85%)
Strand = Plus / Plus

Query: 1502 aaacttggagaagagacgctagaactgctagccaatctgctgctaacaatggcatccct 1561
|||||
Sbjct: 486 aaacttggagaagagatgcaagaagtgctagccagtctgctgctaataatggcattcct 545

Query: 1562 gcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccacc 1621
|||||
Sbjct: 546 gcaccaacttcgaacttgaaccaactcattccagttcaatgctcttggactttccacc 605

Query: 1622 aaggacttgg 1632
|
Sbjct: 606 aaggacttgg 616

Score = 75.8 bits (38), Expect = 2e-09
Identities = 50/54 (92%)
Strand = Plus / Plus

Query: 731 cccgcatgggtgcttctctctctcgttcttctccacgattgcttgtcaatg 784
|||||
Sbjct: 217 cccgaatgggtgcttctctctcgttcttctccacgactgcttgtcaatg 270

Score = 56.0 bits (28), Expect = 0.001
Identities = 118/148 (79%)
Strand = Plus / Plus

Query: 1195 cttcaccggagagaagaacgcaaaccccaacaggaactctgctcgtggattcgaggttat 1254
|||||
Sbjct: 308 cttcaccggagagaaaatgctatcccgaatcggactcagctcggattcgatgtgt 367

Query: 1256 gacaacattaaatcagccgtggagaaagtgtgtccaggagttgttctcctgcgcagatc 1315
||||| || ||||| || || ||||| ||||| ||||| || || || |||||
Sbjct: 310 gacaatataaaatccgcagttgagaaagcttgcctggagtagtctcatgtgctgatc 369

Query: 1316 cttgccatcgctgccagagactct 1339
||||||| |||||
Sbjct: 370 cttgccatcgctgctagagactct 393

Score = 54.0 bits (27), Expect = 0.006
Identities = 27/27 (100%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcaca 1821
||||||| |||||
Sbjct: 574 cacacaattggacaagcaaggtgcaca 600

>gb|DY633234.1| Medicago--03-I06.g1 Subtracted medicago cDNA library specific for
UV-B irradiation Medicago truncatula cDNA clone
Medicago--03-I06, mRNA sequence
Length = 290

Score = 105 bits (53), Expect = 2e-18
Identities = 122/145 (84%)
Strand = Plus / Plus

Query: 1901 catcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttg 1960
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 104 catcaggatcaggtgacaacaatttggcacctcttgatcttcagactcctagttctttg 163

Query: 1961 acaactactacttcaagaacctggttcagaagaagggtctcctccactctgatcagcaac 2020
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 164 acaacaactacttcaagaacctggttcagaacaagggtcttctccattcagaccaacaac 223

Query: 2021 tgttcaacgggtgggtccaccgactc 2045
|| || ||||| ||||| |||||
Sbjct: 224 tttttaacggcgggtccaccaactc 248

>gb|DY633115.1| Medicago--03-I06.b1 Subtracted medicago cDNA library specific for

UV-B irradiation Medicago truncatula cDNA clone
Medicago--03-I06, mRNA sequence
Length = 290

Score = 105 bits (53), Expect = 2e-18
Identities = 122/145 (84%)
Strand = Plus / Minus

Query: 1901 catcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttg 1960
||||||| ||||| ||||||||| ||||||| ||||||||| ||||| | |||||
Sbjct: 187 catcaggatcaggtgacaacaatttggcacctcttgatcttcagactcctagttcttttg 128

Query: 1961 acaactactacttcaagaacctggttcagaagaagggtctcctccactctgatcagcaac 2020
||||| ||||||||| ||||||| ||||||| ||||| || || || |||||
Sbjct: 127 acaacaactacttcaagaacctgttcagaacaagggtcttctccattcagaccaacaac 68

Query: 2021 tgttcaacgggtgggtccaccgactc 2045
| || ||||| ||||||||| |||||
Sbjct: 67 tttttaacggcgggtccaccaactc 43

>gb|BG359643.1| sac26g07.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1051-3398 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 633

Score = 105 bits (53), Expect = 2e-18
Identities = 120/133 (90%), Gaps = 7/133 (5%)
Strand = Plus / Plus

Query: 1508 ggaagaagagacgc-tagaa-ctgctagcc-aatctgct-gctaacaatggca-tccctg 1562
||||||||||| ||||| ||||| || ||||||||| ||||||||| |||||
Sbjct: 334 ggaagaagagacgcctagaaactgctaaccaatctgcttgctaacaatggcaattcctc 393

Query: 1563 caccacttcaaaa-ccttaaccaactcatctcaagatttagcgctcttgactttcca-c 1620
||||||||||| ||||||||||| ||||||||| || ||||||||| |||||
Sbjct: 394 caccacttcaaaaaccttaaccaactcatctcaagattcaccgctcttgactttccacc 453

Query: 1621 caaggacttggtc 1633
||| |||||||||
Sbjct: 454 caaagacttggtc 466

Score = 91.7 bits (46), Expect = 3e-14
Identities = 109/124 (87%), Gaps = 12/124 (9%)
Strand = Plus / Plus

Query: 1162 tgatggttcaattcta-ttggatgacacatcaag--cttcaccggagagaagaa--cgca 1216
|||||
Sbjct: 87 tgatggttcaattctatttggatgacacatcaagnncttcaccggagagaagaanncgca 146

Query: 1217 aaccccaacagg---aactctgctcgtggat--tcgaggttattgaca--acattaaatc 1269
|||||
Sbjct: 147 aaccccaacaggggaacctctgctcgtggatacccgaggtcattgacannacattaaatc 206

Query: 1270 agcc 1273
|||
Sbjct: 207 agcc 210

>gb|GT138697.1| METCC85TF JCVI-MT3 Medicago truncatula cDNA 5', mRNA sequence
Length = 726

Score = 103 bits (52), Expect = 7e-18
Identities = 70/76 (92%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 227 caatctgccatatcaaaagagaccgcgatgggtgcttctcttctgcgtttgttcttccac 286

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 287 gattgctttgttaatg 302

Score = 91.7 bits (46), Expect = 3e-14
Identities = 208/262 (79%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagacc 1851
|||||
Sbjct: 410 ggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacgactcc 469

Gm-c1028-658 5' similar to TR:P93548 P93548 PEROXIDASE
PRECURSOR ;, mRNA sequence
Length = 286

Score = 103 bits (52), Expect = 7e-18
Identities = 103/120 (85%)
Strand = Plus / Plus

Query: 2023 ttcaacggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttc 2082
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 16 ttcaatggtggttccactgactccatagtgctacactacagcaccaacccggcctccttt 75

Query: 2083 tcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctcc 2142
| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 76 ttgccgatttctccgcccatgatccgatgggagacattagtcctcaccggctcc 135

>emb|CU485516.1| CU485516 CUSHIONC_KZOACAC Theobroma cacao cDNA clone KZOACAC4Y017FM1,
mRNA sequence
Length = 540

Score = 101 bits (51), Expect = 3e-17
Identities = 225/283 (79%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaactctggcaccacttgatcttcaaactcc 1949
||||| | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 516 ctgccaaggaacaacaggttcaggggacaacaacttggcacccttgatatccagactcc 457

Query: 1950 aaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccactc 2009
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 456 aacatTTTTGACAACGATTACTTCAAGAACCTCATCAACAGGAGAGGACTCCTCCACTC 397

Query: 2010 tgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaa 2069
|| || | ||||| || || ||||| || ||| | ||||| || ||||| |||||
Sbjct: 396 cgaccaacagctgttcaatgggggtccacggattccttctgtcggggttacagcaaaa 337

Query: 2070 cccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtc 2129
|||| | ||||| | ||| || | | ||| ||||| ||||| ||||| ||||| |||||
Sbjct: 336 cccgagctcctttagtttgcactttgtcaccggcatgatcaagatgggagacatcagtc 277

Query: 2130 tctcactggctccaatggagaatcaggaagaattgtagaagg 2172

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaac 1854
|||||
Sbjct: 556 cacacaattggacaagcaaggtgtacaaatcttagggcacgaatctacaacgagaccaac 615

Query: 1855 ata 1857
|||
Sbjct: 616 ata 618

>gb|BE943474.1| EST423053 MGHG Medicago truncatula cDNA clone pMGHG-15J14, mRNA
sequence
Length = 480

Score = 101 bits (51), Expect = 3e-17
Identities = 138/167 (82%)
Strand = Plus / Plus

Query: 1172 attctattggatgacacatcaagcttcaccggagagaagaacgcaaacccaacaggaac 1231
|||||
Sbjct: 1 attctactagatgacacatcaaaactttaccggagagaagaacgcactcccgaataagaac 60

Query: 1232 tctgctcgtggattcagggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291
|||||
Sbjct: 61 tctgttcgaggattcagtgctgattgacaacataaagacggcggtagagaacgtatgcccc 120

Query: 1292 ggagttgtttctcgcgagatataccttgccatcgtgccagagactc 1338
|||||
Sbjct: 121 ggagttgtatcatgtgctgattccttgccattgctgccacagactc 167

Score = 79.8 bits (40), Expect = 1e-10
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 178 cttggtggcccaacctggaatgtaaaacttggagaagagatgccacaactgctagtcaa 237

Query: 1538 tctgctgtaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 238 tctgatgcaaacactgccatcccaagaccaacttccaaccttaataactcactcaatg 297

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
|||| | |||| |||||||||||||||||| |||| ||||
Sbjct: 298 tttagaatggttggctttccaccaaggacttagtcgattgtc 341

Score = 71.9 bits (36), Expect = 3e-08
Identities = 63/72 (87%)
Strand = Plus / Plus

Query: 1788 agtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattacaacga 1847
|||| |||||||||||||||||||||||||| || || | || |||||| ||
Sbjct: 342 agtgctcacacaattggacaagcaaggtgcacaacatttaggtacgaatctacaatga 401

Query: 1848 gaccaacataga 1859
||||||||||
Sbjct: 402 gaccaacataga 413

>gb|ES840062.1| UFL_061_05 Cotton fiber 0-10 day post anthesis Gossypium hirsutum
cDNA, mRNA sequence
Length = 1368

Score = 99.6 bits (50), Expect = 1e-16
Identities = 221/278 (79%)
Strand = Plus / Plus

Query: 1906 gggtcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaac 1965
|||||||||||||||| || |||| |||| | || |||||| || ||||||
Sbjct: 204 gggtcaggggacaacaatttgtcaccgcttgacatccagactccaacatattttgacaac 263

Query: 1966 tactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttc 2025
| |||||| |||||| | |||| || | |||||| |||| | ||||
Sbjct: 264 aagtacttcaacaacctcatcggcaagaggggctgctccactcggatcaagagttgttc 323

Query: 2026 aacgggtgggtccaccgactccattgtgctggctacagaccaaccgggcaccttctcc 2085
|| || || |||||||||||||| || || |||| | |||||| || ||||
Sbjct: 324 aatgggggatccaccgactccattgtaagggttacagtaaaaaccgagctccttcagc 383

Query: 2086 tctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaat 2145
|||||| | | |||||| |||||||||||||| |||||| || ||

Sbjct: 384 tctgattttgttacagccatgattaagatgggagacattagtcactcactggatcaaag 443

Query: 2146 ggagaaatcaggaagaattgtagaaggattaactaatt 2183

||||| ||||||||||||| || |||||| ||||| |||||

Sbjct: 444 ggagagatcaggaagaactgcagaagggttaattaatt 481

>gb|BI262826.1| NF091E03EC1F1023 Elicited cell culture Medicago truncatula cDNA clone
NF091E03EC 5', mRNA sequence
Length = 409

Score = 99.6 bits (50), Expect = 1e-16

Identities = 108/128 (84%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||||||||||||||| | ||||||||||||||||||||||||||||| | ||

Sbjct: 281 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 340

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276

|| ||||||| || || || || ||||||||| | || || ||||| || ||||||||| |||

Sbjct: 341 aatccaacaaaaattcngcccgtggattcnaagtgatcgacaaaatcaaatcagcagtg 400

Query: 1277 gagaaagt 1284

|||||||

Sbjct: 401 gagaaagt 408

Score = 83.8 bits (42), Expect = 7e-12

Identities = 67/76 (88%)

Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttcac 768

||||||||||||||| || ||||| ||||||||||||||||| | || ||||||||| |||

Sbjct: 206 caatctgccatatcaaaagagactcgcatgggtgcttctcttntgcgttgttcttncac 265

Query: 769 gattgctttgtcaatg 784

||||||||||| ||||

Sbjct: 266 gattgctttgttaatg 281

>gb|AW666202.1| sk33f05.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1028-3994 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 329

Score = 99.6 bits (50), Expect = 1e-16
Identities = 112/133 (84%)
Strand = Plus / Plus

Query: 1497 atgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaatggca 1556
||||| |||||||||||||||||||| | || || || |||||||||||||||| ||||||| ||
Sbjct: 8 atgtgaaacttggagaagagactccaggacggcaagccaatctgctgccaacaatgaca 67

Query: 1557 tcctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgacttt 1616
||||| |||||||||||||||||| |||||||| || || |||||||| |||||| ||||||
Sbjct: 68 tccaagaccacttcaaacctcaaccaacttatttcagatttaatgctctncaacttt 127

Query: 1617 ccaccaaggactt 1629
||||||| ||||||
Sbjct: 128 ccaccaagactt 140

Score = 71.9 bits (36), Expect = 3e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagacc 1851
|||||||||||||| |||||||| |||||||| ||| ||| ||| ||||||||| ||||||
Sbjct: 157 ggtcacacaattgaacaagcaaggtgcacaacctttagaacccaaatctacaacaagacc 216

Query: 1852 aacataga 1859
|||||||
Sbjct: 217 aacataga 224

>gb|G0006531.1| LJGBF85TF JCVI-LJ1 Lotus japonicus cDNA 5', mRNA sequence
Length = 292

Score = 97.6 bits (49), Expect = 4e-16
Identities = 139/165 (84%), Gaps = 3/165 (1%)
Strand = Plus / Plus

Query: 586 tctagattgacaatgtttgtgctctgtttgtcctcatatgggggagtgccaatgcacaa 645

>gb|C0513848.1| s13dSG73C1100082_156358 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 629

Score = 95.6 bits (48), Expect = 2e-15
Identities = 135/164 (82%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| ||||||||||||||||||| || | ||||||| |||
Sbjct: 162 cttggtggcccaacctggaatgtaaaacttggagaagagatgccacgactgctagtcaa 221

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||||| |||| | |||||| | |||| | |||| | ||||| | |||| | |||||
Sbjct: 222 tctgctggaacactgccatcccagcaccaactccaaccttaatgtactcacctcaatg 281

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgct 1641
||| | ||| ||||||||||||||||||| |||| | |||||
Sbjct: 282 ttaagaatgttggctttccaccaaggacttagtgcattgct 325

Score = 89.7 bits (45), Expect = 1e-13
Identities = 132/161 (81%)
Strand = Plus / Plus

Query: 1900 acatcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt 1959
||||||| ||||||||||| || ||||||| ||||||| || ||||| || |||||
Sbjct: 438 acatcaggatcaggggacaataatttggcacctcttgatctccatactcccacttctttt 497

Query: 1960 gacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaa 2019
||||||| |||| | |||||| | |||| | ||||||| || || || || || || || ||
Sbjct: 498 gacaactgtactacaggaaccttgttcaaaacaagggtcttcttcttattcagaccaaca 557

Query: 2020 ctgttcaacgggtgggtccaccgactccattgtgctggcta 2060
|| ||||||| ||||||||||| |||| | || |||||||
Sbjct: 558 cttttcaacggcgggtccaccaactcaatagtgagtggtgcta 598

Score = 81.8 bits (41), Expect = 3e-11
Identities = 116/141 (82%)
Strand = Plus / Plus

Query: 1202 ggagagaagaacgcaaaccccaacaggaactctgctcgtggattcgaggttattgacaac 1261
|||||
Sbjct: 15 ggagagaagaacgcactcccgaataggaactctgttcgaggattcgatgtcattgacaac 74

Query: 1262 attaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagatatccttgcc 1321
|||
Sbjct: 75 ataaagacagatgtagagaacatatgtccaggggttgatcatgtgctgatatcctagcc 134

Query: 1322 atcgtgccagagactctggt 1342
||
Sbjct: 135 attgctgccacagactctggt 155

>gb|AW691930.2| NF050G04ST1F1000 Developing stem Medicago truncatula cDNA clone
NF050G04ST 5', mRNA sequence
Length = 372

Score = 95.6 bits (48), Expect = 2e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttggttctt 764
|||||
Sbjct: 215 agtgcaatccgccatatcaaaggaggcacgaattgggtgcttctatcctccgcttggttctt 274

Query: 765 ccacgattgctttgtcaatg 784
|||||
Sbjct: 275 ccacgattgctttgtcaatg 294

Score = 67.9 bits (34), Expect = 4e-07
Identities = 49/54 (90%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 300 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgca 353

>emb|AJ548283.1| AJ548283 MTAPHEU Medicago truncatula cDNA clone mtaehac110006d12,
mRNA sequence

Length = 322

Score = 87.7 bits (44), Expect = 4e-13
Identities = 62/68 (91%)
Strand = Plus / Minus

Query: 2083 tcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctcc 2142
|||||
Sbjct: 191 tcctctgatttcgtcaccgcccatgatcaagatgggagacattagtcctcaccggtca 132

Query: 2143 aatggaga 2150
|||||
Sbjct: 131 aatggaga 124

>gb|BF520761.1| EST458234 DSIL Medicago truncatula cDNA clone pDSIL-39G8, mRNA
sequence
Length = 535

Score = 87.7 bits (44), Expect = 4e-13
Identities = 143/176 (81%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacc 1222
|||||
Sbjct: 18 gatgggtcaattctactatatgacacttcaaactttaccggagagaagaacgcactgccg 77

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|||
Sbjct: 78 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 137

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactc 1338
|||
Sbjct: 138 gtatgccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 193

Score = 79.8 bits (40), Expect = 1e-10
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||

Sbjct: 204 cttggtggcccaacctggaatgtaaaaacttggagaagagatgccacaactgctagtcaa 263

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
||||| ||| |||| || ||||||| ||| ||||||| ||||||| ||||| |||||

Sbjct: 264 tctgatgcgaacctgccatcccaagaccaactccaaccttaataactcacctcaatg 323

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttggc 1641
|||| | |||| |||||||||||||||||| ||||| |||||

Sbjct: 324 tttagaatgttggcttttccaccaaggacttagtcgattggc 367

Score = 75.8 bits (38), Expect = 2e-09
Identities = 131/162 (80%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggcgcacaaacttcagagcccgcatctacaacga 1847
||||| |||||||||||||||||||||||||| || || | || ||||||| ||

Sbjct: 368 agtgctcacacaattggacaagcaaggcgcacaacatttaggtacgaatctacaatga 427

Query: 1848 gaccaacatagaaaccgcatttgaaggactaggcagcaaagctgcctagaacatcagg 1907
||||||||||| || | ||||| || || ||||| | ||||| | ||||| |

Sbjct: 428 gaccaacatagatacttcttttggctagcacaaggcaatctaattgcccaaagacatcatg 487

Query: 1908 gtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||||||||||||| ||||||| ||||||| || |||||

Sbjct: 488 atcaggggacaacaatttggcacctcttgatctccatactcc 529

>emb|FN039861.1| FN039861 *Petunia axillaris* subsp. *axillaris* pool of root and petal
tissue *Petunia axillaris* subsp. *axillaris* cDNA clone
drs21P0001M16_R.ab1 2007-08-10, mRNA sequence
Length = 485

Score = 85.7 bits (43), Expect = 2e-12
Identities = 118/143 (82%)
Strand = Plus / Minus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||||||||||| | ||||||||||||||||||||| || | |||||||

Sbjct: 400 tcaggttcaggggacaacaacttagcaccacttgatcttcaaactcctacaactttgac 341

Query: 1963 aactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactg 2022
||| || ||||| ||| | | ||||| || | | ||||| |||||
Sbjct: 340 aacagttatttcaagaaccttgtaacagaaagggtctgcttcattctgatcaacaactc 281

Query: 2023 ttcaacggtgggtccaccgactc 2045
|| | | |||| | |||| | |||||
Sbjct: 280 tttaatggtggatccactgactc 258

>emb|FN039860.1| FN039860 *Petunia axillaris* subsp. *axillaris* pool of root and petal
tissue *Petunia axillaris* subsp. *axillaris* cDNA clone
drs21P0001M16_F.ab1 2007-08-10, mRNA sequence
Length = 485

Score = 85.7 bits (43), Expect = 2e-12
Identities = 118/143 (82%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaactctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| | | ||||| ||||| ||||| || | |||||
Sbjct: 85 tcaggttcaggggacaacaacttagcaccacttgatcttcaaactcctacaactttgac 144

Query: 1963 aactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactg 2022
||| || ||||| ||||| ||| | | ||||| || | | ||||| |||||
Sbjct: 145 aacagttatttcaagaaccttgtaacagaaagggtctgcttcattctgatcaacaactc 204

Query: 2023 ttcaacggtgggtccaccgactc 2045
|| | | |||| | |||| | |||||
Sbjct: 205 tttaatggtggatccactgactc 227

>gb|EG559283.1| CR03032H04 Root CR03 cDNA library *Catharanthus roseus* cDNA clone
CR03032H04 5', mRNA sequence
Length = 560

Score = 85.7 bits (43), Expect = 2e-12
Identities = 109/131 (83%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||||| ||||| || | ||||| ||||| ||||| |||||
Sbjct: 376 tggaatgtgaaacttgaagaagagatgcaacaactgcaagccaagctgctgctaacaat 435

Sbjct: 5 tcacaccattggacaagcagcatgcacaaacttcagagctcacatatacaacgaaaccaa 64

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaagctgccctagaacatcagggtcagg 1913
||| ||| | | ||||| | || | ||||| | | ||||| | | ||||| | |||||

Sbjct: 65 catcgacagtggctttgcatgagcaggcaatcaggctgccctcgtagctcaggctcagg 124

Query: 1914 ggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactactactt 1973
||||| ||||| ||||| | ||||| || ||||| || || || || || || || || ||

Sbjct: 125 tgacaacaatctggcacctttggatcttcagacccaaccgtgttcgagaacaactacta 184

Query: 1974 caagaacctcgttcagaagaagggtctcctcactctgatcag 2016
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 185 caagaacctcgtcgtcaagaaggggtcctcactctgatcag 227

>gb|C0498078.1| G. h. fbr-sw07468 G. h. fbr-sw Gossypium hirsutum cDNA, mRNA sequence
Length = 491

Score = 85.7 bits (43), Expect = 2e-12
Identities = 73/83 (87%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 322 gccatgatcaagatgggagacatcagtcctcactggatcaatgggagagatcaggaag 381

Query: 2161 aattgtagaaggattaactaatt 2183
|| ||||| ||||| |||||

Sbjct: 382 aactgtagaagggttaattaatt 404

>gb|EY707107.1| CS00-C3-701-064-H11-CT.F Sweet orange fruit, development stadium (2
of 6) Citrus sinensis cDNA, mRNA sequence
Length = 837

Score = 83.8 bits (42), Expect = 7e-12
Identities = 123/150 (82%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 152 cttggaggcccaagctggcaagtaaaactcgggaaggagagatgctagaactgcaagccta 211

roseus cDNA similar to peroxidase, mRNA sequence
Length = 708

Score = 83.8 bits (42), Expect = 7e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
||||| ||||||||| || ||||||||||||||||||||||||||||| ||||||||| | |||||
Sbjct: 376 ttctactctgattttgctgccgcccatgatcaagatgggagatattagtcctttgactggt 435

Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
|| ||||||||| | ||||| ||||||||| || |||||
Sbjct: 436 tcaaatggagaggttaggaaaaattgtaggagggttaa 473

Score = 46.1 bits (23), Expect = 1.4
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcaca 1821
||||||||||| |||||||||||||
Sbjct: 91 cacacaattggtcaagcaaggtgcaca 117

>gb|FD420140.1| 1_SM-JB_R10-G12_T3_G12_3100394_14_ab1 CrUniGene root Catharanthus
roseus cDNA similar to peroxidase, mRNA sequence
Length = 494

Score = 83.8 bits (42), Expect = 7e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
||||| ||||||||| || ||||||||||||||||||||||||||||| ||||||||| | |||||
Sbjct: 266 ttctactctgattttgctgccgcccatgatcaagatgggagatattagtcctttgactggt 325

Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
|| ||||||||| | ||||| ||||||||| || |||||
Sbjct: 326 tcaaatggagaggttaggaaaaattgtaggagggttaa 363

>gb|DW508346.1| GH_TMIRS_123_D07_F Cotton Normalized Library dT primed Gossypium

hirsutum cDNA, mRNA sequence
Length = 325

Score = 81.8 bits (41), Expect = 3e-11
Identities = 74/85 (87%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||
Sbjct: 160 gccatgatcaagatgggagacattagtcctctcactggatcacgtgggagatcaggaag 219

Query: 2161 aattgtagaaggattaactaatttg 2185
|||
Sbjct: 220 aactgcagaagggtgaactaatttg 244

>gb|GT143205.1| METCC85TR JCVI-MT3 Medicago truncatula cDNA 3', mRNA sequence
Length = 534

Score = 79.8 bits (40), Expect = 1e-10
Identities = 61/68 (89%)
Strand = Plus / Minus

Query: 2083 tcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctcc 2142
|||||
Sbjct: 326 tcctctgatttcgaccgcccatgatcaagatgggagacattagtcctctcactggctcc 267

Query: 2143 aatggaga 2150
|||||
Sbjct: 266 aatggaga 259

>gb|DR280730.1| 157654 CERES-148 Arabidopsis thaliana cDNA clone 124846 5', mRNA
sequence
Length = 461

Score = 79.8 bits (40), Expect = 1e-10
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 229 cgc atgggtgcttctctccttcgcttgttcttccatgattgctttgtcaatg 280

>gb|CN910539.1| 030128ABLC005555HT (ABLC) Braeburn cell culture three days after
subculture Malus x domestica cDNA clone ABLC005555, mRNA
sequence
Length = 643

Score = 79.8 bits (40), Expect = 1e-10
Identities = 205/260 (78%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| | | ||||| | | | ||||| | | | ||||| | | | ||||| | |
Sbjct: 15 tcaggagataacaattggctccacttgaccttcaaaccctacttctttcgacaacaac 74

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||||| ||||| | ||||| | | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 75 tacttcaaaaacctaatccagaataaagggtctcctccactctgaccagcagcttccaat 134

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
||||| ||||| || || | || | | ||||| || | | ||||| |||
Sbjct: 135 ggtggttccaccgattcgatagtgagagcctacagcaacagctacaacgccttcagtct 194

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|| || | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 195 gactttgcgagtgccatgatcaagatgggagacatcaaacctctcactggatccagtggg 254

Query: 2149 gaaatcaggaagaattgtag 2168
|| || ||||| ||||| |||||
Sbjct: 255 gagattaggaagaattgtag 274

>gb|CN908859.1| 030122ABLC003031HT (ABLC) Braeburn cell culture three days after
subculture Malus x domestica cDNA clone ABLC003031, mRNA
sequence
Length = 563

Score = 79.8 bits (40), Expect = 1e-10
Identities = 205/260 (78%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| | | ||||| | | | ||||| | | | ||||| | | | ||||| | |
Sbjct: 15 tcaggagataacaattggctccacttgaccttcaaaccctacttctttcgacaacaac 74

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactggtcaac 2028
||||||| |||| | ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 75 tacttcaaaaacctaataccagaataaagggtctcctccactctgaccagcagctcttcaat 134

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
||||| ||||| || || ||| | | ||||| || | | ||||| |||
Sbjct: 135 ggtggttccaccgattcgatagtgagagcctacagcaacagctacaacgccttcagtct 194

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|| || | ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 195 gactttgcgagtgccatgatcaagatgggagacatcaaacctctcactggatccagtggg 254

Query: 2149 gaaatcaggaagaattgtag 2168
|| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 255 gagattaggaagaattgtag 274

>gb|CN908310.1| 030109ABLC001919HT (ABLC) Braeburn cell culture three days after
subculture Malus x domestica cDNA clone ABLC001919, mRNA
sequence
Length = 627

Score = 79.8 bits (40), Expect = 1e-10
Identities = 205/260 (78%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
||||| || ||||| ||||| ||||| ||||| ||||| || || || || ||||| ||||| ||||| |||||
Sbjct: 15 tcaggagataacaattggctccacttgacctcaaacccctacttctttcgacaacaac 74

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactggtcaac 2028
||||||| ||||| | ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 75 tacttcaaaaacctaataccagaataaagggtctcctccactctgaccagcagctcttcaat 134

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
||||| ||||| || || ||| | | ||||| || | | ||||| |||
Sbjct: 135 ggtggttccaccgattcgatagtgagagcctacagcaacagctacaacgccttcagtct 194

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|| || | ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 195 gactttgcgagtgccatgatcaagatgggagacatcaaacctctcactggatccagtggg 254

Sbjct: 195 gactttgcgagtgccatgatcaagatgggagacatcaaacctctcactggatccagtggg 254

Query: 2149 gaaatcaggaagaattgtag 2168

|| || ||||||||||||||||

Sbjct: 255 gagattaggaagaattgtag 274

>dbj|AU238571.1| AU238571 RAFL17 Arabidopsis thaliana cDNA clone RAFL17-40-J20 5',
mRNA sequence
Length = 647

Score = 79.8 bits (40), Expect = 1e-10
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784

||||||||||||||||||||||| |||||||||||| ||||| ||||||||||||

Sbjct: 226 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 277

>emb|FN019009.1| FN019009 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0005I02_R.ab1 2007-08-10, mRNA sequence
Length = 553

Score = 77.8 bits (39), Expect = 4e-10
Identities = 69/79 (87%)
Strand = Plus / Minus

Query: 706 gtgcaatctgccatatctaaggagaccgcattgggtgcttctctccttcgcttgttcttc 765

||||||||||| || ||||||| || || ||||||||||||||||| ||||||| | |||||||

Sbjct: 427 gtgcaatctgctatcaataaggaaactcgaatgggtgcttctcttcttcgcctattcttc 368

Query: 766 cacgattgctttgtcaatg 784

||||||||||||||||||||||

Sbjct: 367 cacgattgctttgtcaatg 349

Score = 75.8 bits (38), Expect = 2e-09
Identities = 110/134 (82%)
Strand = Plus / Minus

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552

||||||| ||| | ||||||||| || ||||| | ||||| ||||| ||||| |
Sbjct: 142 tggaaatgtaaaattgggaagaagagatgcaagaacagcaagccaagctgctgcaaacagt 83

Query: 1553 ggcacccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggga 1612

|||| | ||| || | || ||||||| | ||||||| | | | | ||| |||
Sbjct: 82 agcattcctccacctacgtctaaccttaatcgactcatctctagtttcagtgctgttggc 23

Query: 1613 ctttcaccaagga 1626

|||||||||||
Sbjct: 22 ctttcaccaagga 9

Score = 54.0 bits (27), Expect = 0.006
Identities = 60/71 (84%)
Strand = Plus / Minus

Query: 1232 tctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291

||||| | ||||| || | ||||||||||||||||| || | ||||||||| ||
Sbjct: 274 tctgctagaggatttgaagtcattgacaacattaaatctgctgtagagaaagtgtgcct 215

Query: 1292 ggagttgtttc 1302

|| |||||||
Sbjct: 214 ggtgttgtttc 204

>emb|FN019008.1| FN019008 *Petunia axillaris* subsp. *axillaris* pool of root and petal
tissue *Petunia axillaris* subsp. *axillaris* cDNA clone
drs31P0005I02_F.ab1 2007-08-10, mRNA sequence
Length = 588

Score = 77.8 bits (39), Expect = 4e-10
Identities = 69/79 (87%)
Strand = Plus / Plus

Query: 706 gtgcaatctgcatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttc 765

||||||||||| || ||||||| || || ||||||||||||||||| ||||| | |||||
Sbjct: 202 gtgcaatctgcatatcaataaggaaactcgaatgggtgcttctctccttcgcctattcttc 261

Query: 766 cacgattgctttgtcaatg 784

|||||||||||||||
Sbjct: 262 cacgattgctttgtcaatg 280

Score = 54.0 bits (27), Expect = 0.006
Identities = 60/71 (84%)
Strand = Plus / Plus

Query: 1232 tctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291
||||| | ||||| || || ||||| ||||| || || ||||| ||||| ||
Sbjct: 355 tctgctagaggatttgaagtcattgacaacattaaatctgctgtagagaaagtgtgcct 414

Query: 1292 ggagttgtttc 1302
|| |||||
Sbjct: 415 ggtgtgtttc 425

Score = 52.0 bits (26), Expect = 0.023
Identities = 82/101 (81%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||| ||| | ||||| || ||||| || ||||| ||||| ||||| ||||| |
Sbjct: 487 tggaatgtaaaattgggaagaagagatgcaagaacagcaagccaagctgctgcaaacagt 546

Query: 1553 ggcattcctgcaccacttcaaaccttaaccaactcatctc 1593
|||| | ||| || || || ||||| | |||||
Sbjct: 547 agcattcctccactacgtctaaccttantcgactcatctc 587

>emb|FN021689.1| FN021689 *Petunia axillaris* subsp. *axillaris* pool of root and petal
tissue *Petunia axillaris* subsp. *axillaris* cDNA clone
drs31P0009N11_R.ab1 2007-08-10, mRNA sequence
Length = 556

Score = 77.8 bits (39), Expect = 4e-10
Identities = 117/143 (81%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaactctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| | ||||| ||||| ||||| || || |||||
Sbjct: 84 tcaggttcaggggacaacaacttagcaccacctgatcttcaaactcctacaaactttgac 143

Query: 1963 aactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactg 2022

|||| | ||||| |||| | | ||||| || | | ||||| |||||
Sbjct: 144 aacagttatttcaagaaccttgtaacagaaagggtctgcttcattctgatcaacaactc 203

Query: 2023 ttcaacggtgggtccaccgactc 2045
|| || ||||| ||||| |||||

Sbjct: 204 tttaatggtggatccactgactc 226

>emb|FN021688.1| FN021688 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0009N11_F.ab1 2007-08-10, mRNA sequence
Length = 526

Score = 77.8 bits (39), Expect = 4e-10
Identities = 117/143 (81%)
Strand = Plus / Minus

Query: 1903 tcagggtcaggggacaacaactctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| | ||||| ||||| ||||| || | |||||
Sbjct: 502 tcagggtcaggggacaacaacttagcaccacctgatcttcaaactcctacaactttgac 443

Query: 1963 aactactacttcaagaacctgcttcagaagaagggtctcctccactctgatcagcaactg 2022
||| || ||||| ||||| || | | ||||| || | | ||||| |||||
Sbjct: 442 aacagttatttcaagaaccttgtaacagaaagggtctgcttcattctgatcaacaactc 383

Query: 2023 ttcaacggtgggtccaccgactc 2045
|| || ||||| ||||| |||||
Sbjct: 382 tttaatggtggatccactgactc 360

>emb|FN034858.1| FN034858 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs13P0012A19_R.ab1 2007-08-10, mRNA sequence
Length = 697

Score = 77.8 bits (39), Expect = 4e-10
Identities = 51/55 (92%)
Strand = Plus / Plus

Query: 730 acccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||| ||||| ||||| ||||| | ||||| ||||| |||||
Sbjct: 214 accggaatgggtgcttctctccttcgcttcttcttccacgattgcttcgtcaatg 268

Score = 71.9 bits (36), Expect = 3e-08
Identities = 54/60 (90%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| |||||||||||||||||||| ||||| || ||||| ||||||||||||||||
Sbjct: 630 tcacactattggacaagcaaggtgcacaaagtttcagggcacgcatttacaacgagaccaa 689

>emb|FN019751.1| FN019751 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0006L16_F.ab1 2007-08-10, mRNA sequence
Length = 604

Score = 77.8 bits (39), Expect = 4e-10
Identities = 51/55 (92%)
Strand = Plus / Plus

Query: 730 acccgcattgggtgcttctctctcttcgcttgttcttccacgattgctttgtcaatg 784
||||| |||||||||||||||||||| | ||||||||||||||||||| |||||||
Sbjct: 211 acccgaatgggtgcttctctctcttcgcttttcttccacgattgcttctgtcaatg 265

>gb|FC869557.1| C31102G05EF AbioticR1 Citrus reshni cDNA clone C31102G05, mRNA
sequence
Length = 706

Score = 77.8 bits (39), Expect = 4e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagaccgcattgggtgcttctctctcttcgcttgttcttc 765
||||||| || || || ||| | ||||||| || |||||||||||||||||||||
Sbjct: 200 gtgcaatctgctatttcaaaagagctcgcatgggagcctctctctcttcgcttgttcttc 259

Query: 766 cacgattgctt 776
|||||||
Sbjct: 260 cacgattgctt 270

Score = 56.0 bits (28), Expect = 0.001
Identities = 122/151 (80%), Gaps = 2/151 (1%)
Strand = Plus / Plus

Query: 1999 ctctccactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggc 2058
|||||
Sbjct: 30 ctctccactccgatcagcagctgttcaacggcggatccactgattcgctggtgcccagc 89

Query: 2059 tacagcaccacccgggacaccttctctctgatttcgccgcccatgatcaagatggga 2118
|||||
Sbjct: 90 tacagcaacagcgaaggcagcttcacttccgatttcgtggcgccgatgatcaggatggga 149

Query: 2119 gacattagtcctctcactggtccaatggagaaatcaggaagaattgtagaaggattaac 2178
|||
Sbjct: 150 gatatcaaacctctcactggaacaatggagaaattaggaagaattgcaggaggatcaac 209

Query: 2179 taa 2181
|||
Sbjct: 210 taa 212

>gb|EG985866.1| GLE049_D04_013 *Cyamopsis tetragonoloba* (L.) Taub seeds at early developmental stage *Cyamopsis tetragonoloba* cDNA, mRNA sequence
Length = 686

Score = 77.8 bits (39), Expect = 4e-10
Identities = 54/59 (91%)
Strand = Plus / Plus

Query: 1151 atgcagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaa 1209
|||||
Sbjct: 610 atgcagggatgtgatggttcgattctactagatgacacatcaagtttcagcggagagaa 668

Score = 65.9 bits (33), Expect = 2e-06
Identities = 51/57 (89%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaatt 789
|||||
Sbjct: 229 cgc atgggtgcttctctgttgcgattgttcttccacgattgctttgttaatgtaatt 285

>gb|EG356679.1| P00462_C7-H9_M13-F_A09_079 *Onu-Ua-pathc Ulmus americana* cDNA, mRNA

||||| ||| |||||
Sbjct: 199 tgatcagcagctcttcaa 182

Score = 71.9 bits (36), Expect = 3e-08
Identities = 54/60 (90%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||||||| ||||||||| ||||| || ||||| ||||||||| |||||
Sbjct: 418 tcacactattggacaagcaaggtgcacaagtttcagggcacgcatttacaacgagaccaa 359

Score = 50.1 bits (25), Expect = 0.092
Identities = 67/81 (82%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||| ||||||||| ||| || ||||| || ||||| || ||||| || |||||||||
Sbjct: 105 atgattaagatgggagactttcgtccccttactggatctaattggcgagatcaggaagaac 46

Query: 2164 tgtagaaggattaactaattt 2184
|| || ||||| |||||||||
Sbjct: 45 tgcaggaggatcaactaattt 25

>emb|FN045147.1| FN045147 *Petunia axillaris* subsp. *axillaris* pool of root and petal
tissue *Petunia axillaris* subsp. *axillaris* cDNA clone
drs21P0009020_F.ab1 2007-08-10, mRNA sequence
Length = 489

Score = 75.8 bits (38), Expect = 2e-09
Identities = 113/138 (81%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaactctggcaccacttgatcttcaactcc 1949
||||| ||||| ||||| ||||||||| ||||||||| ||||||||| || |||||
Sbjct: 318 ctgccaagaacctcaggttcaggggacaacaacttggcaccctcttgatctccagactcc 259

Query: 1950 aaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctctccactc 2009
|| ||||||||| || ||||| || ||||| || ||||||||| |||||||||
Sbjct: 258 tacatactttgacaaccattatttcataaatcttgtaacaaaaagggtctgctccactc 199

Query: 2010 tgatcagcaactgttcaa 2027
 ||||| || ||
Sbjct: 198 tgatcagcagctcttcaa 181

Score = 71.9 bits (36), Expect = 3e-08
Identities = 54/60 (90%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
 ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 417 tcacactattggacaagcaaggtgcacaagtttcagggcacgcatttacaacgagaccaa 358

Score = 50.1 bits (25), Expect = 0.092
Identities = 67/81 (82%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
 ||||| ||||| || || || || || || || ||
Sbjct: 104 atgattaagatgggagcactttcgtccccttactggatctaattggcgagatcaggaagaac 45

Query: 2164 tgtagaaggattaactaattt 2184
 || || ||||| |||||
Sbjct: 44 tgcaggaggatcaactaattt 24

>emb|FN019752.1| FN019752 *Petunia axillaris* subsp. *axillaris* pool of root and petal
tissue *Petunia axillaris* subsp. *axillaris* cDNA clone
drs31P0006L16_R.ab1 2007-08-10, mRNA sequence
Length = 590

Score = 75.8 bits (38), Expect = 2e-09
Identities = 113/138 (81%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaactctggcaccacttgatcttcaaactcc 1949
 ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 301 ctgcccaagaacctcaggttcaggggacaacaactctggcacctcttgatctccagactcc 242

Sbjct: 441 tcaggagataacaatttggctccacttgaccttcaaaccctacttcttttcgacaacaac 500

Query: 1969 tacttcaagaacctcgttcagaagaaggtctctccactctgatcagcaactgttcaac 2028

||||||| ||||| | ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 501 tacttcaaaaacctaataccagaataaaggtctctccactctgaccagcagctcttcaat 560

Query: 2029 ggtgggtccaccga 2042

||||| |||||

Sbjct: 561 ggtggtccaccga 574

Score = 63.9 bits (32), Expect = 6e-06

Identities = 50/56 (89%)

Strand = Plus / Plus

Query: 1798 acaattggacaagcaaggtgcacaaacttcagagcccgcactctacaacgagaccaa 1853

||||||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 330 acaattgggcaagcaaggtgcacatcattcagaccccgcataatacaacgagaccaa 385

Score = 50.1 bits (25), Expect = 0.092

Identities = 100/125 (80%)

Strand = Plus / Plus

Query: 1508 ggaagaagagacgctagaactgctagccaatctgctgctaacaatggcatccctgcacc 1567

||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 186 ggaagaagagacgcaaggactgcaagccaagccgctgctaacaacaacatccccctcca 245

Query: 1568 acttcaaaccttaaccaactcatctcaagatttagcgctcttgactttcaccaaggac 1627

|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 246 acccgaaacctaaaccagctcatctctacattcagtgctgttggtctttccaccagagac 305

Query: 1628 ttggt 1632

|||||

Sbjct: 306 ttggt 310

>gb|EV227910.1| VV_PeA016c06.b1 Vitis vinifera cv. perlette LibA Vitis vinifera cDNA,
mRNA sequence
Length = 1149

Score = 75.8 bits (38), Expect = 2e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 284 tcaggagacaacaacctggcaccctctggatcttcagaccctaccacctttgacaactac 343

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 344 tactacaagaacct 357

>gb|EH047301.1| AS2RM4P1E10.ab1 Roots inoculated with Meloidogyne arenaria (RM)
Arachis stenosperma cDNA 5', mRNA sequence
Length = 725

Score = 75.8 bits (38), Expect = 2e-09
Identities = 164/206 (79%)
Strand = Plus / Plus

Query: 1960 gacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaa 2019
||||| ||||||| ||||||| | ||| || | ||||||| || || |||||||
Sbjct: 80 gacaaccactacttcaacaacctcgtcgaccggaaaggccccctccattccgaccagcaa 139

Query: 2020 ctgttcaacgggtgggtccaccgactccattgtgctggctacagcaccaaccgggcacc 2079
|| ||||||| || || || ||||||| || ||||||| | ||||||| || |
Sbjct: 140 ctettcaacggaggatctactgactccattgttcgctggctacagctcaaaccctagctct 199

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
|| | | ||||| ||| ||||||| ||||||| || ||| |||||||
Sbjct: 200 tttttgccgattttgccagtccatgatcaagatgggagacataaatcccctcactgga 259

Query: 2140 tccaatggagaaatcaggaagaattg 2165
||||| ||||| || || |||||||
Sbjct: 260 tccaaggagagattagaaagaattg 285

>gb|EC991497.1| WIN1142.C21_L14 Muscat Hamburg pre-veraison berry normalized (WIN11)
Vitis vinifera cDNA clone WIN1142_L14 3', mRNA sequence
Length = 465

Score = 75.8 bits (38), Expect = 2e-09

Identities = 65/74 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 449 tcagagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 390

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 389 tactacaagaacct 376

>gb|EC987303.1| WIN1130.C21_E15 Muscat Hamburg pre-veraison berry normalized (WIN11)
Vitis vinifera cDNA clone WIN1130_E15 3', mRNA sequence
Length = 851

Score = 75.8 bits (38), Expect = 2e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 694 tcagagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 753

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 754 tactacaagaacct 767

>gb|EC985323.1| WIN1124.C21_I01 Muscat Hamburg pre-veraison berry normalized (WIN11)
Vitis vinifera cDNA clone WIN1124_I01 3', mRNA sequence
Length = 906

Score = 75.8 bits (38), Expect = 2e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 478 tcagagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 537

Query: 1969 tacttcaagaacct 1982
|||| |||||||

Sbjct: 538 tactacaagaacct 551

>gb|CV861937.1| gonad_EST09518 Embryonic gonad cDNA Library Gallus gallus cDNA 5',
mRNA sequence
Length = 1288

Score = 75.8 bits (38), Expect = 2e-09
Identities = 59/66 (89%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313
||||| ||||| ||||| || ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 348 ttgacaccattaaagaagccgtggagagagagtgccaggagttgtttcctgtgcagata 407

Query: 1314 tccttg 1319
|||||
Sbjct: 408 tccttg 413

>gb|CX309187.1| C18022D10Rv Drought2 Citrus reshni cDNA clone C18022D10, mRNA
sequence
Length = 712

Score = 75.8 bits (38), Expect = 2e-09
Identities = 122/150 (81%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 516 cttggaggcccaagctggcaagtaaaactcgggaaggagagatgctagaactgcaagccta 457

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacttaaccaactcatctcaaga 1597
||||| ||||| || ||||| ||||| || ||| ||||| || ||| ||||| ||||| ||||| |||||
Sbjct: 456 tctgctgctaataagcggcattcctgctcctacctcaaacttgaatcaacctatctctag 397

Query: 1598 tttagcgtcttggactttccaccaaggac 1627
|| | ||||| ||||| ||||| ||||| |||||
Sbjct: 396 ttcaacgtctcggactttccaacaaggac 367

Score = 60.0 bits (30), Expect = 1e-04
Identities = 105/130 (80%)

Strand = Plus / Minus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
||||| ||||||| ||||||| ||||||| ||||||| || || ||||||| ||

Sbjct: 230 cagggcacaacaacttggcaccgcttgatctgcaaactcctacttgttttgacaacaatt 171

Query: 1970 acttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacg 2029
||||| ||||||| || || || ||||||| || ||||||| || ||||||| ||

Sbjct: 170 acttcaggaacctggtcaacagaaaggattgcttcactctgatcaacagctgttcaatg 111

Query: 2030 gtgggtccac 2039
|||||||||

Sbjct: 110 gtgggtccac 101

Score = 46.1 bits (23), Expect = 1.4

Identities = 101/127 (79%)

Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||||| ||| ||||||| |||| ||||||| || ||||||| || || ||

Sbjct: 708 ggatgcatggtcagttctactggacgacacatcatctttcactggagagaaaaatgcg 649

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| ||||| | ||||||| || || ||||||| || || ||||||| || || || ||

Sbjct: 648 aatgccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaagtccgcagtt 589

Query: 1277 gagaaag 1283
|||||||

Sbjct: 588 gagaaag 582

>gb|CA105303.1| SCJFHR1C05E10.g HR1 Saccharum officinarum cDNA clone SCJFHR1C05E10
5', mRNA sequence
Length = 857

Score = 75.8 bits (38), Expect = 2e-09

Identities = 80/94 (85%)

Strand = Plus / Plus

Query: 1889 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948

|||||
Sbjct: 402 gctgccctagaacctcagggttcaggtgacaacaatttggcgcctctggaccttcaaacc 461

Query: 1949 caaccagctttgacaactactacttcaagaacct 1982

|||||
Sbjct: 462 caaccgtctttgagaacaactactacaagaacct 495

Score = 44.1 bits (22), Expect = 5.7
Identities = 40/46 (86%)
Strand = Plus / Plus

Query: 2137 ggctccaatggagaaatcaggaagaattgtagaaggattaactaat 2182

|||||
Sbjct: 650 ggctccaatgggcagatcaggaagaactgcagaagggttaactaat 695

>gb|CA102350.1| SCBGHR1058E08.g HR1 Saccharum officinarum cDNA clone SCBGHR1058E08
5', mRNA sequence
Length = 664

Score = 75.8 bits (38), Expect = 2e-09
Identities = 80/94 (85%)
Strand = Plus / Plus

Query: 1889 gctgccctagaacctcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948

|||||
Sbjct: 402 gctgccctagaacctcagggttcaggtgacaacaatttggcgcctctggaccttcaaacc 461

Query: 1949 caaccagctttgacaactactacttcaagaacct 1982

|||||
Sbjct: 462 caaccgtctttgagaacaactactacaagaacct 495

>gb|CF205258.1| RR890915I0004_IVa_Ra_B09 Vitis sp. RR890915I Vitis hybrid cultivar
cDNA clone RR890915I0004_IVa_Ra_B09 3', mRNA sequence
Length = 746

Score = 75.8 bits (38), Expect = 2e-09
Identities = 65/74 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

5' similar to class III peroxidase [Gossypium hirsutum]
Length = 320, mRNA sequence
Length = 337

Score = 73.8 bits (37), Expect = 6e-09
Identities = 49/53 (92%)
Strand = Plus / Plus

Query: 732 ccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 117 ccgcatgggtgcttctctcgttcgcttgttcttccatgactgtttgtcaatg 169

>emb|CU488677.1| CU488677 DROUGHTLS_KZOACAF Theobroma cacao cDNA clone
KZOACAF8YE10FM1, mRNA sequence
Length = 501

Score = 73.8 bits (37), Expect = 6e-09
Identities = 49/53 (92%)
Strand = Plus / Plus

Query: 732 ccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 269 ccgcatgggtgcttctctcgttcgcttgttcttccatgactgtttgtcaatg 321

>gb|FG154278.1| AGN_RNC104xj04f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 798

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaat 783
|||||
Sbjct: 174 aaggaaaccgcatgggtgcttccctccttcgcctattcttccacgattgcttcgtcaat 233

Query: 784 g 784
|
Sbjct: 234 g 234

Score = 73.8 bits (37), Expect = 6e-09

Score = 73.8 bits (37), Expect = 6e-09
Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||||| |||| | ||| |||| ||||| ||||| ||||| || ||||| || |||||
Sbjct: 434 cttggaggccctaattgggatgtaaaactcggagaagagatgccagaacagcaagccaa 493

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||| | |||| | |||| || | || ||||| ||||| ||||| || ||||| ||
Sbjct: 494 gctgccgcaaacagtagcattcctctccaacttctaaccttaaccggetcatctctagc 553

Query: 1598 tttagcgctcttggactttccaccaagga 1626
|| || ||| |||| ||||| ||||| |||||
Sbjct: 554 ttcagtgctgttggcctttccaccaagga 582

Score = 63.9 bits (32), Expect = 6e-06
Identities = 53/60 (88%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||| ||||| ||||| ||||| | ||||| || ||||| ||||| ||||| |||||
Sbjct: 604 tcacaccattggacaagcaaggtgcactagtttcagggcagcatatacaacgagaccaa 663

>gb|FG156951.1| AGN_RNC026xe21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 921

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcgatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaat 783
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 374 aaggaaaccgcatgggtgcttccctccttcgcttattcttccacgattgcttctgtcaat 433

Query: 784 g 784
|
Sbjct: 434 g 434

Score = 58.0 bits (29), Expect = 4e-04
Identities = 120/149 (80%), Gaps = 1/149 (0%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||||| |||| ||| |||| ||||| ||||| ||||| ||| ||| | || |||||
Sbjct: 625 cttggaggcctaattgggatgtaaaactcggagaagagatgccaga-cagcaagccaa 683

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||| | |||| | |||| ||| | || ||||| ||||| ||||| ||||| ||
Sbjct: 684 gctgccgcaaacagtagcattcctcctccaacttctaaccttaaccggctcatctctagc 743

Query: 1598 tttagcgctcttggactttccaccaagga 1626
|| || ||| |||| ||||| ||||| |||||
Sbjct: 744 ttcagtgctgttggcctttccaccaagga 772

>gb|FG157638.1| AGN_RNC025xk16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 907

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcatgggtgcttctctctctccttgccttgttcttccacgattgctttgcaat 783
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 201 aaggaaaccgcatgggtgcttccctcctcctcgcctattcttccacgattgcttctgcaat 260

Query: 784 g 784
|
Sbjct: 261 g 261

Score = 73.8 bits (37), Expect = 6e-09
Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

Sbjct: 453 cttggaggggcctaattgggatgtaaaactcggaagaagagatgccagaacagcaagccaa 512

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597

Sbjct: 513 gctgccgcaaacagtagcattcctcctccaacttctaaccttaaccggctcatctctagc 572

Query: 1598 tttagcgctcttggactttccaccaagga 1626

Sbjct: 573 ttcagtgtgttggcctttccaccaagga 601

Score = 56.0 bits (28), Expect = 0.001
Identities = 52/60 (86%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853

Sbjct: 623 tcacaccattggacaagcaaaagtgcactagtttcagggcacgcatatacaacgagaccaa 682

>dbj|DB920515.1| DB920515 full-length enriched cassava cDNA library Manihot esculenta
cDNA clone CAS01_002_E19 5', mRNA sequence
Length = 556

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 1497 atgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaatggca 1556

Sbjct: 480 atgttaaacttggagaagagatgctagaactgcaagcctttctgctgcaaataatggca 539

Query: 1557 t 1557

Sbjct: 540 t 540

Score = 65.9 bits (33), Expect = 2e-06
Identities = 45/49 (91%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 221 atgggtgcttcctcctcgttcgcttggttcttccatgattgctttgttaatg 269

Score = 56.0 bits (28), Expect = 0.001
Identities = 70/84 (83%)
Strand = Plus / Plus

Query: 1256 gacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttctgcgcatatc 1315
||||| || ||||| || || ||||| || ||||| ||||| || || || || |||||
Sbjct: 368 gacaatataaaatccgcagttgagaaagcttgcctggagtagtctcatgtgctgatatc 427

Query: 1316 cttgccatcgctgccagagactct 1339
||||| ||||| ||||| ||||| |||||
Sbjct: 428 cttgccatcgctgctagagactct 451

>gb|EB450877.1| KT7C.108P16F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108P16,
mRNA sequence
Length = 785

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaat 783
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 194 aaggaaaccgcatgggtgcttccctccttcgcctattcttccacgattgcttctgcaat 253

Query: 784 g 784
|
Sbjct: 254 g 254

Score = 73.8 bits (37), Expect = 6e-09
Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggcctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||
Sbjct: 263 gccatgatcaagatgggtgacatcaaacctctcaccggctctaattggagaaattcgcaag 322

Query: 2161 aattgtagaaggattaactaa 2181
|||||
Sbjct: 323 aattgtagaaagatcaactaa 343

Score = 71.9 bits (36), Expect = 3e-08
Identities = 87/104 (83%)
Strand = Plus / Plus

Query: 1939 cttcaaactccaaccagctttgacaactactacttcaagaacctcgttcagaagaagggt 1998
|||||
Sbjct: 101 cttcaaaccccaacggcctttgacaacaagtatttcaagaacctgattaacaagaagggc 160

Query: 1999 ctctccactctgatcagcaactgttcaacgggtgggtccaccga 2042
||
Sbjct: 161 ctctccactctgatcagcagcttcaatgggtgggtccgccga 204

>gb|CN782128.1| EST00224 cqseed Chenopodium quinoa cDNA clone S02D05 5' similar to
peroxidase, putative At5g05340, mRNA sequence
Length = 803

Score = 73.8 bits (37), Expect = 6e-09
Identities = 46/49 (93%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgcttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 238 atgggtgcttctctcctacgcttgcttcttccacgattgcttcgcaatg 286

Score = 46.1 bits (23), Expect = 1.4
Identities = 68/83 (81%)
Strand = Plus / Plus

Query: 1521 ctagaactgctagccaatctgctgctaacaatggcatccctgcaccacttcaaactta 1580
||||||| ||||||| | ||| | || | || || ||||| | |
Sbjct: 337 ctagaactgcaagccaatctgctgctaataagcggcttctcctctacctcaaactga 396

Query: 1581 accaactcatctcaagatttagcgctcttggactttccaaccaaggac 1627
| ||||| ||| || | ||||| ||||||| |||||
Sbjct: 397 atcaactcacctctaggttcaacgctctcggactttccaacaaggac 443

>gb|FC874065.1| C31202A05EF BiotPhyR1 Citrus aurantium cDNA clone C31202A05, mRNA
sequence
Length = 689

Score = 71.9 bits (36), Expect = 3e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcatgggtcttctctcttcgcttgttcttccacgattgctt 776
||||||| || ||||||| ||||||| ||||||| |||||||
Sbjct: 228 cgcatgggcctctctcttcgcttgttcttccacgattgctt 271

Score = 56.0 bits (28), Expect = 0.001
Identities = 82/100 (82%)
Strand = Plus / Plus

Query: 1521 ctagaactgctagccaatctgctgctaacaatggcatccctgcaccacttcaaactta 1580
||||||| ||||||| | ||||| ||| | || || ||||| | |
Sbjct: 514 ctagaactgcaagccaatctgctgctaataagcggcattctcctctacctcaaactga 573

Query: 1581 accaactcatctcaagatttagcgctcttggactttccac 1620
| ||||| ||| || | ||||| |||||||
Sbjct: 574 atcaactcacctctaggttcaacgctctcggactttccac 613

Score = 54.0 bits (27), Expect = 0.006
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

Query: 2085 ctctgatttcgccgcccgcgatgatcaagatgggagacattagtcctctcactggctccaa 2144
||||||| || ||||| ||||||||||||||| || ||||||| || ||||| |||||
Sbjct: 33 ctctgattttgctgccgcatgatcaagatgggtgatattagtccttactgggtccaa 92

Query: 2145 tggagaaatcaggaag 2160
||| ||||| |||||
Sbjct: 93 tggcgaataaggaag 108

>gb|EY845171.1| CA26-C1-002-040-C02-CT.F Sour orange leaf, field plant Citrus
aurantium cDNA, mRNA sequence
Length = 812

Score = 71.9 bits (36), Expect = 3e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcattgggtcttctctctctccttcgcttgttcttccacgattgctt 776
||||||| || |||||||||||||||||||||||||||||||||||
Sbjct: 267 cgcattgggcctctctctctccttcgcttgttcttccacgattgctt 310

Score = 60.0 bits (30), Expect = 1e-04
Identities = 120/150 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| || ||| || || ||||| || || ||||| ||||||||| |||||
Sbjct: 510 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 569

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||||| || ||||| ||| || || || ||||| || || ||||| ||| ||
Sbjct: 570 tctgctgctaataagcggcattcctcctctacctcaaacttgaatcaactcacctctagg 629

Query: 1598 tttagcgtcttggactttccaccaaggac 1627
| | ||||| ||||||||| |||||
Sbjct: 630 tccaacgctctcggactttccaacaaggac 659

Score = 54.0 bits (27), Expect = 0.006

Score = 54.0 bits (27), Expect = 0.006
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 286 ggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 345

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| | ||||| || || ||||| ||||| || ||||| ||||| || || ||
Sbjct: 346 gtcccaatcgtaactccgccgaggattcgaggtcatcgacaacattaaagtcgcagtt 405

Query: 1277 gagaaag 1283
|||||||
Sbjct: 406 gagaaag 412

>gb|EY776217.1| CR05-C1-103-015-D05-CT.F Mandarin leaf, infected with Xylella
fastidiosa (stage 2 of 2) Citrus reticulata cDNA, mRNA
sequence
Length = 968

Score = 71.9 bits (36), Expect = 3e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctctcttcgcttgttcttccacgattgctt 776
||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 225 cgcattgggcctctctctcttcgcttgttcttccacgattgctt 268

Score = 54.0 bits (27), Expect = 0.006
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||| ||||| ||||| ||||| |||||
Sbjct: 276 ggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 335

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| | ||||| || || ||||| ||||| || ||||| ||||| || || ||

Sbjct: 336 gtccccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaagtccgcagtt 395

Query: 1277 gagaaag 1283

|||||||

Sbjct: 396 gagaaag 402

>gb|EY725128.1| CS00-C3-703-086-B09-CT.F Sweet orange fruit, development stadium (4 of 6) Citrus sinensis cDNA, mRNA sequence
Length = 840

Score = 71.9 bits (36), Expect = 3e-08

Identities = 42/44 (95%)

Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctt 776

||||||| || ||||||||||||||||||||||||||||||||||

Sbjct: 210 cgc atgggcctctctccttcgcttgttcttccacgattgctt 253

Score = 67.9 bits (34), Expect = 4e-07

Identities = 121/150 (80%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

||||||||||| | ||| | || ||||| | | ||||| ||||||||| |||||||

Sbjct: 453 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 512

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597

||||||||||| | ||||| ||| | || | ||||| | || ||||||| ||| ||

Sbjct: 513 tctgctgctaataagcgcattcctcctctacactcaaacttgaatcaactcacctctagg 572

Query: 1598 tttagcgtcttggactttccaccaaggac 1627

|| | ||||| ||||||||| |||||||

Sbjct: 573 ttcaacgctctcggactttccaacaaggac 602

Score = 54.0 bits (27), Expect = 0.006

Identities = 102/127 (80%)

Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctt 776
||||||| || ||||||||||||||||||||||||||||||||
Sbjct: 512 cgc atgggcctctctccttcgcttgttcttccacgattgctt 469

Score = 60.0 bits (30), Expect = 1e-04
Identities = 105/130 (80%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaac 1213
||||||| ||||| ||| ||||| | || ||||||||| ||||||||||||| ||
Sbjct: 175 cagggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaat 116

Query: 1214 gcaaaccacaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagcc 1273
||| ||||||| | ||||| || | ||||||||||||| || ||||||||||| || ||
Sbjct: 115 gcagtcccaaatcgtaactccgccgcggattcgaggtcatcgacaacattaaagtccgca 56

Query: 1274 gtggagaaag 1283
|| |||||||
Sbjct: 55 gttgagaaag 46

>gb|CV717574.1| UCRC08_0009D08_f Parent Washington Navel Orange Callus cDNA Library
UCRC08-1 Citrus sinensis cDNA clone CS_AEa0009D08, mRNA
sequence
Length = 694

Score = 71.9 bits (36), Expect = 3e-08
Identities = 123/152 (80%)
Strand = Plus / Plus

Query: 1476 agcttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagcc 1535
||||||||||||||| | ||| | || ||||| || || ||||| ||||||||||||| |||||
Sbjct: 120 agcttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagcc 179

Query: 1536 aatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaa 1595
||||||||||||||| | ||||| ||| | || || ||||||| | || ||||||| |||||
Sbjct: 180 aatctgctgctaataagcggcattcctcctcctacactcaaacttgaatcaactcacctcta 239

Query: 1596 gatttagcgtcttggactttccaccaaggac 1627
| || | ||||||| ||||||||||| |||||||
Sbjct: 240 gttcaacgctctcggactttccaacaaggac 271

Score = 46.1 bits (23), Expect = 1.4
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 2005 cactctgatcagcaactgttcaacgggtgggtccac 2039
|||||
Sbjct: 626 cactctgatcaacagctgttcaatgggtgggtccac 660

>gb|CV093292.1| FAMU_USDA_FP_1315 Vitis shuttleworthii L., grape Vitis shuttleworthii
cDNA clone JLVs077_F09 5', mRNA sequence
Length = 666

Score = 71.9 bits (36), Expect = 3e-08
Identities = 101/120 (84%), Gaps = 2/120 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt-gacaacta 1967
|||||
Sbjct: 230 tcaggggacaacaacttgcccctctggatcttcaaactcctac-agcttttgagaaca 288

Query: 1968 ctacttcaagaacctcggttcagaagaagggtctcctcactctgatcagcaactgttcaa 2027
|||||
Sbjct: 289 ctactacaagaacctgatcaagaagaaggacttctcactctgatcagcagctgttcaa 348

Score = 60.0 bits (30), Expect = 1e-04
Identities = 54/62 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattgggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
|||||
Sbjct: 116 cacacaattgggacaagcaaggtgcacatccttcagggtcgcatatacaatgagaccaac 175

Query: 1855 at 1856
||
Sbjct: 176 at 177

Score = 50.1 bits (25), Expect = 0.092
Identities = 58/69 (84%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
|||||
Sbjct: 426 atgatcaagatgggagatatcagccactcactggatcaaacggagagattaggaagaac 485

Query: 2164 tgtagaagg 2172
||
Sbjct: 486 tgcagaagg 494

Score = 48.1 bits (24), Expect = 0.36
Identities = 81/100 (81%)
Strand = Plus / Plus

Query: 1539 ctgctgctaacaatggcatcctgcaccacttcaaaccttaaccaactcatctcaagat 1598
|||||
Sbjct: 6 ctgctgcaaacacagcatcctcctccaacttcaaacctgaaccaactaatctctagtt 65

Query: 1599 ttagcgctcttggactttccaccaaggacttggctgcctt 1638
|
Sbjct: 66 tccaagctcttggcctctcaaccaggacttggctgcctt 105

>gb|C0866271.1| Mdfrt3046b02.y1 Mdfrt Malus x domestica cDNA clone Mdfrt3046b02 5'
similar to TR:Q41326 Q41326 PEROXIDASE ;, mRNA sequence
Length = 509

Score = 71.9 bits (36), Expect = 3e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||
Sbjct: 277 gccatgatcaagatgggagacatcaaacctctcactggatccagtggggagattaggaag 336

Query: 2161 aattgtag 2168
|||||
Sbjct: 337 aattgtag 344

>gb|G0566201.1| Mddb5025B21_e2932.g1 Mddb Malus x domestica cDNA 5' similar to
dbj|BAA82306.1| peroxidase [Nicotiana tabacum], mRNA
sequence
Length = 687

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
|||||
Sbjct: 560 tcacacaattgggcaagcaaggtgtacaactttcagagctcgcatatataacgagaccaa 501

Query: 1854 cat 1856
|||
Sbjct: 500 cat 498

>emb|CU537036.1| CU537036 TISCIVS_KZ0AAQ Theobroma cacao cDNA clone KZ0AAQ5YH15FM1,
mRNA sequence
Length = 744

Score = 69.9 bits (35), Expect = 1e-07
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 463 cttggaggccccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 522

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 523 gctgctgccaacaacagcattcctctccaacttctaactgaacagactcatttctaga 582

Query: 1598 tttagcgcctcttgactttccaccaaggacttggt 1632
|||
Sbjct: 583 ttcaatgctcttgactttccaccaggacatggt 617

Score = 48.1 bits (24), Expect = 0.36
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcaca 1821
 |||||
Sbjct: 633 tcacacaattggactagcaaggtgcaca 660

>emb|CU505430.1| CU505430 PODMEUPA_KZOACAB Theobroma cacao cDNA clone KZOACAB5YF04FM1,
 mRNA sequence
 Length = 769

Score = 69.9 bits (35), Expect = 1e-07
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
 |||||
Sbjct: 455 cttggaggccccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 514

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaacttaaccaactcatctcaaga 1597
 |||||
Sbjct: 515 gctgctgccaacaacagcattcctcctccaacttctaacttgaacagactcatttctaga 574

Query: 1598 tttagcgctcttggactttccaccaaggacttgggt 1632
 |||
Sbjct: 575 ttcaatgctcttggactttccaccaggacatggt 609

Score = 48.1 bits (24), Expect = 0.36
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcaca 1821
 |||||
Sbjct: 625 tcacacaattggactagcaaggtgcaca 652

>emb|CU478688.1| CU478688 COPHAS_KZOAAAL Theobroma cacao cDNA clone KZOAAAL11YB20FM1,
 mRNA sequence
 Length = 642

Score = 69.9 bits (35), Expect = 1e-07
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||| ||||||||||||||||||||| || ||||| || ||||||| |||||||||||||||||
Sbjct: 686 cacacgattggacaagcaaggtgcacgaatttcagggtcgcataatacaacgagaccaa 744

>gb|EB110403.1| 000430AFBC008068HT (AFBC) Royal Gala pre-opened floral bud Malus x
domestica cDNA clone AFBC008068, mRNA sequence
Length = 481

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
||||| ||||||||||||||||||||| ||||| ||||||| ||||| || ||||||| |||||||||
Sbjct: 217 tcacacaattgggcaagcaaggtgtacaactttcagagctcgcataatacaacgagaccaa 276

Query: 1854 cat 1856
|||
Sbjct: 277 cat 279

>gb|DW157696.1| CLVX9795.b1_E02.ab1 CLV(XYZ) lettuce virosa Lactuca virosa cDNA clone
CLVX9795, mRNA sequence
Length = 440

Score = 69.9 bits (35), Expect = 1e-07
Identities = 65/75 (86%)
Strand = Plus / Plus

Query: 2088 tgatttcgccgccgccatgatcaagatgggagacattagtcctctcactggtccaatgg 2147
||||| || ||||||||||||||||||||| ||||| ||| ||||| ||||||||||||||||| ||
Sbjct: 198 tgattttgcgccgccatgatcaacatgggtgatattcgtcccctcactggtccaacgg 257

Query: 2148 agaatcaggaagaa 2162
|| |||||||||||||
Sbjct: 258 cgagatcaggaagaa 272

>gb|DW145800.1| CLVX10900.b1_H13.ab1 CLV(XYZ) lettuce virosa Lactuca virosa cDNA
clone CLVX10900, mRNA sequence
Length = 453

Score = 69.9 bits (35), Expect = 1e-07
Identities = 65/75 (86%)
Strand = Plus / Plus

Query: 2088 tgatttcgccgcccgcacatgatcaagatgggagacattagtcctctcactggctccaatgg 2147
||||||| || |||||||||||||||| ||||| || ||| ||||| |||||||||||||||| ||
Sbjct: 211 tgattttgcggcccgcacatgatcaacatgggtgatattcgtcccctcactggctccaacgg 270

Query: 2148 agaatcaggaagaa 2162
|| ||||||||||||
Sbjct: 271 cgagatcaggaagaa 285

>gb|C0900249.1| Mddb5025b21.y1 Mddb Malus x domestica cDNA clone Mddb5025b21 5'
similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE ;, mRNA sequence
Length = 671

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
|||||||||||| |||||||||| |||| | ||||||| ||||| || ||||||||||||
Sbjct: 344 tcacacaattgggcaagcaaggtgtacaactttcagagctcgcatatataacgagaccaa 403

Query: 1854 cat 1856
|||
Sbjct: 404 cat 406

>gb|C0051719.1| Mdfw2055d05.y1 Mdfw Malus x domestica cDNA clone Mdfw2055d05 5'
similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE ;, mRNA sequence
Length = 537

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgagaccaa 1853
|||||||||||| |||||||||| |||| | ||||||| ||||| || ||||||||||||
Sbjct: 93 tcacacaattgggcaagcaaggtgtacaactttcagagctcgcatatataacgagaccaa 152

Query: 1854 cat 1856

|||
Sbjct: 153 cat 155

>gb|CN880015.1| 010418AASA009843HT (AASA) Royal Gala 10 DAFB fruit Malus x
domestica cDNA clone AASA009843, mRNA sequence
Length = 687

Score = 69.9 bits (35), Expect = 1e-07
Identities = 65/75 (86%)
Strand = Plus / Plus

Query: 710 aatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttcttccacg 769
||||||| |||| ||||| | ||||||||||||||||||||||||| | |||||
Sbjct: 168 aatctgccgatcaaggaaaagcgatgggtgcttctctccttcgctccatttccacg 227

Query: 770 attgctttgtcaatg 784
|||||||||||||||
Sbjct: 228 attgctttgtcaatg 242

Score = 67.9 bits (34), Expect = 4e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| ||||||||||||||||| |||| | ||||||||||||| |||||||||
Sbjct: 608 cacacaataggacaagcaaggtgcaccgtcttccgaaccgcatctacaccgagaccaac 667

Query: 1855 at 1856
||
Sbjct: 668 at 669

>gb|GR871114.1| Pq_F_00457 American ginseng Flower cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 519

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaatcagccgtggagaaagtgtgtccaggagttgttctctgcgagata 1313

||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 354 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 413

Query: 1314 tccttg 1319

|||||
Sbjct: 414 tccttg 419

>gb|GR875194.1| Pq_R_02677 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 453

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313

||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 354 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 413

Query: 1314 tccttg 1319

|||||
Sbjct: 414 tccttg 419

>gb|GR873483.1| Pq_R_00966 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 494

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313

||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 292 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 351

Query: 1314 tccttg 1319

|||||
Sbjct: 352 tccttg 357

>gb|GR873276.1| Pq_R_00759 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence

Length = 557

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313
||||| ||||||| || ||||||| || ||| ||||||||||||||||||| |||||||
Sbjct: 341 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 400

Query: 1314 tccttg 1319
|||||
Sbjct: 401 tccttg 406

>gb|GR871777.1| Pq_F_01120 American ginseng Flower cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 435

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313
||||| ||||||| || ||||||| || ||| ||||||||||||||||||| |||||||
Sbjct: 293 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 352

Query: 1314 tccttg 1319
|||||
Sbjct: 353 tccttg 358

>gb|GR874357.1| Pq_R_01840 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 397

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313
||||| ||||||| || ||||||| || ||| ||||||||||||||||||| |||||||
Sbjct: 315 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 374

Query: 1314 tccttg 1319
 |||||
Sbjct: 375 tccttg 380

>gb|GR874227.1| Pq_R_01710 American ginseng Root cDNA Library Panax quinquefolius
 cDNA 5', mRNA sequence
 Length = 415

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313
 ||||| ||||| || ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 67 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 126

Query: 1314 tccttg 1319
 |||||
Sbjct: 127 tccttg 132

>emb|CU507988.1| CU507988 PODSSHWB1Sb_KZOACD Theobroma cacao cDNA clone
 KZOACD3YE10FM1, mRNA sequence
 Length = 336

Score = 67.9 bits (34), Expect = 4e-07
Identities = 61/70 (87%)
Strand = Plus / Minus

Query: 2103 catgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
 ||||| ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 328 catgatcaagatgggagacatcagtcctcactggatcaaggggagagatcaggaagaa 269

Query: 2163 ttgtagaagg 2172
 || |||||
Sbjct: 268 ctgcagaagg 259

>gb|EY664481.1| CS00-C1-101-067-A09-CT.F Sweet orange leaf, infected with Xylella
 fastidiosa (stage 1 of 2) Citrus sinensis cDNA, mRNA
 sequence
 Length = 677

>gb|EL366609.1| CCES2712.b1_005.ab1 CCE(LMS) endive Cichorium endivia cDNA clone
CCES2712, mRNA sequence
Length = 465

Score = 67.9 bits (34), Expect = 4e-07
Identities = 64/74 (86%)
Strand = Plus / Plus

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||||||||||||| ||||| || ||| ||||| ||||| ||||||||| ||
Sbjct: 267 gatttcgccgccgcatgatcaatatgggtgatattcgtcccctcaccggctccaacggc 326

Query: 2149 gaaatcaggaagaa 2162
|| |||||||||||
Sbjct: 327 gagatcaggaagaa 340

>gb|EH664510.1| 11.2E05 Transformed tobacco Lambda Zap II library Nicotiana tabacum
cDNA 5', mRNA sequence
Length = 1034

Score = 67.9 bits (34), Expect = 4e-07
Identities = 54/61 (88%)
Strand = Plus / Plus

Query: 724 aaggagaccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaat 783
||||| ||||| ||||||||||| ||||||||| | ||||| ||||||||| |||||||
Sbjct: 206 aaggaaaccgcatgggtgcttccctccttcgctattcttccnagattgcttctgtcaat 265

Query: 784 g 784
|
Sbjct: 266 g 266

>gb|EC600006.1| PNSSH3G-1469 panax notoginseng subtracted cDNA libraries Panax
notoginseng cDNA 5' similar to secretory peroxidase, mRNA
sequence
Length = 454

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgagata 1313

||||| ||||| || ||||| || ||| ||||||||||||||| |||||
Sbjct: 30 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 89

Query: 1314 tccttg 1319

|||||
Sbjct: 90 tccttg 95

Database: /usr/local/blast/db/blastlibs/est_others

Posted date: Feb 13, 2010 7:48 AM

Number of letters in database: 29,218,461,503

Number of sequences in database: 51,680,690

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 51680690

Number of Hits to DB: 1,226,019,706

Number of extensions: 77420216

Number of successful extensions: 22531408

Number of sequences better than 10.0: 2217

Number of HSP's gapped: 22531246

Number of HSP's successfully gapped: 2762

Length of query: 3867

Length of database: 29,218,461,503

Length adjustment: 24

Effective length of query: 3843

Effective length of database: 27,978,124,943

Effective search space: 107519934155949

Effective search space used: 107519934155949

X1: 11 (21.8 bits)

X2: 15 (29.7 bits)

X3: 50 (99.1 bits)

S1: 12 (24.3 bits)

S2: 22 (44.1 bits)

BLASTx Output of the Sequence at the Parental Locus of Soybean Event DAS-68416-4 against GenBank Non-redundant Protein Sequences (nr)

BLASTX 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Query= 68416_parent_locus
(3867 letters)

Database: /usr/local/blast/db/blastlibs/nr
10,432,217 sequences; 3,559,509,877 total letters

Searching..... done

Sequences producing significant alignments:	Score	E
	(bits)	Value
gb ACU17608.1 unknown [Glycine max]	249	2e-63
gb ACU17865.1 unknown [Glycine max]	242	2e-61
gb AAP76387.1 class III peroxidase [Gossypium hirsutum]	218	4e-54
gb AB077632.1 peroxidase [Medicago truncatula]	217	1e-53
dbj BAA82306.1 peroxidase [Nicotiana tabacum]	212	3e-52
ref XP_002278996.1 PREDICTED: hypothetical protein [Vitis vinif...	211	7e-52
gb AAX44001.2 putative secretory peroxidase [Catharanthus roseus]	209	2e-51
gb AAP42508.1 anionic peroxidase swpb3 [Ipomoea batatas]	209	2e-51
gb ABR23054.1 basic peroxidase swpb4 [Ipomoea batatas]	209	2e-51
gb ACU23245.1 unknown [Glycine max]	208	4e-51
gb ACM47317.1 peroxidase [Capsicum annuum]	205	4e-50
ref XP_002328991.1 predicted protein [Populus trichocarpa] >gi ...	204	5e-50
ref XP_002269918.1 PREDICTED: hypothetical protein [Vitis vinif...	204	5e-50
emb CAD67479.1 peroxidase [Asparagus officinalis]	203	2e-49
ref NP_196153.1 peroxidase, putative [Arabidopsis thaliana] >gi ...	202	3e-49
dbj BAF27413.2 Os11g0112400 [Oryza sativa Japonica Group]	201	8e-49
ref NP_001065568.1 Os11g0112400 [Oryza sativa (japonica cultiva...	201	8e-49
gb EAY79693.1 hypothetical protein OsI_34840 [Oryza sativa Indi...	199	2e-48
ref NP_001065971.1 Os12g0112000 [Oryza sativa (japonica cultiva...	199	2e-48
ref XP_002450132.1 hypothetical protein SORBIDRAFT_05g001000 [S...	199	3e-48
gb ACT35473.1 peroxidase 52 [Brassica rapa]	197	1e-47
ref XP_002441703.1 hypothetical protein SORBIDRAFT_08g000990 [S...	196	2e-47
ref XP_002450133.1 hypothetical protein SORBIDRAFT_05g001010 [S...	196	2e-47
gb ABV24960.2 putative secretory peroxidase [Catharanthus roseus]	196	2e-47
sp P00434.3 PERP7_BRARA RecName: Full=Peroxidase P7; AltName: Fu...	196	2e-47

gb AAD37423.1 AF149281_1 peroxidase 6 [Phaseolus vulgaris]	195	4e-47
ref XP_002520835.1 Peroxidase 52 precursor, putative [Ricinus c...	194	5e-47
ref XP_002319968.1 predicted protein [Populus trichocarpa] >gi ...	193	1e-46
ref NP_001151940.1 peroxidase 52 [Zea mays] >gi 195651251 gb AC...	191	5e-46
ref XP_002489046.1 hypothetical protein SORBIDRAFT_0246s002010 ...	190	1e-45
ref XP_002441702.1 hypothetical protein SORBIDRAFT_08g000980 [S...	190	1e-45
gb AAA96137.1 peroxidase [Stylosanthes humilis]	190	1e-45
gb AAL93151.1 AF485265_1 class III peroxidase [Gossypium hirsutum]	189	2e-45
emb CAD67478.1 peroxidase [Asparagus officinalis]	188	4e-45
gb AAR31108.1 peroxidase precursor [Quercus suber]	188	5e-45
gb AAR31106.1 peroxidase precursor [Quercus suber]	187	1e-44
ref NP_001131000.1 hypothetical protein LOC100192105 [Zea mays]...	186	1e-44
gb AAD43561.1 AF155124_1 bacterial-induced peroxidase precursor ...	185	3e-44
gb ACN33662.1 unknown [Zea mays]	184	6e-44
emb CBI25393.1 unnamed protein product [Vitis vinifera]	184	1e-43
gb ACU23223.1 unknown [Glycine max]	182	3e-43
emb CAA71491.1 peroxidase [Spinacia oleracea]	182	3e-43
gb ABK21858.1 unknown [Picea sitchensis]	180	1e-42
emb CAD67477.1 peroxidase [Asparagus officinalis]	179	2e-42
emb CAA62597.1 korean-radish isoperoxidase [Raphanus sativus]	179	2e-42
gb AC090366.1 peroxidase precursor [Triticum aestivum]	179	2e-42
gb ACN34270.1 unknown [Zea mays]	179	3e-42
gb ACU24215.1 unknown [Glycine max]	178	5e-42
gb AAB48184.1 peroxidase precursor [Linum usitatissimum]	178	5e-42
emb CBI27506.1 unnamed protein product [Vitis vinifera]	177	7e-42
ref XP_002274550.1 PREDICTED: hypothetical protein [Vitis vinif...	177	7e-42
gb ACN42168.1 peroxidase 1 [Sesuvium portulacastrum]	177	9e-42
ref XP_002269058.1 PREDICTED: hypothetical protein [Vitis vinif...	177	1e-41
emb CBI27505.1 unnamed protein product [Vitis vinifera]	177	1e-41
emb CAL25300.1 properoxidase [Picea abies]	176	2e-41
ref XP_002269145.1 PREDICTED: hypothetical protein [Vitis vinif...	175	3e-41
gb ACJ85500.1 unknown [Medicago truncatula]	174	8e-41
emb CAN80097.1 hypothetical protein [Vitis vinifera]	173	2e-40
emb CBI27503.1 unnamed protein product [Vitis vinifera]	172	2e-40
emb CBI27502.1 unnamed protein product [Vitis vinifera]	172	2e-40
ref XP_002269169.1 PREDICTED: hypothetical protein [Vitis vinif...	172	2e-40
gb AA013838.1 AF405326_1 peroxidase 2 [Lupinus albus]	172	2e-40
gb ABA96220.1 Cationic peroxidase 1 precursor, putative, expres...	172	2e-40
tpe CAH69378.1 TPA: class III peroxidase 136 precursor [Oryza s...	172	2e-40
ref XP_002269216.1 PREDICTED: hypothetical protein [Vitis vinif...	172	3e-40
emb CAH10839.1 peroxidase [Picea abies]	172	3e-40
ref XP_002266365.1 PREDICTED: hypothetical protein [Vitis vinif...	172	4e-40
ref NP_001106040.1 plasma membrane-bound peroxidase 2b precurs...	172	4e-40
gb EAY82023.1 hypothetical protein OsI_37207 [Oryza sativa Indi...	171	5e-40
gb ABA91154.1 Cationic peroxidase 1 precursor, putative, expres...	171	5e-40
ref NP_001065566.1 Os11g0112200 [Oryza sativa (japonica cultiva...	171	5e-40
gb EEE67815.1 hypothetical protein OsJ_25569 [Oryza sativa Japo...	171	6e-40
ref NP_001060628.1 Os07g0677200 [Oryza sativa (japonica cultiva...	171	6e-40
tpe CAH69353.1 TPA: class III peroxidase 111 precursor [Oryza s...	171	6e-40

emb	CBI27501.1	unnamed protein product [Vitis vinifera]	170	1e-39
ref	XP_002269266.1	PREDICTED: hypothetical protein [Vitis vinif...	170	1e-39
ref	XP_002509730.1	Lignin-forming anionic peroxidase precursor,...	170	1e-39
emb	CBI18066.1	unnamed protein product [Vitis vinifera]	170	1e-39
ref	XP_002268259.1	PREDICTED: hypothetical protein [Vitis vinif...	170	1e-39
ref	XP_002299006.1	predicted protein [Populus trichocarpa] >gi ...	170	1e-39
ref	XP_002333334.1	predicted protein [Populus trichocarpa] >gi ...	170	1e-39
ref	XP_002285723.1	PREDICTED: hypothetical protein [Vitis vinif...	170	1e-39
emb	CAA46916.1	peroxidase [Oryza sativa (japonica cultivar-grou...	170	1e-39
ref	XP_002319967.1	predicted protein [Populus trichocarpa] >gi ...	169	2e-39
gb	ABK24123.1	unknown [Picea sitchensis]	169	3e-39
gb	AAA20473.1	peroxidase [Cenchrus ciliaris]	169	3e-39
gb	ABK23423.1	unknown [Picea sitchensis]	168	4e-39
ref	NP_001060629.1	Os07g0677300 [Oryza sativa (japonica cultiva...	168	4e-39
gb	ACJ11762.1	class III peroxidase [Gossypium hirsutum]	168	5e-39
gb	ABK25962.1	unknown [Picea sitchensis]	168	5e-39
gb	EAZ05133.1	hypothetical protein OsI_27326 [Oryza sativa Indi...	168	5e-39
ref	NP_001046400.1	Os02g0240100 [Oryza sativa (japonica cultiva...	168	5e-39
gb	AAC49818.1	peroxidase [Oryza sativa Indica Group]	168	5e-39
dbj	BAD28869.1	putative bacterial-induced peroxidase precursor ...	168	5e-39
ref	XP_002274693.1	PREDICTED: hypothetical protein [Vitis vinif...	167	7e-39
gb	EEC82680.1	hypothetical protein OsI_27324 [Oryza sativa Indi...	167	7e-39
ref	NP_001060626.1	Os07g0676900 [Oryza sativa (japonica cultiva...	167	7e-39
emb	CAH10840.1	peroxidase [Picea abies]	167	7e-39
dbj	BAC83101.1	putative peroxidase precursor [Oryza sativa Japo...	167	7e-39
tpe	CAH69351.1	TPA: class III peroxidase 109 precursor [Oryza s...	167	7e-39
ref	XP_002451848.1	hypothetical protein SORBIDRAFT_04g008620 [S...	167	9e-39
gb	ACN33811.1	unknown [Zea mays]	167	9e-39
gb	ABR18139.1	unknown [Picea sitchensis]	167	9e-39
sp	A2YPX3.2	PER2_ORYSI RecName: Full=Peroxidase 2; Flags: Precu...	167	1e-38
ref	XP_002461208.1	hypothetical protein SORBIDRAFT_02g042850 [S...	166	2e-38
ref	XP_002320417.1	predicted protein [Populus trichocarpa] >gi ...	166	2e-38
ref	NP_001130666.1	hypothetical protein LOC100191769 [Zea mays]...	166	2e-38
ref	NP_200648.1	peroxidase, putative [Arabidopsis thaliana] >gi ...	166	2e-38
ref	XP_002338628.1	predicted protein [Populus trichocarpa] >gi ...	166	2e-38
ref	XP_002336344.1	predicted protein [Populus trichocarpa] >gi ...	166	2e-38
emb	CAA71493.1	peroxidase [Spinacia oleracea]	166	2e-38
gb	AAX53172.1	peroxidase [Populus alba x Populus tremula var. g...	166	2e-38
ref	XP_002509738.1	Lignin-forming anionic peroxidase precursor,...	166	3e-38
ref	XP_002453592.1	hypothetical protein SORBIDRAFT_04g008630 [S...	165	4e-38
gb	ACN60163.1	class III peroxidase [Tamarix hispida]	164	8e-38
ref	XP_002450134.1	hypothetical protein SORBIDRAFT_05g001030 [S...	163	1e-37
gb	AAC05277.1	peroxidase FLXPER4 [Linum usitatissimum]	163	1e-37
ref	XP_002269343.1	PREDICTED: hypothetical protein [Vitis vinif...	163	2e-37
gb	EAY85148.1	hypothetical protein OsI_06503 [Oryza sativa Indi...	163	2e-37
ref	XP_002269301.1	PREDICTED: hypothetical protein [Vitis vinif...	162	2e-37
gb	AAD37428.1	AF149278_1 peroxidase 3 precursor [Phaseolus vulga...	162	2e-37
ref	XP_002334243.1	predicted protein [Populus trichocarpa] >gi ...	162	3e-37
ref	XP_002438530.1	hypothetical protein SORBIDRAFT_10g021630 [S...	162	4e-37

ref	XP_002281755.1	PREDICTED: hypothetical protein [Vitis vinif...	162	4e-37
ref	XP_002437128.1	hypothetical protein SORBIDRAFT_10g021610 [S...	161	5e-37
ref	XP_002517727.1	Cationic peroxidase 1 precursor, putative [R...	160	9e-37
ref	NP_001057822.1	Os06g0547400 [Oryza sativa (japonica cultiva...	160	9e-37
ref	XP_002285724.1	PREDICTED: hypothetical protein [Vitis vinif...	160	1e-36
ref	XP_002521867.1	Lignin-forming anionic peroxidase precursor,...	160	1e-36
emb	CAH10841.1	peroxidase [Picea abies]	160	1e-36
gb	EEE67814.1	hypothetical protein OsJ_25568 [Oryza sativa Japo...	160	1e-36
tpe	CAH69352.1	TPA: class III peroxidase 110 precursor [Oryza s...	160	1e-36
ref	NP_001060627.1	Os07g0677100 [Oryza sativa (japonica cultiva...	160	1e-36
gb	ABD66594.1	peroxidase [Litchi chinensis]	159	2e-36
emb	CBI19219.1	unnamed protein product [Vitis vinifera]	159	2e-36
ref	XP_002334317.1	predicted protein [Populus trichocarpa] >gi ...	159	2e-36
emb	CAN73051.1	hypothetical protein [Vitis vinifera]	159	2e-36
gb	EEE67818.1	hypothetical protein OsJ_25573 [Oryza sativa Japo...	159	3e-36
gb	EEE56633.1	hypothetical protein OsJ_06032 [Oryza sativa Japo...	159	3e-36
ref	XP_002281731.1	PREDICTED: hypothetical protein [Vitis vinif...	159	3e-36
gb	EAZ05136.1	hypothetical protein OsI_27329 [Oryza sativa Indi...	159	3e-36
ref	NP_001046402.1	Os02g0240500 [Oryza sativa (japonica cultiva...	159	3e-36
ref	NP_001060630.1	Os07g0677400 [Oryza sativa (japonica cultiva...	159	3e-36
emb	CAA59487.1	peroxidase [Triticum aestivum] >gi 193074375 gb ...	159	3e-36
gb	AAB02554.1	cationic peroxidase [Stylosanthes humilis]	159	3e-36
sp	P16147.2	PERX_LUPPO RecName: Full=Peroxidase >gi 1345541 emb ...	159	3e-36
dbj	BAA77389.1	peroxidase 3 [Scutellaria baicalensis]	159	3e-36
ref	XP_002461207.1	hypothetical protein SORBIDRAFT_02g042840 [S...	158	4e-36
gb	EEC82684.1	hypothetical protein OsI_27330 [Oryza sativa Indi...	158	4e-36
gb	AAW52720.1	peroxidase 6 [Triticum monococcum]	158	4e-36
gb	AAQ55292.1	class III peroxidase GvPx2b [Vitis vinifera]	158	4e-36
gb	AAF65464.2	AF247700_1 peroxidase POC1 [Oryza sativa Indica Gr...	158	4e-36
ref	XP_002311022.1	predicted protein [Populus trichocarpa] >gi ...	158	6e-36
gb	EEE67819.1	hypothetical protein OsJ_25574 [Oryza sativa Japo...	158	6e-36
ref	NP_001147216.1	LOC100280824 [Zea mays] >gi 195608630 gb ACG...	158	6e-36
ref	NP_001060631.1	Os07g0677500 [Oryza sativa (japonica cultiva...	158	6e-36
pdb	1SCH A Chain A, Peanut Peroxidase >gi 1633131 pdb 1SCH B Cha...		158	6e-36
sp	P22195.2	PER1_ARAHY RecName: Full=Cationic peroxidase 1; AltN...	158	6e-36
gb	ACU22965.1	unknown [Glycine max]	157	7e-36
ref	XP_002311955.1	predicted protein [Populus trichocarpa] >gi ...	157	7e-36
gb	AAM61588.1	peroxidase [Arabidopsis thaliana]	157	7e-36
ref	NP_200647.1	peroxidase, putative [Arabidopsis thaliana] >gi...	157	7e-36
ref	XP_002460939.1	hypothetical protein SORBIDRAFT_02g037840 [S...	157	1e-35
ref	XP_002334018.1	predicted protein [Populus trichocarpa] >gi ...	157	1e-35
gb	EAY85151.1	hypothetical protein OsI_06506 [Oryza sativa Indi...	157	1e-35
emb	CAH10842.1	peroxidase [Picea abies]	157	1e-35
emb	CBI22007.1	unnamed protein product [Vitis vinifera]	157	1e-35
ref	XP_002283995.1	PREDICTED: hypothetical protein [Vitis vinif...	157	1e-35
emb	CAN81400.1	hypothetical protein [Vitis vinifera]	157	1e-35
emb	CAN63655.1	hypothetical protein [Vitis vinifera]	157	1e-35
gb	AAA20472.1	peroxidase [Cenchrus ciliaris]	156	2e-35
gb	ACF08096.1	class III peroxidase [Triticum aestivum]	156	2e-35

ref XP_002461211.1	hypothetical protein SORBIDRAFT_02g042870 [S...	156	2e-35
sp Q02200.1 PERX_NICSY	RecName: Full=Lignin-forming anionic pero...	156	2e-35
ref XP_002437129.1	hypothetical protein SORBIDRAFT_10g021620 [S...	155	3e-35
gb AAW52718.1	peroxidase 4 [Triticum monococcum]	155	3e-35
gb ACI03401.1	peroxidase 1 [Litchi chinensis]	155	4e-35
ref XP_002284007.1	PREDICTED: hypothetical protein [Vitis vinif...	155	4e-35
ref XP_002323054.1	predicted protein [Populus trichocarpa] >gi ...	155	4e-35
gb EEC82681.1	hypothetical protein OsI_27325 [Oryza sativa Indi...	155	4e-35
gb EAZ01280.1	hypothetical protein OsI_23303 [Oryza sativa Indi...	155	4e-35
gb AAV89058.1	class III peroxidase [Phelipanche ramosa]	155	4e-35
gb AAW52719.1	peroxidase 5 [Triticum monococcum]	155	4e-35
gb AAC49819.1	peroxidase [Oryza sativa Indica Group]	155	4e-35
dbj BAD97435.1	peroxidase [Pisum sativum]	155	4e-35
ref NP_001057821.1	Os06g0547100 [Oryza sativa (japonica cultiva...	155	4e-35
emb CBI19220.1	unnamed protein product [Vitis vinifera]	155	5e-35
gb ACN30737.1	unknown [Zea mays]	155	5e-35
gb ACG40622.1	peroxidase 2 precursor [Zea mays]	155	5e-35
emb CAN83972.1	hypothetical protein [Vitis vinifera]	154	6e-35
ref XP_002509737.1	Lignin-forming anionic peroxidase precursor,...	154	8e-35
ref XP_002268412.1	PREDICTED: hypothetical protein [Vitis vinif...	154	8e-35
dbj BAD36900.1	peroxidase [Lotus japonicus]	154	8e-35
gb ACN26131.1	unknown [Zea mays]	154	1e-34
gb ACF08094.1	class III peroxidase [Triticum aestivum]	153	1e-34
ref XP_002509733.1	Lignin-forming anionic peroxidase precursor,...	153	1e-34
ref XP_002319407.1	predicted protein [Populus trichocarpa] >gi ...	153	1e-34
dbj BAA77388.1	peroxidase 2 [Scutellaria baicalensis]	153	1e-34
gb ACF08095.1	class III peroxidase [Triticum aestivum]	153	2e-34
gb EAZ01279.1	hypothetical protein OsI_23302 [Oryza sativa Indi...	153	2e-34
ref NP_001046392.1	Os02g0236600 [Oryza sativa (japonica cultiva...	152	2e-34
gb EAZ37287.1	hypothetical protein OsJ_21626 [Oryza sativa Japo...	152	2e-34
gb ABD47726.1	peroxidase [Eucalyptus globulus subsp. globulus]	152	2e-34
ref NP_001057820.1	Os06g0546500 [Oryza sativa (japonica cultiva...	152	2e-34
ref XP_002438534.1	hypothetical protein SORBIDRAFT_10g021650 [S...	152	3e-34
ref NP_001140437.1	hypothetical protein LOC100272496 [Zea mays]...	152	3e-34
gb ACF82414.1	unknown [Zea mays]	152	3e-34
dbj BAF19735.2	Os06g0547100 [Oryza sativa Japonica Group]	152	4e-34
ref XP_002438533.1	hypothetical protein SORBIDRAFT_10g021640 [S...	151	5e-34
gb ACE00594.1	lignin biosynthetic peroxidase [Leucaena leucocep...	151	5e-34
emb CBI19221.1	unnamed protein product [Vitis vinifera]	151	7e-34
ref XP_002451846.1	hypothetical protein SORBIDRAFT_04g008590 [S...	151	7e-34
emb CAL25299.1	properoxidase [Picea abies]	151	7e-34
emb CBI15847.1	unnamed protein product [Vitis vinifera]	150	9e-34
ref XP_002451850.1	hypothetical protein SORBIDRAFT_04g008650 [S...	150	9e-34
ref XP_002276796.1	PREDICTED: hypothetical protein [Vitis vinif...	150	9e-34
gb EAZ22364.1	hypothetical protein OsJ_06022 [Oryza sativa Japo...	150	9e-34
gb EAY85141.1	hypothetical protein OsI_06496 [Oryza sativa Indi...	150	9e-34
tpe CAH69268.1	TPA: class III peroxidase 26 precursor [Oryza sa...	150	9e-34
ref NP_001046393.1	Os02g0236800 [Oryza sativa (japonica cultiva...	150	9e-34
gb ABK22680.1	unknown [Picea sitchensis]	150	1e-33

emb CAN61440.1	hypothetical protein [Vitis vinifera]	150	1e-33
gb AAC31550.1	peroxidase PXC2 precursor [Avena sativa]	150	1e-33
gb AAC31551.1	peroxidase PXC6 precursor [Avena sativa]	150	1e-33
emb CAA71492.1	peroxidase [Spinacia oleracea]	149	3e-33
ref NP_001054096.1	Os04g0651000 [Oryza sativa (japonica cultiva...	149	3e-33
ref XP_002308244.1	predicted protein [Populus trichocarpa] >gi ...	149	3e-33
emb CBI19222.1	unnamed protein product [Vitis vinifera]	148	4e-33
ref XP_002467656.1	hypothetical protein SORBIDRAFT_01g031740 [S...	148	4e-33
gb EEE61812.1	hypothetical protein OsJ_16433 [Oryza sativa Japo...	148	4e-33
gb EEC78144.1	hypothetical protein OsI_17703 [Oryza sativa Indi...	148	4e-33
emb CAJ86184.1	H0212B02.16 [Oryza sativa (indica cultivar-group...	148	4e-33
gb EAZ22372.1	hypothetical protein OsJ_06030 [Oryza sativa Japo...	148	4e-33
ref NP_001046401.1	Os02g0240300 [Oryza sativa (japonica cultiva...	148	4e-33
gb ABK21983.1	unknown [Picea sitchensis]	148	6e-33
ref XP_002461210.1	hypothetical protein SORBIDRAFT_02g042860 [S...	148	6e-33
emb CBI18065.1	unnamed protein product [Vitis vinifera]	147	8e-33
gb ACF08091.1	class III peroxidase [Triticum aestivum]	147	8e-33
gb EAY85149.1	hypothetical protein OsI_06504 [Oryza sativa Indi...	147	8e-33
gb AAW52716.1	peroxidase 2 [Triticum monococcum]	147	8e-33
gb AAA32972.1	peroxidase [Hordeum vulgare]	147	8e-33
emb CBI22008.1	unnamed protein product [Vitis vinifera]	147	1e-32
gb ACD70388.1	class III peroxidase [Triticum aestivum]	147	1e-32
gb ABF48527.1	cell wall peroxidase [Capsicum annuum] >gi 110348...	147	1e-32
gb ACF08092.1	class III peroxidase [Triticum aestivum]	146	2e-32
gb ACN37032.1	unknown [Zea mays]	146	2e-32
sp P27337.1	PER1_HORVU RecName: Full=Peroxidase 1; Flags: Precur...	146	2e-32
gb ABV24961.1	peroxidase [Catharanthus roseus]	146	2e-32
emb CAL25298.1	properoxidase [Picea abies]	146	2e-32
gb ACF08089.1	class III peroxidase [Triticum aestivum]	146	2e-32
ref XP_002467893.1	hypothetical protein SORBIDRAFT_01g036000 [S...	145	3e-32
gb EEC75221.1	hypothetical protein OsI_11488 [Oryza sativa Indi...	145	3e-32
gb ABF95843.1	Peroxidase 52 precursor, putative, expressed [Ory...	145	3e-32
tpe CAH69282.1	TPA: class III peroxidase 40 precursor [Oryza sa...	145	3e-32
ref XP_002531319.1	Peroxidase 2 precursor, putative [Ricinus co...	145	3e-32
ref NP_001147254.1	peroxidase 52 [Zea mays] >gi 195609124 gb AC...	145	3e-32
ref XP_002465306.1	hypothetical protein SORBIDRAFT_01g035990 [S...	145	4e-32
emb CAA39486.1	peroxidase [Triticum aestivum]	145	4e-32
gb ACR36744.1	unknown [Zea mays]	145	5e-32
ref XP_002323056.1	predicted protein [Populus trichocarpa] >gi ...	145	5e-32
gb ACF88317.1	unknown [Zea mays]	145	5e-32
gb AAZ42168.1	lignin peroxidase-like [Cucumis sativus]	145	5e-32
gb AAB48986.1	peroxidase precursor [Medicago truncatula]	144	6e-32
ref XP_002521852.1	Lignin-forming anionic peroxidase precursor,...	144	6e-32
ref NP_001106020.1	plasma membrane-bound peroxidase 3-2 precurs...	144	6e-32
ref XP_002521866.1	Lignin-forming anionic peroxidase precursor,...	144	8e-32
ref XP_002521851.1	Lignin-forming anionic peroxidase precursor,...	144	8e-32
gb EEC75545.1	hypothetical protein OsI_12177 [Oryza sativa Indi...	144	8e-32
ref NP_001050435.1	Os03g0434800 [Oryza sativa (japonica cultiva...	144	8e-32
gb AAU89207.1	peroxidase, putative [Oryza sativa Japonica Group...	144	8e-32

gb ACU21160.1	unknown [Glycine max]	144	8e-32
gb ACF08090.1	class III peroxidase [Triticum aestivum]	144	1e-31
emb CAA59484.1	pox1 [Triticum aestivum]	144	1e-31
gb AAW52715.1	peroxidase 1 [Triticum monococcum]	143	1e-31
ref NP_001042342.1	Os01g0205900 [Oryza sativa (japonica cultiva...]	143	1e-31
tpe CAH69245.1	TPA: class III peroxidase 2 precursor [Oryza sat...]	143	1e-31
gb ACU20213.1	unknown [Glycine max]	143	2e-31
gb EEC75220.1	hypothetical protein OsI_11487 [Oryza sativa Indi...]	143	2e-31
emb CAB99487.1	peroxidase [Hordeum vulgare subsp. vulgare]	143	2e-31
ref NP_001050059.1	Os03g0339300 [Oryza sativa (japonica cultiva...]	143	2e-31
emb CAD92857.1	peroxidase [Picea abies]	142	2e-31
gb ACF08086.1	class III peroxidase [Triticum aestivum]	142	2e-31
emb CAN80096.1	hypothetical protein [Vitis vinifera]	142	2e-31
gb AAB97854.1	ferriprotein porphyrin-containing peroxidase [Str...]	142	2e-31
emb CAC81821.1	peroxidase [Beta vulgaris]	142	3e-31
gb ACF08083.1	class III peroxidase [Triticum aestivum]	142	3e-31
ref NP_001106019.1	LOC100101533 precursor [Zea mays] >gi 221272...]	142	3e-31
ref NP_172906.1	anionic peroxidase, putative [Arabidopsis thali...]	142	3e-31
gb ACF70708.1	root peroxidase [Triticum aestivum]	142	4e-31
gb ACF70706.1	root peroxidase [Triticum aestivum]	142	4e-31
ref NP_001050434.1	Os03g0434500 [Oryza sativa (japonica cultiva...]	142	4e-31
gb AAU89205.1	peroxidase, putative [Oryza sativa Japonica Group...]	142	4e-31
gb EEC70139.1	hypothetical protein OsI_00829 [Oryza sativa Indi...]	141	5e-31
ref XP_002319422.1	predicted protein [Populus trichocarpa] >gi ...]	141	7e-31
gb ACF70710.1	root peroxidase [Triticum aestivum]	140	9e-31
gb ACF70709.1	root peroxidase [Triticum aestivum]	140	9e-31
gb ACF70705.1	root peroxidase [Triticum aestivum] >gi 194425605...]	140	9e-31
gb ACF70701.1	root peroxidase [Triticum aestivum]	140	9e-31
gb AAM76682.1	AF387866_1 peroxidase [Triticum aestivum]	140	9e-31
ref XP_002448660.1	hypothetical protein SORBIDRAFT_06g030940 [S...]	140	1e-30
gb AAM65211.1	peroxidase [Arabidopsis thaliana] >gi 42494611 gb...]	140	1e-30
gb ACF08087.1	class III peroxidase [Triticum aestivum]	140	1e-30
ref XP_002270068.1	PREDICTED: hypothetical protein [Vitis vinif...]	140	1e-30
ref XP_002323055.1	predicted protein [Populus trichocarpa] >gi ...]	140	1e-30
gb AAF43956.1	AC012188_33 Strong similarity to an Anionic Peroxi...]	140	1e-30
gb AAF63165.1	AC010657_1 T5E21.5 [Arabidopsis thaliana]	140	1e-30
ref NP_172907.1	anionic peroxidase, putative [Arabidopsis thali...]	140	1e-30
ref NP_001147443.1	peroxidase 52 [Zea mays] >gi 195611432 gb AC...]	140	2e-30
gb ACF08085.1	class III peroxidase [Aegilops ventricosa]	140	2e-30
gb ACF70703.1	root peroxidase [Triticum aestivum]	140	2e-30
gb ACT78791.1	putative peroxidase [Cucumis sativus]	139	2e-30
gb ACD87898.1	class III peroxidase [Aegilops ventricosa]	139	2e-30
gb ACF70707.1	root peroxidase [Triticum aestivum]	139	2e-30
emb CAN61439.1	hypothetical protein [Vitis vinifera]	139	2e-30
gb AAW52717.1	peroxidase 3 [Triticum monococcum] >gi 193074352 ...]	139	2e-30
sp Q05855.1	PER1_WHEAT RecName: Full=Peroxidase; AltName: Full=W...]	139	2e-30
gb ACF08084.1	class III peroxidase [Triticum aestivum]	139	3e-30
ref XP_002521868.1	Lignin-forming anionic peroxidase precursor,...]	139	3e-30
gb ACF70702.1	root peroxidase [Triticum aestivum]	139	3e-30

ref XP_002327780.1 predicted protein [Populus trichocarpa] >gi ...	139	4e-30
gb EEE54081.1 hypothetical protein OsJ_00811 [Oryza sativa Japo...	139	4e-30
gb AAQ55233.1 peroxidase [Orobanche cernua var. cumana]	138	5e-30
emb CAN80051.1 hypothetical protein [Vitis vinifera]	138	6e-30
ref XP_002521850.1 Peroxidase 30 precursor, putative [Ricinus c...	138	6e-30
gb ABR13314.1 putative peroxidase class III [Prunus dulcis]	138	6e-30
ref XP_002530724.1 Peroxidase 53 precursor, putative [Ricinus c...	137	8e-30
emb CAA59485.1 peroxidase [Triticum aestivum]	137	8e-30
gb ABK59095.1 peroxidase 1 [Sesbania rostrata]	137	1e-29
gb AAP42504.1 anionic peroxidase swpa5 [Ipomoea batatas]	137	1e-29
emb CBI27504.1 unnamed protein product [Vitis vinifera]	136	2e-29
emb CBI17443.1 unnamed protein product [Vitis vinifera]	136	2e-29
gb ACU23405.1 unknown [Glycine max]	136	2e-29
ref XP_002521512.1 Peroxidase 72 precursor, putative [Ricinus c...	136	2e-29
ref XP_002275309.1 PREDICTED: hypothetical protein [Vitis vinif...	136	2e-29
ref XP_002531320.1 Cationic peroxidase 1 precursor, putative [R...	136	2e-29
gb ABG49114.1 peroxidase [Dimocarpus longan]	136	2e-29
gb AAP42506.1 anionic peroxidase swpb1 [Ipomoea batatas]	136	2e-29
gb ACU24350.1 unknown [Glycine max]	135	3e-29
gb ACU21179.1 unknown [Glycine max]	135	3e-29
ref XP_002310274.1 predicted protein [Populus trichocarpa] >gi ...	135	3e-29
gb ABR17414.1 unknown [Picea sitchensis]	135	3e-29
gb AAB97853.1 ferriprotein porphyrin-containing peroxidase [Str...	135	3e-29
ref XP_002322726.1 predicted protein [Populus trichocarpa] >gi ...	135	5e-29
gb ACI22425.1 pericarp peroxidase 3 [Litchi chinensis]	134	7e-29
ref XP_002304885.1 predicted protein [Populus trichocarpa] >gi ...	134	9e-29
gb ABR17480.1 unknown [Picea sitchensis]	134	9e-29
gb ABZ80408.1 class III peroxidase [Casuarina glauca]	134	9e-29
gb AAK52085.1 peroxidase [Nicotiana tabacum]	134	9e-29
ref XP_002455406.1 hypothetical protein SORBIDRAFT_03g010250 [S...	134	1e-28
ref XP_002455405.1 hypothetical protein SORBIDRAFT_03g010240 [S...	134	1e-28
gb ACG44598.1 peroxidase 72 precursor [Zea mays]	134	1e-28
ref NP_001136736.1 hypothetical protein LOC100216875 [Zea mays]...	134	1e-28
ref NP_195361.1 peroxidase, putative [Arabidopsis thaliana] >gi ...	134	1e-28
gb ABR23055.1 basic peroxidase swpb5 [Ipomoea batatas]	133	1e-28
gb EAY85142.1 hypothetical protein OsI_06497 [Oryza sativa Indi...	133	1e-28
gb AAC49822.1 peroxidase [Oryza sativa Indica Group]	133	1e-28
gb ACU21377.1 unknown [Glycine max]	133	2e-28
ref NP_001148509.1 peroxidase 72 [Zea mays] >gi 195619908 gb AC...	132	3e-28
gb ABK26974.1 unknown [Picea sitchensis]	132	3e-28
gb AAF63025.1 AF244922_1 peroxidase prx13 precursor [Spinacia ol...	132	3e-28
gb AAM61616.1 putative peroxidase [Arabidopsis thaliana]	132	3e-28
ref NP_179407.1 peroxidase, putative [Arabidopsis thaliana] >gi ...	132	3e-28
emb CBI27500.1 unnamed protein product [Vitis vinifera]	132	3e-28
gb AAP42507.1 anionic peroxidase swpb2 [Ipomoea batatas]	132	3e-28
gb ABV26013.1 peroxidase [Musa acuminata]	132	4e-28
sp Q9LEH3.1 PER15_IPOBA RecName: Full=Peroxidase 15; Short=Prx15...	132	4e-28
ref XP_002300745.1 predicted protein [Populus trichocarpa] >gi ...	131	6e-28
gb ABC60345.1 putative peroxidase [Musa acuminata AAA Group]	131	6e-28

emb CAA66964.1	peroxidase [Arabidopsis thaliana] >gi 1429215 em...	131	6e-28
gb AAR15704.3	peroxidase [Brassica napus]	131	7e-28
gb AAM63684.1	peroxidase, putative [Arabidopsis thaliana]	131	7e-28
ref NP_175117.1	peroxidase, putative [Arabidopsis thaliana] >gi...	131	7e-28
ref NP_001050060.1	Os03g0339400 [Oryza sativa (japonica cultiva...	131	7e-28
sp Q4W1I8.1	PER1_ZINEL RecName: Full=Basic peroxidase; AltName: ...	131	7e-28
sp Q4W1I9.1	PER2_ZINEL RecName: Full=Basic peroxidase; AltName: ...	131	7e-28
gb AAF63026.1	AF244923_1 peroxidase prx14 precursor [Spinacia ol...	130	1e-27
ref NP_001046394.1	Os02g0237000 [Oryza sativa (japonica cultiva...	130	1e-27
dbj BAD27600.1	putative bacterial-induced peroxidase precursor ...	130	1e-27
ref NP_201440.1	peroxidase 72 (PER72) (P72) (PRXR8) [Arabidopsi...	130	1e-27
gb ABB45838.1	hypothetical protein [Thellungiella halophila]	130	2e-27
gb AAS00456.1	acid isoperoxidase [Brassica napus]	129	2e-27
emb CBI25854.1	unnamed protein product [Vitis vinifera]	129	3e-27
ref XP_002281048.1	PREDICTED: hypothetical protein [Vitis vinif...	129	3e-27
ref XP_002263033.1	PREDICTED: hypothetical protein [Vitis vinif...	129	4e-27
ref XP_002510443.1	Peroxidase 9 precursor, putative [Ricinus co...	129	4e-27
emb CBI15846.1	unnamed protein product [Vitis vinifera]	128	5e-27
ref XP_002457158.1	hypothetical protein SORBIDRAFT_03g002370 [S...	128	5e-27
ref XP_002455760.1	hypothetical protein SORBIDRAFT_03g024460 [S...	128	5e-27
ref XP_002438468.1	hypothetical protein SORBIDRAFT_10g020100 [S...	128	5e-27
gb ABI37011.1	peroxidase [Oryza sativa]	128	6e-27
emb CBI16459.1	unnamed protein product [Vitis vinifera]	127	8e-27
ref XP_002285642.1	PREDICTED: hypothetical protein [Vitis vinif...	127	8e-27
gb EAY73397.1	hypothetical protein OsI_01277 [Oryza sativa Indi...	127	8e-27
ref NP_001042657.1	Os01g0263300 [Oryza sativa (japonica cultiva...	127	8e-27
emb CBI16466.1	unnamed protein product [Vitis vinifera]	127	1e-26
ref XP_002463385.1	hypothetical protein SORBIDRAFT_02g042880 [S...	127	1e-26
ref XP_002285649.1	PREDICTED: hypothetical protein [Vitis vinif...	127	1e-26
gb ABI97032.1	peroxidase [Solanum tuberosum]	127	1e-26
gb AAU04440.2	secreted peroxidase [Phelipanche ramosa]	127	1e-26
dbj BAG55221.1	peroxidase 2 [Sesbania rostrata]	127	1e-26
ref NP_001151639.1	peroxidase 68 [Zea mays] >gi 195648284 gb AC...	127	1e-26
gb EAY74439.1	hypothetical protein OsI_02330 [Oryza sativa Indi...	127	1e-26
ref XP_002269425.1	PREDICTED: hypothetical protein [Vitis vinif...	126	2e-26
ref NP_001043276.1	Os01g0543100 [Oryza sativa (japonica cultiva...	126	2e-26
dbj BAB89258.1	putative peroxidase ATP6a [Oryza sativa Japonica...	126	2e-26
dbj BAA94962.1	peroxidase [Asparagus officinalis]	125	3e-26
ref NP_179406.1	peroxidase, putative [Arabidopsis thaliana] >gi...	125	5e-26
emb CBI27497.1	unnamed protein product [Vitis vinifera]	124	7e-26
gb AAM28296.1	peroxidase [Ananas comosus]	124	7e-26
gb ABD47725.1	peroxidase [Eucalyptus globulus subsp. globulus]	124	7e-26
gb ACF88307.1	unknown [Zea mays]	124	9e-26
gb EAZ22365.1	hypothetical protein OsJ_06023 [Oryza sativa Japo...	123	2e-25
ref NP_564948.1	peroxidase, putative [Arabidopsis thaliana] >gi...	122	3e-25
emb CAH69540.1	putative peroxidase [Zinnia elegans]	122	4e-25
ref XP_002312356.1	predicted protein [Populus trichocarpa] >gi ...	121	6e-25
dbj BAD43011.1	peroxidase ATP23a [Arabidopsis thaliana]	121	6e-25
emb CAH69535.1	putative peroxidase [Zinnia elegans]	121	8e-25

gb AA013837.1 AF403735_1	extensin peroxidase [Lupinus albus]	121	8e-25
ref XP_002457609.1	hypothetical protein SORBIDRAFT_03g010230 [S...	120	1e-24
emb CAB65334.1	SPI2 protein [Picea abies]	120	1e-24
gb ACF22712.1	peroxidase precursor [Brachypodium distachyon]	120	2e-24
ref XP_002315983.1	predicted protein [Populus trichocarpa] >gi ...	120	2e-24
emb CAM31942.1	hypothetical protein [Lolium perenne]	120	2e-24
ref XP_002438233.1	hypothetical protein SORBIDRAFT_10g010040 [S...	119	2e-24
ref XP_002451847.1	hypothetical protein SORBIDRAFT_04g008600 [S...	119	2e-24
ref NP_190668.2	electron carrier/ heme binding / peroxidase [Ar...	119	3e-24
emb CAB62621.1	peroxidase-like protein [Arabidopsis thaliana] >...	119	3e-24
gb EAZ05138.1	hypothetical protein OsI_27331 [Oryza sativa Indi...	119	3e-24
ref NP_001060632.1	Os07g0677600 [Oryza sativa (japonica cultiva...	119	3e-24
emb CBI27438.1	unnamed protein product [Vitis vinifera]	119	4e-24
ref XP_002270660.1	PREDICTED: hypothetical protein [Vitis vinif...	119	4e-24
emb CAN65777.1	hypothetical protein [Vitis vinifera]	119	4e-24
gb EAY89162.1	hypothetical protein OsI_10658 [Oryza sativa Indi...	118	5e-24
ref NP_001042655.1	Os01g0263000 [Oryza sativa (japonica cultiva...	118	5e-24
ref NP_001049480.1	Os03g0234500 [Oryza sativa (japonica cultiva...	118	5e-24
ref XP_002509732.1	Lignin-forming anionic peroxidase precursor,...	118	5e-24
ref XP_002509731.1	Lignin-forming anionic peroxidase precursor,...	118	5e-24
gb EEC70836.1	hypothetical protein OsI_02331 [Oryza sativa Indi...	118	6e-24
emb CAH55694.1	putative peroxidase [Lolium perenne]	117	8e-24
emb CAH55692.1	putative peroxidase [Festuca pratensis]	117	8e-24
ref NP_001057377.1	Os06g0274800 [Oryza sativa (japonica cultiva...	117	1e-23
ref XP_002509735.1	Lignin-forming anionic peroxidase precursor,...	117	1e-23
gb ACF08088.1	class III peroxidase [Aegilops ventricosa]	116	2e-23
gb ACG43658.1	hypothetical protein [Zea mays]	116	2e-23
gb ACF80021.1	unknown [Zea mays]	116	2e-23
ref NP_001130123.1	hypothetical protein LOC100191217 [Zea mays]...	116	2e-23
ref XP_002304020.1	predicted protein [Populus trichocarpa] >gi ...	115	3e-23
ref XP_002306459.1	predicted protein [Populus trichocarpa] >gi ...	115	4e-23
gb ABF95842.1	Peroxidase 2 precursor, putative, expressed [Oryz...	115	4e-23
emb CAA59486.1	peroxidase [Triticum aestivum]	115	5e-23
dbj BAA01992.1	peroxidase [Nicotiana tabacum]	114	9e-23
ref XP_002529736.1	Peroxidase 27 precursor, putative [Ricinus c...	114	1e-22
gb ACJ84393.1	unknown [Medicago truncatula]	114	1e-22
gb ACU23010.1	unknown [Glycine max]	113	2e-22
ref XP_001751508.1	predicted protein [Physcomitrella patens sub...	112	4e-22
gb AA013839.1 AF405327_1	peroxidase 1 [Lupinus albus]	112	5e-22
gb AAL58444.1 AF455807_1	anionic peroxidase [Nicotiana tomentososi...	112	5e-22
ref XP_002464560.1	hypothetical protein SORBIDRAFT_01g020830 [S...	111	6e-22
gb ACF70704.1	root peroxidase [Triticum aestivum]	111	6e-22
dbj BAD97439.1	peroxidase [Pisum sativum]	111	6e-22
gb AAQ67366.1	POD9 precursor [Gossypium hirsutum]	111	6e-22
ref XP_002309830.1	predicted protein [Populus trichocarpa] >gi ...	111	8e-22
gb EEE59027.1	hypothetical protein OsJ_10774 [Oryza sativa Japo...	111	8e-22
gb AAA34101.1	peroxidase [Nicotiana tabacum]	110	1e-21
sp P11965.1 PERX_TOBAC	RecName: Full=Lignin-forming anionic pero...	110	1e-21
emb CBI28955.1	unnamed protein product [Vitis vinifera]	110	1e-21

ref XP_002274157.1 PREDICTED: hypothetical protein [Vitis vinif...	110	1e-21
sp P15003.1 PER1_SOLLC RecName: Full=Suberization-associated ani...	110	1e-21
gb EAZ22371.1 hypothetical protein OsJ_06029 [Oryza sativa Japo...	110	2e-21
gb ABK22032.1 unknown [Picea sitchensis]	109	2e-21
ref XP_001783974.1 predicted protein [Physcomitrella patens sub...	108	4e-21
gb EAZ37178.1 hypothetical protein OsJ_21519 [Oryza sativa Japo...	108	4e-21
emb CBI28956.1 unnamed protein product [Vitis vinifera]	108	5e-21
gb ACJ11761.1 class III peroxidase [Gossypium hirsutum]	108	5e-21
dbj BAF08306.2 Os02g0236600 [Oryza sativa Japonica Group]	108	5e-21
gb EAZ01154.1 hypothetical protein OsI_23183 [Oryza sativa Indi...	108	5e-21
tpe CAH69331.1 TPA: class III peroxidase 89 precursor [Oryza sa...	108	5e-21
ref NP_001058379.1 Os06g0681600 [Oryza sativa (japonica cultiva...	108	5e-21
dbj BAD45811.1 putative bacterial-induced peroxidase precursor ...	108	5e-21
ref NP_001057744.1 Os06g0521200 [Oryza sativa (japonica cultiva...	108	5e-21
gb EAZ01158.1 hypothetical protein OsI_23186 [Oryza sativa Indi...	108	7e-21
gb ACJ11766.1 class III peroxidase [Gossypium hirsutum]	108	7e-21
ref XP_002443277.1 hypothetical protein SORBIDRAFT_08g016840 [S...	107	1e-20
emb CAA50597.1 peroxidase [Solanum lycopersicum]	107	1e-20
emb CAB67121.1 peroxidase [Solanum lycopersicum]	107	1e-20
ref XP_002465968.1 hypothetical protein SORBIDRAFT_01g049140 [S...	107	1e-20
gb ACU20287.1 unknown [Glycine max]	107	1e-20
gb EEE65802.1 hypothetical protein OsJ_21515 [Oryza sativa Japo...	107	1e-20
sp P12437.2 PERX_SOLTU RecName: Full=Suberization-associated ani...	107	1e-20
dbj BAD98313.2 peroxidase [Nicotiana tabacum]	107	1e-20
dbj BAD98314.1 peroxidase [Nicotiana tabacum]	107	1e-20
ref NP_001057745.1 Os06g0521400 [Oryza sativa (japonica cultiva...	107	1e-20
sp P15004.1 PER2_SOLLC RecName: Full=Suberization-associated ani...	107	1e-20
gb AAA33837.1 anionic peroxidase [Solanum tuberosum] >gi 228610...	107	1e-20
ref XP_002336172.1 predicted protein [Populus trichocarpa] >gi ...	107	1e-20
ref NP_001136722.1 hypothetical protein LOC100216859 [Zea mays]...	107	1e-20
ref XP_002516846.1 Peroxidase 24 precursor, putative [Ricinus c...	106	2e-20
ref NP_001140982.1 hypothetical protein LOC100273061 [Zea mays]...	106	2e-20
gb ABU63712.1 lignin peroxidase [Garcinia mangostana]	106	2e-20
emb CBI25927.1 unnamed protein product [Vitis vinifera]	106	3e-20

>gb|ACU17608.1| unknown [Glycine max]

Length = 320

Score = 249 bits (635), Expect = 2e-63

Identities = 120/124 (96%), Positives = 121/124 (97%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRARIYNETNI TAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV
Sbjct: 197 QARCTNFRARIYNETNIGTAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
QKKG LHSDQQLFNGGSTDSIVRGYSTNPGTF SDDFAAAMIKMGDISPLTGSNGE+RKNC
Sbjct: 257 QKKGFLHSDQQLFNGGSTDSIVRGYSTNPGTFPSDFAAAMIKMGDISPLTGSNGEVRKNC 316

Query: 2167 RRIN 2178
RRIN
Sbjct: 317 RRIN 320

Score = 213 bits (543), Expect = 1e-52
Identities = 118/165 (71%), Positives = 120/165 (72%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI
Sbjct: 70 VNGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSVQI+ G PTWNVKLG
Sbjct: 130 RDSVQILGG-----PTWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG
Sbjct: 147 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 191

Score = 145 bits (365), Expect = 5e-32
Identities = 70/71 (98%), Positives = 70/71 (98%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASL 750
MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKS VQSAISKETRMGASL
Sbjct: 1 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKS VQSAISKETRMGASL 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>gb|ACU17865.1| unknown [Glycine max]
Length = 320

Score = 242 bits (618), Expect = 2e-61
Identities = 117/124 (94%), Positives = 120/124 (96%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCTNFRARIYNE+NI+TAFAR RQQSCPRTSGSGDNNLA LDLQTPT FDNYYFKNLV
Sbjct: 197 QARCTNFRARIYNESNIDTAFARARQQSCPRTSGSGDNNLATLDLQTPTFEFDNYYFKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
QKKGLLHSDQQLFNGGSTDSIVRGYSTNP +FSSDFAAAMIKMGDISPLTGSNGEIRKNC
Sbjct: 257 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPSSFSSDFAAAMIKMGDISPLTGSNGEIRKNC 316

Query: 2167 RRIN 2178
RRIN
Sbjct: 317 RRIN 320

Score = 208 bits (530), Expect = 4e-51
Identities = 114/165 (69%), Positives = 119/165 (72%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTSSFTGEKNANPNRNSARG+EVIDNIKSAVEK CPGVVSCADILAI AA
Sbjct: 70 VNGCDGSILLDDTSSFTGEKNANPNRNSARGYEVIDNIKSAVEKACPGVVSCADILAI AA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDSVQI+ GGP+WNVK+G
Sbjct: 130 RDSVQIL-----GGPSWNVKVG 146

Query: 1511 RR DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RR DARTASQSAANNGIP PTSNLNQLISRFSALGLSTKDLVALSG
Sbjct: 147 RR DARTASQSAANNGIP PPTS NLNQLISRFSALGLSTKDLVALSG 191

Score = 138 bits (347), Expect = 6e-30
Identities = 68/71 (95%), Positives = 69/71 (97%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MASFCSRLTICLALFVLI GSANAQLSTNFYHSCPNLFS+VKSTVQSAISKETRMGASL
Sbjct: 1 MASFCSRLTICLALFVLILGSANAQLSTNFYHSCPNLFSTVKSTVQSAISKETRMGASL 60

Query: 751 LRLFFHDCFVN 783
LR FFHDCFVN
Sbjct: 61 LRPFFHDCFVN 71

>gb|AAP76387.1| class III peroxidase [Gossypium hirsutum]
Length = 330

Score = 218 bits (556), Expect = 4e-54
Identities = 100/124 (80%), Positives = 116/124 (93%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT+FRARIYNE+NI+ +FA+TRQ++CPRT+GSGDNNLAPLD+QTPTSFDN YFKNL+
Sbjct: 207 QARCTSFARIYNESNIDASFAQTRQRNCPRTTSGDNNLAPLDIQTPTSFDNNYFKNLI 266

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQQLFNGGSTDSIVRGY +P +F+SDF AAMIKMGDISPLTGS GEIRKNC

Sbjct: 267 SQRGLLHSDQQLFNGGSTDSIVRGYGNPSSFNDFVAAMIKMGDISPLTGSRGEIRKNC 326

Query: 2167 RRIN 2178

RR+N

Sbjct: 327 RRVN 330

Score = 196 bits (499), Expect = 1e-47
Identities = 107/169 (63%), Positives = 117/169 (69%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEKNANPNRNS+RGF+V+DNIKSAVE VCPGVVSCADILAIAA

Sbjct: 80 VNGCDGSVLLDDTSSFTGEKNANPNRNSRGFVDVVDNIKSAVENVCPGVVSCADILAIAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I LGGP W VKLG

Sbjct: 140 RDSVEI-----LGGPKWAVKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDAR+ASQSAANNGIP PTSNLN+L SRF+ALGLST+DLVALSG I

Sbjct: 157 RRDARSASQSAANNGIPPTSNLRLTSRFNALGLSTRDLVALSGAHTI 205

Score = 100 bits (248), Expect = 2e-18
Identities = 51/75 (68%), Positives = 58/75 (77%)
Frame = +1

Query: 559 SKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRM 738
+K+ AS S+ + L L V + GS NAQLSTNFY SCPNL S+VKSTV SAI+KE RM

Sbjct: 7 TKMGSASSFSKFCLTLLLLVDVLGSTNAQLSTNFYSKSCPPLLSTVKSTVTSAINKEARM 66

Query: 739 GASLLRRLFHDCFVN 783

GASLLRRLFHDCFVN

Sbjct: 67 GASLLRRLFHDCFVN 81

>gb|AB077632.1| peroxidase [Medicago truncatula]

Length = 322

Score = 217 bits (552), Expect = 1e-53
Identities = 104/124 (83%), Positives = 112/124 (90%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPSFDNYYFKNLV 1986
QARCTNFRARIYNETNI A A TRQ +CP+ SGSGDNNLAPLDLQTP+SFDN YFKNLV

Sbjct: 199 QARCTNFRARIYNETNINAAXASTRQSNCPKASGSGDNNLAPLDLQTPSSFDNYYFKNLV 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLLHSDQQLFNGGST+SIV GYST+P +FSSDFAAAMIKMG+I PLTGSNGEIRKNC

Sbjct: 259 QNKGLLHSDQQLFNGGSTNSIVSGYSTSPSSFSSDFAAAMIKMGNIKPLTGSNGEIRKNC 318

Query: 2167 RRIN 2178

R+ N

Sbjct: 319 RKTN 322

Score = 188 bits (478), Expect = 4e-45
Identities = 105/169 (62%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGEKNANPNRNSARGF+VIDNIK+AVE VCPGVVSCADILAIAA

Sbjct: 72 VNGCDGSILLDDTSSFTGEKNANPNRNSARGFDVIDNIKTAVENVCPGVVSCADILAIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
DSV I+ G PTWNVKLG

Sbjct: 132 ADSVAILGG-----PTWNVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDA+TASQSAAN IPAPTSNLN L S FSA+GLS+KDLV LSG I

Sbjct: 149 RRDAKTASQSAANTAIPAPTSNLNLTSMFSAVGLSSKDLVTLGSAHTI 197

Score = 100 bits (249), Expect = 1e-18
Identities = 52/68 (76%), Positives = 58/68 (85%), Gaps = 1/68 (1%)
Frame = +1

Query: 583 CSRLT-ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRL 759
CSRLT I L L VLI GSANAQLSTNFY +CP L ++VKST+Q+AISKE RMGAS+LRL

Sbjct: 6 CSRLTMISLVLSVLIIGSANAQLSTNFYSKTCPKLSTTVKSTLQTAISKEARMGASILRL 65

Query: 760 FFHDCFVN 783

FFHDCFVN

Sbjct: 66 FFHDCFVN 73

>dbj|BAA82306.1| peroxidase [Nicotiana tabacum]

Length = 321

Score = 212 bits (540), Expect = 3e-52
Identities = 102/125 (81%), Positives = 110/125 (88%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETN-IETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT+FRARIYNETN ++ +FARTRQ +CPR+SGSGDNNLAPLDLQTP FDN YFKNL
Sbjct: 197 QARCTSFARIYNETNLDASFARTRQSNCPRSSGSGDNNLAPLDLQTPNKFDNYYFKNL 256

Query: 1984 VQKKGLLHSDQQFLNFGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
V KKGLLHSDQQFLNFGGS DSIV YS NP +FSSDF AMIKMGDI PLTGSNGEIRKN
Sbjct: 257 VDKKGLLHSDQQFLNFGGSADSIIVTSYNNPSSSFSSDFVTAMIKMGDIRPLTGSNGEIRKN 316

Query: 2164 CRRIN 2178
CRR+N
Sbjct: 317 CRRLN 321

Score = 187 bits (476), Expect = 7e-45
Identities = 105/169 (62%), Positives = 113/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDTSSFTGEK A PN NSARGFEVIDNIKSAVEKVCPGVVSCADILA+ A
Sbjct: 70 VNGCDGSLLDDTSSFTGEKRAAPNVNSARGFEVIDNIKSAVEKVCPGVVSCADILAVTA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP WNVKLG
Sbjct: 130 RDSVVI-----LGGPNWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTASQSAAN+GIP TSNLN+LIS FSA+GLSTKD+VALSG I
Sbjct: 147 RRDSRTASQSAANSIPPATSNLRLISSFSAVGLSTKDMVALSGAHTI 195

Score = 91.3 bits (225), Expect = 8e-16
Identities = 46/71 (64%), Positives = 53/71 (74%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS + L L+ GS++AQLST FY SCP L+ +VKS VQSAI+KETRMGASL
Sbjct: 1 MASLKINAI VLFILVSLIGSSAQLSTGFYSKSCP KLYQTVKSAVQSAINKETRMGASL 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>ref|XP_002278996.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 321

Score = 211 bits (536), Expect = 7e-52
Identities = 98/124 (79%), Positives = 112/124 (90%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNETNI+ +FA+TRQ +CPR SGSGDNNLAPLDLQTPT+F+N Y+KNL+
Sbjct: 198 QARCTSFARIYNETNIDNSFAKTRQSNCPRASGSGDNNLAPLDLQTPTAFENNYKNI 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQLFNGGSTDSIVR YS + F++ F A MIKMGDISPLTGSNGEIRKNC
Sbjct: 258 KKKGLLHSDQQLFNGGSTDSIVRKYSNSRSNFNAHFVAGMIKMGDISPLTGSNGEIRKNC 317

Query: 2167 RRIN 2178
RR+N
Sbjct: 318 RRVN 321

Score = 184 bits (466), Expect = 1e-43
Identities = 100/169 (59%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSF GEKNA PN NS RGF+V+D+IKS VE CPGVVSCAD+LAIAA
Sbjct: 71 VNGCDGSVLLDDTSSFIGEKNAAPNANSVRGFVDDIKSKVETACPGVVSCADVLAIAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDSV I+ GGP+WNVKLG
Sbjct: 131 RDSVVIL-----GGPSWNVKLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IP PTSNLNQLISRF ALGLST+DLVAL+G+ I
Sbjct: 148 RRDARTASQAANNSIPPPTSNLNQLISRFAQALGLSTRDLVALAGSHTI 196

Score = 90.1 bits (222), Expect = 2e-15
Identities = 46/72 (63%), Positives = 56/72 (77%), Gaps = 1/72 (1%)
Frame = +1

Query: 571 MASFCSRLTIC-LALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGAS 747
MAS S + I +AL +L GS+ AQLST++Y SCP LF +VKS V+SA++KE RMGAS
Sbjct: 1 MASPSSYMAIVTMALLILFLGSSTAQLSTDYYSQSCPFLFPTVKS AVKSAVAKEARMGAS 60

Query: 748 LLRLFFHDCFVN 783

LLRFFHDCFVN
Sbjct: 61 LLRFFHDCFVN 72

>gb|AAx44001.2| putative secretory peroxidase [Catharanthus roseus]
Length = 318

Score = 209 bits (533), Expect = 2e-51
Identities = 101/125 (80%), Positives = 113/125 (90%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETN-IETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCTNFRARIYNETN ++ A A+TR+ +CPR SGS DNNLAPLDLQTP +FDN Y+KNL
Sbjct: 194 QARCTNFRARIYNETNLDAAALQTRRSNCPRPSGSRDNNLAPLDLQTPRAFDDNNYYKNL 253

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
V ++GLLHSDQQLFNGGSTDSIVR YS NP +F+SDFAAAMIKMGDISPLTGSNG+IRKN
Sbjct: 254 VNRRLHSDQQLFNGGSTDSIVRSYSGNPASFASDFAAAMIKMGDISPLTGSNGQIRKN 313

Query: 2164 CRRIN 2178
CRRIN
Sbjct: 314 CRRIN 318

Score = 191 bits (484), Expect = 8e-46
Identities = 106/169 (62%), Positives = 114/169 (67%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGEK A PN NSARGFEV+DNKSAVE VCPGVVSCADILAIAA
Sbjct: 67 VNGCDGSILLDDTSSFTGEKRAAPNFSARGFEVVDNIKSAVENVCPGVVSCADILAIAA 126

Query: 1331 RDSVQIVSGQTTNKNLNL*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSVQI+ GGP+WNVKLG
Sbjct: 127 RDSVQIL-----GGPSWNVKLG 143

Query: 1511 RRDARTASQAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDA TASQ+AANN IP PTSNLN L+SRF+ALGLST DLVALSG+ I
Sbjct: 144 RRDATTASQAANNSIPPPTSNLNLVSRFNALGLSTNDLVALSGSHTI 192

Score = 85.1 bits (209), Expect = 6e-14
Identities = 42/61 (68%), Positives = 52/61 (85%), Gaps = 1/61 (1%)
Frame = +1

Query: 604 LALFVL-IWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
L +F+L + GS++AQLST++Y SCPN+F++VKS V SAI KE RMGASLLRFFHDCFV

Sbjct: 8 LGIFLLFLIGSSSAQLSTDYYSKSCPNTVKSQVHSAILKEARMGASLLRRLFHDCFV 67

Query: 781 N 783
N

Sbjct: 68 N 68

>gb|AAP42508.1| anionic peroxidase swpb3 [Ipomoea batatas]
Length = 320

Score = 209 bits (533), Expect = 2e-51
Identities = 100/124 (80%), Positives = 110/124 (88%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRARIYNE+NI+++FA+++R+ +CPR SGSGDNNLAPLDLQTP FDN Y+ NLV
Sbjct: 197 QARCTNFRARIYNESNIDSSFAQSRKGNCPRASGSGDNNLAPLDLQTPIKFDNYYVNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS VRGYSTNP F SFAAAMIKMGDI PLTG+NGEIRKNC
Sbjct: 257 NKKGLLHSDQQLFNGVSTDSTVRGYSTNPSKFKSDFAAAMIKMGDIKPLTGNGEIRKNC 316

Query: 2167 RRIN 2178
RR N

Sbjct: 317 RRRN 320

Score = 184 bits (467), Expect = 7e-44
Identities = 103/169 (60%), Positives = 113/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTSSFTGEK A PN SARGFEVID I KSAVEKVC PGVVSCADILAI A+
Sbjct: 70 VNGCDGSILLDDTSSFTGEKRAAPNFQSARGFEVIDQIKSAVEKVC PGVVSCADILAI AS 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS ++ LGGP+WNVKLG
Sbjct: 130 RDS-----TVTLGGPSWNVKLG 146

Query: 1511 RRDARTASQAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IPAPTSNLN+LIS FSA+GLST D+V LSG+ I
Sbjct: 147 RRDARTASQAAANNSIPAPTSNLNRLISSFSAVGLSTNDMVVLSGSHTI 195

Score = 82.8 bits (203), Expect = 3e-13
Identities = 42/71 (59%), Positives = 48/71 (67%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA LT L +++ G +AQLS FY SCP LF +V S V+SAI KE RMGASL
Sbjct: 1 MAVSVKALTAVLLCVLVLVGGCSAQLSPGFYSKSCPFLQTVNSVVRSAIQKEARMGASL 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>gb|ABR23054.1| basic peroxidase swpb4 [Ipomoea batatas]
Length = 320

Score = 209 bits (532), Expect = 2e-51
Identities = 100/124 (80%), Positives = 110/124 (88%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRARIYNE+NI+++FA+++R+ +CPR SGSGDNNLAPLDLQTP FDN Y+ NLV
Sbjct: 197 QARCTNFRARIYNESNIDSSFAQSRKGNCPRASGSGDNNLAPLDLQTPIKFDNYYVNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS VRGYSTNP F SDFAAAMIKMGDI PLTG+NGEIRKNC
Sbjct: 257 NKKGLLHSDQQLFNGVSTDSTVRGYSTNPSKFRSDFAAAMIKMGDIKPLTGNGEIRKNC 316

Query: 2167 RRIN 2178
RR N
Sbjct: 317 RRRN 320

Score = 182 bits (462), Expect = 3e-43
Identities = 102/169 (60%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGEK A PN SARGFEVID IKSAVEKVCPGVVSCADILAIA+
Sbjct: 70 VNGCDGSILLDDTSSFTGEKRAAPNFQSARGFEVIDQIKSAVEKVCPGVVSCADILAIAS 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS ++ LGGP+WNVKLG
Sbjct: 130 RDS-----TVTLGGPSWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDAR ASQ+AANN IPAPTSNLN+LIS FSA+GLST D+V LSG+ I
Sbjct: 147 RRDARAASQAAANNSIPAPTSNLNRLISSFSAVGLSTNDMVVLSGSHTI 195

Score = 80.5 bits (197), Expect = 1e-12
Identities = 40/62 (64%), Positives = 46/62 (74%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPNIFFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777
+ L + VL+ G +AQLS FY SCP LF +V S V+SAI KE RMGASLLRLLFFHDCF
Sbjct: 11 VLLCVLVLV-GGCSAQLSPGFYSKSCPFLFQTVNSVVRSAIQKEARMGASLLRLLFFHDCF 69

Query: 778 VN 783
VN
Sbjct: 70 VN 71

>gb|ACU23245.1| unknown [Glycine max]
Length = 326

Score = 208 bits (530), Expect = 4e-51
Identities = 95/124 (76%), Positives = 111/124 (89%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FRARIYNE+NI+++FAR RQ CPRTSGSGDNNLAP+D TPT FDN+YFKNL+
Sbjct: 203 QARCTTFRARIYNESNIDSSFARMRQSRCPRTSGSGDNNLAPIDFATPTFFDNHYFKNLI 262

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
QKKG +HSDQ+LFNGGSTDS+V YSTNP +F +DF+AAMI+MGDISPLTGS GEIR+NC
Sbjct: 263 QKKGFIHSDQELFNGGSTDSLVTYSTNPASFFADFSAAAMIRMGDISPLTGSERGEIRENC 322

Query: 2167 RRIN 2178
RR+N
Sbjct: 323 RRVN 326

Score = 200 bits (509), Expect = 1e-48
Identities = 111/165 (67%), Positives = 116/165 (70%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTSSFTGEKNA PNRNSARGFEVID I KSAVEKVC PGVVSCADILAI AA
Sbjct: 76 VNGCDGSILLDDTSSFTGEKNAGPNRNSARGFEVIDQIKSAVEKVC PGVVSCADILAI AA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDSV+I L GPTW+VKLG
Sbjct: 136 RDSVEI-----LRGPTWDVKLG 152

Query: 1511 RR DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+RTASQSAANNGIP PTSNLNQLISRF+ LGLSTKDLVALSG
Sbjct: 153 RRDSRTASQSAANNGIPRPTSNLNQLISRFTLGLSTKDLVALSG 197

Score = 100 bits (248), Expect = 2e-18
Identities = 53/77 (68%), Positives = 57/77 (74%), Gaps = 6/77 (7%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGS-----ANAQLSTNFYHSCPNLFSSVKSTVQSAISKET 732
MAS CS I LAL VL+ G+ AN L TNFY SCF LF +VK TV+SAISKET
Sbjct: 1 MASSCSSMITLALLVLVLTNTSSANANPTLHTNFYSSCPKLFDTVKRTVESAIKSKET 60

Query: 733 RMGASLLRLFFHDCFVN 783
RMGASLLRLFFHDCFVN
Sbjct: 61 RMGASLLRLFFHDCFVN 77

>gb|ACM47317.1| peroxidase [Capsicum annuum]
Length = 324

Score = 205 bits (521), Expect = 4e-50
Identities = 100/125 (80%), Positives = 108/125 (86%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETN-IETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNL 1983
QARCT+FRARIYNETN I+++FA TRQ++CPR SGSGDNNLAPLDLQTPT FDN YFKNL
Sbjct: 200 QARCTSFARIYNETNNIDSSFATTRQRNCPRNSGSGDNNLAPLDLQTPTKFDNNYFKNL 259

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKN 2163
V K+GLLHSDQQLFNGGS DSIV YS NP +FSSDF AMIKMGD PLTGSNGEIRKN
Sbjct: 260 VSKRGLLHSDQQLFNGGSADSI VTSYSNNPSSFSDFVTAMIKMGDNRPLTGSNGEIRKN 319

Query: 2164 CRRIN 2178
CR N
Sbjct: 320 CRTRN 324

Score = 184 bits (468), Expect = 6e-44
Identities = 104/169 (61%), Positives = 109/169 (64%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEK A PN NS RGFEVIDNIKSAVEK CPGVVSCADILAI A
Sbjct: 73 VNGCDGSLLDDTSSFTGEKRAAPNVNSVRGFEVIDNIKSAVEKACPGVVSCADILAITA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP WNVKLG
Sbjct: 133 RDSVVI-----LGGPNWNVKLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ AAN+ IP PTSNLNQLIS FSA+GLST D+VALSG I
Sbjct: 150 RRDARTASQGAANSSIPPPTSNLNQLISSFSAVGLSTTDMVALSGAHTI 198

Score = 89.4 bits (220), Expect = 3e-15
Identities = 44/60 (73%), Positives = 51/60 (85%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
L + L+ S++AQLSTNFY SCP LF +VKSTVQSAI++ETRMGASLLRLLFFHDCFVN
Sbjct: 15 LVVVLLIVSSSAQLSTNFYSKSCP KLFQTVKSTVQSAINRETRMGASLLRLLFFHDCFVN 74

>ref|XP_002328991.1| predicted protein [Populus trichocarpa]
gb|EEE77576.1| predicted protein [Populus trichocarpa]
Length = 322

Score = 204 bits (520), Expect = 5e-50
Identities = 96/124 (77%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCTNFRARIYNET I+++ A+TR+ +CPRTSGSGDNNLAPLDLQTPT F+N Y+KNL+
Sbjct: 199 QARCTNFRARIYNETTIDSSLAQTRRSNCPRTSGSGDNNLAPLDLQTPTRFENNYK NLI 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQQLFNGGSTDSIV YS+N TF SDF A MIKMGDI PLTGS GEIR NC
Sbjct: 259 NRRGLLHSDQQLFNGGSTDSIVSTYSSNENTFRSDFVAGMIKMGDIRPLTGSRGEIRNNC 318

Query: 2167 RRIN 2178
RRIN
Sbjct: 319 RRIN 322

Score = 194 bits (493), Expect = 7e-47
Identities = 107/169 (63%), Positives = 116/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEK VCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEKNA PN+NSARGFEVIDNIKSAVEK CPGVVSCADILAIAA
Sbjct: 72 VNGCDGSLLDDTSSFTGEKNAAPKNNSARGFEVIDNIKSAVEKACPGVVSCADILAIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I LGGP W+VKLG
Sbjct: 132 RDSTVI-----LGGPEWDVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IP PTSNLNQLISRF+ALGLST+D+VALSG+ I
Sbjct: 149 RRDARTASQAAANNSIPRPTSNLNQLISRFNALGLSTRDMVALSGSHTI 197

Score = 87.8 bits (216), Expect = 9e-15
Identities = 43/70 (61%), Positives = 52/70 (74%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANAQLSTNFYHSCP NFLSSVKSTVQSAISKETRMGASLL 753
+SF + L +L GS+NAQLS +FY SCP+L S+VK VQSAI+KE RMGAS+L
Sbjct: 4 SSFSKAIIVTLAILVMLSMGSSNAQLSIDFYKSCP HLLSTVKPVVQSAINKEARMGASIL 63

Query: 754 RLFFHDCFVN 783
RLFFHDCFVN
Sbjct: 64 RLFFHDCFVN 73

>ref|XP_002269918.1| PREDICTED: hypothetical protein [Vitis vinifera]
sp|A7NY33.1|PER4_VITVI RecName: Full=Peroxidase 4; Flags: Precursor
emb|CBI15844.1| unnamed protein product [Vitis vinifera]
Length = 321

Score = 204 bits (520), Expect = 5e-50
Identities = 94/124 (75%), Positives = 110/124 (88%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCT+FRARIYNETNI+++FA+TRQ SCP SGSGDNNLAPLDLQTPT+FDNYY+KNL+
Sbjct: 198 QARCTSF RARIYNETNIDSSFAKTRQASCPSASGSGDNNLAPLDLQTPTTFDNYYYKNLI 257

Query: 1987 QKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L+NGGSTDS V+ Y NP TF+SDF A MIKMGDI+PLTGS GEIRK+C
Sbjct: 258 NQKGLLHSDQVLYNGGSTDSTVKTYVNNPKTFTSDFVAGMIKMGDITPLTGSEGEIRKSC 317

Query: 2167 RRIN 2178
++N
Sbjct: 318 GKVN 321

Score = 165 bits (417), Expect = 5e-38
Identities = 92/169 (54%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEK VCPGVVSCADILAI 1330
+ GCD S+LLDDTSSFTGE+ A PN+NS RG VIDNIKS VE VCPGVVSCADI+AIAA
Sbjct: 71 VNGCDASVLLDDTSSFTGEQTAVPNKNSIRGLNVIDNIKSQVESVCPGVVSCADIIAIAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W+VKLG
Sbjct: 131 RDSVVI-----LGGPDWDVKLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS S ANN IP PTS+L+ LIS+F A GLST+D+VALSG I
Sbjct: 148 RRDSKTASLSGANNIPPTSSLSNLISKFQAQGLSTRDMVALSGAHTI 196

Score = 90.5 bits (223), Expect = 1e-15
Identities = 44/70 (62%), Positives = 54/70 (77%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPFLFSSVKSTVQSAISKETRMGASLL 753
+S S + + L + L GS++AQLSTNFY +CP +F +VKS VQSA+SKE RMGASLL
Sbjct: 3 SSSFSIVVVALGVLALFAGSSSAQLSTNFYSKTCPKVFDTVKSGVQSAVSKERRMGASLL 62

Query: 754 RLFFHDCFVN 783
RLFFHDCFVN
Sbjct: 63 RLFFHDCFVN 72

>emb|CAD67479.1| peroxidase [Asparagus officinalis]
Length = 320

Score = 203 bits (516), Expect = 2e-49
Identities = 95/124 (76%), Positives = 109/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA +YN+T+I+ FA+TRQ +CP TSGSGDNNLAPLDLQTP +FDN YFKNLV
Sbjct: 197 QARCTNFRAHVYNDTIDATFAKTRQSNCPSTSGSGDNNLAPLDLQTPVAFDNNYFKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQ+F+GGST+S V YST+P T+SSDF AAMIKMGDISPLTG +GEIRKNC
Sbjct: 257 SKKGLLHSDQQVFGGSTNSQVSTYSTPSTWSSDFVAAMIKMGDISPLTGKSGEIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKTN 320

Score = 169 bits (427), Expect = 3e-39
Identities = 92/169 (54%), Positives = 107/169 (63%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGS+LLDDTSSFTGEKNA PN+ S RGF+VID IK+AVE+ CPGVVSCADILA+ A
Sbjct: 70 VNGCDGSLLLDDTSSFTGEKNAIPNKGSVRGFDVIDKIKTAVEQACPGVVSCADILAVTA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV ++ G PTWNVKLG
Sbjct: 130 RDSVLLGG-----PTWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTASQS ANN IP PTS+L+ LIS+FSA GLS K++VAL G I
Sbjct: 147 RRDSRTASQSGANNIPPTSSLSNLISKFSAQGLSAKEMVALVGAHTI 195

Score = 80.1 bits (196), Expect = 2e-12
Identities = 42/73 (57%), Positives = 52/73 (71%)
Frame = +1

Query: 565 LTMASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
+ +SF S I L + + +++AQL+ NFY SCP LF ++KS VQSAIS E RMGA
Sbjct: 1 MASSSFKSLAPISLVSYV--RASSAQLTPNFYSSCPTLFPPTIKSVVQSAISSEKRMGA 58

Query: 745 SLLRLLFFHDCFVN 783
SLLRLLFFHDCFVN
Sbjct: 59 SLLRLLFFHDCFVN 71

>ref|NP_196153.1| peroxidase, putative [Arabidopsis thaliana]
sp|Q9FLC0.1|PER52_ARATH RecName: Full=Peroxidase 52; Short=Atperox P52; AltName: Full=ATP49;
Flags: Precursor
dbj|BAB09977.1| peroxidase [Arabidopsis thaliana]
gb|AAL38746.1| putative peroxidase [Arabidopsis thaliana]
Length = 324

Score = 202 bits (513), Expect = 3e-49
Identities = 97/124 (78%), Positives = 107/124 (86%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RCTNFRARIYNETNI AFA TRQ++CPR SGSGD NLAPLD+ T SFDN YFKNL+
Sbjct: 201 QSRCTNFRARIYNETNINAAFATTRQRTCPRASGSGDGNLAPLDVTTAASFDNYYFKNLM 260

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ LFNNGGSTDSIVRGYS NP +F+SDF AAMIKMGDISPLTGS+GEIRK C
Sbjct: 261 TQRGLLHSDQVLFNNGGSTDSIVRGYSNPNSSFNDFTAAMIKMGDISPLTGSNGEIRKVC 320

Query: 2167 RRIN 2178
R N
Sbjct: 321 GRN 324

Score = 187 bits (476), Expect = 7e-45
Identities = 104/169 (61%), Positives = 115/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGE+NA PNRNSARGF VIDNIKSAVEK CPGVVSCADILAI
Sbjct: 74 VNGCDGSILLDDTSSFTGEQNAAPNRNSARGFNVIDNIKSAVEKACPGVVSCADILAI 133

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 134 RDSV-----VALGGPNWNVKVG 150

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AAAN+ IPAPTS+L+QLIS FSA+GLST+D+VALSG I
Sbjct: 151 RRDARTASQAANSNIPAPTSLSQLISSFSAVGLSTRDMVALSGAHTI 199

Score = 78.2 bits (191), Expect = 7e-12
Identities = 38/66 (57%), Positives = 50/66 (75%), Gaps = 4/66 (6%)
Frame = +1

Query: 598 ICLALFVLIWGSAN----AQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLF 765
+ L + +L+ G N AQL+TNFY SCPNL S+V++ V+SA++ E RMGAS+LRLFF
Sbjct: 10 LVLVVTLLLQGDNNYVVEAQLTTNFYSTPCPNLLSTVQTAVKSAVNSEARMGASILRRLF 69

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 70 HDCFVN 75

>dbj|BAF27413.2| Os11g0112400 [Oryza sativa Japonica Group]
Length = 136

Score = 201 bits (510), Expect = 8e-49
Identities = 93/124 (75%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA +RQ CPR+SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 13 QARCTNFRAHIYNETNIDSGFAMSRQSGCPRSSGSGDNNLAPLDLQTPTVFENYYKNLV 72

Query: 1987 QKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 73 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMKMGDITPLTGSNGEIRKNC 132

Query: 2167 RRIN 2178
RRIN
Sbjct: 133 RRIN 136

>ref|NP_001065568.1| Os11g0112400 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69372.1| TPA: class III peroxidase 130 precursor [Oryza sativa (japonica
cultivar-group)]
gb|ABA91159.1| Peroxidase 52 precursor, putative, expressed [Oryza sativa (japonica
cultivar-group)]
gb|EAZ00524.1| hypothetical protein OsI_22542 [Oryza sativa Indica Group]
gb|EAZ17186.1| hypothetical protein OsJ_32693 [Oryza sativa Japonica Group]
dbj|BAH01350.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 324

Score = 201 bits (510), Expect = 8e-49
Identities = 93/124 (75%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA +RQ CPR+SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 201 QARCTNFRAHIYNETNIDSGFAMSRQSGCPRSSGSGDNNLAPLDLQTPTVFENNYKLV 260

Query: 1987 QKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 261 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMKMGDITPLTGSNGEIRKNC 320

Query: 2167 RRIN 2178
RRIN
Sbjct: 321 RRIN 324

Score = 166 bits (419), Expect = 3e-38
Identities = 94/169 (55%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT+SFTGEK ANPN S RGFEVID IKSAVE +CPGVVSCADILAI AA
Sbjct: 74 VQGCDASLLDDTASFTGEKMANPNNGSVRGFEVIDAIKSAVETICPGVVSCADILAI AA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 134 RDSVAI-----LGGPSWDVKVG 150

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG+ I
Sbjct: 151 RRDSRTASLSGANNNIPPTSGLANLTSLFAAQGLSQKDMVALSGSHTI 199

Score = 75.5 bits (184), Expect = 5e-11
Identities = 35/75 (46%), Positives = 56/75 (74%)
Frame = +1

Query: 556 LSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETR 735
+++ T ++ CS L + + + + + G ++AQLS +FY +SCP +F +VK +QSAI+ E R
Sbjct: 1 MAQPTSSARCS-LVVMVVVVLAVAGGSSAQLSPSFYSYSCPGVFDVAVKCGMQSAIANEKR 59

Query: 736 MGASLLRLFFHDCFV 780
+GAS++RLFFHDCFV
Sbjct: 60 IGASIVRLFFHDCFV 74

>gb|EAY79693.1| hypothetical protein OsI_34840 [Oryza sativa Indica Group]
Length = 329

Score = 199 bits (507), Expect = 2e-48
Identities = 93/124 (75%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA RQ CPR SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 206 QARCTNFRAHIYNETNIDSGFAMRRQSGCPRNSGSGDNNLAPLDLQTPTVFENNYKLV 265

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 266 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMKMGDITPLTGSNGEIRKNC 325

Query: 2167 RRIN 2178
RRIN
Sbjct: 326 RRIN 329

Score = 166 bits (421), Expect = 2e-38
Identities = 94/169 (55%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDT+SFTGEK ANPN S RGFEVID IKSVE +CPGVVSCADILAIAA
Sbjct: 79 VQGCDASLLDDTASFTGEKTANPNNGSVRGFEVIDAIKSAVETICPGVVSCADILAIAA 138

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 139 RDSVAI-----LGGPSWDVKVG 155

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG+ I
Sbjct: 156 RRDSRTASLSGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGSHTI 204

Score = 70.1 bits (170), Expect = 2e-09
Identities = 31/61 (50%), Positives = 47/61 (77%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCF 777
+ + + + G + AQLS +FY SCP +F++VK +QSAI++E R+GAS++RLFFHDCF
Sbjct: 19 VVVVVVLAVAGGSWAQLSPSFYSFSCPGVFNVAVKRGMQSAIAREKRIGASIVRLFFHDCF 78

Query: 778 V 780
V
Sbjct: 79 V 79

>ref|NP_001065971.1| Os12g0112000 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69377.1| TPA: class III peroxidase 135 precursor [Oryza sativa (japonica
cultivar-group)]
gb|ABA96259.1| Peroxidase 52 precursor, putative, expressed [Oryza sativa (japonica
cultivar-group)]
dbj|BAF28990.1| Os12g0112000 [Oryza sativa Japonica Group]
gb|EAZ19424.1| hypothetical protein OsJ_34981 [Oryza sativa Japonica Group]
dbj|BAG91443.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 327

Score = 199 bits (507), Expect = 2e-48
Identities = 93/124 (75%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA RQ CPR SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 204 QARCTNFRAHIYNETNIDSGFAMRRQSGCPRNSGSGDNNLAPLDLQTPTVFENNYKLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 264 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMKMGDITPLTGSNGEIRKNC 323

Query: 2167 RRIN 2178
RRIN
Sbjct: 324 RRIN 327

Score = 164 bits (415), Expect = 8e-38
Identities = 93/169 (55%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT+SFTGEK ANPN S RGFEVID I KSAVE +CPGVVSCADILAI AA
Sbjct: 77 VQGCDASLLDDTASFTGEKTANPNNGSVRGFEVIDAIKSAVETICPGVVSCADILAI AA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 137 RDSVAI-----LGGPSWDVKVG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A LS KD+VALSG+ I
Sbjct: 154 RRDSRTASLSGANNIPPTSGLANLTSLFAAQALSQKDMVALSGSHTI 202

Score = 72.8 bits (177), Expect = 3e-10
Identities = 32/63 (50%), Positives = 49/63 (77%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + + + + G + AQLS +FY +SCP +F++VK +QSAI++E R+GAS++RRLFHD
Sbjct: 15 LVVMVVVVLAVAGGSWAQLSPSFYSYSCPGVFNNAVKRGMQSAIAREKRIGASIVRRLFHD 74

Query: 772 CFV 780
CFV
Sbjct: 75 CFV 77

>ref|XP_002450132.1| hypothetical protein SORBIDRAFT_05g001000 [Sorghum bicolor]
gb|EES09120.1| hypothetical protein SORBIDRAFT_05g001000 [Sorghum bicolor]
Length = 331

Score = 199 bits (505), Expect = 3e-48
Identities = 93/124 (75%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA +YN+TNI+ FARTRQ CPRTSGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 208 QARCTNFRAHVYNDTNIDGTFARTRQSGCPRTSGSGDNNLAPLDLQTPTVFENNYKLV 267

Query: 1987 QKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFNNG+TD+ V+ Y ++ TF SDF MIKMGDI+PLTGSNG+IRKNC
Sbjct: 268 CKKGLLHSDQELFNNGATDAQVQSYISSQSTFFSDFVTGMKMGDITPLTGSNGQIRKNC 327

Query: 2167 RRIN 2178
R IN
Sbjct: 328 RMIN 331

Score = 160 bits (404), Expect = 1e-36
Identities = 92/169 (54%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LLDDT+SF GEK A PN S RGFVID +KSAVEKVCPGVVSCADILAIAA
Sbjct: 81 VQGCDASLLDDTASFQGEKMATPNNGSVRGFEVIDAVKSAVEKVCPGVVSCADILAIAA 140

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 141 RDSVVI-----LGGPSWDVKVG 157

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 158 RRDSTTASFSGANNNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 206

Score = 82.8 bits (203), Expect = 3e-13
Identities = 39/74 (52%), Positives = 55/74 (74%)
Frame = +1

Query: 559 SKLTMASFCRSLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRM 738
+K + + S L + L L ++ G+++AQLST+FY SCP ++ SVKS +QSAI+ E RM
Sbjct: 8 TKCSSCSASGLALLLLVLMAGTSSAQLSTSFYSSSCPGVYDSVKSAIQSAIATEQRM 67

Query: 739 GASLLRRLFHDCFV 780
GAS++RRLFHDCFV
Sbjct: 68 GASIVRRLFHDCFV 81

>gb|ACT35473.1| peroxidase 52 [Brassica rapa]
Length = 306

Score = 197 bits (500), Expect = 1e-47
Identities = 93/124 (75%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RCTNFR R+YNETNI AFA RQ+SCPR +GSGD NLAPLD+ + +FDN YFKNLV
Sbjct: 183 QSRCTNFRTRVYNETNINAFAFATLRQRSCPRAAGSGDGNLAPLDVNSANTFDNSYFKNLV 242

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGSTDSIV GYS NP +FSSDF AAMIKMGDISPLTGS+GEIRK C
Sbjct: 243 AQRGLLHSDQELFNGGSTDSIVTGYSNPNSSSFSSDFTAAMIKMGDISPLTGSNGEIRKVC 302

Query: 2167 RRIN 2178
R N

Sbjct: 303 GRN 306

Score = 189 bits (481), Expect = 2e-45
Identities = 104/169 (61%), Positives = 115/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGE+NANPNRNSARGF VIDNIK+AVE CPGVVSCADILAI 115
Sbjct: 56 VNGCDGSILLDDTSSFTGEQANPNRNSARGFNVIDNIKTAVEAACPGVVSCADILAI 115

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 116 RDSVVL-----LGGPNWNVKVG 132

Query: 1511 RRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IPAPTS+L+QLIS FSA+GLST+D+VALSG I
Sbjct: 133 RRDARTASQAANNIPAPTSLSQLISSFSAVGLSTRDMVALSGAHTI 181

Score = 75.9 bits (185), Expect = 4e-11
Identities = 34/48 (70%), Positives = 41/48 (85%)
Frame = +1

Query: 640 AQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
AQL+TNFY SCPNL S+V+STV+SA+ + R GAS+LRLFFHDCFVN
Sbjct: 10 AQLTTFYSTSCPNNLSTVRSTVKS AVDSQPRTGASILRLLFFHDCFVN 57

>ref|XP_002441703.1| hypothetical protein SORBIDRAFT_08g000990 [Sorghum bicolor]
gb|EES15541.1| hypothetical protein SORBIDRAFT_08g000990 [Sorghum bicolor]
Length = 328

Score = 196 bits (498), Expect = 2e-47
Identities = 92/123 (74%), Positives = 105/123 (85%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
ARCTNFRA IYN+TNI+ +FAR+RQ CPRTSGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 206 ARCTNFRAHIYNDTNIDGSFARSRSQVCPRTSGSGDNNLAPLDLQPTVFENNYKLVY 265

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KKG+LHSDQ+LFNGGSTD+ V+ Y ++ F +DF MIKMGDI PLTGSNGEIRKNCR
Sbjct: 266 KKGILHSDQELFNGGSTDAQVQSYVSSQSAFFADFVTGMIKMGDIPLTGSNGEIRKNCR 325

Query: 2170 RIN 2178
RIN

Sbjct: 326 RIN 328

Score = 164 bits (415), Expect = 8e-38
Identities = 95/169 (56%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT SF GEK ANPN SARGFEVID IKS AV+KVC PGVVSCADILAI AA
Sbjct: 78 VQGCDASLLDDTPSFQGEKMANPNNGSARGFEVIDAIKSAVDKVC PGVVSCADILAI AA 137

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 138 RDSVVI-----LGGPSWDVKVG 154

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 155 RRDSRTASFSGANNIPPTSGLVNLTSLFAAQGLSQKDMVALSGAHTI 203

Score = 77.4 bits (189), Expect = 1e-11
Identities = 36/61 (59%), Positives = 50/61 (81%), Gaps = 2/61 (3%)
Frame = +1

Query: 604 LALFVLI--WGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR LFFHDCF 777
L L VL+ G+++AQL T+FY HSCP ++ +V+S +Q+AI+++E RMGAS+LRLFFHDCF
Sbjct: 18 LLLLVL LAGTGTSSAQLCTSFYSHSCPGVYDAVRSVLQAAIAREQRMGASILR LFFHDCF 77

Query: 778 V 780
V
Sbjct: 78 V 78

>ref|XP_002450133.1| hypothetical protein SORBIDRAFT_05g001010 [Sorghum bicolor]
gb|EES09121.1| hypothetical protein SORBIDRAFT_05g001010 [Sorghum bicolor]
Length = 328

Score = 196 bits (498), Expect = 2e-47
Identities = 89/124 (71%), Positives = 107/124 (86%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCTNFRA IYN+T+I +AFA+TRQ CP TSG+GDNNLAPLDLQTPT F+N Y+KNL+
Sbjct: 205 QARCTNFRAHIYNDTDINSAFAKTRQSGCPSTSGAGDNNLAPLDLQTPTVFENNYKNNL 264

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y + TF +DF MIKMGDI+PLTGSNG+IRKNC

Sbjct: 265 SKKGLLHSDQELFNGGATDTLVQSYVGSQSTFFTFDVTGMIKMGDITPLTGSNGQIRKNC 324

Query: 2167 RRIN 2178
RR+N

Sbjct: 325 RRVN 328

Score = 159 bits (401), Expect = 3e-36
Identities = 91/169 (53%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDT++F GEK A PN S RGFEVID +KSAVEKVC PGVVSCADILAIAA

Sbjct: 78 VQGCDASLLDDTATFQGEKMATPNNGSVRGFEVIDAVKSAVEKVC PGVVSCADILAIAA 137

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G

Sbjct: 138 RDSVVI-----LGGPSWDVKVG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I

Sbjct: 155 RRDSTTASFSGANNNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 203

Score = 77.4 bits (189), Expect = 1e-11
Identities = 38/70 (54%), Positives = 52/70 (74%), Gaps = 1/70 (1%)
Frame = +1

Query: 574 ASFC SRLTICLALFVL-IWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
AS S + L L L + G+++AQLST FY +SCP ++ +VKS ++SAI+ E RMGAS+

Sbjct: 9 ASSSSAAALLLLLLALAVAGTSSAQLSTGFYSYSCPGVYGAVKSVMKSAIANEKRMGASI 68

Query: 751 LRLFFHDCFV 780

+RLFFHDCFV

Sbjct: 69 VRLFFHDCFV 78

>gb|ABV24960.2| putative secretory peroxidase [Catharanthus roseus]
Length = 330

Score = 196 bits (498), Expect = 2e-47
Identities = 92/124 (74%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT FRARIYNE+NIET+FARTRQ +CP +G+GDN+LAPLDLQ+P FD Y+KNL+

Sbjct: 207 QARCTVFRARIYNESNIETSFARTRQGNCLPTGNGDNLAPLDLQSPNGFDINYYKNLI 266

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+L+NGGST+S+V YS + F SDFAAAMIKMGDISPLTGSNGE+RKNC
Sbjct: 267 NKKGLLHSDQELYNGGSTNSLVEAYSKDTKAFYSDFAAAMIKMGDISPLTGSNGEVRKNC 326

Query: 2167 RRIN 2178
RR+N
Sbjct: 327 RRVN 330

Score = 164 bits (414), Expect = 1e-37
Identities = 92/169 (54%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+QGCDGSILLDDTSS GEK A PN S RGF+V+DNIS VEKVCPCGVVSCADILAI
Sbjct: 80 VQGCDGSILLDDTSSLRGEKTAGPNVGSVRGFDVVDNIKSDVEKVCPCGVVSCADILAI 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W VK+G
Sbjct: 140 RDSV-----VALGGPSWKVKVG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS S AN+ IP PTSNL LIS F A+GLS KD+V LSG+ I
Sbjct: 157 RRDSKTASLSGANSRIPPPTSNLRLISSFQAVGLSAKDMVVLSGSHTI 205

Score = 72.4 bits (176), Expect = 4e-10
Identities = 37/77 (48%), Positives = 52/77 (67%), Gaps = 3/77 (3%)
Frame = +1

Query: 559 SKLTMASFCSRLTICLALFVL---IWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKE 729
S + +SF S I + + VL + S + QLS+ FY +CP ++++V+ V+SA+SKE
Sbjct: 4 SSSSSSSFSNFGIVIMVIVLSIIMRSCSGQLSSEFYSKTCPQVYNTVRKGVESAVSKE 63

Query: 730 TRMGASLLRLFFHDCFV 780
RMGASLLRL FHDCFV
Sbjct: 64 KRMGASLLRLHFHDCFV 80

>sp|P00434.3|PERP7_BRARA RecName: Full=Peroxidase P7; AltName: Full=TP7
Length = 296

Score = 196 bits (498), Expect = 2e-47
Identities = 93/124 (75%), Positives = 107/124 (86%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRSTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC NFRAR+YNETNI AFA RQ+SCPR +GSGD NLAPLD+ + TSFDN YFKNL+
Sbjct: 173 QSRCVNFRRARVYNETNINAAAFATLRQSRCPRAAAGSGDANLAPLDINSATSFDNSYFKNLM 232

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPFTSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ LFNGGSTDSIVRGYS +P +F+SDFAAAMIKMGDISPLTGS+GEIRK C
Sbjct: 233 AQRGLLHSDQVLFNGGSTDSIVRGYSNSPSSFNDFAAAMIKMGDISPLTGSSGEIRKVC 292

Query: 2167 RRIN 2178
+ N
Sbjct: 293 GKTN 296

Score = 179 bits (455), Expect = 2e-42
Identities = 99/169 (58%), Positives = 114/169 (67%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKCPGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGE+NA PNRNSARGF VI++IKSAVEK CPGVVSCADILAIAA
Sbjct: 46 VNGCDGSILLDDTSSFTGEQNAGPNRNSARGFTVINDIKSAVEKACPGVVSCADILAIAA 105

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 106 RDSV-----VQLGGPNWNVKVG 122

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDA+TASQ+AAAN+ IPAP+ +L+QLIS FSA+GLST+D+VALSG I
Sbjct: 123 RRDAKTASQAAANSNIPAPMSLSQLISSFSAVGLSTRDMVALSGAHTI 171

Score = 76.6 bits (187), Expect = 2e-11
Identities = 35/47 (74%), Positives = 41/47 (87%)
Frame = +1

Query: 643 QLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCFVN 783
QL+TNFY SCPNL S+VKS V+SA+S + RMGAS+LRLFFHDCFVN
Sbjct: 1 QLSTNFYSTSCPNNLSTVKSGVKS AVSSQPRMGASILRFFHDCFVN 47

>gb|AAD37423.1|AF149281_1 peroxidase 6 [Phaseolus vulgaris]
Length = 128

Score = 195 bits (495), Expect = 4e-47
Identities = 106/165 (64%), Positives = 116/165 (70%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKCPGVVSCADILAIAA 1330

+ GCDGSILLDDTSSFTGEKNA PN+NSARGF+VID IKSAVE+VCPGVVSCADILAIAA
Sbjct: 7 VNGCDGSILLDDTSSFTGEKNARPNKNSARGFDVIDKIKSAVEEVCPGVVSCADILAIAA 66

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGP+WNVKLG

Sbjct: 67 RDSVHIL-----GGPSWNVKLG 83

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRD+RTASQSAANNGIP PTSN+NQLISRF++LGLS KDLVALSG
Sbjct: 84 RRDSRTASQSAANNGIPPTSNVNLISRFSNLGLSPKDLVALSG 128

>ref|XP_002520835.1| Peroxidase 52 precursor, putative [Ricinus communis]
gb|EEF41544.1| Peroxidase 52 precursor, putative [Ricinus communis]
Length = 318

Score = 194 bits (494), Expect = 5e-47
Identities = 109/169 (64%), Positives = 115/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKCPGVVSCADILAIAA 1330

+ GCDGSILLDDTSSFTGE+ A PNRNS RGFEVID+IKSAVEK CPGVVSCADILAIAA
Sbjct: 70 VNGCDGSILLDDTSSFTGEQTAVPNRNSVRGFEVIDSIKSAVEKACPGVVSCADILAIAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I+ GGP+WNVKLG

Sbjct: 130 RDSTAIL-----GGPSWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDARTAS SAANNGIPAPTSNLNQLISRFSALGLST+DLVALSG I
Sbjct: 147 RRDARTASLSAANNGIPAPTSNLNQLISRFSALGLSTRDLVALSGAHTI 195

Score = 193 bits (490), Expect = 2e-46
Identities = 93/124 (75%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCTNFR RIYN+TNI+++FA+TR+ +CP T G DNNLAPLDLQTPTSFDN YFKNL+
Sbjct: 197 QARCTNFRTRIYNDTIDSSFAQTRRSNCPSTGG--DNNLAPLDLQTPTSFDNYYFKNLL 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166

+KGLLHSDQ+LFN GSTDSIVR YS TF SDF A MIKMGDISPLTGS GEIRKNC
Sbjct: 255 VQKGLLHSDQELFNGGSTDSIVRTYSNGQSTFFSDFVAGMIKMGDISPLTGSQGEIRKNC 314

Query: 2167 RRIN 2178

++N
Sbjct: 315 GKVN 318

Score = 88.2 bits (217), Expect = 7e-15
Identities = 43/63 (68%), Positives = 50/63 (79%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDC 774
TI +L+ +NAQLSTNFY SCPNLFS+VK VQSAI++E RMGASL+RLFFHDC
Sbjct: 9 TIVTLSLLLVSISNAQLSTNFYSKPCPNLFSTVKPVVQSAINQEKRMGASLVRLFFHDC 68

Query: 775 FVN 783
FVN
Sbjct: 69 FVN 71

>ref|XP_002319968.1| predicted protein [Populus trichocarpa]
gb|EEE95891.1| predicted protein [Populus trichocarpa]
Length = 325

Score = 193 bits (491), Expect = 1e-46
Identities = 92/124 (74%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNETNI+++FA TRQ++CP GDN LAPLD+QTPTSFDN Y+KNL+
Sbjct: 202 QARCTSFARIYNETNIDSSFATTRQKNCPPGPKGDNKLAPLDVQTPTSFDNKYYKNLI 261

Query: 1987 QKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ LFNGGSTDS+VR YS+NP TFSSDF AMIKMGDI PLTGS GEIRK C
Sbjct: 262 SQKGLLHSDQVLFNGGSTDSLVRTYSSNPKTFSSDFVTAMIKMGDIDPLTGSQGEIRKIC 321

Query: 2167 RRIN 2178
+ N
Sbjct: 322 SKRN 325

Score = 160 bits (406), Expect = 9e-37
Identities = 91/170 (53%), Positives = 107/170 (62%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
++GCDGSILL+DTSSFTGE+ A PN NS RGF V+ IKS VEKVCPG+VSCADI+AIAA
Sbjct: 74 VKGCDGSILLEDTSSFTGEQTAGPNNSVRGFNVVAKIKSQVEKVCPGIVSCADIVAIAA 133

Query: 1331 RDSVQIVSGQTTNKNLTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I LGGP WNVKLG
Sbjct: 134 RDSTVI-----LGGPFWNVKLG 150

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS SAAN+G IP PTS L+ LI+RF++ GLS KD+VALSG+ I
Sbjct: 151 RRDSKTASLSAANSVIPPPTSTLSNLINRFNSKGLSVKDMVALSGSHTI 200

Score = 86.7 bits (213), Expect = 2e-14
Identities = 44/70 (62%), Positives = 55/70 (78%), Gaps = 1/70 (1%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGS-ANAQLSTNFYHSCPFLFSSVKSTVQSAISKETRMGASL 750
+SF S + I F++I+ S ++AQLSTNFY SCP +F +VKS VQSA+SKE RMGASL
Sbjct: 5 SSFSSYMAIFTLAFLVIFTSHSSAQLSTNFYSKCPKVFVAVKSVVQSAVSKERRMGASL 64

Query: 751 LRLFFHDCFV 780
+RLFFHDCFV
Sbjct: 65 VRLFFHDCFV 74

>ref|NP_001151940.1| peroxidase 52 [Zea mays]
gb|ACG45093.1| peroxidase 52 precursor [Zea mays]
Length = 334

Score = 191 bits (486), Expect = 5e-46
Identities = 89/126 (70%), Positives = 106/126 (84%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSG--SGDNNLAPLDLQTPTSFDNYYFKN 1980
QARCTNFRA +YN+TNI+ +FARTRQ CPR+S SGDNNLAPLDLQTPT FDN Y+KN
Sbjct: 209 QARCTNFRAHVYNDTNIDGSFARTRQSGCPRSSSGSSGDNNLAPLDLQTP TVFDNYYKN 268

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
LV KKGLLHSDQ+LFNGG+TD++V+ Y++ F SDF M+KMGDI+PLTGS G+IRK
Sbjct: 269 LVCKKGLLHSDQELFNGGATDALVQSYASGQSEFFSDFVTGMVKMGDITPLTGS GGQIRK 328

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 329 NCRRVN 334

Score = 162 bits (409), Expect = 4e-37
Identities = 93/169 (55%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LLDDT SF GEK ANPN S RGFEVID +KSAVEKVC PGVVSCADILAI
Sbjct: 82 VQGCDASLLDDTSPFQGEKMANPNNGSVRGFEVIDAVKSAVEKVC PGVVSCADILAI 141

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGPTW+VK+G
Sbjct: 142 RDSVVIL-----GGPTWDVKVG 158

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 159 RRDSTTASFGANNIPPTSGLANLTSFAAQGLSQKDMVALSGAHTI 207

Score = 79.0 bits (193), Expect = 4e-12
Identities = 36/59 (61%), Positives = 47/59 (79%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCP NFLFSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
LAL + G+++AQLST FY SCP ++ +VKS VQSA++ E RMGAS++RLFFHDCFV
Sbjct: 24 LALLMAAAGTSSAQLSTGFYSSSCPGVYDAVKSVVQSAVASEQRMGASIVRLFFHDCFV 82

>ref|XP_002489046.1| hypothetical protein SORBIDRAFT_0246s002010 [Sorghum bicolor]
gb|EES20431.1| hypothetical protein SORBIDRAFT_0246s002010 [Sorghum bicolor]
Length = 320

Score = 190 bits (483), Expect = 1e-45
Identities = 88/124 (70%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR IYN+TN++ AFARTRQ CP TSG+GDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 197 QARCTNFRDHIYNDTNVDGAFARTRQSGCPSTSGTGDNNLAPLDLQTPTVFENDYYKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFNGG+TD++V+ Y ++ F +DF MIKMGDI+PLTGS GEIRKNC
Sbjct: 257 SNMGLLHSDQELFNGGATDALVQSYVSSQSAFFADFVTGMKMGDITPLTGSAGEIRKNC 316

Query: 2167 RRIN 2178
RRIN
Sbjct: 317 RRIN 320

Score = 155 bits (392), Expect = 4e-35
Identities = 90/169 (53%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKPCPGVVSCADILAI 1330
+QGCD S+LLDDT++F GEK A PN S RGFEVID KSAVE VCPGVVSCADILAI
Sbjct: 70 VQGCDASLLDDTATFQGEKMATPNNGSVRGFEVIDAAKSAVENVCPGVVSCADILAI 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 130 RDSVVI-----LGGPSWDVKVG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 147 RRDSTTASFSGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 195

Score = 73.9 bits (180), Expect = 1e-10
Identities = 38/70 (54%), Positives = 47/70 (67%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ L + L G++ AQLST FY SCP L+S+VK VQSAI E R+GAS+
Sbjct: 1 MAAQSIALWLLTTTALQAGTSAQLSTGFYSSSCPGLYSAVKPVVQSAIDSEKRVGASI 60

Query: 751 LRLFFHDCFV 780
+RLFFHDCFV
Sbjct: 61 VRLFFHDCFV 70

>ref|XP_002441702.1| hypothetical protein SORBIDRAFT_08g000980 [Sorghum bicolor]
gb|EES15540.1| hypothetical protein SORBIDRAFT_08g000980 [Sorghum bicolor]
Length = 131

Score = 190 bits (483), Expect = 1e-45
Identities = 88/124 (70%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR IYN+TN++ AFARTRQ CP TSG+GDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 8 QARCTNFRDHIYNDTNVDGAFARTRQSGCPSTSGTGDNNLAPLDLQTPTVFENDYYKNLV 67

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFNGG+TD++V+ Y ++ F +DF MIKMGDI+PLTGS GEIRKNC
Sbjct: 68 SNMGLLHSDQELFNGGATDALVQSYVSSQSAFFADFVTGMIKMGDITPLTGSAGEIRKNC 127

Query: 2167 RRIN 2178
RRIN
Sbjct: 128 RRIN 131

>gb|AAA96137.1| peroxidase [Stylosanthes humilis]
Length = 136

Score = 190 bits (483), Expect = 1e-45

Identities = 87/124 (70%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FR IYN+T+I+ +FA+ RQ++CPR SG+GD+NLAPLDLQTPT F+N Y+KNL+

Sbjct: 13 QARCTSRFGHIYNDTIDPSFAKLRRQKNCPRQSGTGDSNLAPLDLQTPHFENNYKLI 72

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS+V+ YS N F+SDF MIKMGD+ PLTGS GEIRKNC

Sbjct: 73 NKKGLLHSDQELFNGGSTDSLVTYKSNKAFTSDFVPGMIKMGDLLPLTGSKEIRKNC 132

Query: 2167 RRIN 2178

RR+N

Sbjct: 133 RRMN 136

>gb|AAL93151.1|AF485265_1 class III peroxidase [Gossypium hirsutum]
Length = 320

Score = 189 bits (480), Expect = 2e-45
Identities = 91/124 (73%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIYN+T I+T+FA+TR+ SCPRT GSGDNNLAPLDL TP SFD+ YF+NL+

Sbjct: 197 KARCLVFRNRIYNDTIIDTSFAKTRRSSCPRTSGSGDNNLAPLDLATPNSFDSKYFENLL 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS+V+ YS+N F SDF AAMIKMGDI PLTGSNGEIRKNC

Sbjct: 257 NKKGLLHSDQELFNGGSTDSLVTYSSNVKKFYSDFAAMIKMGDIKPLTGSNGEIRKNC 316

Query: 2167 RRIN 2178

+ N

Sbjct: 317 GKPN 320

Score = 160 bits (404), Expect = 1e-36
Identities = 92/170 (54%), Positives = 106/170 (62%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGE+ A PN S RGFEV+D IK+ VEKVCPCGVVSCADILAIAA

Sbjct: 69 VNGCDGSVLLDDTSSFTGEQTATPNNGSLRGFEVVDEIKAKVEKVCPCGVVSCADILAIAA 128

Query: 1331 RDSVQIVSGQTTNKNLTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W+VKLG

Sbjct: 129 RDSVVI-----LGGPDWDVKLG 145

Query: 1511 RRDARTASQSAANNGI-PAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS S AN+G+ P ++NL+QLIS F A GLSTKD+VALSG I
Sbjct: 146 RRDSKTASFSDANSGVLPPLGSANLSQLISLFAQQLSTKDMVALSGAHTI 195

Score = 76.6 bits (187), Expect = 2e-11
Identities = 34/60 (56%), Positives = 48/60 (80%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCPFLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
+ +++++ + AQLSTNFY SCP + S+V+ V++A+SKE R+GASLLRLLFFHDCFVN
Sbjct: 11 VGVWMMMGSGSYAQLSTNFYSKSCPVLSTVELVVETAVSKEQRLGASLLRLLFFHDCFVN 70

>emb|CAD67478.1| peroxidase [Asparagus officinalis]
Length = 301

Score = 188 bits (478), Expect = 4e-45
Identities = 87/124 (70%), Positives = 104/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT+FR IYN+ +I+ +FA RQ+ CPR SGSGD NLAPLDLQTPT+FDN Y+KNL+
Sbjct: 178 QARCTSFRGHIYNDADIDASFASLRQKICPRKSGSGDTNLAPLDLQTPTAFDNNYYKNLI 237

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFN G+TDS+V+ YS + G+F+SDF AMIKMGDISPLTGS GEIRK C
Sbjct: 238 NKKGLLHSDQELFNGGATDSLVSYSNSEGSFNSDFVKAMIKMGDISPLTGSKEIRKIC 297

Query: 2167 RRIN 2178
+IN
Sbjct: 298 SKIN 301

Score = 161 bits (407), Expect = 7e-37
Identities = 90/169 (53%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILL DT++F GE++A PN S RGF+VID IK+AVE CPGVVSCADILA+AA
Sbjct: 51 VNGCDGSILLADTANFRGEQHAGPNNGSVRGFKVIDKIKTAVENACPGVVSCADILAVAA 110

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W VKLG
Sbjct: 111 RDSVVI-----LGGPDWVKVKG 127

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDARTAS + ANN IP PTS+L+ LIS+F+A GLSTKD+VALSG I
Sbjct: 128 RRDARTASATLANNIPPTSSLSNLISKFAAQLSTKDMVALSGAHTI 176

Score = 82.4 bits (202), Expect = 4e-13
Identities = 37/52 (71%), Positives = 45/52 (86%)
Frame = +1

Query: 628 GSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
GS++A LSTNFY SCP +FS++K +QSAI+KE RMGAS+LRLFFHDCFVN
Sbjct: 1 GSSSAHLSTNFYSSSCPVKVFSTIKPVLQSAIAKEKRMGASILRLLFFHDCFVN 52

>gb|AAR31108.1| peroxidase precursor [Quercus suber]
Length = 330

Score = 188 bits (477), Expect = 5e-45
Identities = 88/125 (70%), Positives = 107/125 (85%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSG-SGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT FR RIY + NI+++FA+TRQ CP+T+G GDN +APLDLQTPT+FDNYY+KNL
Sbjct: 205 QARCTVFRDRIYKDKNIDSSFAKTRQNKCPKTTGLPGDNKIAPLDLQTPTAFDNYYYKNL 264

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+++KGLL SDQQLFNGGSTDS+V+ YS + TF SDF AMIKMGDI PLTGS+GEIRKN
Sbjct: 265 IKEKGLLRSDQQLFNGGSTDSLVKKYSQDTKTFYSDFVNAMIKMGDIQPLTGSSGEIRKN 324

Query: 2164 CRRIN 2178
CR++N
Sbjct: 325 CRKVN 329

Score = 162 bits (409), Expect = 4e-37
Identities = 93/166 (56%), Positives = 103/166 (62%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDT +FTGEK A PN S R FEV+D IKS VEK CPGVVSCADILAIAA
Sbjct: 77 VNGCDGSILLDDTPTFTGEKTARPNNGSIRAFEVVDEIKSKVEKECPGVVSCADILAIAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I LGGP W+VKLG
Sbjct: 137 RDSVKI-----LGGPKWDVKLG 153

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD++TAS SAAN+G IP PTS L LI+RF A GLSTKD+VALSG

Sbjct: 154 RRDSKTASFAANSVIPPPTSTLGNLINRFKAKGLSTKDMVALSG 199

Score = 84.3 bits (207), Expect = 1e-13
Identities = 39/64 (60%), Positives = 51/64 (79%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ V+ G+++A+LSTNFY SCP +FS+V+S V SA+SK+ R GASLLRL FHD
Sbjct: 15 LIVSLAVLVIFTGNSSAKLSTNFYSKSCPVKVSTVQSVVHSAVSKQPRQGASLLRLHFHD 74

Query: 772 CFVN 783
CFVN
Sbjct: 75 CFVN 78

>gb|AAR31106.1| peroxidase precursor [Quercus suber]
Length = 330

Score = 187 bits (474), Expect = 1e-44
Identities = 87/125 (69%), Positives = 108/125 (86%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSG-SGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT FR RIY + NI+++FA+TRQ +CP+T+G GDN +APLDLQTPT+FDNYY+KNL
Sbjct: 205 QARCTVFRDRIYKDKNIDSSFAKTRQNTCPKTTGLPGDNKIAPLDLQTPTAFDNYYKKNL 264

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKN 2163
+++KGLL SDQQLFNGGSTDS+V+ YS + +F SDF AMIKMGDI PLTGS+GEIRKN
Sbjct: 265 IKQKGLLRSDQQLFNGGSTDSLVKKYSQDTKSFYSDFVNAMIKMGDIQPLTGSSGEIRKN 324

Query: 2164 CRRIN 2178
CR++N
Sbjct: 325 CRKVN 329

Score = 162 bits (410), Expect = 3e-37
Identities = 92/170 (54%), Positives = 105/170 (61%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDT +FTGEK A PN+ S RGFE +D IKS VEK CPGVVSCADILAIAA
Sbjct: 77 VNGCDGSVLLDDTPTFTGEKTAGPNKGSIRGFVFEVDEIKSKVEKECPGVVSCADILAIAA 136

Query: 1331 RDSVQIVSGQTTNKNLTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I LGGP W+VKLG
Sbjct: 137 RDSVKI-----LGGPKWDVKLG 153

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS AAN+G IP PTS L+ LI+RF A GLSTKD+VALSG I
Sbjct: 154 RRDSKTASLKAANSVIPPPTSTLSNLINRFKAKGLSTKDMVALSGAHTI 203

Score = 87.8 bits (216), Expect = 9e-15
Identities = 41/64 (64%), Positives = 52/64 (81%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ V+ G+++A+LSTNFYY SCP +FS+V+S V SAISK+ R GASLLRL FHD
Sbjct: 15 LIVSLAVLVIFSGNSSAKLSTNFYKSCPVKVSTVQSVVHSAISKQPRQGASLLRRLFHD 74

Query: 772 CFVN 783
CFVN
Sbjct: 75 CFVN 78

>ref|NP_001131000.1| hypothetical protein LOC100192105 [Zea mays]
gb|ACF79421.1| unknown [Zea mays]
gb|ACL53914.1| unknown [Zea mays]
Length = 320

Score = 186 bits (473), Expect = 1e-44
Identities = 89/126 (70%), Positives = 107/126 (84%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG-DNNLAPLDLQTPTSFDNYYFKNL 1983
QARCTNFRA IYN+T+I+ AFARTRQ CP TSG+G DNNLAPLDLQTPT F+N Y++NL
Sbjct: 195 QARCTNFRAHIYNDTDIDAAFARTRQSGCPSTSGAGGDNNLAPLDLQTPTVFENNYRNL 254

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS-NGEIRK 2160
+ KKGLLHSDQ+LFNGG+TD++V+ Y + F +DF A MIKMGDI+PLTGS NG+IRK
Sbjct: 255 LAKKGLLHSDQELFNGGATDALVQSYVGSQSAFFADVFAGMIKMGDITPLTGSNNGQIRK 314

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 315 NCRRVN 320

Score = 160 bits (406), Expect = 9e-37
Identities = 92/169 (54%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKCPGVVSCADILAIAA 1330
+QGCD S+LLDDT SF GEK ANPN S RGFEVID +KSAVEK+CPGVVSCADILAIAA

Sbjct: 68 VQGCASLLLDTPSFQGEKMANPNNGSVRGFEVIDAVKSAVEKLCPGVVSCADILAIAA 127

Query: 1331 RDSVQIVSGGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGPTWNVKLG 1510
RDSV I+ GGPTW+VK+G

Sbjct: 128 RDSVVIL-----GGPTWDVKVG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I

Sbjct: 145 RRDSTTASFGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 193

Score = 81.6 bits (200), Expect = 7e-13
Identities = 37/65 (56%), Positives = 51/65 (78%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLF 765
+R L L + + G+++AQLST FY +SCP ++ +VKS +QSAI++E RMGAS+LRLFF

Sbjct: 4 TRAAATLLLLLALAGTSSAQLSTGFYSYSCPGVYGAVKSVMSAIAREKRMGASILRRLF 63

Query: 766 HDCFV 780

HDCFV

Sbjct: 64 HDCFV 68

>gb|AAD43561.1|AF155124_1 bacterial-induced peroxidase precursor [Gossypium hirsutum]
Length = 316

Score = 185 bits (470), Expect = 3e-44
Identities = 86/123 (69%), Positives = 104/123 (84%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
ARCT FR RIYN+TNI+ FA TR+ +CP + GDNNLAPLD+QTPT FDN YF+NLV

Sbjct: 196 ARCTTFRGRIYNDTNIDANFAATRRANCP--ASGGDNNLAPLDIQTPTFRFDNDYFRNLVA 253

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++VR YS NP TFS+DFAAAM+KMG+ISPLTG+ GEIR+NCR

Sbjct: 254 RRGLLHSDQELFNGGSQDALVRTYSNNPATFSADFAAAMVKMGNISPLTGTQGEIRRNCR 313

Query: 2170 RIN 2178

+N

Sbjct: 314 VVN 316

Score = 159 bits (403), Expect = 2e-36
Identities = 90/165 (54%), Positives = 101/165 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDT++FTGEKNA PNRNSARGFEVID IK+ VE C VSCADILA+AA
Sbjct: 68 VNGCDGSILLDDTATFTGEKNAVPNRNSARGFEVIDTIKTNVEAAC SATVSCADILALAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++ GGPTW V LG
Sbjct: 128 RDGVALL-----GGPTWQVPLG 144

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAANN IP+P +NL L S F+A GLST+DL ALSG
Sbjct: 145 RRDARTASQSAANNQIPSPFANLATLTSSFAAKGLSTRDLTALSG 189

Score = 76.6 bits (187), Expect = 2e-11
Identities = 35/62 (56%), Positives = 48/62 (77%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR LFFHDCF 777
+ L + +L +ANAQLS NFY SCPNL + V++ + A+++ETR+GAS+LRLFFHDCF
Sbjct: 8 VTLIVMLSCHAANAQLSPNFYASSCPNLQTIVRNAMSRVNRRETRIGASILR LFFHDCF 67

Query: 778 VN 783
VN
Sbjct: 68 VN 69

>gb|ACN33662.1| unknown [Zea mays]
Length = 320

Score = 184 bits (468), Expect = 6e-44
Identities = 88/126 (69%), Positives = 107/126 (84%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG-DNNLAPLDLQTPTSFDNYYFKNL 1983
QARCTNFRA IYN+T+I+ AFARTRQ CP TSG+G D+NLAPLDLQTPT F+N Y++NL
Sbjct: 195 QARCTNFRAHIYNDTDIDAAFARTRQSGCPSTSGAGGDSNLAPLDLQTPTVFENNYRNL 254

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS-NGEIRK 2160
+ KKGLLHSDQ+LFNGG+TD++V+ Y + F +DF A MIKMGDI+PLTGS NG+IRK
Sbjct: 255 LAKKGLLHSDQELFNGGATDALVQSYVGSQSAFFADVFAGMIKMGDITPLTGSNNGQIRK 314

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 315 NCRRVN 320

Score = 160 bits (406), Expect = 9e-37
Identities = 92/169 (54%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LLDDT SF GEK ANPN S RGFVID +KSAVEK+CPGVVSCADILAIAA
Sbjct: 68 VQGCDASLLDDTSPFQGEKMANPNNGSVRGFEVIDAVKSAVEKLCPGVVSCADILAIAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGPTW+VK+G
Sbjct: 128 RDSVVIL-----GGPTWDVKVG 144

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 145 RRDSTTASFSGANNIPPTSGLANLTSFAAQGLSQKDMVALSGAHTI 193

Score = 81.6 bits (200), Expect = 7e-13
Identities = 37/65 (56%), Positives = 51/65 (78%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLF 765
+R L L + + G+++AQLST FY +SCP ++ +VKS +QSAI++E RMGAS+LRLFF
Sbjct: 4 TRAAATLLLLLALAGTSSAQLSTGFYSYSCPGVYGAVKSVMQSAIAREKRMGASILRRLF 63

Query: 766 HDCFV 780
HDCFV
Sbjct: 64 HDCFV 68

>emb|CBI25393.1| unnamed protein product [Vitis vinifera]
Length = 179

Score = 184 bits (466), Expect = 1e-43
Identities = 100/169 (59%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSF GEKNA PN NS RGF+V+D+IKS VE CPGVVSCAD+LAIAA
Sbjct: 15 VNGCDGSVLLDDTSSFIGEKNAAPNANSVRGFVDDIKSKVETACPGVVSCADVLAIAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGP+WNVKLG
Sbjct: 75 RDSVVIL-----GGPSWNVKLG 91

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IP PTSNLNQLISRF ALGLST+DLVAL+G+ I
Sbjct: 92 RRDARTASQAANNSIPPPTSNLNLISRFAALGLSTRDLVALAGSHTI 140

Score = 57.8 bits (138), Expect = 1e-05
Identities = 24/31 (77%), Positives = 29/31 (93%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR 1899
QARCT+FRARIYNETNI+ +FA+TRQ +CPR
Sbjct: 142 QARCTSFARIYNETNIDNSFAKTRQSNCP 172

Score = 38.1 bits (87), Expect = 8.5
Identities = 16/16 (100%), Positives = 16/16 (100%)
Frame = +1

Query: 736 MGASLLRLLFFHDCFVN 783
MGASLLRLLFFHDCFVN
Sbjct: 1 MGASLLRLLFFHDCFVN 16

>gb|ACU23223.1| unknown [Glycine max]
Length = 328

Score = 182 bits (462), Expect = 3e-43
Identities = 86/124 (69%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR RIYN+TNI+ FA RQ+ CPRT+G+GDNNLA LD +TP FDN YFKNL+
Sbjct: 205 KARCTSFDRRIYNTNIDRTFALARQRRCPRTNGTGDNNLANLDFRTPNHFDNYYFKNLL 264

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GLL+SDQ LFNNGGSTDS+VR YS N F +DF AMI+MGDI PLTGS GEIRKNC
Sbjct: 265 IKRGLLNSDQVLFNGGSTDSLVRTYSQNNKAFDTDFVKAMIRMGDIKPLTGSQGEIRKNC 324

Query: 2167 RRIN 2178
RR+N
Sbjct: 325 RRVN 328

Score = 152 bits (383), Expect = 4e-34
Identities = 88/166 (53%), Positives = 100/166 (60%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCDGSILLDDT +F GEK A N NS RGFEVID IKS VEK+CPGVVSCADIL IA+

Sbjct: 77 VQCGDGSILLDDTPTFQGEKTAANNNSVRGFEVIDAIKSEVEKICPGVWSCADILDIAS 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W V+LG

Sbjct: 137 RDSVVL-----LGGPFWKVRLG 153

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+RTA+ +AAN G IP PTSNL LI+RF GLS +D+VALSG

Sbjct: 154 RRDSRTANFTAANTGVIPPTSNTLNLTRFRDQGLSARDMVALSG 199

Score = 87.0 bits (214), Expect = 2e-14
Identities = 39/77 (50%), Positives = 59/77 (76%)
Frame = +1

Query: 550 VCLSKLTMASFCRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKE 729
+ LS + +SF S + LA+ +L+ G+++A LS NFY +CPN+F++VKS V+SA+ +E

Sbjct: 1 MALSPIRSSSFSSSAIVALAVLLLLTGTSSANLSKNFYSKTCPNVFNTVKS VVKS AVVRE 60

Query: 730 TRMGASLLRLFFHDCFV 780
R+GAS++RLFFHDCFV

Sbjct: 61 PRIGASIVRLFFHDCFV 77

>emb|CAA71491.1| peroxidase [Spinacia oleracea]
Length = 323

Score = 182 bits (462), Expect = 3e-43
Identities = 84/123 (68%), Positives = 102/123 (82%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCTNFR IYN++NI+ FA TR+ SCPR +G+GD NLAP+D+QTP +FDN Y+KNLV

Sbjct: 201 ARCTNFRDHIYNDNSNIDPNAATRKAACPRPTGTGDFNLAPMDIQTPTFDNDYYKNLVA 260

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLLHSDQ+L+NGGS DS+V+ YSTN F DFAAAMI+MGD+ PLTG+NGEIR NCR

Sbjct: 261 KRGLLHSDQELYNGGSQDSLKMYSTNQALFFQDFAAAMIRMGDLKPLTGTNGEIRNNCR 320

Query: 2170 RIN 2178
IN

Sbjct: 321 VIN 323

Score = 123 bits (308), Expect = 2e-25
Identities = 74/166 (44%), Positives = 89/166 (53%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRN-SARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+ GCDGS+LLDDT + GEK A PNRN S RGFEVID IKS VE C G VSCADILA+A
Sbjct: 72 VNGCDGSVLLDDTPTSQGEKMAFPNRNNSIRGFEVIDATKSNVEAACSGTVSCADILALA 131

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD VQ++ G PTWNVKL
Sbjct: 132 ARDGVQLLGG-----PTWNVKL 148

Query: 1508 GRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRDARTA+ + AN +P + L L F+ L+ +++ ALSG
Sbjct: 149 GRRDARTANMTLANLNLPPGNAPLANLTELAFARQNLNIREMTALSG 194

Score = 66.6 bits (161), Expect = 2e-08
Identities = 32/60 (53%), Positives = 46/60 (76%), Gaps = 1/60 (1%)
Frame = +1

Query: 607 ALFVLIWGSANAQL-STNFYYHSCP NFLSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
++ +L+ G+++A L +FY SCPN+ V +T++ A+SKE RMGAS+LRLFFHDCFVN
Sbjct: 14 SIILLAGTSDAWLRKPHFYASSCPNVEQIVFNTMKQAVSKEPRMGASILRLLFFHDCFVN 73

>gb|ABK21858.1| unknown [Picea sitchensis]
Length = 326

Score = 180 bits (457), Expect = 1e-42
Identities = 86/124 (69%), Positives = 104/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR RI++E+NI+ +FAR RQ +CP T G D+NLAPLDL TPT+FDN Y+KNL
Sbjct: 205 QARCTNFRNRHSESNI DLSFARARQANCPSTGG--DDNLAPLDLLTPTTFDNYYKNLE 262

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+++GLLHSDQQLFNGGSTD++V Y+T P FS DFA AM+KMG I PLTG+NGEIRKNC
Sbjct: 263 RRRGLLHSDQQLFNGGSTDNLVSFYTTYPIAFSIDFAVAMVKMGSI EPLTGNGEIRKNC 322

Query: 2167 RRIN 2178
R+IN
Sbjct: 323 RKIN 326

Score = 153 bits (386), Expect = 2e-34
Identities = 88/169 (52%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI AA 1330
+ GCDGSILLDDTS+F GEK A PN+NS RGFEVID IK+ VE CPGVVSCADI+AIAA
Sbjct: 78 VNGCDGSILLDDTSTFQGEKTAVPNKNSVRGFEVIDAIKTQVEAACPGVVSCADIVAIAA 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + LGGPTW V LG
Sbjct: 138 RDAV-----VQLGGPTWLVLLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ +P P SNL+ LIS F + GLS +DLVALSG+ I
Sbjct: 155 RRDSTTASLSAANSNLPPPASNLSALISSFQSHGLSIRDLVALSGSHTI 203

Score = 67.8 bits (164), Expect = 1e-08
Identities = 35/65 (53%), Positives = 42/65 (64%)
Frame = +1

Query: 589 RLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFH 768
R +CL + V + + QL FY SCP+ FS V S V A++KE RMGASLLRL FH
Sbjct: 16 RSLLLCLLILVRL-SAVYGQLCPRFYDISCPSAFSIVNSVVTQAVAKEKRMGASLLR LFFH 74

Query: 769 DCFVN 783
DCFVN
Sbjct: 75 DCFVN 79

>emb|CAD67477.1| peroxidase [Asparagus officinalis]
Length = 315

Score = 179 bits (455), Expect = 2e-42
Identities = 82/124 (66%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCT+FR+ IYN+++I+ +FA R+ +CP+ SGSGD NLAPLDLQTPT+FDN Y++NLV
Sbjct: 192 QARCTSF RSHIYNDSDIDPSFATLRKSNCPKQSGSGDMNLAPLDLQTPTTFDNNYYRNLV 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGL+HSDQ+LFNGGSTDS+V+ YS G F S F MIKMGD+SPL GSNGEIRK C
Sbjct: 252 VKKGLMHSDQELFNGGSTDSLKSYSDGTGKFYSAFVEGMIKMGDVSPLVGSNGEIRKIC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 162 bits (409), Expect = 4e-37

Identities = 92/169 (54%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILL DT F GE++ANPN SARGF+VID IK+AVEK CPGVVSCADILAIAA

Sbjct: 65 VNGCDGSILLADTPHFVGEQHANPNRNSARGFKVIDRIKTAVEKACPGVVSCADILAIAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W+VKLG

Sbjct: 125 RDSVVI-----LGGPNWDVKLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+RTA+++AANN IP PTS+L L S F+A GLSTKD+VALSG I

Sbjct: 142 RRDSRTANKTAANNEIPPTSSLANLTSLFAAKGLSTKDMVALSGAHTI 190

Score = 82.8 bits (203), Expect = 3e-13
Identities = 40/64 (62%), Positives = 51/64 (79%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L I L+L ++ S+NAQLST FY +SCPN+F+++K +Q AI KE RMGAS+LRLFHD

Sbjct: 6 LAIILSLCIV---SSNAQLSTTFYSNSCPNVFTTIKPVLQHAIEKEKRMGASILRRLFHD 62

Query: 772 CFVN 783
CFVN

Sbjct: 63 CFVN 66

>emb|CAA62597.1| korean-radish isoperoxidase [Raphanus sativus]
Length = 315

Score = 179 bits (455), Expect = 2e-42
Identities = 89/124 (71%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RCTNFR RIYNETNI AFA RQ+SCPR + PLD+ +PTSFDN YFKNL+

Sbjct: 193 QSRCTNFRTRIYNETNINAAFATLRQKSCPRAAFRR-RKPQLDINSPTSFDNSYFKNLM 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ LFNNGGSTDSIVRGYS +P +F+SDFAAAMIKMGDISPLTGS+GEIRK C

Sbjct: 252 AQRGLLHSDQVLFNGGSTDSIVRGYSNSPSSFNDSFAAAMIKMGDISPLTGSSGEIRKVC 311

Query: 2167 RRIN 2178
R N

Sbjct: 312 GRN 315

Score = 176 bits (445), Expect = 3e-41
Identities = 99/169 (58%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKPCPGVVSCADILAI 1330
+ GCDGSILLDDTS FTGE+NA PNRNSARGF VIDNIKSAVEK CPGVVSCADILAI
Sbjct: 67 VNGCDGSILLDDTS-FTGEQNAGPNRNSARGFNVIDNIKSAVEKACPGVVSCADILAI 125

Query: 1331 RDSVQIVSGQTTNKNLNL*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 126 RDSV-----VQLGGPNWNVKVG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDA+TASQ+AAAN+ IPAP+ +L+QLIS F A+GLST+D+VALSG I
Sbjct: 143 RRDARTASQAAANSNIPAPSM SLSQLISSFRAVGLSTRDMVALSGAHTI 191

Score = 82.8 bits (203), Expect = 3e-13
Identities = 39/66 (59%), Positives = 49/66 (74%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLF 765
S + I + + L+ AQL+TNFY SCPNL S+VKS V+SA+S + RMGAS+LRLFF
Sbjct: 3 SNIAILLVIVITLLLQGGEAQLTTFYSTSCPNLLSTVKSGVKS AVSSQPRMGASILLRRLF 62

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 63 HDCFVN 68

>gb|AC090366.1| peroxidase precursor [Triticum aestivum]
Length = 180

Score = 179 bits (454), Expect = 2e-42
Identities = 83/123 (67%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCTNFR IYN+TNI+ FAR+RQ CP +GS DNNLAPLDLQT T F+N+Y+KNLVQ
Sbjct: 58 ARCTNFRDHIYNDTNIDAGFARSRQSGCPHATGSRDNNLAPLDLQTLTVFENHYYKNLVQ 117

Query: 1990 KKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLLHSDQ+LFNGG+ D++VR Y + F DF MI MGDI+PLTGSNG+IR NCR
Sbjct: 118 KRGLLHSDQELFNNGAADALVREYVGSQS AFFQDFVEGMIMMGDITPLTGSNGQIRMNCR 177

Query: 2170 RIN 2178

RIN
Sbjct: 178 RIN 180

Score = 64.7 bits (156), Expect = 8e-08
Identities = 33/55 (60%), Positives = 38/55 (69%)
Frame = +2

Query: 1493 WNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
W VK+GRRD+ TAS + A N IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 1 WEVKMGRRDSTTASFNGAENNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 55

>gb|ACN34270.1| unknown [Zea mays]
Length = 332

Score = 179 bits (453), Expect = 3e-42
Identities = 85/127 (66%), Positives = 103/127 (81%), Gaps = 3/127 (2%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG---DNNLAPLDLQTPTSFDNYYFK 1977
QARCTNFRA +YN+TNI+ AFAR R+ CP + SG DNNLAPLDLQTPT F+N Y++
Sbjct: 206 QARCTNFRAHVYNDTNIDGAFARARRSVCPAAASSGSGGDNNLAPLDLQTPTVFENDYYR 265

Query: 1978 NLVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSGEIR 2157
NLV +KGLLHSDQ+LFNG +TD+ V+ Y ++ F +DF A M+KMGDISPLTGSGEIR
Sbjct: 266 NLVCRKGLLHSDQELFNGAATDAQVQAYVSSQSAFFADVFAGMVKMGDISPLTGSSGEIR 325

Query: 2158 KNCRRIN 2178
KNCRRIN
Sbjct: 326 KNCRRIN 332

Score = 159 bits (401), Expect = 3e-36
Identities = 92/169 (54%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAREKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDT SF GEK A PN S RGFEVID IKS AV+K CPGVVSCADILAIAA
Sbjct: 79 VQGCDASLLDDTSPSQGEKMAKPNGSVRGFEVIDA IKS AVDKACPGVVSCADILAIAA 138

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W+VKLG
Sbjct: 139 RDSV-----VTLGGPNWDVKLG 155

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG I

Sbjct: 156 RRDSRTASFGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 204

Score = 76.6 bits (187), Expect = 2e-11
Identities = 35/61 (57%), Positives = 47/61 (77%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCF 777
+ LAL +++AQLST FY HSCP + +V+S +Q+AI+++E RMGAS+LRLFHDCF
Sbjct: 19 LLLALLAAGTSTSSAQLSTGFYSHSCPGVHDAVRSVLQAAIAREQRMGASILRRLFHDCF 78

Query: 778 V 780
V
Sbjct: 79 V 79

>gb|ACU24215.1| unknown [Glycine max]
Length = 329

Score = 178 bits (451), Expect = 5e-42
Identities = 85/124 (68%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR RIYN+TNI+ FA RQ+ CPRT+G+GDNNLA LD +TP FDN YFKNL
Sbjct: 206 KARCTSFDRRIYNQTNIDRTFALARQRRCPRTNGTGDNNLANLDFRTPNHFDNYYFKNLF 265

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GLL+ DQ LFNGGSTDS+VR YS N F DF AMI+MGDI PLTGS GEIRKNC
Sbjct: 266 IKRGLLNFDQVLFNGGSTDSLVRTYSQNKAFDFVVKAMIRMGDIKPLTGSQGEIRKNC 325

Query: 2167 RRIN 2178
RR+N
Sbjct: 326 RRVN 329

Score = 152 bits (383), Expect = 4e-34
Identities = 86/166 (51%), Positives = 102/166 (61%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCDGSILLDDT +F GEK A N NS RG+E+ID+IKS VEK+CPGVVSCADIL IA+
Sbjct: 78 VQGCDGSILLDDTPTFQGEKTAANNNSVRGYELIDDIKSKVEKICPGVVSCADILDIAS 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNV+LG
Sbjct: 138 RDSVVL-----LGGPFWNVRLG 154

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+R+A+ +AAN G IP PTSNL LI+RF GLS +D+VALSG
Sbjct: 155 RRDSRSANFTAANTGVIPPTSNTLNLI TRFQDQGLSARDMVALSG 200

Score = 80.1 bits (196), Expect = 2e-12
Identities = 39/78 (50%), Positives = 59/78 (75%), Gaps = 1/78 (1%)
Frame = +1

Query: 550 VCLSKLTMASFCSRLTIC-LALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISK 726
+ LS + ++F S I LA+ +L+ +++A LS NFY +CPN+F++VKS V+SA++K
Sbjct: 1 MALSPIRSSTFSSSSAIVTLAVLLLLTRTSSATLSKNFYSKTCPNVFNTVKS VVKS AVAK 60

Query: 727 ETRMGASLLRRLFHDCFV 780
E R+GAS++RRLFHDCFV
Sbjct: 61 EPRIGASIVRRLFHDCFV 78

>gb|AAB48184.1| peroxidase precursor [Linum usitatissimum]
Length = 323

Score = 178 bits (451), Expect = 5e-42
Identities = 83/123 (67%), Positives = 100/123 (81%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC +FR RIYNETNI+ +FA +++CP SGD+NLAPLDL+TPTSFDN Y+ NL++
Sbjct: 201 ARCVSFRDRIYNETNIDPSFASQSEENCPLAPNSGDDNLAPLDLKTPTSFDNYYNNLIE 260

Query: 1990 KKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
+KGLLHSDQ LFNNGSTDS+VR YS +P F++DFAAAM+KMGDI PLTGS GEIR C
Sbjct: 261 QKGLLHSDQVLFNNGSTDSLRSYSQSPKRFAADFAAAMVKMGDIKPLTGSQGEIRNVCS 320

Query: 2170 RIN 2178
R N
Sbjct: 321 RPN 323

Score = 143 bits (361), Expect = 1e-31
Identities = 82/170 (48%), Positives = 101/170 (59%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILL+DT SFTGE+ A PN S RG+ VI++IKS VE+VCPGVVSCADI+AIAA
Sbjct: 72 VNGCDGSILLEDDTSSFTGEQTAAPNNGSVRGYVIEDIKSKEVQCPGVVSCADIVAIAA 131

Query: 1331 RDSVQIVSQTTNKNLNL*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I GQ +W VK+G
Sbjct: 132 RDSTVIAGGQ-----SWEVKVG 148

Query: 1511 RRDARTASQSAANNGI-PAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS +AAN+G+ PAPTS+LN+LI F GLS D+V LSG+ I
Sbjct: 149 RRDSKTASFNAANSVLPAPTSNLNELIKSFGDQGLSANDMVVLSGSHTI 198

Score = 73.9 bits (180), Expect = 1e-10
Identities = 37/66 (56%), Positives = 45/66 (68%), Gaps = 2/66 (3%)
Frame = +1

Query: 592 LTICLALFVLIWGSANA--QLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
L CL L V + G+ QLST+FY SCP L +V+ V+SA+ KETR+ ASLLRL F
Sbjct: 8 LRSCLVLLVAVCGAGKCGWQLSTDFYSESCPMLMDTVRCEVESAVDKETRIAASLLRLHF 67

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 68 HDCFVN 73

>emb|CBI27506.1| unnamed protein product [Vitis vinifera]
Length = 266

Score = 177 bits (450), Expect = 7e-42
Identities = 89/125 (71%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RI+ N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 142 QARCVTFRDRIHDNGTNI DAGFASTRRRRCPVDNGNGDDNLAPLDLVT P NSFDNYYFKNL 201

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS + TFSSDFAAAM+KMGDI PLTGSNGEIRK
Sbjct: 202 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSRSTFSSDFAAAMVKMGDIPLTGSNGEIRKL 261

Query: 2164 CRRIN 2178
C IN
Sbjct: 262 CNAIN 266

Score = 138 bits (347), Expect = 6e-30
Identities = 77/169 (45%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAIAA 1330

+QGCD SILLDD+++ EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 15 VQGCDA SILLDD SATI QSEKNAPNNNSVRGFEVIDNVKSQVESICPGVVSCADILAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDS S+ +GGPTW VKLG

Sbjct: 75 RDS-----SVA VGGPTWTVKLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P+ L++L+S FS+ GL+T+++VALSG+ I

Sbjct: 92 RRDSTTSGLSQA AANLPSFRDGLDKLVSLFSSKGLNTREMV ALSGSH TI 140

>ref|XP_002274550.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 320

Score = 177 bits (450), Expect = 7e-42
Identities = 89/125 (71%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RI+ N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL

Sbjct: 196 QARC VTRDRIHDNGTNI DAGFASTRRRRC PVDNGDNNLAPLDLVTPNSFDNYYFKNL 255

Query: 1984 VQKGLLHSDQQLFN GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFN GGSTDSIV YS + TFSSDFAAAM+KMGDI PLTGSNGEIRK

Sbjct: 256 IQRKGLLQSDQVLFN GGSTDSIVTEYSKSRSTFSSDFAAAMV KMGDIDPLTGSNGEIRKL 315

Query: 2164 CRRIN 2178
C IN

Sbjct: 316 CNAIN 320

Score = 138 bits (347), Expect = 6e-30
Identities = 77/169 (45%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLDD+++ EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA

Sbjct: 69 VQGCDA SILLDD SATI QSEKNAPNNNSVRGFEVIDNVKSQVESICPGVVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDS S+ +GGPTW VKLG

Sbjct: 129 RDS-----SVA VGGPTWTVKLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P+ L++L+S FS+ GL+T+++VALSG+ I

Sbjct: 146 RRDSTTSGLSQA AANLPSFRDGLDKLVSLFSSKGLNTREMV ALSGSH TI 194

Score = 62.0 bits (149), Expect = 5e-07
Identities = 25/47 (53%), Positives = 38/47 (80%)
Frame = +1

Query: 640 AQLSTNFYHHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
AQLS+ FY ++CP S++++ +++A+S+E RM ASL+RL FHDCFV
Sbjct: 23 AQLSSKFYDNTCPKALSTIRTAIRTAVSRERRMAASLIRLHFHDCFV 69

>gb|ACN42168.1| peroxidase 1 [Sesuvium portulacastrum]
Length = 318

Score = 177 bits (449), Expect = 9e-42
Identities = 83/124 (66%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYN+++I +FA++ + +CP +G+GDNNLAPLD QTP FD+ YF+ LV
Sbjct: 195 QARCTNFRAHIYNDSINASFASLKANCPKNGTGDNNLAPLDPQTPNKFHDHIYFQGLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KK LHSQ+L NG ST S ++ YSTNP FSSDF +MIKMGDI PLTGSNGEIRKNC
Sbjct: 255 NKKAPLHSDQELTNGASTSSWIQKYSTNPSLFSDFGSMIKMGDIKPLTGSNGEIRKNC 314

Query: 2167 RRIN 2178
RRIN
Sbjct: 315 RRIN 318

Score = 157 bits (398), Expect = 7e-36
Identities = 89/165 (53%), Positives = 105/165 (63%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS LLDDTSSF GEK+A+PN SARGFEVID IK+AVE+VCPGVVSCADILA+ A
Sbjct: 68 VNGCDGSNLLDDTSSFKGEKSASPNFQSARGFEVIDQIKAAVERVCPGVVSCADILAVTA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW+VKLG
Sbjct: 128 RDSV-----VGLGGPTWDVKLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTA+Q+AAAN+ IP +S+L++LIS F GL+ KDLVAL G
Sbjct: 145 RRDARTANQAAANSSIPPASSLSRLISSFQNGQLTIKDLVALYG 189

Score = 86.3 bits (212), Expect = 3e-14
Identities = 46/68 (67%), Positives = 55/68 (80%), Gaps = 2/68 (2%)
Frame = +1

Query: 586 SRLTICLAL-FVLIW-GSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLRL 759
+RLT LAL FV+++ GS++AQL+TNFY SCP+LF V+ VQSAI KE RMGASLLRL
Sbjct: 2 ARLTCFLALAFVIVFVGSSSAQLTTNFYEKSCPHLFPVVRDQVQSAIRKEARMGASLLRL 61

Query: 760 FFHDCFVN 783
FHDCFVN
Sbjct: 62 HFHDCFVN 69

>ref|XP_002269058.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 319

Score = 177 bits (448), Expect = 1e-41
Identities = 88/125 (70%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP TSG GD+N+A LDL TP SFDN YFKNL
Sbjct: 195 QARCVTFRDRIYDNGTDIDAGFASTRRRRC PATSGDGDNNIAALDLVTPNSFDNYYFKNL 254

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTDSIV GYS +P TFSSDFA+AM+KMG+I PLTGS GEIRK
Sbjct: 255 IQKKGLLQSDQVLFSGGSTDSIVTGYSKSPSTFSSDFASAMVKMGNIEPLTGSAGEIRKL 314

Query: 2164 CRRIN 2178
C IN
Sbjct: 315 CSAIN 319

Score = 127 bits (318), Expect = 1e-26
Identities = 73/169 (43%), Positives = 94/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKS AVEKVC PGVVSCADILAIAA 1330
+QGCD SILL+D+SS EKNA N NS RG++VID++KS VE +CPG+VSCADILA+AA
Sbjct: 68 VQGDASILLNDSSSIQSEKNAPNNLSVRGYDVIDDKSEVESICPGIVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GP T WNVKLG 1510
RD+ VSG PTW V LG
Sbjct: 128 RDASVAVSG-----PTWTVNLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P + L++LIS F + GLS +D+VALSG+ I

Sbjct: 145 RRDSTTSGLSQAATNLPNFSDDLRLISLFGSKGLSERDMVALSGSHTI 193

Score = 63.9 bits (154), Expect = 1e-07
Identities = 28/57 (49%), Positives = 42/57 (73%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRRLFHDFV 780
LF+ AQLS++FY ++CP S++++ V++A+S+E RM ASL+RL FHDFV
Sbjct: 12 LFIFSNMPCEAQLSSSFYDNTCPKALSTIRTAVRTAVSRERRMAASLIRLHFHDFV 68

>emb|CBI27505.1| unnamed protein product [Vitis vinifera]
Length = 302

Score = 177 bits (448), Expect = 1e-41
Identities = 88/125 (70%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP TSG GD+N+A LDL TP SFDN YFKNL
Sbjct: 178 QARCVTRDRIDYDNGTDIDAGFASTRRRRCPATSGDGDNNIAALDLVTPNSFDNYYFKNL 237

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTDSIV GYS +P TFSSDFA+AM+KMG+I PLTGS GEIRK
Sbjct: 238 IQKKGLLQSDQVLFSGGSTDSIVTGYSKSPSTFSSDFASAMVKGNIPLTGSAGEIRKL 297

Query: 2164 CRRIN 2178
C IN
Sbjct: 298 CSAIN 302

Score = 127 bits (318), Expect = 1e-26
Identities = 73/169 (43%), Positives = 94/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILATAA 1330
+QGCD SILL+D+SS EKNA N NS RG++VID++KS VE +CPG+VSCADILA+AA
Sbjct: 51 VQGCDASILLNDSSSIQSEKNAPNNLNSVRGYDVIDDVKSEVESICPGIVSCADILAVAA 110

Query: 1331 RDSVQIVSGQTTNKNLTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VSG PTW V LG
Sbjct: 111 RDASVAVSG-----PTWTVNLG 127

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P + L++LIS F + GLS +D+VALSG+ I
Sbjct: 128 RRDSTTSGLSQAATNLPNFSDDLRLISLFGSKGLSERDMVALSGSHTI 176

Score = 62.8 bits (151), Expect = 3e-07
Identities = 26/47 (55%), Positives = 39/47 (82%)
Frame = +1

Query: 640 AQLSTNFYHSCP NFLSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
AQLS++FY ++CP S++++ V++A+S+E RM ASL+RL FHDCFV
Sbjct: 5 AQLSSSFYDNTCPKALSTIRTAVRTAVSRERRMAASLIRLHFHDCFV 51

>emb|CAL25300.1| properoxidase [Picea abies]
Length = 310

Score = 176 bits (447), Expect = 2e-41
Identities = 81/124 (65%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARC NFRA IYNETNI++ ++ + Q CP T+GSGD+NL+PLD TPT+FD Y+ NL
Sbjct: 187 QARCVNFRAHIYNETNIDSTYSTSLQSKCPSTAGSGDSNLSPLDYVTP TAFDKNYYSNLK 246

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS V Y++N +F SDFAAAM+KMG+I PLTG++G+IRKNC
Sbjct: 247 SKKGLLHSDQELFNGGSTDSQVTTYASNQNSFFSDFAAAMVKMGNIKPLTGTSGQIRKNC 306

Query: 2167 RRIN 2178
R+ N
Sbjct: 307 RKPN 310

Score = 159 bits (401), Expect = 3e-36
Identities = 88/165 (53%), Positives = 103/165 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AA 1330
+ GCDGS+LLDD+S+ TGEK ANPN NSARGF+VID IKS VEK C GVVSCADILAI+A
Sbjct: 60 VNGCDGSVLLDDSSITITGEKTANPNANSARGFDVIDTIKSNEKACSGVVSCADILAI SA 119

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 120 RDSV-----VELGGPSWTVM LG 136

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+ TAS++ ANN IP PTS+L+ LIS F A GLSTK++VALSG
Sbjct: 137 RRDSTASKNGANNIPPTSSLSNLISLFAQGLSTKEMVALSG 181

Score = 69.7 bits (169), Expect = 3e-09
Identities = 32/51 (62%), Positives = 38/51 (74%)
Frame = +1

Query: 631 SANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFVN 783
+AN QLS+ FY SCP S VK+ V+ A++ E RMGASLLR L F H D C F V N
Sbjct: 11 TANGQLSSTFYAQCPTALS VVKA AVRQAVANEKRMGASLLR L F H D C F V N 61

>ref|XP_002269145.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 331

Score = 175 bits (444), Expect = 3e-41
Identities = 87/125 (69%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARC V T F R D R I Y G N G T N I D A G F A S T R R R R C P A D N G N G D D N L A P L D L V T P N S F D N N Y F K N L 266

Query: 1984 VQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS GEIRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGEIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 136 bits (343), Expect = 2e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGC DASILLDD SPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 63.5 bits (153), Expect = 2e-07
Identities = 32/72 (44%), Positives = 49/72 (68%), Gaps = 1/72 (1%)
Frame = +1

Query: 568 TMAFCSRLTICLA-LFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGA 744
T S S I +A L +L AQLS++FY ++CP+ S++++ +++A+S+E RM A
Sbjct: 9 TWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNTCPSALSTIRTAIRTAIVSRERRMAA 68

Query: 745 SLLRLLFFHDCFV 780
SL+RL FHDCFV
Sbjct: 69 SLIRLHFHDCFV 80

>gb|ACJ85500.1| unknown [Medicago truncatula]
Length = 229

Score = 174 bits (441), Expect = 8e-41
Identities = 99/169 (58%), Positives = 106/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTS+FTGEKNA PN+NS RGF+VIDNIK+AVE VCPGVVSCADILAIAA
Sbjct: 72 VNGCDGSILLDDTSNFTGEKNALPNKNSVRGFDVIDNIKTAVENVCPGVVSCADILAIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
DSV I+ G PTWNVKLG
Sbjct: 132 TDSVAILGG-----PTWNVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDA TASQS AN IP PTSNLN L S F +GLSTKDLVALSG I
Sbjct: 149 RRDATTASQSDANTAIPRPTSNLNILTSMFKNVGLSTKDLVALSGAHTI 197

Score = 95.1 bits (235), Expect = 6e-17
Identities = 49/68 (72%), Positives = 55/68 (80%), Gaps = 1/68 (1%)
Frame = +1

Query: 583 CSRLTI-CLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRL 759
CSR+T+ L LFVLI GS NAQLSTNFY +CP L S V+ VQSAISKE R+GAS+LRL
Sbjct: 6 CSRITMFSLVLFVLIIGSVNAQLSTNFYSKTCPKLSSIVQRQVQSAISKEARIGASILRL 65

Query: 760 FFHDCFVN 783
FFHDCFVN
Sbjct: 66 FFHDCFVN 73

Score = 43.1 bits (100), Expect = 0.26
Identities = 18/24 (75%), Positives = 21/24 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFART 1878
QA+CT FR RIYNETNI+T+FA T
Sbjct: 199 QAKCTTFRVRIYNETNIDTSFAST 222

>emb|CAN80097.1| hypothetical protein [Vitis vinifera]
Length = 331

Score = 173 bits (438), Expect = 2e-40
Identities = 86/125 (68%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSVSGSDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYNGTNI DAGFASTRRRRCPADNGNGDDNLAPLDLVTNPSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS G IRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGXIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 136 bits (343), Expect = 2e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGC DASILLDDSP TIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNLNI*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 63.9 bits (154), Expect = 1e-07

Identities = 32/78 (41%), Positives = 52/78 (66%), Gaps = 8/78 (10%)
Frame = +1

Query: 571 MASFC SRLTICLA-LFVLIWG-----SANAQLSTNFYHSCP NLFSSVKSTVQSAISK 726
+A+ SR C++ F+L+ G AQLS++FY + CP+ S++++ +++A+S+
Sbjct: 3 LAAGSSRWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNXCPSALSTIRTAIRTAVSR 62

Query: 727 ETRMGASLLRLFFHDCFV 780
E RM ASL+RL FHDCFV
Sbjct: 63 ERRMAASLIRLHFHDCFV 80

>emb|CBI27503.1| unnamed protein product [Vitis vinifera]
Length = 357

Score = 172 bits (437), Expect = 2e-40
Identities = 85/121 (70%), Positives = 97/121 (80%), Gaps = 1/121 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYNGTNI DAGFASTRRRRC PADNGGDDNLAPLDLVTPNSFDNYYFKNL 266

Query: 1984 VQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS GEIRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKGDI EPLIGSAGEIRKF 326

Query: 2164 C 2166
C
Sbjct: 327 C 327

Score = 136 bits (343), Expect = 2e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGCDASILLDDSP TIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 63.5 bits (153), Expect = 2e-07
Identities = 32/72 (44%), Positives = 49/72 (68%), Gaps = 1/72 (1%)
Frame = +1

Query: 568 TMAFCSRLTICLA-LFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
T S S I +A L +L AQLS++FY ++CP+ S++++ +++A+S+E RM A
Sbjct: 9 TWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNTCPSALSTIRTAIRTAVSRERRMAA 68

Query: 745 SLLRLLFFHDCFV 780
SL+RL FHDCFV
Sbjct: 69 SLIRLHFHDCFV 80

>emb|CBI27502.1| unnamed protein product [Vitis vinifera]
Length = 266

Score = 172 bits (437), Expect = 2e-40
Identities = 86/125 (68%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 142 QARCVTFRDRIYNGTNDAGFASTRRRRCPADNGGDDNLAPLDLVTSPNSFDNYYFKNL 201

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS G IRK
Sbjct: 202 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGVIRKF 261

Query: 2164 CRRIN 2178
C IN
Sbjct: 262 CNVIN 266

Score = 136 bits (343), Expect = 2e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 15 VQGCDASILLDDSPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI* LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 75 RDA-----SVAVGGPTWTLKLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 92 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 140

>ref|XP_002269169.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 331

Score = 172 bits (437), Expect = 2e-40
Identities = 86/125 (68%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYNGTNIIDAGFASTRRRRCPADNGGDDNLAPLDLVTPNSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS G IRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFFSAMVKMGDIEPLIGSAGVIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 136 bits (343), Expect = 2e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGCDASILLDDSPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 64.7 bits (156), Expect = 8e-08
Identities = 32/78 (41%), Positives = 53/78 (67%), Gaps = 8/78 (10%)
Frame = +1

Query: 571 MASFCSRLTICLA-LFVLIWG-----SANAQLSTNFYHSCPNLFSSVKSTVQSAISK 726
+A+ SR C++ F+L+ G AQLS++FY ++CP+ S++++ +++A+S+

Sbjct: 3 LAAGSSRWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNACPSALSTIRTAIRTAIVSR 62

Query: 727 ETRMGASLLRLLFFHDCFV 780
E RM ASL+RL FHDCFV

Sbjct: 63 ERRMAASLIRLHFHDCFV 80

>gb|AA013838.1|AF405326_1 peroxidase 2 [Lupinus albus]
Length = 260

Score = 172 bits (437), Expect = 2e-40
Identities = 81/126 (64%), Positives = 102/126 (80%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG--DNNLAPLDLQTPTSFDNYYFKN 1980
+ARC+++R RIY++TNI+ FA++RQ++CPR S DNN+A LD +TPT FDN Y+KN

Sbjct: 135 KARCSSYRDRIYDDTNIDKLFKSRQRNCPRKSSGTVKDNNVAVLDFKTPTHFDNLYYKN 194

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ KKGLLHSDQ+LFNGGSTDS+V YS N F+SDF AMIKMG+I PLTGSNG+IRK

Sbjct: 195 LINKKGLLHSDQQLFNGGSTDSLVTTYSNNEKAFNSDFVTAMIKMGNIKPLTGSNGQIRK 254

Query: 2161 NCRRIN 2178
+CRR N

Sbjct: 255 HCRRAN 260

Score = 155 bits (392), Expect = 4e-35
Identities = 92/170 (54%), Positives = 102/170 (60%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTSSF GEK A PN NS RGFEVID IKS VE+ CPGVVSCADI+AIAA

Sbjct: 7 VNGCDGSILLDDTSSFRGEKTAPPNNNSVRGFEVIDAIKSKVEEACPGVVSCADIVAIAA 66

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I LGGP WNVK+G

Sbjct: 67 RDSTAI-----LGGPYWNVKVG 83

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS S A++G IP P S L+ LISRF A GLS KD+VALSG I

Sbjct: 84 RRDSKTASFSDASSGVIPPPFSTLSNLISRFAQGLSIKDMVALS GAHTI 133

>gb|ABA96220.1| Cationic peroxidase 1 precursor, putative, expressed [Oryza sativa
(japonica cultivar-group)]

gb|EAY79691.1| hypothetical protein OsI_34838 [Oryza sativa Indica Group]

gb|EAZ19422.1| hypothetical protein OsJ_34979 [Oryza sativa Japonica Group]

Length = 291

Score = 172 bits (437), Expect = 2e-40
Identities = 78/124 (62%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 170 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYAFDNFYKKNL 227

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AAM+KMG+I+P+TGS+G+IRKNC
Sbjct: 228 NKKGVLHSDQQLFNGGSADSQTTTYSNMATFFTFSAAMVKMGNINPITGSSGQIRKNC 287

Query: 2167 RRIN 2178
R++N
Sbjct: 288 RKNV 291

Score = 146 bits (369), Expect = 2e-32
Identities = 82/170 (48%), Positives = 98/170 (57%)
Frame = +2

Query: 1148 QMQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
++ GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ +E +CP VVSCADILA+A
Sbjct: 42 RIAGCDGSVLLDDTPTFTGEKTAAPNNSLRGFDVIDNIKAHIEGICPQVVSCADILAVA 101

Query: 1328 ARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
AR+SV + LGGPTW V+L
Sbjct: 102 ARESV-----VALGGPTWVVQL 118

Query: 1508 GRRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
GRRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 119 GRRDSTTASLDTANNDIPAPTFDLGDLTKSFSNKGLSATDMIALSGAHTI 168

>tpe|CAH69378.1| TPA: class III peroxidase 136 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 317

Score = 172 bits (437), Expect = 2e-40
Identities = 78/124 (62%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 196 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYAFDNFYKKNL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AAM+KMG+I+P+TGS+G+IRKNC
Sbjct: 254 NKKGVLHSDQQLFNGGSADSQTTTYSSNMATFFTFDSAAMVKMGNINPITGSSGQIRKNC 313

Query: 2167 RRIN 2178
R++N
Sbjct: 314 RKNV 317

Score = 146 bits (369), Expect = 2e-32
Identities = 82/169 (48%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ +E +CP VVSCADILA+AA
Sbjct: 69 VNGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFVIDNIKAHIEGICPQVVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
R+SV + LGGPTW V+LG
Sbjct: 129 RESV-----VALGGPTWVWQLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 146 RRDSTTASLDTANNDIPAPTFDLGDLTKSFSNKGLSATDMIALSGAHTI 194

Score = 71.2 bits (173), Expect = 9e-10
Identities = 35/62 (56%), Positives = 45/62 (72%), Gaps = 1/62 (1%)
Frame = +1

Query: 601 CLALFVLIWGS-ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCF 777
C A+ +L + +AQLS NFY SCPN +++ V+SAI++E RMGASLLRL FHDCF
Sbjct: 9 CSAIALLFAANLVSQAQLSANFYDKSCPALPTIRI AVRSAIARENRMGASLLRFFHDCF 68

Query: 778 VN 783
VN
Sbjct: 69 VN 70

>ref|XP_002269216.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 199

Score = 172 bits (436), Expect = 3e-40
Identities = 86/125 (68%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983

QARC R RIY N TNI+T FA TR++ CP +G+GD+NLAPLD+ TP SFDN YFKNL
Sbjct: 75 QARCVTVRDRIYDNGTNIIDTGFASRRRRCPVDNGNGDDNLAPLDVVTPNSFDNYYFKNL 134

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSS+FA+AM+KMGDI PL GS GEIRK

Sbjct: 135 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSEFASAMVKMGDIEPLLSAGEIRKI 194

Query: 2164 CRRIN 2178

C IN

Sbjct: 195 CNVIN 199

Score = 38.9 bits (89), Expect = 5.0
Identities = 22/42 (52%), Positives = 31/42 (73%)
Frame = +2

Query: 1532 SQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

SQ+AAAN +P+ L++LI FS+ GLST+D+VALSG+ I

Sbjct: 34 SQAAAN--LPSFRDGLDRLIPLFSSKGLSTRDMVALSGSHTI 73

>emb|CAH10839.1| peroxidase [Picea abies]
Length = 317

Score = 172 bits (436), Expect = 3e-40
Identities = 83/124 (66%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT FRARIYNE+NI+T+FA + + SCP S GDN L+PLDL TPT+FDN Y+ +L

Sbjct: 196 QARCTTFRARIYNESNIDTSFATSVKSSCP--SAGGDNTLSPLDLATPTTFDNKYITDLG 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

+KGLLHSDQQLF+GGST+S V YS N TF +DFAAAM+KMG+ISPLTG++G+IRKNC

Sbjct: 254 NRKGLLHSDQQLFSGGSTNSQVTTYSANQNTFFTFDFAAAMVKMGNISPLTGTSGQIRKNC 313

Query: 2167 RRIN 2178

R+ N

Sbjct: 314 RKAN 317

Score = 158 bits (400), Expect = 4e-36
Identities = 91/165 (55%), Positives = 100/165 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330

+ GCDGSILLDD S+FTGEK A PN NS RGF+VID IK+ VE C GVVSCADILAI A

Sbjct: 69 VNGCDGSILLDDNSTFTGEKTALPNANSVRGFDVIDTIKTQVEAACSGVWSCADILAIVA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG

Sbjct: 129 RDSV-----VQLGGPTWTVLLG 145

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS SAANN IP+P SNL+ LIS F+A GLSTKDLVALSG

Sbjct: 146 RRDSTTASLSAANNIPSPASNLSALISSFTAHLSTKDLVALSG 190

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/64 (48%), Positives = 41/64 (64%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHD 771
+ +C+ I +A+ QL++ FY CP S VK+ V A++ E RMGASLLRL FHD

Sbjct: 7 IVLCVLCISSINNAAHGQLTSTFYNKLCPTALSIVKAAVNKAVNNEKRMGASLLRHFHD 66

Query: 772 CFVN 783

CFVN

Sbjct: 67 CFVN 70

>ref|XP_002266365.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 328

Score = 172 bits (435), Expect = 4e-40
Identities = 81/124 (65%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT FR RIYNE NI+ +F + Q +CP S GDN L+PLD QTPT+FDN Y+ NLV

Sbjct: 207 QARCTTFRTRIYNEANIDASFKTSLQANCP--SSGGDNTLSPLDTQTPTTFDNAYYTNLV 264

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNGGSTD++V YST TF +DFA AM+KMG++SPLTG++G+IR NC

Sbjct: 265 NKKGLLHSDQQLFNGGSTDAVVNTYSTRSTTFFTFANAMVKMGNLSPLTGTSGQIRTNC 324

Query: 2167 RRIN 2178

R+ N

Sbjct: 325 RKTN 328

Score = 147 bits (372), Expect = 8e-33
Identities = 83/169 (49%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILATAA 1330
+ GCD SILLDDTS+FTGEK A PN NS RG+EV+D IKS +E CPGVVSCADILA+AA
Sbjct: 80 VNGCDASILLDDTSNFTGEKTAGPNANSVRGYEVVDTIKSQLEASCPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GP+W V+LG
Sbjct: 140 RDSV-----VALRGPSSWVRLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ IPAPT NL+ LIS F+ G + +++VALSG+ I
Sbjct: 157 RRDSTTASLSAANSNIPAPTLNLSGLISAFTNKGFNAREMVALSGSHTI 205

Score = 76.3 bits (186), Expect = 3e-11
Identities = 35/52 (67%), Positives = 40/52 (76%)
Frame = +1

Query: 628 GSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783
G A+AQL+TNFY +CPN S +KS V SA+ E RMGASLLRL FHDCFVN
Sbjct: 30 GMASAQLTTFYAKTCPNALSIIKSAVNSAVKSEARMGASLLRRLFHDCFVN 81

>ref|NP_001106040.1| plasma membrane-bound peroxidase 2b precursor [Zea mays]
sp|A5H452.1|PER70_MAIZE RecName: Full=Peroxidase 70; AltName: Full=Plasma membrane-bound
peroxidase 2b; Short=pmPOX2b; Flags: Precursor
gb|ABN48843.1| plasma membrane-bound peroxidase 2b [Zea mays]
Length = 321

Score = 172 bits (435), Expect = 4e-40
Identities = 77/123 (62%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
A+C NFRA IYN+TN+ AFA R+ +CP +G+GD NLAPLD TPT+FDN Y+ NL+
Sbjct: 199 AQCKNFRAHIYNDTNVNAAFATLRRANCPAAAGNGDGNLAPLDTATPTAFDNAYYTLLA 258

Query: 1990 KKGLLHSDQQLFNGGSTDIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQQLFNGG+TD +VR Y++ P FS DFAAAMI+MG+ISPLTG+ G+IR+ C
Sbjct: 259 QRGLLHSDQQLFNGGATDGLVRTYASTPRRFSRDFAAAMIRMGNISPLTGTGQGI RRACS 318

Query: 2170 RIN 2178
R+N
Sbjct: 319 RVN 321

Score = 140 bits (353), Expect = 1e-30

Identities = 80/169 (47%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCDGS+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE VCPGVVSCADILA+AA

Sbjct: 71 VQGCDGSVLLNDTATFTGEQTANPNVGSIRFGVVDNIKAQVEAVCPGVVSCADILAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 131 RDSV-----VALGGPSWRVLLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS + AN+ +PAP+ +L L + F+ LS DLVALSG I

Sbjct: 148 RRDSTTASLALANSDLPAPSLDLANLTAAFAKKRLSRTDLVALSGAHTI 196

Score = 68.2 bits (165), Expect = 8e-09
Identities = 34/72 (47%), Positives = 49/72 (68%)
Frame = +1

Query: 565 LTMASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744

+ +SF S L++ + L + A+AQLS FY SCP +++K+ V +A+++E RMGA

Sbjct: 1 MASSSFTS-L SVMVLLCLAAA AVASAQLSPTFYRSRCPRALATIKA AVTAAVAQEARMGA 59

Query: 745 SLLRRLFHDCFV 780

SLLRL FHDCFV

Sbjct: 60 SLLRLHFHDCFV 71

>gb|EAY82023.1| hypothetical protein OsI_37207 [Oryza sativa Indica Group]
gb|EAZ17184.1| hypothetical protein OsJ_32691 [Oryza sativa Japonica Group]
Length = 291

Score = 171 bits (434), Expect = 5e-40
Identities = 78/124 (62%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+

Sbjct: 170 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYTFDNFYKLL 227

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

KKG+LHSDQQLFNGGS DS YS+N TF +DF+AA++KMG+I PLTGS+G+IRKNC

Sbjct: 228 NKKGVLHSDQQLFNGGSADSQTTTYSNMATFFTFSSAAIVKMGNI DPLTGSSGQIRKNC 287

Query: 2167 RRIN 2178

R++N

Sbjct: 288 RKNV 291

Score = 146 bits (368), Expect = 2e-32
Identities = 83/167 (49%), Positives = 95/167 (56%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ VE +CP VVSCADILA+AARD
Sbjct: 45 GCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAQVEGICPQVVSCADILAVAARD 104

Query: 1337 SVQIVSQGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + GGPTW V+LGRR
Sbjct: 105 SVFAL-----GGPTWVVLGRR 121

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 122 DSTTASLDTANNDIPAPTLDLGLTKSFSNKGLSATDMIALSGAHTI 168

>gb|ABA91154.1| Cationic peroxidase 1 precursor, putative, expressed [Oryza sativa
(japonica cultivar-group)]
Length = 254

Score = 171 bits (434), Expect = 5e-40
Identities = 78/124 (62%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 133 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTG--DNNISPLDASTPYTFDNFYKLL 190

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AA++KMG+I PLTGS+G+IRKNC
Sbjct: 191 NKKGVLSHSDQQLFNGGSADSQTTTYSSNMATFFTFSSAAIVKMGNDPLTGSSGQIRKNC 250

Query: 2167 RRIN 2178
R++N
Sbjct: 251 RKNV 254

Score = 148 bits (374), Expect = 4e-33
Identities = 84/169 (49%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI A 1330
M+GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ VE +CP VVSCADILA+AA
Sbjct: 6 MKGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAQVEGICPQVVSCADILAVAA 65

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGPTWNVKLG 1510
RDSV + GGPTW V+LG
Sbjct: 66 RDSVFAL-----GGPTWVWVQLG 82

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 83 RRDSTTASLDTANNDIPAPTLDLGDLTKSFSNKGLSATDMIALSGAHTI 131

>ref|NP_001065566.1| Os11g0112200 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69373.1| TPA: class III peroxidase 131 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF27411.1| Os11g0112200 [Oryza sativa Japonica Group]
Length = 317

Score = 171 bits (434), Expect = 5e-40
Identities = 78/124 (62%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 196 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTG--DNNISPLDASTPYTFDNFYKKNL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AA++KMG+I PLTGS+G+IRKNC
Sbjct: 254 NKKGV LHSDQQLFNGGSADSQTTTYSSNMATFFTFDSAAIVKMGNDPLTGSSGQIRKNC 313

Query: 2167 RRIN 2178
R++N
Sbjct: 314 RKNV 317

Score = 146 bits (369), Expect = 2e-32
Identities = 83/169 (49%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCVGVVSCADILAI 1330
+ GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ VE +CP VVSCADILA+AA
Sbjct: 69 VNGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAQVEGICPVVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGPTWNVKLG 1510
RDSV + GGPTW V+LG
Sbjct: 129 RDSVFAL-----GGPTWVWVQLG 145

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 146 RRDSTTASLDTANNDIPAPTLDLGDLTKSFSNKGLSATDMIALSGAHTI 194

Score = 74.7 bits (182), Expect = 8e-11
Identities = 36/67 (53%), Positives = 48/67 (71%)
Frame = +1

Query: 583 CSRLTICLALFVLIWGSANAQLSTNFYHSCP NFLSSVKSTVQSAISKETRMGASLLRLF 762
CS ++ A ++ +AQLS NFY SCPN S+++ V+SA++KE RMGASLLRL
Sbjct: 9 CSVIALLF AAHLV-----SAQLSANFYDKSCP NALSTIRTAVRS AVAKENRMGASLLRLH 63

Query: 763 FHDCFVN 783
FHDCFVN
Sbjct: 64 FHDCFVN 70

>gb|EEE67815.1| hypothetical protein OsJ_25569 [Oryza sativa Japonica Group]
Length = 324

Score = 171 bits (433), Expect = 6e-40
Identities = 78/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAPLD TP +FDN Y+ NL+
Sbjct: 200 QAQCQNFDRRIYNETNIDSAFATQRQANCPRPTGSGDSNLAPLDTTTPNAFDNAYYSNLL 259

Query: 1987 QKKGLLHSDQQLFNNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNNGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 260 SNKGLLHSDQVLFNNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQGQIRLSC 319

Query: 2167 RRIN 2178
++N
Sbjct: 320 SKVN 323

Score = 116 bits (290), Expect = 2e-23
Identities = 71/167 (42%), Positives = 86/167 (51%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AARD
Sbjct: 80 GCDASVLLSGQ-----EQNAGPNVGLRGSVIDNAKARVEAICNQTVSCADILAVAARD 134

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 135 SV-----VALGGPSWTVLLGRR 151

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 152 DSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 198

Score = 71.6 bits (174), Expect = 7e-10
Identities = 34/69 (49%), Positives = 46/69 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
Sbjct: 7 SLSLMLLVAAAMASVASAQLSATFYDTSCPINALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFVNVIY 792
HDCFV +
Sbjct: 67 HDCFVQASF 75

>ref|NP_001060628.1| Os07g0677200 [Oryza sativa (japonica cultivar-group)]
dbj|BAC83103.1| peroxidase [Oryza sativa Japonica Group]
dbj|BAF22542.1| Os07g0677200 [Oryza sativa Japonica Group]
dbj|BAG93342.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG96895.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 317

Score = 171 bits (433), Expect = 6e-40
Identities = 78/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAPLD TP +FDN Y+ NL+
Sbjct: 193 QAQCQNFRDRIYNETNIDSAFATQRQANCPRPTSGGDSNLAPLDTTTPNAFDNAYYSNLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 253 SNKGLLHSDQVLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQQIRLSC 312

Query: 2167 RRIN 2178
++N
Sbjct: 313 SKVN 316

Score = 118 bits (296), Expect = 5e-24
Identities = 72/169 (42%), Positives = 88/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+QGCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AA
Sbjct: 71 VQGCDASVLLSGQ-----EQNAGPNVGLRGFVSDNAKARVEAICNQTVSCADILAVAA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 126 RDSV-----VALGGPSWTVLLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I

Sbjct: 143 RRDSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 191

Score = 71.2 bits (173), Expect = 9e-10
Identities = 34/65 (52%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F

Sbjct: 7 SLSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITAAVNSEARMGASLLRLHF 66

Query: 766 HDCFV 780
HDCFV

Sbjct: 67 HDCFV 71

>tpe|CAH69353.1| TPA: class III peroxidase 111 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 323

Score = 171 bits (433), Expect = 6e-40
Identities = 78/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAPLD TP +FDN Y+ NL+

Sbjct: 199 QAQCQNFDRRIYNETNIDSAFATQRQANCPRPTGSGDSNLAPLDTTTPNAFDNAYYSNLL 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C

Sbjct: 259 SNKGLLHSDQVLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTGQIRLSC 318

Query: 2167 RRIN 2178
++N

Sbjct: 319 SKVN 322

Score = 113 bits (283), Expect = 2e-22

Identities = 69/162 (42%), Positives = 84/162 (51%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AARD

Sbjct: 80 GCDASVLLSGQ-----EQNAGPNVGLRGSVIDNAKARVEAICNQT VSCADILAVAARD 134

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR

Sbjct: 135 SV-----VALGGPSWTVLLGRR 151

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALS 1642

D+ TAS++ AN +PAP+S+L +LI FS GL D+VALS

Sbjct: 152 DSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALS 193

Score = 71.6 bits (174), Expect = 7e-10
Identities = 34/69 (49%), Positives = 46/69 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F

Sbjct: 7 SLSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFVNVIY 792

HDCFV +

Sbjct: 67 HDCFVQASF 75

>emb|CBI27501.1| unnamed protein product [Vitis vinifera]
Length = 265

Score = 170 bits (431), Expect = 1e-39
Identities = 82/124 (66%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YN T+I+ FA TR++ CP +G+GD NLAPL+L TP SFDN YFKNL+

Sbjct: 142 QARCVTFRDRVYNGTDIDAGFASTRRRRCPADNGNGDANLAPLELVTPNSFDNYYFKNLI 201

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q+KGLL SDQ LF+GGSTD+IV YS +P TF SDF A+AM+KMGDI PLTGS G IRK C

Sbjct: 202 QRKGLLQSDQVLFSGGSTDTIVNEYSKPKTFRSDFASAMVKMGDIEPLTGSAGVIRKFC 261

Query: 2167 RRIN 2178

IN

Sbjct: 262 NVIN 265

Score = 134 bits (337), Expect = 9e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLDD+SS EKNA N NS RG+EVIDNIKS VE +CPGVVSCADI+A+AA
Sbjct: 15 VQGCDASILLDDSSSIQSEKNAPNNLSVRGYEVIDNIKSKVESICPGVVSCADIVAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VS GPTW VKLG
Sbjct: 75 RDASVAVS-----GPTWTVKLG 91

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P+ +L++L+S F + GLS +D+VALSG+ I
Sbjct: 92 RRDSTTSGLSLAATNLPSFRDSLDKLVSLFGSKGLSARDMVALSGSHTI 140

>ref|XP_002269266.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 326

Score = 170 bits (431), Expect = 1e-39
Identities = 82/124 (66%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YN T+I+ FA TR++ CP +G+GD NLAPL+L TP SFDN YFKNL+
Sbjct: 203 QARCVTFRDRVYNGTDIDAGFASTRRRRCPADNGNGDANLAPLELVTPNSFDNYYFKNLI 262

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q+KGLL SDQ LF+GGSTD+IV YS +P TF SDF+A+AM+KMGDI PLTGS G IRK C
Sbjct: 263 QRKGLLQSDQVLFSGGSTDTIVNEYSKSPKTFRSDFASAMVKMGDIEPLTGSAGVIRKFC 322

Query: 2167 RRIN 2178
IN
Sbjct: 323 NVIN 326

Score = 134 bits (337), Expect = 9e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLDD+SS EKNA N NS RG+EVIDNIKS VE +CPGVVSCADI+A+AA
Sbjct: 76 VQGCDASILLDDSSSIQSEKNAPNNLSVRGYEVIDNIKSKVESICPGVVSCADIVAVAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

Sbjct: 136 RD+ VS GPTW VKLG
RDASVAVS-----GPTWTVKLG 152

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P+ +L++L+S F + GLS +D+VALSG+ I

Sbjct: 153 RRDSTTSGLSLAATNLPFRDSDLKLVSLFGSKGLSARDMVALSGSHTI 201

Score = 62.4 bits (150), Expect = 4e-07
Identities = 31/69 (44%), Positives = 46/69 (66%), Gaps = 1/69 (1%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGS-ANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLL 753
S S I LA+F+++ AQLS FY +CP +++++ V++A+S+E RM ASL+

Sbjct: 8 SCISPACIFLAVFLILSNMPCEAQLSPTFYDDTCPTALTIRTAVRTAVSRERRMAASLI 67

Query: 754 RLFFHDCFV 780

RL FHDCFV

Sbjct: 68 RLHFHDCFV 76

>ref|XP_002509730.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
gb|EEF51117.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
Length = 323

Score = 170 bits (431), Expect = 1e-39
Identities = 82/125 (65%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIYN ++I+ FA TR++ CP +G+GD NLA LDL TP SFDN YF+NL

Sbjct: 199 QARCLTFRGRIYNNASDIDAGFASTRRRRQCPANNGNGDGNLAALDLVTPNSFDNYYFRNL 258

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTD+IV YS +P TFSSDFA+AM+KMGDI PLTGS GEIR+

Sbjct: 259 IQKKGLLQSDQVLFSGGSTDNIVNEYSRSPSTFSSDFASAMVKMGDIEPLTGSQGEIRRL 318

Query: 2164 CRRIN 2178

C +N

Sbjct: 319 CNVVN 323

Score = 141 bits (355), Expect = 7e-31
Identities = 79/169 (46%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILATAA 1330
+QGCDGSILLDDTSS TGEK A N NS RGF+VIDN K+ VE +CPG+VSCADI+A+AA
Sbjct: 72 VQGCDGSILLDDTSSMTGEKFARNNNNSVRGFQVIDNAKAQVESICPGIVSCADIVAVAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W VKLG
Sbjct: 132 RDA-----SVAVGGPSWTVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ +ASQ A+ +P T +L LIS F GLS +D+VALSG I
Sbjct: 149 RRDSTSASQRLADANLPGFTDSLESLSLFRKGLSARDMVALSGAHTI 197

Score = 74.7 bits (182), Expect = 8e-11
Identities = 33/67 (49%), Positives = 51/67 (76%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRL 759
F +R+ + + L VL ++AQLS+NFY ++CPN S++++ ++SA+S+E RM ASL+RL
Sbjct: 6 FFRNRMVLTIFLIVLSSMQSHAQLSSNFYDNTCPNALSTIRTAIRSAVSRERRMSASLRL 65

Query: 760 FFHDCFV 780
FHDCFV
Sbjct: 66 HFHDCFV 72

>emb|CBI18066.1| unnamed protein product [Vitis vinifera]
Length = 263

Score = 170 bits (430), Expect = 1e-39
Identities = 81/124 (65%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETNI+ +F + Q +CP S GDNNL+PLD ++PT+FDN YF NLV
Sbjct: 142 QARCTNFRDRLYNETNIDASFQSSLQANCP--SSGGDNNLSPLDTKSPTTFDNAYFTNLV 199

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLFNGGSTDS V YST TF +DFA A++KMG++SPLTG++G+IR NC
Sbjct: 200 NNKGLLHSDQQLFNGGSTDSQVTTYSTKSTFFTFDFANAIVKMGNSPLTGTSGQIRTNC 259

Query: 2167 RRIN 2178
R+ N
Sbjct: 260 RKTN 263

Score = 150 bits (379), Expect = 1e-33
Identities = 86/169 (50%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCD SILLDDTS+FTGEK A PN NS RGF+VID IKS VE CPGVVSCADILA+ A
Sbjct: 15 VNGCDASILLDDTSNFTGEKTAVPNANSVRGFVDITIKSQVESSCPGVVSCADILAVVA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 75 RDSV-----VALGGPSWTVRLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ IPAPT NL+ LIS FS G S ++VALSG+ I
Sbjct: 92 RRDSTTASLSTANS DIPAPTLNLSGLISSFSNKGFSANEMVALSGSHTI 140

>ref|XP_002268259.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 298

Score = 170 bits (430), Expect = 1e-39
Identities = 81/124 (65%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETNI+ +F + Q +CP S GDNNL+PLD ++PT+FDN YF NLV
Sbjct: 177 QARCTNFRDRLYNETNIDASFQSSLQANCP--SSGGDNNLSPLDTKSPPTFDNAYFTNLV 234

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLFNGGSTDS V YST TF +DFA A++KMG++SPLTG++G+IR NC
Sbjct: 235 NNKGLLHSDQQLFNGGSTDSQVTTYSTKSTFFTFDFANAIVKMGNSPLTGTSGQIRTNC 294

Query: 2167 RRIN 2178
R+ N
Sbjct: 295 RKTN 298

Score = 150 bits (380), Expect = 9e-34
Identities = 86/169 (50%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
++GCD SILLDDTS+FTGEK A PN NS RGF+VID IKS VE CPGVVSCADILA+ A
Sbjct: 50 VKGCDASILLDDTSNFTGEKTAVPNANSVRGFVDITIKSQVESSCPGVVSCADILAVVA 109

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 110 RDSV-----VALGGPSWTVRLG 126

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ IPAPT NL+ LIS FS G S ++VALSG+ I
Sbjct: 127 RRDSTTASLSTANS DIPAPTLNLSGLISSFSNKGFSANEMVALSGSHTI 175

Score = 71.2 bits (173), Expect = 9e-10
Identities = 32/49 (65%), Positives = 39/49 (79%)
Frame = +1

Query: 634 ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFV 780
A+AQL+TN+Y SCPN S +KS V +A++ E RMGASLLRL FHDCFV
Sbjct: 2 ASAQLTTNYSSCPNALSIIKSAVNTAVNNEARMGASLLRRLFHDCFV 50

>ref|XP_002299006.1| predicted protein [Populus trichocarpa]
gb|EEE83811.1| predicted protein [Populus trichocarpa]
Length = 322

Score = 170 bits (430), Expect = 1e-39
Identities = 82/125 (65%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N ++I+ FA TR+++CP SG+G+NNLAPLDL TP SFDN YF+NL
Sbjct: 198 QARCVTFRGRIYDNSSDIDAGFASTRRRNCPSASGNGNNLAPLDLVTPNSFDNYYFRNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q++GLL SDQ LF+G STDSIV YS NP FSSDFAAAM++MGDI PLTGS GEIR+
Sbjct: 258 IQRRLQSDQVLFSGQSTDSIVTEYSRNP SLFSSDFAAAMLRMGDIEPLTGSQGEIRRV 317

Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CSVVN 322

Score = 126 bits (317), Expect = 2e-26
Identities = 72/169 (42%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SI+LD++ S EK + N NS RGFEVID+ K+ VE +CPGVVSCADI A+AA
Sbjct: 71 VQGCDASIMLDNPSIDSEKFSFNNSIRGFEVIDDAKAQVESICPGVVSCADIAAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W V+LG
Sbjct: 131 RDA-----SVAVGGPSWTVRLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS+S A++ IP T++L LI F+ GLS +D+VALSG+ I
Sbjct: 148 RRDSTTASRSLADSDIPRATTSLVNLI GMFNGKGLSERDMVALSGSHTI 196

Score = 66.2 bits (160), Expect = 3e-08
Identities = 32/69 (46%), Positives = 47/69 (68%), Gaps = 4/69 (5%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSA----NAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLL 753
SRL++ +F L S+ AQLS+NFY +CPN +++++ ++ A+S E RM ASL+
Sbjct: 3 SRLSLACVVFSLFLISSCLPCQAQLSSNFYDSTCPNALT TIRTAIRRAVSSERRMAASLI 62

Query: 754 RLFHDFCV 780
RL FHDFCV
Sbjct: 63 RLHFHDFCV 71

>ref|XP_002333334.1| predicted protein [Populus trichocarpa]
gb|EEE74658.1| predicted protein [Populus trichocarpa]
Length = 322

Score = 170 bits (430), Expect = 1e-39
Identities = 82/125 (65%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N ++I+ FA TR+++CP SG+G+NNLAPLDL TP SFDN YF+NL
Sbjct: 198 QARCVTFRGR IYDNSSDIDAGFASTRRRNCPSASGNGNNLAPLDLVTPNSFDNYYFRNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q++GLL SDQ LF+G STDSIV YS NP FSSDFAAAM++MGDI PLTGS GEIR+
Sbjct: 258 IQRRGLLQSDQVLFSGQSTDSIVTEYSRNP SLFSSDFAAAMLRMGDIEPLTGSQGEIRRV 317

Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CSVVN 322

Score = 126 bits (316), Expect = 2e-26
Identities = 71/169 (42%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SI+LD++ S EK + N NS RGFEV+D+ K+ VE +CPGVVSCADI A+AA
Sbjct: 71 VQGCDASIMLDNSPSIDSEKFSFSNNNSIRGFEVVDDAKAQVESICPGVVSCADIAAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W V+LG
Sbjct: 131 RDA-----SVAVGGPSWTVRLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS+S A++ IP T++L LI F+ GLS +D+VALSG+ I
Sbjct: 148 RRDSTTASRSLADSDIPRATTSVNLIGMFNGKGLSERDMVALSGSHTI 196

Score = 66.2 bits (160), Expect = 3e-08
Identities = 32/69 (46%), Positives = 47/69 (68%), Gaps = 4/69 (5%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSA----NAQLSTNFYHSCP NFLSSVKSTVQSAISKETRMGASLL 753
SRL++ +F L S+ AQLS+NFY +CPN +++++ ++ A+S E RM ASL+
Sbjct: 3 SRLSLACVVFSLFLISSCLPCQAQLSSNFYDSTCPNALTTIRTAIRRAVSSERRMAASLI 62

Query: 754 RLFFHDCFV 780
RL FHDCFV
Sbjct: 63 RLHFHDCFV 71

>ref|XP_002285723.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 317

Score = 170 bits (430), Expect = 1e-39
Identities = 84/124 (67%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR+RIYNETNI+ AFA ++Q+ CP T G DNNL+ LD +T T FDN YF+NL
Sbjct: 195 KARCTSFRRSRIYNETNIDAAFATSKQKICPSTGG--DNNLSDLD-ETTTVFDNVYFRNLK 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQL+NGGSTDSIV YSTN TF +D A AMIKMG++SPLTG+NGEIR +C
Sbjct: 252 AKKGLLHSDQQLYNGGSTDSIVETYSTNSATFFTDVANAMIKMGNLSPLTGTNGEIRTDC 311

Query: 2167 RRIN 2178
++IN
Sbjct: 312 KKIN 315

Score = 155 bits (391), Expect = 5e-35
Identities = 85/167 (50%), Positives = 103/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD SILLDDT+SFTGEK A PN++S RG+EVID IKS VE +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILLDDTASFTGEKTAGPNKDSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW ++LGRR
Sbjct: 130 SV-----VALGGPTWTLQLGRR 146

Query: 1517 DARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN+ +P P S+L+ LISRFS G +TK++VALSGT I
Sbjct: 147 DSTTASLSTANS DLPASPDLSTLISRFSNKGFTTKEMVALSGTHTI 193

Score = 75.1 bits (183), Expect = 6e-11
Identities = 38/70 (54%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+NFY SCP S++++ V +A++KE RMGASL
Sbjct: 1 MASLSLFSLFCVFSFLL--GMAHAQLSSNFYASSCPKALSTIRAAVNNAVAKERRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>emb|CAA46916.1| peroxidase [Oryza sativa (japonica cultivar-group)]
prf||1909367A peroxidase
Length = 317

Score = 170 bits (430), Expect = 1e-39
Identities = 77/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAP+D TP +FDN Y+ NL+
Sbjct: 193 QAQCQNFDRRIYNETNIDSAFATQRQANCPRTSGGDSNLAPVDTTTPNAFDNAYYSNLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 253 SNKGLLHSDQVLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQGI RLSL 312

Query: 2167 RRIN 2178
++N
Sbjct: 313 SKVN 316

Score = 118 bits (296), Expect = 5e-24
Identities = 72/169 (42%), Positives = 88/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AA

Sbjct: 71 VQGCDASVLLSGQ-----EQNAGPNVGLRGRFVIDNAKARVEAICNQTVCADILAVAA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 126 RDSV-----VALGGPSWTVLLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 143 RRDSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 191

Score = 71.2 bits (173), Expect = 9e-10
Identities = 34/65 (52%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F

Sbjct: 7 SLSLMLLVAAAMASVASAQLSATFYDTSCPINALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFV 780
HDCFV

Sbjct: 67 HDCFV 71

>ref|XP_002319967.1| predicted protein [Populus trichocarpa]
gb|EEE95890.1| predicted protein [Populus trichocarpa]
Length = 312

Score = 169 bits (429), Expect = 2e-39
Identities = 82/120 (68%), Positives = 94/120 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q +C FRARIYNETNI+ +FA RQ+ CP T+G D+NLAPLD QTP FDN Y+KNL+

Sbjct: 191 QTKCKTFRARIYNETNIDKSFATMRQKMCPLTTG--DDNLAPLDFQTPNVFDNYYKNLI 248

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ LF+G STDS+VR YS NP F SFAAAM+KMGDI P TG+ GEIRK C

Sbjct: 249 HKKGLLHSDQVLFSGESTDSLVRTYSNPNPDIFFSFAAAMVKMGDIDPRTGTRGEIRKCC 308

Score = 140 bits (352), Expect = 2e-30
Identities = 75/169 (44%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
++GCD SILL+DT++F GE+ A PN NS RG+ V+ IKS +EKVCPG+VSCADI+ IAA

Sbjct: 64 VKGCDASILLEDATATFKGEQGAGPNNSVRGYNVVAKIKSKLEKVCPCGIVSCADIVVIA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS ++ LGGP W VKLG

Sbjct: 124 RDS-----TVLLGGPYWKV KLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TA+ +AA+ +P+ TS ++QLI RF + GLS D+VALSG+ I

Sbjct: 141 RRDSKTANMNAASKSLPSDTSTVSQLIKRFKSKGLSATDMVALSGSHTI 189

Score = 84.3 bits (207), Expect = 1e-13
Identities = 40/63 (63%), Positives = 51/63 (80%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHD 771
+++ LAL ++ S++A LST+FY SCP LF +VKS VQSAI+KE RMGASL+RLFFHD

Sbjct: 2 VSVTLALLLIYTSSSSAHLSTDFYDKSCPQLFGTVKSVVQSAIAKERRMGASLVRLFFHD 61

Query: 772 CFV 780
CFV

Sbjct: 62 CFV 64

>gb|ABK24123.1| unknown [Picea sitchensis]
Length = 208

Score = 169 bits (427), Expect = 3e-39
Identities = 81/124 (65%), Positives = 100/124 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
+ARCT+FR IYN++NI+TA+A++ Q CPR+ G DN L+PLD QTPT F+N Y+KNLV

Sbjct: 87 KARCTFRDHIYNSNIDTAYAKSLQAKCPRSGG--DNRLSPLDYQTPTKFENNYKLV 144

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNG STDS+V YS N F +DFAAAMIKMG+I PLTGS G+IRKNC

Sbjct: 145 ARKGLLHSDQELFNGVSTDSLVTKYKSNLKL FENDFAAAMIKMGNIMPLTGSQGIIRKNC 204

Query: 2167 RRIN 2178
R+ N

Sbjct: 205 RKRN 208

Score = 91.7 bits (226), Expect = 6e-16
Identities = 54/124 (43%), Positives = 66/124 (53%)
Frame = +2

Query: 1274 VEKVC PGV VSCADILAI AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRT 1453
+EK C GVVSCADILA+AARDSV
Sbjct: 1 MEKACSGVVSCADILAVAARDSV----- 23

Query: 1454 FC*F*SI*LGGPTWNVKLGRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLV 1633
+ LGGPTW V LGRRD+ TA+++AAN IPAPT+NL L S+F A GLS +++V
Sbjct: 24 -----VTLGGPTWTVMLGRRDSGTANRTAANTNIPAPTANLANLTSKFGAQLSKREMV 77

Query: 1634 ALSG 1645
LSG
Sbjct: 78 VLSG 81

>gb|AAA20473.1| peroxidase [Cenchrus ciliaris]
Length = 313

Score = 169 bits (427), Expect = 3e-39
Identities = 78/124 (62%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR IYN+TNI T FA + + +CPR +GSGD NLA LD TP +FDN YFKNL+
Sbjct: 190 QAQCLNFRDHIYNDTNINTGFASLKCANCPRTGSGDGNLASLDTSTPYTFDNAYFKNLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGSTD+ VR +++NP FSS FAAAM+KM +SPLTGS G+IR C
Sbjct: 250 SQKGLLHSDQELFNGGSTDNVTRNFASNPSAFSSAFAAAMVKMASLSPLTGSQQIRLTC 309

Query: 2167 RRIN 2178
+ N
Sbjct: 310 SKAN 313

Score = 103 bits (258), Expect = 1e-19
Identities = 67/170 (39%), Positives = 85/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI A 1330
+QGCD S+LLD GE+ A PN S RGF+VI NIK+ VE +C VSCADILA+ A
Sbjct: 66 VQGCDASVLLDSG----GEQGAIPNAGSLRGFDVIANIKAQVEAICKQTVSCADILAVGA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
R SV + LGGP+W V LG
Sbjct: 122 RHSV-----VALGGPSWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTS--NLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ + S + AN+ +PA S NL+QLI F G + ++VALSG I
Sbjct: 139 RRDSTSGSAALANSDLPASRSFNLSQLIGSFDNKGFTATEMVALSGAHTI 188

Score = 73.2 bits (178), Expect = 2e-10
Identities = 39/70 (55%), Positives = 47/70 (67%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L + + A+AQLS FY SCPN S++KS V +A+ KE RMGASL
Sbjct: 1 MASSVSGLLLMLCMAAV----ASAQLSATFYDTSCPNALSTIKSAVTA AVKKNRMGASL 56

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 57 LRLHFHDCFV 66

>gb|ABK23423.1| unknown [*Picea sitchensis*]
Length = 318

Score = 168 bits (426), Expect = 4e-39
Identities = 81/124 (65%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNE+NI+T+ A + CPRT G DN L+PLDL TP +FD +Y+ NL
Sbjct: 197 QARCTSFARIYNESNIDTSLATAVKPKCPRTGG--DNTLSPLDLATPITFDKHYCNLR 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNGGSTDS V YSTN F +DFAAAM+ MG+I PLTG++G+IR+NC
Sbjct: 255 SKKGLLHSDQQLFNGGSTDSQVTTYSTNQNNFFTFDFAAAMVNMGNIKPLTGTSGQIRRNC 314

Query: 2167 RRIN 2178
R+ N
Sbjct: 315 RKS N 318

Score = 149 bits (377), Expect = 2e-33
Identities = 86/169 (50%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAIAA 1330

+ GCDGSILLDD S+FTGEK A PN NS RG++VID IK+ VE C GVVSCADI+AIAA
 Sbjct: 70 VNGCDGSILLDDNSTFTGEKTATPNNSVRYDVIDTIKTQVEAACSGVVSCADIVAIAA 129
 Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGPTWNVKLG 1510
 RDSV + LGGPTW V LG
 Sbjct: 130 RDSV-----VALGGPTWTVLLG 146
 Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ TAS +AAN+ IP+P SNL+ LIS F + LS KDLVALSG I
 Sbjct: 147 RRDSTTASFNAANSSIPSPASNLSTLISSFRSHNLSPKDLVALSGAHTI 195

Score = 66.6 bits (161), Expect = 2e-08
 Identities = 33/64 (51%), Positives = 44/64 (68%), Gaps = 2/64 (3%)
 Frame = +1

Query: 598 ICLALFVL--IWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHD 771
 I + LF++ I + QL++ FY SCP S V++ V+ A++KE RMGASLLRL FHD
 Sbjct: 8 IPIVLFIIICSIPNIVHGQLTSTFYSESCPRALSIVQAAVEQAVAKERRMGASLLRHFHD 67

Query: 772 CFVN 783
 CFVN
 Sbjct: 68 CFVN 71

>ref|NP_001060629.1| Os07g0677300 [Oryza sativa (japonica cultivar-group)]
 sp|Q0D3N0.1|PER2_ORYSJ RecName: Full=Peroxidase 2; Flags: Precursor
 dbj|BAA03911.1| peroxidase [Oryza sativa Japonica Group]
 dbj|BAC79528.1| peroxidase [Oryza sativa Japonica Group]
 dbj|BAC83104.1| peroxidase [Oryza sativa Japonica Group]
 tpe|CAH69354.1| TPA: class III peroxidase 112 precursor [Oryza sativa (japonica
 cultivar-group)]
 dbj|BAF22543.1| Os07g0677300 [Oryza sativa Japonica Group]
 dbj|BAG93552.1| unnamed protein product [Oryza sativa Japonica Group]
 gb|EEE67816.1| hypothetical protein OsJ_25570 [Oryza sativa Japonica Group]
 Length = 314

Score = 168 bits (426), Expect = 4e-39
 Identities = 76/124 (61%), Positives = 99/124 (79%)
 Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
 QA+C NFR R+YNETNI+++FA + +CPR +GSGD+NLAPLD TP +FD+ Y+ NL+
 Sbjct: 191 QAQCQNFDRRLYNETNIDSSFATALKANCPRTGSGDSNLAPLDTTTPNAFDSAYYTNLL 250

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
 KLLHSDQ LFNGGSTD+ VR +S+N F+S F AAM+KMG+ISPLTG+ G+IR NC
 Sbjct: 251 SNKGLLHSDQQLFNGGSTDNTVRNFSSNTAAFNSAFTAAMVKMGNISPLTGTGQIRLNC 310

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQLF+GGSTDS V YS+N G+F++DFA AM+KMG++SPLTG++G+IR NC
Sbjct: 260 GQKGLLHSDQQLFSGGSTDSQVNAYSSNLGSFTTDFANAMVKMGNLSPLTGTSGQIRTNC 319

Query: 2167 RRIN 2178
R+ N
Sbjct: 320 RKAN 323

Score = 152 bits (384), Expect = 3e-34
Identities = 87/169 (51%), Positives = 103/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDT++ TGEK A PN NSARGFEVID IKS VE +CPGVVSCADI+A+AA
Sbjct: 75 VNGCDGSILLDDTANMTGEKTAVPNSNSARGFEVIDTIKSQVESLCPGVVSCADIVAVAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 135 RDSV-----VALGGPSWIVLLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ IPAPT NL+ LI+ FS G + K++VALSG+ I
Sbjct: 152 RRDSTTASLSAANSNIPAPTLNLSGLITAFSNKGFTAKEMVALSGSHTI 200

Score = 72.0 bits (175), Expect = 5e-10
Identities = 39/75 (52%), Positives = 48/75 (64%)
Frame = +1

Query: 559 SKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRM 738
SK S R + + LF+L+ A AQLS+ FY +CP S++KS V SA+S E RM
Sbjct: 3 SKTCSPSNKLRFLLMVLFLLM-NMATAQLSSTFYSTTCPRALSTIKSAVNSAVSNEARM 61

Query: 739 GASLLRRLFHDCFVN 783
GASL RL FHDCFVN
Sbjct: 62 GASLPRLHFHDCFVN 76

>gb|ABK25962.1| unknown [Picea sitchensis]
Length = 323

Score = 168 bits (425), Expect = 5e-39
Identities = 79/124 (63%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986

QARC NFRA IYN+TNI + ++ + + CP T+GSGDNNL+PLD +PT+FD Y+ NL
Sbjct: 200 QARCFNFRAHIYNDTNILSTYSTSLRSKCPPTNGSGDNNLSPLDYVSPTAFDKNYYCNLK 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS V Y++N F SDFAAAM+KMG+I PLTG++G+IRKNC

Sbjct: 260 IKKGLLHSDQELFNGGSTDSQVTTYASNQNIFFSDFAAAMVKGNIKPLTGTSGQIRKNC 319

Query: 2167 RRIN 2178

R+ N

Sbjct: 320 RKPN 323

Score = 153 bits (387), Expect = 1e-34
Identities = 87/169 (51%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDD+S TGEK A PN NSARGF+VID IKS VEK C GVVSCADILAIAA

Sbjct: 73 VNGCDGSVLLDDSSKITGEKTAVPNANSARGFDVIDTIKSQVEKSCSGVVSCADILAIAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 133 RDSV-----VELGGPSWTVLLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS+S ANN IP PTS+L+++IS F A GLS K++VAL+G I

Sbjct: 150 RRDSTTASKSGANNIPPTSSLSKIISLFAQQGLSAKEMVALAGAHTI 198

Score = 69.3 bits (168), Expect = 3e-09
Identities = 36/65 (55%), Positives = 45/65 (69%), Gaps = 4/65 (6%)
Frame = +1

Query: 601 CLALFVLIWGS----ANAQLSTNFYHSCP NFLSSVKSTVQSAISKETRMGASLLRLFFH 768
C+A+ V I S ++ QLS+ FY SCP S VK+ V+ A++KE RMGASLLRL FH

Sbjct: 10 CIAVMVFIICSIANLSHGQLSSTFYDKSCPAALS VVKA AVKQAVAKEQRMGASLLRLHFH 69

Query: 769 DCFVN 783

DCFVN

Sbjct: 70 DCFVN 74

>gb|EAZ05133.1| hypothetical protein OsI_27326 [Oryza sativa Indica Group]
Length = 324

Score = 168 bits (425), Expect = 5e-39
Identities = 77/124 (62%), Positives = 97/124 (78%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLA LD TP +FDN Y+ NL+

Sbjct: 200 QAQCQNFRDRIYNETNIDSAFATQRQANCPRTGSGDSNLAALDITTPNAFDNAYYSNLL 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNNGS D+ VR ++N FSS F AM+KMG+ISPLTG+ G+IR +C

Sbjct: 260 SNKGLLHSDQVLFNNGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQQIRLSC 319

Query: 2167 RRIN 2178

++N

Sbjct: 320 SKVN 323

Score = 116 bits (290), Expect = 2e-23

Identities = 71/167 (42%), Positives = 86/167 (51%)

Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCVGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AARD

Sbjct: 80 GCDASVLLSQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAARD 134

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR

Sbjct: 135 SV-----VALGGPSWTVLLGRR 151

Query: 1517 DARTASQSAANNGIPAPTSNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I

Sbjct: 152 DSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 198

Score = 71.6 bits (174), Expect = 7e-10

Identities = 34/69 (49%), Positives = 46/69 (66%)

Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F

Sbjct: 7 SSLSLMLLVAAAMASVASAQLSATFYDTSCPINALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFVNVIY 792

HDCFV +

Sbjct: 67 HDCFVQASF 75

>ref|NP_001046400.1| Os02g0240100 [Oryza sativa (japonica cultivar-group)]

Length = 335

Score = 168 bits (425), Expect = 5e-39
Identities = 74/123 (60%), Positives = 101/123 (82%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
++C NFR R+YN+TNI+ AFA R++ CP GSGD++LAPLD QT FDN Y++NL+
Sbjct: 211 SQCANFRDRVYNDTNIDPAFAALRRRGCPAAPGSGDSSLAPLDAQTNVFDNAYYRNLLA 270

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++V+ YS+NP F++DFAAAMIKMG+I PLTG+ G+IR++CR
Sbjct: 271 QRGLLHSDQELFNGGSQDALVQQYSSNPALFAADFAAAMIKMGNIKPLTGAAGQIRRSR 330

Query: 2170 RIN 2178
+N
Sbjct: 331 AVN 333

Score = 134 bits (337), Expect = 9e-29
Identities = 80/171 (46%), Positives = 97/171 (56%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD SILLDD +SF GEK A PN NS RG++VID IK VE +CPGVVSCADI+A+
Sbjct: 81 VQGCDASILLDDVPATSFVGEKTAFPNVNSVRGYDVIDQIKRNVLLCPGVVSCADIVAL 140

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 141 AARDSTAL-----LGGPSWAVP 157

Query: 1505 LRRRDARTASQSAANNIPAPTSNQLISRFSALGLSTKDLVALSGTKHI 1657
LRRRD+ TAS SAAN+ +PAP+S+L LI+ F GLS +D+ ALSG I
Sbjct: 158 LRRRDSTTASLSAANSDLPAPSSDLATLIAGFGNKGLSPRDMTALSGAHTI 208

Score = 70.1 bits (170), Expect = 2e-09
Identities = 42/82 (51%), Positives = 52/82 (63%), Gaps = 4/82 (4%)
Frame = +1

Query: 547 LVCLSKLTMASFCSRLTICLALFVLIWGSANA----QLSTNFYHSCP NLFSSVKSTVQS 714
L+ + ++TMAS S CL F L+ +A A QLST FY SCP L V++TV
Sbjct: 1 LIKICEITMASRSS-WHCCLLAFFLLSSAAGAAYGQQLSTTFYAASCP TLQVVVRATVLG 59

Query: 715 AISKETRMGASLLRFFHDCFV 780
A+ E RMGASL+RFFHDCFV
Sbjct: 60 ALLAERRMGASLVRFFHDCFV 81

>gb|AAC49818.1| peroxidase [Oryza sativa Indica Group]
Length = 317

Score = 168 bits (425), Expect = 5e-39
Identities = 77/124 (62%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLA LD TP +FDN Y+ NL+
Sbjct: 193 QAQCQNFRDRIYNETNIDSAFATQRQANCPRPTGSGDSNLAALDTPNAFDNAYYSNLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNNGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 253 SNKGLLHSDQVLFNNGSADNTRNFASNAAAFSSAFTTAMVKMGNISPLTGTQGIQLSC 312

Query: 2167 RRIN 2178
++N
Sbjct: 313 SKVN 316

Score = 118 bits (296), Expect = 5e-24
Identities = 72/169 (42%), Positives = 88/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AA
Sbjct: 71 VQGCDASVLLSGQ-----EQNAGPNVGLRGFVSDNAKARVEAICNQTVSCADILAVAA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 126 RDSV-----VALGGPSWTVLLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 143 RRDSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 191

Score = 71.2 bits (173), Expect = 9e-10
Identities = 34/65 (52%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
Sbjct: 7 SSSLMLLVAAAMASVASAQLSATFYDTPSCPNALSTIKSVITA AVNSEARMGASLLRLLHF 66

Query: 766 HDCFV 780

HDCFV
Sbjct: 67 HDCFV 71

>dbj|BAD28869.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69272.1| TPA: class III peroxidase 30 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAG98261.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAF08314.2| Os02g0240100 [Oryza sativa Japonica Group]
Length = 327

Score = 168 bits (425), Expect = 5e-39
Identities = 74/123 (60%), Positives = 101/123 (82%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
++C NFR R+YN+TNI+ AFA R++ CP GSGD++LAPLD QT FDN Y++NL+
Sbjct: 203 SQCANFRDRVYNDTNIDPAFAALRRRGCPAAPGSGDSSLAPLDAQTNVFDNAYYRNLLA 262

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++V+ YS+NP F++DFAAAMIKMG+I PLTG+ G+IR++CR
Sbjct: 263 QRGLLHSDQELFNGGSQDALVQQYSSNPALFAADFAAAMIKMGNIKPLTGAAGQIRRSR 322

Query: 2170 RIN 2178
+N
Sbjct: 323 AVN 325

Score = 134 bits (337), Expect = 9e-29
Identities = 80/171 (46%), Positives = 97/171 (56%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD SILLDD +SF GEK A PN NS RG++VID IK VE +CPGVVSCADI+A+
Sbjct: 73 VQGC DASILLDDVPATSFVGEKTAFPNVNSVRGYDVIDQIKRNVELLCPGVVSCADIVAL 132

Query: 1325 AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 133 AARDSTAL-----LGGPSWAVP 149

Query: 1505 LRRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
LRRRD+ TAS SAAN+ +PAP+S+L LI+ F GLS +D+ ALSG I
Sbjct: 150 LRRRDSTTASLSAANS DLPAPSSDLATLIAGFGNKGLSPRDMTALSGAHTI 200

Score = 66.6 bits (161), Expect = 2e-08

Identities = 36/64 (56%), Positives = 42/64 (65%), Gaps = 4/64 (6%)
Frame = +1

Query: 601 CLALFVLIWGSANA----QLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFH 768
CL F L+ +A A QLST FY SCP L V++TV A+ E RMGASL+RLFFH
Sbjct: 10 CLLAFFLLSSAAGAAYGQQLSTTFYAASCPTLQVVVRATVLGALLAERRMGASLVRLFFH 69

Query: 769 DCFV 780
DCFV
Sbjct: 70 DCFV 73

>ref|XP_002274693.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 324

Score = 167 bits (424), Expect = 7e-39
Identities = 85/125 (68%), Positives = 96/125 (76%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP +G GD+NLA LDL TP SFDN YFKNL
Sbjct: 200 QARCVTFRDRIYDNGTDIDAGFASTRRRRCPADNGDGDNNLAALDLVTPNSFDNYYFKNL 259

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTDSIV YS N TFSSDFA AM+KMGDI PLTG+ GEIR+
Sbjct: 260 IQKKGLLQSDQVLFSGGSTDSIVSEYSKNRKTFSDFALAMVKMGDIEPLTGAAGEIREF 319

Query: 2164 CRRIN 2178
C IN
Sbjct: 320 CNAIN 324

Score = 136 bits (343), Expect = 2e-29
Identities = 76/169 (44%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAIAA 1330
+QGCD SILLDD+SS EKNA N NSARG+EVI ++KS VE +CPG+VSCADILA+AA
Sbjct: 73 VQGCDASILLDDSSSIQSEKNAPNNLNSARGYEV IHDVKSQVESICPGIVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RD+ S+ +GGPTW VKLG
Sbjct: 133 RDA-----SVAVGGPTWTVKLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S ++ +P+ +L++LIS F + GLST+D+VALSG+ I
Sbjct: 150 RRDSTTSGLSQVSSNLPSFRDSLRLISLFGSKGLSTRDMVALSGSHTI 198

Score = 63.2 bits (152), Expect = 2e-07
Identities = 31/73 (42%), Positives = 46/73 (63%), Gaps = 3/73 (4%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGS---ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMG 741
M S C + + VL+ S AQLS++FY ++CP S++++ + A+S+E RM
Sbjct: 1 MGSIAGNYGACIFVAVLLILSIMPCEAQLSSSFYDNTCPKALSTIRTATRKAVSRERRMA 60

Query: 742 ASLLRRLFHDCFV 780
ASL+RL FHDCFV
Sbjct: 61 ASLIRLHFHDCFV 73

>gb|EEC82680.1| hypothetical protein OsI_27324 [Oryza sativa Indica Group]
Length = 318

Score = 167 bits (424), Expect = 7e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+
Sbjct: 195 QAQCQNFDRRLYNETNIDAAFAAALKASCPRPTGSGDGNLAPLDTTPTAFDNAYYTLL 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C
Sbjct: 255 SNKGLLHSDQVLFNGGAVDGGVRSYASGPSRFRRDFAAAMVKMGNIAPLTGTGQGI RLVLC 314

Query: 2167 RRIN 2178
++N
Sbjct: 315 SKVN 318

Score = 130 bits (327), Expect = 1e-27
Identities = 73/165 (44%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AA
Sbjct: 68 VQGCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 128 RDSV-----VALGGPSWRVLLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRD+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG
Sbjct: 145 RRDSTTASLALANSDLPPPSFDVANLTAAFAAKGLSQADMVALSG 189

Score = 64.3 bits (155), Expect = 1e-07
Identities = 32/63 (50%), Positives = 43/63 (68%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L +CLAL + G QLS FY SCP + +++ V++A+++E RMGASLLRL FHD
Sbjct: 9 LLLCLALAGSVSGQ---QLSATFYRSRCPRALAIIRAGVRAAVAQEPRMGASLLRRLFHD 65

Query: 772 CFV 780
CFV
Sbjct: 66 CFV 68

>ref|NP_001060626.1| Os07g0676900 [Oryza sativa (japonica cultivar-group)]
dbj|BAF22540.1| Os07g0676900 [Oryza sativa Japonica Group]
Length = 333

Score = 167 bits (424), Expect = 7e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+
Sbjct: 210 QAQCQNFRDRLYNETNIDAAFAAALKASCPRTSGSGDGNLAPLDTTPTAFDNAYYTLL 269

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNNG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C
Sbjct: 270 SNKGLLHSDQVLFNGGAVDGGVRSYASGSPRFRDFAAAMVKMGNIAPLTGTGGQIRLVC 329

Query: 2167 RRIN 2178
++N
Sbjct: 330 SKVN 333

Score = 130 bits (327), Expect = 1e-27
Identities = 73/165 (44%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVWSCADILAI AA 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AA
Sbjct: 83 VQGCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNLTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDSV + LGGP+W V LG
Sbjct: 143 RDSV-----VALGGPSWRVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG

Sbjct: 160 RRDSTTASLALANSDLPPPSFDVANLTASFAAKGLSQADMVALSG 204

Score = 68.6 bits (166), Expect = 6e-09
Identities = 38/74 (51%), Positives = 50/74 (67%), Gaps = 1/74 (1%)
Frame = +1

Query: 562 KLTMASFCS-RLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRM 738
+LTMAS S L +CLAL + G QLS FY SCP + +++ V++A+++E RM
Sbjct: 13 RLTMASCLSVLLLLCLALAGSVSGQ---QLSATFYRSCPRALAIIRAGVRAAVAQEP RM 69

Query: 739 GASLLRLLFFHDCFV 780
GASLLRLL FHD CFV
Sbjct: 70 GASLLRLLHFHDCFV 83

>emb|CAH10840.1| peroxidase [Picea abies]
Length = 320

Score = 167 bits (424), Expect = 7e-39
Identities = 81/124 (65%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYNE+NI AFA + + +CP S GDN L+PLD+ TPT+FDN Y+ NL
Sbjct: 199 QSRCAFFRTRIYNESNINAAFATSVKPNCP--SAGGDNTLSPLDVVPTTTFDNKYYSNLK 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGNGEIRKNC 2166
+KGLLHSDQQLFNGGSTDS V YSTN +F +DFAAAM+KMG+ISPLTG++G+IRKNC
Sbjct: 257 VQKGLLHSDQQLFNGGSTDSQVTTYSTNQNSFFTFDFAAAMVKMGNISPLTGTSGQIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKAN 320

Score = 151 bits (381), Expect = 7e-34
Identities = 87/169 (51%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDD ++FTGEK A PN NSARGF+VID IK+ VE C GVVSCADIL IAA

Sbjct: 72 VNGCDGSILLDDNATFTGEKTAGPNANSARGFDVIDTIKTQVEAACSGVWSCADILTIAA 131

Query: 1331 RDSVQIVSGGTTNKNLNLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS+ + L GPTW V LG

Sbjct: 132 RDSI-----VELQGPTWTVMLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAANN IP+P S+L+ LI+ F GLSTKDLVALSG I

Sbjct: 149 RRDSPTASLSAANNIPASSLSTLITSFQNHGLSTKDLVALSGAHTI 197

Score = 69.3 bits (168), Expect = 3e-09
Identities = 34/70 (48%), Positives = 46/70 (65%), Gaps = 5/70 (7%)
Frame = +1

Query: 589 RLTICLALFVLIWGS-----ANAQLSTNFYHSCPFLFSSVKSTVQSAISKETRMGASLL 753
R +C+ + ++ S N QLS+ FY SCP + S VK+ V+ A++KE RMGASL+

Sbjct: 4 RTLVCIGVMVLLCSININAVNGQLSSTFYAKSCPVRQSIKTVVKQAVAKEKRMGASLV 63

Query: 754 RLFFHDCFVN 783
RL FHDCFVN

Sbjct: 64 RLHFHDCFVN 73

>dbj|BAC83101.1| putative peroxidase precursor [Oryza sativa Japonica Group]
gb|EEE67813.1| hypothetical protein OsJ_25567 [Oryza sativa Japonica Group]
Length = 318

Score = 167 bits (424), Expect = 7e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+

Sbjct: 195 QAQCQNFDRRLYNETNIDAAFAAALKASCPRTGSGDGNLAPLDTTPTAFDNAYYTLL 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C

Sbjct: 255 SNKGLLHSDQVLFNGGAVDGGVRSYASGSPRRRDFAAAMVKMGNIAPLTGTGQIRLVC 314

Query: 2167 RRIN 2178
++N

Sbjct: 315 SKVN 318

Score = 130 bits (327), Expect = 1e-27
Identities = 73/165 (44%), Positives = 94/165 (56%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AA
Sbjct: 68 VQGCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 128 RDSV-----VALGGPSWRVLLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG
Sbjct: 145 RRDSTTASLALANSDLPPPSFDVANLTASFAAKGLSQADMVALSG 189

Score = 64.3 bits (155), Expect = 1e-07
Identities = 32/63 (50%), Positives = 43/63 (68%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L +CLAL + G QLS FY SCP + +++ V++A+++E RMGASLLRL FHD
Sbjct: 9 LLLCLALAGSVSGQ---QLSATFYRSRCPRALAIRAGVRAAVAQEPRMGASLLRLHFHD 65

Query: 772 CFV 780
CFV
Sbjct: 66 CFV 68

>tpe|CAH69351.1| TPA: class III peroxidase 109 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 322

Score = 167 bits (424), Expect = 7e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+
Sbjct: 199 QAQCQNFRDRLYNETNIDAAFAAALKASCPRTSGSGDGNLAPLDTTTPTAFDNAYYTPLL 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNNG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C
Sbjct: 259 SNKGLLHSDQVLFNGGAVDQVRSYASGPSRFRRDFAAAMVKMGNIAPLTGTGQIRLVC 318

Query: 2167 RRIN 2178
++N
Sbjct: 319 SKVN 322

Score = 128 bits (321), Expect = 6e-27
Identities = 72/163 (44%), Positives = 92/163 (56%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AARD
Sbjct: 74 GCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAARD 133

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 134 SV-----VALGGPSWRVLLGRR 150

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
D+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG
Sbjct: 151 DSTTASLALANSDLPPPSFDVANLTASFAAKGLSQADMVALSG 193

Score = 64.3 bits (155), Expect = 1e-07
Identities = 32/63 (50%), Positives = 43/63 (68%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L +CLAL + G QLS FY SCP + +++ V++A+++E RMGASLLRL FHD
Sbjct: 9 LLLCLALAGSVSGQ---QLSATFYRSRCPRALAIRAGVRAAVAQEPRMGASLLRRLFHD 65

Query: 772 CFV 780
CFV
Sbjct: 66 CFV 68

>ref|XP_002451848.1| hypothetical protein SORBIDRAFT_04g008620 [Sorghum bicolor]
gb|EES04824.1| hypothetical protein SORBIDRAFT_04g008620 [Sorghum bicolor]
Length = 278

Score = 167 bits (423), Expect = 9e-39
Identities = 79/124 (63%), Positives = 100/124 (80%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG-DNNLAPLDLQTPTSFNYYFKNLV 1986
++C NFR IYN+T+I+ AFA RQ+SCP G+G D NLA LD+QT FDN Y++NL+
Sbjct: 153 SQCNFRGHIYNDTDIDAAFAALRQRSCPAAPGTGGDTNLAALDVQTQLVFDNAYYRNL 212

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GLLHSDQ+LFNGGS D++VR YS+NP F+SDFAAAMIKMG+ISPLTG+ G+IR NC
Sbjct: 213 AKRGLLHSDQELFNGGSQDALVRQYSSNPALFASDFAAAMIKGNISPLTG TAGQIRANC 272

Query: 2167 RRIN 2178
R +N
Sbjct: 273 RVVN 276

Score = 134 bits (338), Expect = 7e-29
Identities = 78/169 (46%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCDGSILLDD SF GEK A PN NS RGF+VID IK+ VE +CPGVVSCADI+A+AA
Sbjct: 25 VQGCDGSILLDDVGSFVGEKGAGPNVNSVRGFDVIDQIKTNVELICPGVVSCADIVALAA 84

Query: 1331 RDSVQIVSGQTNNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
R F + LGGP+W V LG
Sbjct: 85 R-----FGTFLGGPSWAVPLG 101

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P+P S L L++ F GLS DL ALSG I
Sbjct: 102 RRDSTTASLTLANSIDLSPASGLATLVAFGNKGLSPGDLTALSGAHTI 150

Score = 39.3 bits (90), Expect = 3.8
Identities = 17/22 (77%), Positives = 19/22 (86%)
Frame = +1

Query: 715 AISKETRMGASLLRFFHDCFV 780
A+ E RMGASL+RLFFHDCFV
Sbjct: 4 ALLAERRMGASLVRLFFHDCFV 25

>gb|ACN33811.1| unknown [Zea mays]
Length = 320

Score = 167 bits (423), Expect = 9e-39
Identities = 77/124 (62%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR IYN+TNI FA + + +CPR +GSGD NLAPLD TP SFDN Y+ NL+
Sbjct: 197 QAQCKNFRDHIYNDTNINQGFASSLKANCPRPTGSGDGNLAPLDTTTPYSFDNAYYSNLL 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGSTD+ VR +++N FSS FAAAM+KMG++SPLTGS G+IR C
Sbjct: 257 SQKGLLHSDQELFNGGSTDNVTRNFASNSAAFSSAFAAAMVKGMLSPLTGSQQIRLTC 316

Query: 2167 RRIN 2178

+N
Sbjct: 317 STVN 320

Score = 118 bits (296), Expect = 5e-24
Identities = 72/171 (42%), Positives = 89/171 (52%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1324
+QGCD S+LL D ++ FTGE+ A PN S RGF+VI NIK+ VE VC VSCADILA+
Sbjct: 68 VQGCDAVLLADNAATGFTGEQGAAPNAGSLRGRFDVIANIKAQVEAVCKQTVSCADILAV 127

Query: 1325 AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDSV + LGGP+W V
Sbjct: 128 AARDSV-----VALGGPSWTVP 144

Query: 1505 LRRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
LRRRD+ TAS S AN+ +P P NL QLI+ F G + ++ LSG I
Sbjct: 145 LRRRDSTTASLSLANSIDLPPFFNLGQLITAFGNKGFTATEMATLSGAHTI 195

Score = 75.1 bits (183), Expect = 6e-11
Identities = 36/65 (55%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCP NFLSSVKSTVQSAISKETRMGASLLRLFF 765
S ++ CL L + + A+AQLS FY SCPN S++K V +A+ KE RMGASLLRL F
Sbjct: 4 SSVSSCLLLLCLAAVASAQLSPTFYDSSCPNALSTIKIAVNAAVQKENRMGASLLRLHF 63

Query: 766 HDCFV 780
HDCFV
Sbjct: 64 HDCFV 68

>gb|ABR18139.1| unknown [Picea sitchensis]
Length = 327

Score = 167 bits (423), Expect = 9e-39
Identities = 83/124 (66%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR RIYNE+NI FA R+ +CP T G DNNLAPLDL TPT+FDN Y+ NL
Sbjct: 206 QARCTNFRNRIYNESNIALLFAGLRKANCPVTGG--DNNLAPLDLFTPTAFDNSYNNLQ 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ GLLHSDQQLF GGSTD+ V Y+ +P F +DFAAAM+KMG+I PLT +NGEIRKNC

Sbjct: 264 FQNGLLHSDQQLFKGGSTDNRVSFYAVHPDAFFNDFAAAMVKMGNIKPLTVNNGEIRKNC 323

Query: 2167 RRIN 2178
R+IN

Sbjct: 324 RKIN 327

Score = 162 bits (410), Expect = 3e-37
Identities = 91/169 (53%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTS+FTGEK ANPN NS RGF+VID IK+ VE C GVVSCADI+AIAA

Sbjct: 79 VNGCDGSILLDDTSTFTGEKTANPNNSVRGFDVIDTIKTQVEATCSGVVSCADIVAIAA 138

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG

Sbjct: 139 RDSV-----VQLGGPTWTVMGL 155

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ +AS+SAANN IP PTSNL+ LIS F A GL+T+D+VALSG+ I

Sbjct: 156 RRDSTSASKSAANNIPPTSNSALISFFQAQGLTTEDMVALSGSHTI 204

Score = 76.3 bits (186), Expect = 3e-11
Identities = 39/78 (50%), Positives = 52/78 (66%), Gaps = 4/78 (5%)
Frame = +1

Query: 562 KLTMASFCS---RLTICLALFVLIWG-SANAQLSTNFYHSCPNLFPSSVKSTVQSAISKE 729
++ MA F + R+ +C++L V++ S QL +FY SCPN+ S V S V A++KE

Sbjct: 3 RIVMAFFSTMGIRIIVCISLLVIVCSTSVYVQLCPDFYDKSCPNVLSIVNSVVMQAVAKE 62

Query: 730 TRMGASLLRLLFFHDCFVN 783

RMGASLLRL FHDCFVN

Sbjct: 63 KRMGASLLRLLHFHDCFVN 80

>sp|A2YPX3.2|PER2_ORYSI RecName: Full=Peroxidase 2; Flags: Precursor
gb|AAC49821.1| peroxidase [Oryza sativa Indica Group]
gb|EEC82682.1| hypothetical protein OsI_27327 [Oryza sativa Indica Group]
Length = 314

Score = 167 bits (422), Expect = 1e-38
Identities = 75/124 (60%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFNYYFKNLV 1986

QA+C NFR R+YNETNI+++FA + +CPR +GSGD+NLAPLD TP +FD+ Y+ NL+
Sbjct: 191 QAQCQNFRDRLYNETNIDSSFATALKANCPRPTGSGDSNLAPLDTTTPNAFDSAYYTNLL 250

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGSTD+ VR +S+N F+S F AM+KMG+ISPLTG+ G+IR NC

Sbjct: 251 SNKGLLHSDQVLFNGGSTDNTVRNFSSNTAAFNSAFTVAMVKGNISPLTGTQGQIRLNC 310

Query: 2167 RRIN 2178
++N

Sbjct: 311 SKVN 314

Score = 121 bits (303), Expect = 8e-25
Identities = 72/169 (42%), Positives = 89/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGF V+DNIK+ VE +C VSCADILA+AA

Sbjct: 69 VQGCDAVLLSGQ-----EQNAGPNAGSLRGFNVVDNIKTQVEAICSQTVSCADILAVAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 124 RDSV-----VALGGPSWTVLLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA++S AN +PAP+S+L +LI FS GL D+VALSG I

Sbjct: 141 RRDSTTANESQANTDLPAPSSSLAELIGNFSRGLDVTDMVALSGAHTI 189

Score = 70.5 bits (171), Expect = 2e-09
Identities = 36/70 (51%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S +++ L + + +A+AQLS FY SCPN S++KS V +A++ E RMGASL

Sbjct: 1 MAS-ASSVSLMLLVAAAMASAASAQLSATFYDTSCPNALSTIKSAVTA AVNSEPRMGASL 59

Query: 751 LRLFFHDCFV 780
+RL FHDCFV

Sbjct: 60 VRLHFHDCFV 69

>ref|XP_002461208.1| hypothetical protein SORBIDRAFT_02g042850 [Sorghum bicolor]
gb|EER97729.1| hypothetical protein SORBIDRAFT_02g042850 [Sorghum bicolor]
Length = 319

Score = 166 bits (421), Expect = 2e-38

Identities = 76/124 (61%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR IYN+TNI +AFA + + +CPR++GSGD NLAPLD TP FDN Y+ NL+

Sbjct: 196 QAQCQFFRDHIYNDTNINSAFATSLKANCPRTSGSGDGNLAPLDTTPYKFDNAYYSNLL 255

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGSTD+ VR +++N FSS FAAAM+KMG++SPLTGS G+IR C

Sbjct: 256 NQKGLLHSDQELFNGGSTDNTVRNFASNSAAFSSAFAAAMVKMGNLSPLTGSQGGIIRLTC 315

Query: 2167 RRIN 2178

++N

Sbjct: 316 SKVN 319

Score = 118 bits (296), Expect = 5e-24
Identities = 71/171 (41%), Positives = 89/171 (52%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD S+LL D ++ FTGE+ A PN S RGF+VI NIK+ VE +C VSCADILA+

Sbjct: 67 VQGCDASVLLADNAATGFTGEQGALPNAGSLRQFDVIANIKTQVEAICKQTVSCADILAV 126

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDSV + LGGP+W V

Sbjct: 127 AARDSV-----VALGGPSWTVP 143

Query: 1505 LRRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

LRRRD+ TAS S AN+ +P P+ NL QLI F G + ++ LSG I

Sbjct: 144 LRRRDSTTASLSLANSDLPPPSFNLEQLIKAFGNKGFTATEMATLSGAHTI 194

Score = 74.7 bits (182), Expect = 8e-11
Identities = 36/59 (61%), Positives = 43/59 (72%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780

L LF+ + A+AQLS FY SCPN S++KS V +A+ KE RMGASLLRL FHDCFV

Sbjct: 9 LLLFLCLAAVASAQLSPTFYDTSCPNALSTIKSAVNAAVQKENRMGASLLRLLHFHDCFV 67

>ref|XP_002320417.1| predicted protein [Populus trichocarpa]
gb|EEE98732.1| predicted protein [Populus trichocarpa]
Length = 316

Score = 166 bits (421), Expect = 2e-38

Identities = 82/123 (66%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCT FR RIYN+TNI+ +FA TR+ SCP + GD LAPLD T T FDN Y+ NLV

Sbjct: 197 ARCTFRNRRIYNDTNIDASFATRRASCP--ASGGDATLAPLD-GTQTRFDNYYTNLVA 253

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++VR YSTN TF+ DFAAAM+KMG+ISPLTG NGEIR+NCR

Sbjct: 254 RRGLLHSDQELFNGGSQDALVRTYSTNGATFARDFAAAMVKMGNISPLTGRNGEIRRNCR 313

Query: 2170 RIN 2178

+N

Sbjct: 314 VVN 316

Score = 157 bits (396), Expect = 1e-35
Identities = 89/165 (53%), Positives = 100/165 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDT++FTGEKNANPNRNSARGFEVID IK+ VE C VSCADILA+AA

Sbjct: 69 VNGCDGSILLDDTATFTGEKNANPNRNSARGFEVIDT IKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + GGP+W V LG

Sbjct: 129 RDGVVL-----RGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRDARTASQSAAN+ IP+P S+L LIS FSA GLS D+ ALSG

Sbjct: 146 RRDARTASQSAANSQIPSPASSLATLISMFSAKGLSAGDMTALSG 190

Score = 62.8 bits (151), Expect = 3e-07
Identities = 32/78 (41%), Positives = 45/78 (57%)
Frame = +1

Query: 550 VCLSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQS AISKE 729

+C+ L +SFCS AQLS FY +CPNL + V++ + A++ +

Sbjct: 10 LCVVPLLASSFCS-----AQLSATFYASTCPNLQTIVRNAMTGAVNGQ 52

Query: 730 TRMGASLLRLLFFHDCFVN 783

R+ AS+LRLFFHDCFVN

Sbjct: 53 PRLAASILRLLFFHDCFVN 70

>ref|NP_001130666.1| hypothetical protein LOC100191769 [Zea mays]

gb|ACF78975.1| unknown [Zea mays]
Length = 324

Score = 166 bits (421), Expect = 2e-38
Identities = 77/123 (62%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
++C NFRA IYN+T+I+ AFA RQ++CP G+GD++LAPLD+QT FDN Y++NL+
Sbjct: 200 SQCQNFRAHIYNDTDIDPAFASLRQRTCPAAPGTGDS SLAPLDVQTQLVFDNAYYRNLLA 259

Query: 1990 KKGLLHSDQQLFNNGSSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+G LL SDQ LFNNGS D++VR YS NP F+SDFA AMIKMG+ISPLTG+ G+IR NCR
Sbjct: 260 KRGLLRSDQALFNNGSQDALVRQYSANPALFASDFANAMIKMGNISPLTG TAGQIRANCR 319

Query: 2170 RIN 2178
+N
Sbjct: 320 VVN 322

Score = 134 bits (338), Expect = 7e-29
Identities = 77/169 (45%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCDGSILLDD SF GEK A PN NS RGF+VID IK+ VE +CPGVVSCADI+A+AA
Sbjct: 72 VQGCDGSILLDDVGSFVGEKGAGPNVNSLRGFDVIDQIKANVELICPGVVSCADIVALAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD + LGGP+W V LG
Sbjct: 132 RDGTFL-----LGGPSWAVPLG 148

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P+P S L L++ F GL DL ALSG I
Sbjct: 149 RRDSTTASLALANS DLPSPVSGLAALLAAFGNKGLGPGDLTALSGAHTI 197

Score = 63.9 bits (154), Expect = 1e-07
Identities = 36/72 (50%), Positives = 48/72 (66%), Gaps = 2/72 (2%)
Frame = +1

Query: 571 MASFCSRLTICLA--LFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
MASF + LA LF+L + QLS++FY +CP L V++T+ +A+ E RMGA
Sbjct: 1 MASFRTSWHCLLAACFL LASAAHQQLSSSFYAATCPTLELIVRTTMLTALLAERRMGA 60

Query: 745 SLLRLFFHDCFV 780
SL+RLFFHDCFV

Sbjct: 61 SLVRLFFHDCFV 72

>ref|NP_200648.1| peroxidase, putative [Arabidopsis thaliana]
sp|Q9LVL1.1|PER68_ARATH RecName: Full=Peroxidase 68; Short=Atperox P68; Flags: Precursor
dbj|BAA96931.1| peroxidase [Arabidopsis thaliana]
dbj|BAC42892.1| putative peroxidase [Arabidopsis thaliana]
gb|AAP40354.1| putative peroxidase [Arabidopsis thaliana]
Length = 325

Score = 166 bits (421), Expect = 2e-38
Identities = 82/124 (66%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RIYN TNI+ +FA +R++SCP +GSGDNN A LDL+TP FD YF LV
Sbjct: 202 QARCVTFRSRIYNSTNIDLSFALSRRRSCPAATGSGDNNAAILDRLTPEKFDGSYFMQLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
+GLL SDQ LFNGGSTDSIV YS + F DF AAMIKMGDISPLTGSNG+IR++C
Sbjct: 262 NHRGLLTSQVLFNGGSTDSIVVYSYRSVQAFYRDFVAAMIKMGDISPLTGSNGQIRRSC 321

Query: 2167 RRIN 2178
RR N
Sbjct: 322 RRPN 325

Score = 144 bits (362), Expect = 1e-31
Identities = 85/170 (50%), Positives = 99/170 (58%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD SILLDDT SF GEK A PN NS RG+EVID IKS VE++CPGVVSCADILAI A
Sbjct: 74 VNGCDASILLDDTRSFLGEKTAGPNNNSVRGYEVIDAIKSRVERLCPGVVSCADILAITA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + +GG W+VKLG
Sbjct: 134 RDSVLL-----MGGRGWSVKLG 150

Query: 1511 RRDARTASQSAANNGI-PAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+G+ P PTS L+ LI+ F A GLS +D+VALSG I
Sbjct: 151 RRDSITASFSTANSGLVPPPTSTLDNLINLFRANGLSPRDMVALS GAHTI 200

Score = 73.2 bits (178), Expect = 2e-10
Identities = 36/66 (54%), Positives = 47/66 (71%), Gaps = 1/66 (1%)
Frame = +1

Query: 589 RLTICLALFVLIWGS-ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLF 765
R + LF+++ GS A AQL T+FY SCP+L +V+ VQ ++KE R+ ASLLRRLF
Sbjct: 10 RAAFVLLFVIMLGSQAQAQLRDTFYSDSCPSLLPTVRRVVQREVAKERRIAASLLRRLF 69

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 70 HDCFVN 75

>ref|XP_002338628.1| predicted protein [Populus trichocarpa]
gb|EEF10179.1| predicted protein [Populus trichocarpa]
Length = 183

Score = 166 bits (420), Expect = 2e-38
Identities = 83/124 (66%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR G NLAPLDL TP SFDN YFKNL+
Sbjct: 62 QAQCFTFRDRIYNASNIDAGFASTRKRRCPRAGGQA--NLAPLDLVTNPSFDNYYFKNLM 119

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLL SDQ LFNGGSTDSIV YS NP FSSDFA+AMIKMGDI PLTGS G+IR+ C
Sbjct: 120 RNKGLLQSDQVLFNGGSTDSIVSEYSRNPAPKFSDFASAMIKMGDIRPLTGSAGQIRRIC 179

Query: 2167 RRIN 2178
+N
Sbjct: 180 SAVN 183

Score = 65.5 bits (158), Expect = 5e-08
Identities = 31/57 (54%), Positives = 43/57 (75%)
Frame = +2

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
+GGP+W VK GRRD+ TAS++ AN +PA L++LISRF GL+ +D+VALSG+
Sbjct: 1 VGGPSWAVKFGRRDSTASRTLANAELPAFFDRLDRLISRFAQKGLTARDMVALSGS 57

>ref|XP_002336344.1| predicted protein [Populus trichocarpa]
gb|EEE73229.1| predicted protein [Populus trichocarpa]
Length = 316

Score = 166 bits (420), Expect = 2e-38
Identities = 83/124 (66%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR G NLAPLDL TP SFDN YFKNL+
Sbjct: 195 QAQCFTFRDRIYNASNIDAGFASTRKRRCPRAGGQA--NLAPLDLVTNPSFDNYYFKNLM 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLL SDQ LFNGGSTDSIV YS NP FSSDFA+AMIKMGDI PLTGS G+IR+ C
Sbjct: 253 RNKGLLQSDQVLFNGGSTDSIVSEYSRNPAPKFSDFASAMIKMGDIRPLTGSAGQIRRIC 312

Query: 2167 RRIN 2178
+N
Sbjct: 313 SAVN 316

Score = 135 bits (339), Expect = 5e-29
Identities = 76/166 (45%), Positives = 97/166 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLD+TSS EK A N+NSARG+EVID K+ VEK+CPGVVSCADI+A+AA
Sbjct: 68 VQGDASILLDETSSIKSEKTAGANKNSARGYEVIDKAKAEVEKICPGVVSCADIIAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP+W VKLG
Sbjct: 128 RDA-----SAYVGGPSWAVKLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS + A +PA + +L +LISRF GL+ +D+VALSG+
Sbjct: 145 RRDSTTASPTLAITELPAFSDDLGRLISRFFQKGLTARDMVALSGS 190

Score = 63.5 bits (153), Expect = 2e-07
Identities = 26/50 (52%), Positives = 40/50 (80%)
Frame = +1

Query: 631 SANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
+ A+LS+ FY+ SCPN S++++ +++AI++E RM ASL+RL FHDCFV
Sbjct: 19 ACQAKLSSTFYHKSCPNAESAIRTAIRTAIRERRMAASLIRLHFHDCFV 68

>emb|CAA71493.1| peroxidase [Spinacia oleracea]
Length = 309

Score = 166 bits (420), Expect = 2e-38
Identities = 76/123 (61%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARC +FR IYN+T+I+ F TR+ +CP ++ +G+ NLAPLDLQ+PT FDN Y+KNL+
Sbjct: 187 ARCVSFRHHIYNDTDIDANFEATRKCNCPLSNNTGNTNLAPLDLQSPKFDNSYYKNLIA 246

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLLHSDQ+L+NGGS D++V YS + F+ DF AA+IKMG+ISPLTGS+GEIRKNCR

Sbjct: 247 KRGLLHSDQELYNGGSQDALVTRYSKSNAAFKDFVAAIIKMGNISPLTGSSGEIRKNCR 306

Query: 2170 RIN 2178

IN

Sbjct: 307 FIN 309

Score = 131 bits (329), Expect = 7e-28
Identities = 79/170 (46%), Positives = 95/170 (55%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRN-SARGFEVIDNIKSAVEKVC PGVVSCADILAIA 1327
+ GCD S+LLDDTS+FTGEK A NRN S RGFEVID+IK+ VE C VSCADILA+A

Sbjct: 58 VNGCDASLLDDTSTFTGEKTAISNRNNSVRGFEVIDSIKTNVEASCKATVSCADILALA 117

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD V + LGGP+W V L

Sbjct: 118 ARDGVFL-----LGGPSWKVPL 134

Query: 1508 GRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

GRRDARTAS +AA N +P +S+L+ L + F+ GLS KD+ ALSG I

Sbjct: 135 GRRDARTASLTAATNNLPPASSSLSNLTLFNNKGLSPKDMTALSGAHTI 184

Score = 70.9 bits (172), Expect = 1e-09
Identities = 32/50 (64%), Positives = 39/50 (78%)
Frame = +1

Query: 634 ANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFVN 783

+NAQLS+ Y SCPNL V+ T++ A+ KE RMGAS+LRLFFHDCFVN

Sbjct: 10 SNAQLSSKHYASSCPNLEKIVRKTMKQAVQKEQRMGASILR LFFHDCFVN 59

>gb|AAX53172.1| peroxidase [Populus alba x Populus tremula var. glandulosa]
Length = 316

Score = 166 bits (420), Expect = 2e-38
Identities = 81/123 (65%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARCT FR RIYN+TNI+ +FA TR+ SCP + GD LAPLD T T FDN Y+ NLV

Sbjct: 197 ARCTTFRNRIYNDTNIDASFATRRASCP--ASGGDATLAPLD-GTQTRFDNYYTNLVA 253

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++VR YSTN TF+ DFAAAM++MG+ISPLTG+NGEIR+NCR

Sbjct: 254 RRGLLHSDQELFNGGSQDALVRTYSTNGATFARDFAAAMVRMGNISPLTGTNGEIRRNCR 313

Query: 2170 RIN 2178
+N

Sbjct: 314 VVN 316

Score = 159 bits (402), Expect = 3e-36
Identities = 90/165 (54%), Positives = 101/165 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDT++FTGEKNANPNRNSARGFEVID IK+ VE C VSCADILA+AA

Sbjct: 69 VNGCDGSILLDDTATFTGEKNANPNRNSARGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG

Sbjct: 129 RDGVVL-----LGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAAN+ IP+P S+L LIS FSA GLS D+ ALSG

Sbjct: 146 RRDARTASQSAANSQIPSPASSLATLISMFSAKGLSAGDMTALSG 190

Score = 63.2 bits (152), Expect = 2e-07
Identities = 32/78 (41%), Positives = 45/78 (57%)
Frame = +1

Query: 550 VCLSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQS AISKE 729
+C+ L +SFCS AQLS FY +CPNL + V++ + A++ +

Sbjct: 10 LCIVPLLASSFCS-----AQLSATFYASTCPNLQTIVRNAMTGAVNGQ 52

Query: 730 TRMGASLLRLLFFHDCFVN 783
R+ AS+LRLFFHDCFVN

Sbjct: 53 PRLAASILRLLFFHDCFVN 70

>ref|XP_002509738.1| Lignin-forming anionic peroxidase precursor, putative [Ricin
communis]

gb|EEF51125.1| Lignin-forming anionic peroxidase precursor, putative [Ricin
communis]

Length = 320

Score = 166 bits (419), Expect = 3e-38
Identities = 80/125 (64%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIYN ++I+ FA TR+ CP SGSGD+NLAPLDL TP FDN YF+NL

Sbjct: 196 QAQCVTFRGRIYNNASDIDAGFAATTRSQCPAASGSGDSNLAPLDLVTNIFDNNYFRNL 255

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GG+TDSIV YS + FSSDFA+AM+KMG+ISPLTGS G+IR+

Sbjct: 256 IQKKGLLQSDQVLFSGGATDSIVNQYSRDSVSSDFASAMVKMGNISPLTGSQQIRRV 315

Query: 2164 CRRIN 2178
C +N

Sbjct: 316 CNVVN 320

Score = 137 bits (346), Expect = 8e-30
Identities = 77/169 (45%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCDGSILLDDT + TGEK A N NS RGF+VIDNIKS +E CPG+VSCADI+A+AA

Sbjct: 69 VQGCDGSILLDDTPTMTGEKTARNNANSVRGFDVIDNIKSQLESRCPGIVSCADIVAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ GP+W+V LG

Sbjct: 129 RDA-----SVAASGPSWSVNLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS+S A++ +PA T +L++L S F + GLS +D+VALSG I

Sbjct: 146 RRDSTTASRSLADSNLPAFTDSLDRLTSLFGSKGLSQRDMVALSGAHTI 194

Score = 70.1 bits (170), Expect = 2e-09
Identities = 32/67 (47%), Positives = 49/67 (73%), Gaps = 2/67 (2%)
Frame = +1

Query: 586 SRLTICLALFVLIWGS--ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRL 759
SRL++ + ++I+ S AQLS+NFY ++CP+ S++K + +A+S+E RM ASL+RL

Sbjct: 3 SRLSLLCMVLMIFSSLPCQAQLSSNFYDNTCPSALSTIKGAISTAVSREQRMAASLIRL 62

Query: 760 FFHDCFV 780
FHDCFV

Sbjct: 63 HFHDCFV 69

>ref|XP_002453592.1| hypothetical protein SORBIDRAFT_04g008630 [Sorghum bicolor]
gb|EES06568.1| hypothetical protein SORBIDRAFT_04g008630 [Sorghum bicolor]
Length = 321

Score = 165 bits (418), Expect = 4e-38
Identities = 76/123 (61%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A C +FR IYN+TN++ AFA RQ++CP SGSGD NLAPLD+QT FDN Y++NL+
Sbjct: 197 AECEDFRGHIYNDTNVDPFAALRQRNCPAESGSGDTNLAPLDVQTRYVFDNAYYRNLMV 256

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++V+ YST+PG F+S F AAMIKMG+I LTGS G+IR +CR
Sbjct: 257 RQGLLHSDQELFNGGSQDALVQQYSTDPGLFASHFVAAMIKMGNIGTLTGSQGGIRADCR 316

Query: 2170 RIN 2178
+N
Sbjct: 317 VVN 319

Score = 135 bits (339), Expect = 5e-29
Identities = 81/169 (47%), Positives = 92/169 (54%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCDGSILLDD SF GEK A PN S RG+EVID IK+ VE VCPGVVSCADI+A+AARD
Sbjct: 72 GCDGSILLDDAGSFVGEKTALPNA-SIRGYEVIDQIKANVEAVCPGVVSCADIVALAARD 130

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
++ GGPTW V LGRR
Sbjct: 131 GTVLL-----GGPTWAVPLGRR 147

Query: 1517 DARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHISH 1663
D+ TAS S AN+ IPAPT NL+ LI F GLS D+ ALSG I +
Sbjct: 148 DSTTASLSQANS DIPAPTLNLDLILAFGKKGLSPADMTALSGAHTIGY 196

Score = 60.8 bits (146), Expect = 1e-06
Identities = 34/70 (48%), Positives = 40/70 (57%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA L CL L + QL+ FY SCP L V++T+ AI + RMGASL
Sbjct: 1 MACSFRALLHCLLALSCLSTAYGGQLTPTFYALSCPALEPIVRTTMTKAIINDRRMGASL 60

Query: 751 LRLFFHDCFV 780

LRLFFHDCFV
Sbjct: 61 LRLFFHDCFV 70

>gb|ACN60163.1| class III peroxidase [Tamarix hispida]
Length = 320

Score = 164 bits (415), Expect = 8e-38
Identities = 77/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNETNI ++FA++ Q +CP T G DNNL+PLD +PT+FD Y+ +L+
Sbjct: 199 QARCTSFARIYNETNINSSFAKSLQANCPSTGG--DNNLSPLDTSSPTTFDVGYYTDLI 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQL+NGGSTDS V YS++ TF +DF +MI MG+ISPLTGS G++R NC
Sbjct: 257 GQKGLLHSDQQLYNGGSTDSQVTSYSSSSSTFLTDFGTSMINMGNISPLTGSRGQVRTNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKTN 320

Score = 125 bits (313), Expect = 5e-26
Identities = 78/170 (45%), Positives = 89/170 (52%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGS-ILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIA 1327
+ GCD S + K A PN S RGF+V+D IKS VE VCPGVV CADILA+A
Sbjct: 71 VNGCDASGSIRRHCQLHRKRKTAQPNNGLRGFVVDTIKSKVESVCPGVVPCADILAVA 130

Query: 1328 ARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGG +W V L
Sbjct: 131 ARDSV-----VALGGKSWGVL 147

Query: 1508 GRRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
GRRD+ TAS SAAN GIPAPT NL+ LI+ FS +GLSTKDLV LSG I
Sbjct: 148 GRRDSTTASLSAANTGIPAPTLNLSGLITSFNSVGLSTKDLVVLGAHTI 197

>ref|XP_002450134.1| hypothetical protein SORBIDRAFT_05g001030 [Sorghum bicolor]
gb|EES09122.1| hypothetical protein SORBIDRAFT_05g001030 [Sorghum bicolor]
Length = 317

Score = 163 bits (413), Expect = 1e-37
Identities = 76/124 (61%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+E NI+T+ A + + +CP +G DNN++PLD TP FDN+Y+KNL+
Sbjct: 196 QARCVNFRDRIYSEANIDTSLATSLKTCNPKTG--DNNISPLDASTPYVFDNFYKKNLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N F +DF+ AM+KM +ISPLTGS+G+IRKNC
Sbjct: 254 NKKGVLHSDQQLFNGGSADSQTTTYSSNMAKFFTFSTAMLKMSNISPLTGSSGQIRKNC 313

Query: 2167 RRIN 2178
RR+N
Sbjct: 314 RRVN 317

Score = 147 bits (370), Expect = 1e-32
Identities = 81/165 (49%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVSCADILAI AA 1330
+ GCDGS+LLDDT +FTGEK A PN NS RGF+VID+IK+ +E++CP VVSCADI+A+AA
Sbjct: 69 VNGCDGSVLLDDTPTFTGEKTAVPNNSLRGFVIDSIKAQLERICPQVVSCADIVAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 129 RDSV-----VALGGPTWAVNLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+ TAS AANN IPAPT +L L FS GLS D++ALSG
Sbjct: 146 RRDSL TASLDAANNDIPAPTLDLTDLTKSFSNKGLSASDMIALSG 190

Score = 68.9 bits (167), Expect = 4e-09
Identities = 36/71 (50%), Positives = 47/71 (66%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS LALF ++QL+ NFY SCPN ++++ V+SA+++E RMGASL
Sbjct: 1 MASHKPLTCSVLALFFAA-SLVSSQLNANFYDKSCPALYTIQTAVRS AVAREN RMGASL 59

Query: 751 LRLFFHDCFVN 783
LRL FHDCFVN
Sbjct: 60 LRLHFHDCFVN 70

>gb|AAC05277.1| peroxidase FLXPER4 [Linum usitatissimum]
Length = 305

Score = 163 bits (413), Expect = 1e-37
Identities = 81/124 (65%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYN+TNI+ AFA TR+ +CP+ +G+G N LAPLD TPT FDN Y+++LV

Sbjct: 185 QARCTTFRQRIYNDTNIDPAFATRRGNCPQ-AGAGAN-LAPLD-GTPTQFDNRYQDLV 241

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFN G+ D++VR YS N TF++DFAAAM++MG+ISPLTG+NGEIR NC

Sbjct: 242 ARRGLLHSDQELFNNGTQDALVRTYSNNAATFATDFAAAMVRMGNISPLTG+NGEIRFNC 301

Query: 2167 RRIN 2178
RR N

Sbjct: 302 RRPN 305

Score = 144 bits (362), Expect = 1e-31
Identities = 80/169 (47%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDT++FTGEKNA PN+NS RGF++ID IK+ VE C VSCADILA+AA

Sbjct: 58 VNGCDGSLLLDDTATFTGEKNAGPNQNSVRGFDIIDT IKTRVEAACNATVSCADILALAA 117

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V +V GGPTW V LG

Sbjct: 118 RDGVVLV-----GGPTWTVPLG 134

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAAN IPAP S+L + + F+ GL+ +D+ LSG I

Sbjct: 135 RRDARTASQSAANAQIPAPGSSLGTITNLFTNKGLTARDVTILSGAHTI 183

Score = 65.1 bits (157), Expect = 6e-08
Identities = 29/55 (52%), Positives = 39/55 (70%)
Frame = +1

Query: 619 LIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
L+ S +AQL+ NFY SCP L + V++ + A++ E RM AS+LRL FHDCFVN

Sbjct: 5 LLASSGSAQLAANFYATSCPTLLTIVRNAMTQAVNSENMAASILRLLHFHDCFVN 59

>ref|XP_002269343.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 331

Score = 163 bits (412), Expect = 2e-37

Identities = 81/125 (64%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP +G+GD+NLAPL+L TP SFDN YFKNL

Sbjct: 207 QARCVTFRDRIYDNGTDIDAGFASTRRRRCPANNGGDDNLAPLELVTPNSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+++KGLL SDQ LF+GGSTD+IV YS +P TF SDFA+AM+KMGDI LTGS G IRK

Sbjct: 267 IRRKGLLQSDQVLFSGGSTDTIVNEYSKSPKTFRSDFASAMVKMGDIEALTGSAGVIRKF 326

Query: 2164 CRRIN 2178

C IN

Sbjct: 327 CNVIN 331

Score = 132 bits (332), Expect = 3e-28
Identities = 76/169 (44%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SILLDD+SS EKNA N NS RG+EVIDNIKS VE +CPGVVSCADI+A+AA

Sbjct: 80 VQGC DASILLDDSSSIQSEKNAPNNLNSVRGYEVIDNIKSKVESLCPGVVSCADIVAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VS GPTW V+LG

Sbjct: 140 RDASVAVS-----GPTWTVRLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ T+ S A +P+ +L++L+S F + GLS +D+VALSG+ I

Sbjct: 157 RRDSTTSGLSQAATNLPSFRDSLDKLVSLFGSKGLSARDMVALSGSHTI 205

Score = 63.5 bits (153), Expect = 2e-07
Identities = 31/69 (44%), Positives = 46/69 (66%), Gaps = 1/69 (1%)
Frame = +1

Query: 577 SFC SRLTICLALFVLIWGS-ANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753
S S I LA+F+++ A LS FY H+CP +++++ V++A+S+E RM ASL+

Sbjct: 12 SCISPACIFLAVFLILSNMPCEAHLSPTFYDHTCPRALTTIQTAVRTAVSRERRMAASLI 71

Query: 754 RLFFHDCFV 780

RL FHDCFV

Sbjct: 72 RLHFHDCFV 80

>gb|EAY85148.1| hypothetical protein OsI_06503 [Oryza sativa Indica Group]

Length = 323

Score = 163 bits (412), Expect = 2e-37
Identities = 74/123 (60%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
++C NFR RIYN+TNI+ AFA R+ CP GSGD +LAPLD T FDN Y++NL+
Sbjct: 199 SQCANFRDRIYNDTNIDPAFAALRRGGCPAAPGSGDTS LAPLDALTQNVFDNAYYRNLLA 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGS D++V+ YS+NP F++DFAAAMIKMG+I+PLTG+ G+IR++CR
Sbjct: 259 QRGLLHSDQVLFNGGSQDALVQQYSSNPALFAADFAAAMIKMGNINPLTGAAGQIRRSCR 318

Query: 2170 RIN 2178
+N
Sbjct: 319 AVN 321

Score = 139 bits (349), Expect = 4e-30
Identities = 80/171 (46%), Positives = 99/171 (57%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD SILLDD +SF GEK A PN NS RG++VID IK VE +CPGVVSCADI+A+
Sbjct: 69 VQGCDASILLDDVPATSFVGEKTAFPNVNSVRGYDVIDQIKRRVELLCPGVVSCADIVAL 128

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 129 AARDSTAL-----LGGPSWEVP 145

Query: 1505 LRRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
LRRRD+ TAS SAAN+ +PAP+S+L L++RF + GLS +D+ ALSG I
Sbjct: 146 LRRRDSTTASLSAANSDLPAPSSDLATLVARFGSKGLSPRDMTALSGAHTI 196

Score = 69.7 bits (169), Expect = 3e-09
Identities = 35/60 (58%), Positives = 41/60 (68%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
CL F L+ +A QLST FY SCP L V++TV S + E RMGASL+RLFFHDCFV
Sbjct: 10 CLLAFFLLSSAACGQLSTTFYAASCP TLQLVVRATV LSTLLAERRMGASLVR LFFHDCFV 69

>ref|XP_002269301.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 213

Score = 162 bits (411), Expect = 2e-37
Identities = 81/124 (65%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q RC FR RIYN T+I+ FA TR++ CP +G+GD NLAPL+L TP SFDN YFKNL+
Sbjct: 90 QGRCVTFRDRIYNGTDIDAGFASTRRRRCPADNGNGDANLAPLELVTPNSFDNYYFKNLI 149

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q+KGLL SDQ LF+GGSTDSIV YS +P TF SDFA+AM+KMGDI PLT S G IRK
Sbjct: 150 QRKGLLQSDQVLFSGGSTDSIVNEYSKSPKTFRSDFASAMLKMGDIEPLTRSAGVIRKIFY 209

Query: 2167 RRIN 2178
IN
Sbjct: 210 NVIN 213

Score = 62.0 bits (149), Expect = 5e-07
Identities = 30/60 (50%), Positives = 42/60 (70%)
Frame = +2

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
+ GPTW VKLGRRD+ T+ S A +P+ +L++LIS F + GLS +D+VALSG+ I
Sbjct: 29 VSGPTWTVKLGRRDSTTSGLSLAATNLPSFRDSLKLI SLFGSKGLSARDMVALSGSHTI 88

>gb|AAD37428.1|AF149278_1 peroxidase 3 precursor [Phaseolus vulgaris]
Length = 324

Score = 162 bits (411), Expect = 2e-37
Identities = 78/126 (61%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG--DNNLAPLDLQTPTSFDNYYFKN 1980
+ARC + +RIYNE NIE+ FA+ RQ++CPR S DNN+APL+ +TP FDN Y+KN
Sbjct: 199 KARCAVYGSRIYNEKNIESLFAKARQKNCPRNSNGTPKDNNVAPLEFKTPNHFDNYYKN 258

Query: 1981 LVQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ KKGLLHSDQ LF+GGSTDS+VR YS + F SDF AMIKMG+I PLTGSNG+IR+
Sbjct: 259 LINKKGLLHSDQVLFDDGGSTDSLVRAYSNDQRAFESDFVTAMIKMGNIKPLTGSNGQIRR 318

Query: 2161 NCRRIN 2178
C R N
Sbjct: 319 LCGRPN 324

Score = 126 bits (317), Expect = 2e-26
Identities = 79/170 (46%), Positives = 93/170 (54%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+ GCDGS+LLD SS EK A PN S RG+EVID IKS VE +CPG+VSCADI+AIAA
Sbjct: 74 VNGCDGSVLLDGPSS---EKTAPPNDKSLRGYEVIDAIKSKVEALCPGIVSCADIVAIAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W VKLG
Sbjct: 131 RDSVNI-----LGGPFWKVKLG 147

Query: 1511 RRDARTA-SQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T Q A++ +P+P S+L+ LIS F GLS KD+VALSG I
Sbjct: 148 RRDSSTGFFQLASSGALPSPASSLDTLISSFKDQGLSAKDMVALSGAHTI 197

Score = 83.6 bits (205), Expect = 2e-13
Identities = 42/67 (62%), Positives = 50/67 (74%), Gaps = 1/67 (1%)
Frame = +1

Query: 586 SRLTICLALFVL-IWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLF 762
S T +A F L + GS++AQLS NFY CP + +VKS VQSA++KE RMGASLLRLF
Sbjct: 9 STTFAIAFFTLFLIGSSSAQLSENFYAKKCPKVLVAVKSVVQSAVAKEPRMGASLLRLF 68

Query: 763 FHDCFVN 783
FHDCFVN
Sbjct: 69 FHDCFVN 75

>ref|XP_002334243.1| predicted protein [Populus trichocarpa]
gb|EEF07510.1| predicted protein [Populus trichocarpa]
Length = 317

Score = 162 bits (410), Expect = 3e-37
Identities = 80/124 (64%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RI+++ NI+ FA TR++ CP D+ LAPLDL TP SFDN YFKNL+
Sbjct: 196 QAQCFTFRDRIHSDNNIDAGFASTRKRRCLVGS--DSTLAPLDLVTPNVFDNYYFKNLM 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
QKKGLL SDQ+LF+GGSTDSIV YS NP FSSDFA+AMIKMGDISPLTG+ G+IR+ C
Sbjct: 254 QKKGLLQSDQELFSGGSTDSIVSEYSRNPAPKFSDFASAMIKMGDISPLTGTAGQIRRIC 313

Query: 2167 RRIN 2178
+N

Sbjct: 314 SAVN 317

Score = 133 bits (335), Expect = 1e-28
Identities = 76/166 (45%), Positives = 95/166 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLD+TSS EK A N NS RG+EVID KS VEK+CPGVVSCADI+A+AA
Sbjct: 69 VQGCDA SILLDETSSIQSEKTAGGNNSVRGYEVIDKAKSKVEKICPGVVSCADIIAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP+W VKLG
Sbjct: 129 RDA-----SAYVGGPSWAVKLG 145

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS + A +PA + +L +LISRF GL+ +D+VALSG+
Sbjct: 146 RRDSTTASPTLAITELPAFSDDLGRLISRFRQKGLTARDMVALSGS 191

Score = 62.0 bits (149), Expect = 5e-07
Identities = 28/57 (49%), Positives = 42/57 (73%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRRLFHDCFV 780
LF+L + A+LS+ FY SCP S++++ +++AI++E RM ASL+RL FHDCFV
Sbjct: 13 LFLSTTACQAKLSSAFYDKSCPKAESAIRTAIRTAIARERRMAASLIRLHFHDCFV 69

>ref|XP_002438530.1| hypothetical protein SORBIDRAFT_10g021630 [Sorghum bicolor]
gb|EER89897.1| hypothetical protein SORBIDRAFT_10g021630 [Sorghum bicolor]
Length = 329

Score = 162 bits (409), Expect = 4e-37
Identities = 73/126 (57%), Positives = 100/126 (79%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS--GSGDNNLAPLDLQTPTSFDNYYFKN 1980
QARCT FR+RIY +TNI FA RQQ+CP+ S G+GD LAP+D++TP +FDN Y++N
Sbjct: 204 QARCTTFRSRIYGDTNINATFASLRQQTCPQASDGGAGDAALAPIDVRTPEAFDNAYYQN 263

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ ++GL HSDQ+LFNGGS D++V+ YS N F++DFA AM++MG ISPLTG+ GE+R
Sbjct: 264 LMARQGLFHSDQQLFNGGSQDALVKKYSGNAAMFAADFAKAMVRMG AISPLTGTQGEVRL 323

Query: 2161 NCRRIN 2178
+CR++N

Sbjct: 324 DCRKVN 329

Score = 141 bits (356), Expect = 5e-31
Identities = 79/165 (47%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 77 VNGCDASILLDDTATFTGEKNAGPNANSVRGYEVIDAIKTQEASCNATVSCADILALAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ GGPTW V LG
Sbjct: 137 RDAVNLL-----GGPTWTVYLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQS AN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 154 RRDARTASQSDANGNLPGPSLTLVTMFGNKGLSARDMTALSG 198

Score = 69.3 bits (168), Expect = 3e-09
Identities = 35/66 (53%), Positives = 48/66 (72%), Gaps = 2/66 (3%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQ--LSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFF 765
LT+ L +L+ G+A A LST+FY CPN+ S V++ + SA++ E RMGAS+LR+FF
Sbjct: 13 LTVAAVLSLLMAGAAAAGGLSTSFYSKCKPNVQSIVRAGMASAVAAEKRMGASILRMFF 72

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 73 HDCFVN 78

>ref|XP_002281755.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 317

Score = 162 bits (409), Expect = 4e-37
Identities = 78/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD+QT FDN Y++NL+
Sbjct: 196 QAQCFTFRSRIYNDTNIDPNFAATRRSTCP-VSG-GNSNLAPLDIQTMNKFDNYYQNLN 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR YS N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TQRGLLHSDQELFNGGSQDALVRTYSANNALFFGDFAAAMVKMSNISPLTG+NGEIRSNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RVVN 317

Score = 152 bits (383), Expect = 4e-34
Identities = 85/169 (50%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACKATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 129 RDGVVL-----LGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTA+QSAANN +PAP +NL+ LIS F+A GL+ D+ ALSG+ I
Sbjct: 146 RRDARTANQSAANNDLPAPFANLSALISGFAAKGLNADDMTALSGSHTI 194

Score = 70.9 bits (172), Expect = 1e-09
Identities = 37/71 (52%), Positives = 47/71 (66%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MASF + + + VL S NAQLS NFY +CPN+ V+ + A+ +E RMGAS+
Sbjct: 1 MASFTNSFVFSIISVLAC-SINAQLSPNFYASTCPNVQKIVRVEMVQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>ref|XP_002437128.1| hypothetical protein SORBIDRAFT_10g021610 [Sorghum bicolor]
gb|EER88495.1| hypothetical protein SORBIDRAFT_10g021610 [Sorghum bicolor]
Length = 314

Score = 161 bits (408), Expect = 5e-37
Identities = 76/125 (60%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFART-RQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT FR+RIY +TNI +FA RQQ+CP++ G G NLAP+D+QTPT FD Y+ NL
Sbjct: 191 QARCTTFRSRIYGDNTNINASFAAALRQQTCPQSGGDG--NLAPMDVQTPTRFDTDYNTNL 248

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ ++GL HSDQ+LFNGGS D++VR YS NP F+SDF AAMIKMG++ LTG+ G+IR+N
Sbjct: 249 LSQRGLFHSDQELFNGGSQDALVRQYSANPSLFNSDFMAAMIKMGVGVLTGTAGQIRRN 308

Query: 2164 CRRIN 2178
CR +N
Sbjct: 309 CRVVN 313

Score = 134 bits (336), Expect = 1e-28
Identities = 80/169 (47%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCDGSILLD GEK A PN NSARGFEVID IK+ VE CPGVVSCADILA+AA
Sbjct: 68 VQGCDGSILLDAG----GEKTAGPNANSARGFEVIDTIKTNVEAACPGVVSCADILALAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD ++ G PTWNV LG
Sbjct: 124 RDGTNLLGG-----PTWNVPLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P T++L LIS FS GLS +D+ ALSG I
Sbjct: 141 RRDSTTASASLANSNLPQSTASLGTLISLFSRQGLSARDMTALSGAHTI 189

Score = 71.6 bits (174), Expect = 7e-10
Identities = 36/60 (60%), Positives = 42/60 (70%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
CL L+ A+AQLST FY SCPNL S V+ + A+S + RMGASLLRFFHDCFV
Sbjct: 9 CLVAISLLSCVAHAQLSTTFYASSCPNLQSI VRRAMIQALSNDQRMGASLLRFFHDCFV 68

>ref|XP_002517727.1| Cationic peroxidase 1 precursor, putative [Ricinus communis]
gb|EEF44659.1| Cationic peroxidase 1 precursor, putative [Ricinus communis]
Length = 264

Score = 160 bits (406), Expect = 9e-37
Identities = 79/124 (63%), Positives = 100/124 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YNETNI++A A + + CP T+GS D+NL+PLD +P FDN YFKNLV
Sbjct: 143 QARCLMFRGRLYNETNIDSALATSLKSDCP--TTGS--DDNLSPLDATSPVIFDNSYFKNLV 200

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLF+GGST+S V+ YST+P TF +DFA AMIKMG +SPLTG++G+IR +C
Sbjct: 201 NKGGLLHSDQQLFSGGSTNSQVKTYSTDPFTFYADFANAMIKMGKLSPLTGTGQIRTDC 260

Query: 2167 RRIN 2178
R++N
Sbjct: 261 RKNV 264

Score = 140 bits (354), Expect = 9e-31
Identities = 80/170 (47%), Positives = 98/170 (57%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTS-SFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI A 1327
+ GCD S+LLDD S SFTGEK A PN NS RGF+VID IKS VE +CPGVVSCADILA+A
Sbjct: 15 VNGCDASVLLDDISPSTGEKTAGPNANSLRGFDVIDTIKSQVESICPGVVSCADILAVA 74

Query: 1328 ARDSVQIVSQGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGP+W V+L
Sbjct: 75 ARDSV-----VALGGPSWQVEL 91

Query: 1508 GRRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
GRRD+ TAS AAN +P+P +L+ LIS S G + K++VAL+G+ I
Sbjct: 92 GRRDSTTASYDAANTDLPSPMLDSDLISALSRKGFTAKEMVALAGSHTI 141

>ref|NP_001057822.1| Os06g0547400 [Oryza sativa (japonica cultivar-group)]
dbj|BAD54122.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69328.1| TPA: class III peroxidase 86 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAF19736.1| Os06g0547400 [Oryza sativa Japonica Group]
gb|EEC80780.1| hypothetical protein OsI_23305 [Oryza sativa Indica Group]
gb|EEE65851.1| hypothetical protein OsJ_21628 [Oryza sativa Japonica Group]
Length = 324

Score = 160 bits (406), Expect = 9e-37
Identities = 74/124 (59%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFNYYFKNLV 1986
+A+C FR+RIY E NI +FA RQQ+CPR+ G D NLAP D+QTP +FDN Y++NLV
Sbjct: 203 RAQCQFFRSRIYTERNINASFASLRQQTCPRSGG--DANLAPFDVQTPDAFDNAYYQNLV 260

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D +VR YSTNP FSSDF +AM+KMG++ P +G+ E+R NC
Sbjct: 261 SQRLLHSDQELFNGGSQDGLVRQYSTNPSQFSSDFVSAMVKMGNLLPSSGTATEVRLNC 320

Query: 2167 RRIN 2178
R++N
Sbjct: 321 RKNV 324

Score = 149 bits (375), Expect = 3e-33
Identities = 84/169 (49%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGKFNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTS+FTGK+A PN NSARGFEVID IK+ VE C VSCADILA+AA
Sbjct: 76 VNGCDGSILLDDTSTFTGKFSAGPNANSARGFEVIDAIKTQVEASCKATVSCADILALAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGPTWNVKLG 1510
RD V ++ GGPTW+V LG
Sbjct: 136 RDGVNLL-----GGPTWSVALG 152

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
R+D+RTASQSAAN+ +P P S+L LIS F GLS +D+ ALSG I
Sbjct: 153 RKDSRTASQSAANSLPGGSSLATLISMFGNQGLSARDMTALSGAHTI 201

Score = 73.2 bits (178), Expect = 2e-10
Identities = 36/63 (57%), Positives = 47/63 (74%), Gaps = 1/63 (1%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQ-LSTNFYHSCPFLFSSVKSTVQSAISKETRMGASLLRRLFHDC 774
+ + + VL+ G+A AQ LS NFY +CPNL + V+S + SA+ E RMGAS+LRLFHDC
Sbjct: 15 VAVVVAVLLGGAAEAQQLSPNFYSRTCPLATIVRSGMASAVRTEPRMGASILRRLFHDC 74

Query: 775 FVN 783
FVN
Sbjct: 75 FVN 77

>ref|XP_002285724.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 318

Score = 160 bits (405), Expect = 1e-36
Identities = 78/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR IYN+T+I+ AFA ++Q+ CPR+ G D+NL+PLD T T FDN YF+ L
Sbjct: 196 KARCTSFRNHIYNDTIDPAFAASKQKICPRSGG--DDNLSPLD-GTTTVFDNVYFRGLK 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ+L+NGGSTDSIV YS N TF D A AM+KMG+ISPLTG+NG+IR NC
Sbjct: 253 EKKGLLHSDQELYNGGSTDSIVETYSINTATFFRDVANAMVKMGNISPLTGNGQIRTNC 312

Query: 2167 RRIN 2178
R++N
Sbjct: 313 RKNV 316

Score = 155 bits (391), Expect = 5e-35
Identities = 86/167 (51%), Positives = 100/167 (59%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG+EVID IKS VE +CPGVVSCADI+A+AARD
Sbjct: 71 GCDASILLDDTATFTGEKTAGPNNNSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 130

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1516
SV + LGGPTW V+LGRR
Sbjct: 131 SV-----VALGGPTWTVRLGR 147

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS SAA +P P NL+QLIS FS GL+TK++V LSGT I
Sbjct: 148 DSTTASFAARTDLPGNLNSQLISAFSKKGLTTKEMVVLSGHTI 194

Score = 66.6 bits (161), Expect = 2e-08
Identities = 32/58 (55%), Positives = 41/58 (70%), Gaps = 1/58 (1%)
Frame = +1

Query: 610 LFVLIWGSANAQ-LSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
+F L+ G A+A LS NFY SCP ++++ V A++KE RMGASLLRL FHDCFV
Sbjct: 12 IFSLLGMAHAHYLSPNFYARSCPRLPTIRTAVNKAVAKEKRMGASLLRLLFHDCFV 69

>ref|XP_002521867.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
gb|EEF40503.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
Length = 326

Score = 160 bits (405), Expect = 1e-36
Identities = 83/125 (66%), Positives = 96/125 (76%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIY N T I+ FA TR++SCP G D NLAPLDL TP SFDN YFKNL

Sbjct: 204 QAQCFTFRDRIYSNGTEIDAGFASTRKRSCPAVGG--DANLAPLDLVTNPNSFDNNYFKNL 261

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ L +GGSTDSIV GYS +P TFSSDFA+AMIKMG+I PLTG+ G+IR+

Sbjct: 262 MQRKGLLESQILLSGGSTDSIVSGYSRSPSTFSSDFASAMIKMGIDPLTGTAGQIRRI 321

Query: 2164 CRRIN 2178
C IN

Sbjct: 322 CSAIN 326

Score = 137 bits (344), Expect = 1e-29
Identities = 75/165 (45%), Positives = 99/165 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLD+TS+ EK A PN++SARG+EVID K+ VEK+CPGVVSCADIL++AA

Sbjct: 77 IQGCDASVLLDETSTIESEKTALPNKDSARGYEVIDKAKTEVEKICPGVVSCADILSVAA 136

Query: 1331 RDSVQIVSGQTTNKNLTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDS S +GGP+W V LG

Sbjct: 137 RDS-----SAYVGGPSWTVMLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS++ AN+ +P+ L++LISRF + GLS +D+VALSG

Sbjct: 154 RRDSTTASRTLANSFELPSFKDGLDRLISRFSKGLSARDMVALSG 198

Score = 60.8 bits (146), Expect = 1e-06
Identities = 27/56 (48%), Positives = 44/56 (78%), Gaps = 1/56 (1%)
Frame = +1

Query: 616 VLIWGA-NAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
+LI G+A +AQL++ FY CPN S+++++++I+ E RM ASL+RL FHDCF+

Sbjct: 22 LLILGTACHAQLTSTFYDSLCPNALSTIRTSIRNSIAAERRMAASLIRLHFHDCFV 77

>emb|CAH10841.1| peroxidase [Picea abies]
Length = 320

Score = 160 bits (405), Expect = 1e-36
Identities = 78/124 (62%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYNE+NI AFA + + +CP S GDN L+PLD+ TP F+N Y+ NL

Sbjct: 199 QSRCAFFRTRIYNESNINAAFATSVKANCP--SAGGDNTLSPLDVVTPIKFNKYYGNLK 256

Query: 1987 QKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQLFNGGSTDS V YSTN +F +DFAAAM+KM +ISPLTG++G+IRKNC
Sbjct: 257 IQKGLLHSDQQLFNGGSTDSQVTAYSTNQNSFFTFDFAAAMVKMSNISPLTGTSGQIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKAN 320

Score = 154 bits (388), Expect = 1e-34
Identities = 89/169 (52%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGSILLDD ++FTGEK A PN NSARGF+VID IK+ VE C GVVSCADIL IAA
Sbjct: 72 VSGCDGSILLDDNATFTGEKTAGPNANSARGFDVIDTIKTQVEAACSGVVSCADILTIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GPTW V LG
Sbjct: 132 RDSV-----VELQGPTWTVMLG 148

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAANN IP+P S+L+ LIS F GLSTKDLVALSG I
Sbjct: 149 RRDSTTASLSAANNIPSPASSLSALISSFKGHGLSTKDLVALSGAHTI 197

Score = 62.8 bits (151), Expect = 3e-07
Identities = 33/70 (47%), Positives = 43/70 (61%), Gaps = 5/70 (7%)
Frame = +1

Query: 589 RLTICLALFVLIWGSAN-----AQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLL 753
R +C+ + + S N QLS+ FY SCP S VK V+ A++KE RMGASL+
Sbjct: 4 RNLICIGIMAVFVCSININAVSGQLSSTFYDKSCPRAQSIKRVVKQALAKEKRMGASLV 63

Query: 754 RLFHDFCFVN 783
RL FHDFCV+
Sbjct: 64 RLHFHDFCFVS 73

>gb|EEE67814.1| hypothetical protein OsJ_25568 [Oryza sativa Japonica Group]
Length = 135

Score = 160 bits (404), Expect = 1e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFDN Y+ NL+
Sbjct: 12 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTPYSFDNAYYSNLL 71

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PLTGS G+IR +C
Sbjct: 72 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLTGSQQIRLSC 131

Query: 2167 RRIN 2178
++N
Sbjct: 132 SKVN 135

>tpe|CAH69352.1| TPA: class III peroxidase 110 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 313

Score = 160 bits (404), Expect = 1e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFDN Y+ NL+
Sbjct: 190 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTPYSFDNAYYSNLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PLTGS G+IR +C
Sbjct: 250 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLTGSQQIRLSC 309

Query: 2167 RRIN 2178
++N
Sbjct: 310 SKVN 313

Score = 127 bits (319), Expect = 1e-26
Identities = 74/175 (42%), Positives = 94/175 (53%)
Frame = +2

Query: 1118 AS*ILMSKH*QMCGDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV 1297
AS + + H GCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C
Sbjct: 53 ASLLRLHFHDFVGCDA SVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQT 112

Query: 1298 VSCADILAI AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI* 1477
VSCADILA+AARDSV +
Sbjct: 113 VSCADILAVAARDSV-----VA 129

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALS 1642
LGGP+W V LGRRD+ TAS +ANN +P P +L LI F G S D+VALS

Sbjct: 130 LGGPSWTVGLGRDSTTASMSANNDLPPFFDLENLIKAFGDKGFSVTDMVALS 184

Score = 67.0 bits (162), Expect = 2e-08
Identities = 31/62 (50%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASLLRLLFFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC
Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTAAVNNEPRMGASLLRLLHFHDC 63

Query: 775 FV 780
FV
Sbjct: 64 FV 65

>ref|NP_001060627.1| Os07g0677100 [Oryza sativa (japonica cultivar-group)]
dbj|BAC83102.1| peroxidase [Oryza sativa Japonica Group]
dbj|BAF22541.1| Os07g0677100 [Oryza sativa Japonica Group]
dbj|BAG95220.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 315

Score = 160 bits (404), Expect = 1e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFDN Y+ NL+
Sbjct: 192 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTPYFDNAYYSNLL 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR ++N FSS F++AM+KM ++ PLTGS G+IR +C
Sbjct: 252 SNKGLLHSDQVLFNGNSTDNTVRNFAFNRAAFSSAMVKMANLGPLTGSQQGQIRLSC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 132 bits (331), Expect = 4e-28
Identities = 74/169 (43%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C VSCADILA+AA
Sbjct: 65 VQGCDASVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQTVSCADILAVAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 125 RDSV-----VALGGPSWTVGLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS +ANN +P P +L LI F G S D+VALSG I
Sbjct: 142 RRSTTASMDSANNDLPPPFDFLENLIKAFGDKGFSVTDMVALSGAHTI 190

Score = 67.0 bits (162), Expect = 2e-08
Identities = 31/62 (50%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPFLSSVKSTVQSAISKETRMGASLLRRLFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC
Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTAANNNEPRMGASLLRRLFHDC 63

Query: 775 FV 780
FV
Sbjct: 64 FV 65

>gb|ABD66594.1| peroxidase [Litchi chinensis]
Length = 234

Score = 159 bits (403), Expect = 2e-36
Identities = 88/169 (52%), Positives = 103/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTS+F GEK A PN NS RGF V+D IK+ +EK CPGVVSCAD+LAIAA
Sbjct: 4 VDGCDGSLLDDTSTFVGEKTAVPNNNSVRGFNVVDQIKAKLEKACPGVVSCADLLAIAA 63

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 64 RDSV-----VHLGGPSWTVRLG 80

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS++ AN IP PTSNL+ LIS FSA GLS KDLVALSG I
Sbjct: 81 RRDSKTASRALANTSIPPPTSNSALISSFSAQGLSLKDLVALSGAHTI 129

Score = 113 bits (283), Expect = 2e-22
Identities = 54/98 (55%), Positives = 69/98 (70%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARCT+FR IYN+TNI+++FA + ++ CPR+ DN LA LD QTP FD Y+ NL++
Sbjct: 132 ARCTSFRGHIYNDTNIDSSFAMSLRRKCPRSGN--DNALANLDRQTPFCFDKLYYDNLK 189

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAA 2103
KKGLLHSDQ+LF GGS D V+ Y+ N F DFA A

Sbjct: 190 KKGLLHSDQELFKGGSADPFVKKYANNTSAFFKDFAGA 227

>emb|CBI19219.1| unnamed protein product [Vitis vinifera]
Length = 446

Score = 159 bits (403), Expect = 2e-36
Identities = 81/138 (58%), Positives = 105/138 (76%), Gaps = 1/138 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR IYN+T+I+ AFA ++Q+ CPR+ G D+NL+PLD T T FDN YF+ L

Sbjct: 194 KARCTSFRNHIYNDTDIDPAFAASKQKICPRSGG--DDNLSPLD-GTTTVFDNVYFRGLK 250

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ+L+NGGSTDSIV YS N TF D A AM+KMG+ISPLTG+NG+IR NC

Sbjct: 251 EKKGLLHSDQELYNGGSTDSIVETYSINTATFFRDVANAMVKMGNISPLTGNGQIRTNC 310

Query: 2167 RRIN*F-DSVLNIKGPTH 2217

R+I + + I+ PT+

Sbjct: 311 RKIQCIGPTPIEIRNPTN 328

Score = 155 bits (391), Expect = 5e-35
Identities = 86/167 (51%), Positives = 100/167 (59%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG+EVID IKS VE +CPGVVSCADI+A+AARD

Sbjct: 69 GCDASILLDDTATFTGEKTAGPNNSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 128

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V+LGRR

Sbjct: 129 SV-----VALGGPTWTVRLGRR 145

Query: 1517 DARTASQSAANNGIPAPTSNLSRFSALGLSTKDLVALSGTKHI 1657

D+ TAS SAA +P P NL+QLIS FS GL+TK++V LSGT I

Sbjct: 146 DSTTASFAARTDLPGNLNSQLISAFSKKGLTTKEMVVLSGHTI 192

Score = 65.1 bits (157), Expect = 6e-08
Identities = 31/57 (54%), Positives = 40/57 (70%), Gaps = 1/57 (1%)

Frame = +1

Query: 610 LFVLIWGSANAQ-LSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777
+F L+ G A+A LS NFY SCP +++++ V A++KE RMGASLLRL FHDCF
Sbjct: 12 IFSLLLGMAHAHYLSPNFYARSCPRLPTIRTAVNKAVAKEKRMGASLLRLLHFHDCF 68

>ref|XP_002334317.1| predicted protein [Populus trichocarpa]
gb|EEF08174.1| predicted protein [Populus trichocarpa]
Length = 224

Score = 159 bits (403), Expect = 2e-36
Identities = 80/124 (64%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR D LAPLDL TP SFDN YFKNL+
Sbjct: 103 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGS--DATLAPLDLVT PNSFDNYYFKNLM 160

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS+G+IR+ C
Sbjct: 161 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPFRSDFGSAMIKMGDIGLLTGSSGQIRRIC 220

Query: 2167 RRIN 2178
+N
Sbjct: 221 SAVN 224

Score = 99.4 bits (246), Expect = 3e-18
Identities = 59/140 (42%), Positives = 77/140 (55%)
Frame = +2

Query: 1229 NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARDSVQIVSGQTTNKNTLN*I IKLYIS 1408
NSARG+ VID K+ VEK+CPGVVSCADI+A+AARD+
Sbjct: 2 NSARGYNVIDKAKTEVEKICPGVVSCADIIA VAARDA----- 38

Query: 1409 KLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQL 1588
S +GGP++ VKLGRRD+ TAS++ AN +PA +L L
Sbjct: 39 -----SAYVGGPSYAVKLGRRDSTASRTLANAELPAFFESLES L 78

Query: 1589 ISRFSALGLSTKDLVALSGT 1648
ISRF GL+ +D+VALSG+
Sbjct: 79 ISRFQKKGLTARDMVALSGS 98

>emb|CAN73051.1| hypothetical protein [Vitis vinifera]
Length = 297

Score = 159 bits (403), Expect = 2e-36
Identities = 77/124 (62%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD+QT FDN Y++NL

Sbjct: 176 QAQCFTFRSRIYNDTNIDPNFAATTRSTCP-VSG-GNSNLAPLDIQTMNKFNDNKYYENLE 233

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++VR YS N F DFAAAM+KM +ISPLTG+NGEIR NC

Sbjct: 234 AQRGLFHSDQELFNGGSQDALVRAYSANNALFFXDFAAAMVKMSNISPLTGTNGEIRSNC 293

Query: 2167 RRIN 2178
R +N

Sbjct: 294 RVVN 297

Score = 151 bits (382), Expect = 5e-34
Identities = 85/169 (50%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA

Sbjct: 49 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACNATVSCADILALAA 108

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG

Sbjct: 109 RDGVVL-----LGGPSWTVPLG 125

Query: 1511 RRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTA+QSAANN +PAP +NL+ LIS F+A GL+ D+ ALSG+ I

Sbjct: 126 RRDARTANQSAANNLPPFANLSALISGFAAKGLNADDMTALSGSHTI 174

Score = 62.4 bits (150), Expect = 4e-07
Identities = 28/49 (57%), Positives = 36/49 (73%)
Frame = +1

Query: 637 NAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783
N +LS NFY +CPN+ V+ + A+ +E RMGAS+LRLFHDCFVN

Sbjct: 2 NYKLSPNFYASTCPNVQKIVRVEMVQAVIREPRMGASILRRLFHDCFVN 50

>gb|EEE67818.1| hypothetical protein OsJ_25573 [Oryza sativa Japonica Group]
Length = 323

Score = 159 bits (402), Expect = 3e-36

Identities = 72/123 (58%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC FR R+YNETNI+ AFA + +CP T GSGD NLAPLD TPT+FDN Y++NL+

Sbjct: 200 ARCRGFRTRLYNETNIDAAFAAALKANCPATPGSGDGNLAPLDTTTPTAFDNAYYRNLLS 259

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KGLLHSDQ+LF+ GSTD+ VR +++++ F + FA AM+KMG+ISPLTG+ G+IR C

Sbjct: 260 NKGLLHSDQELFSNGSTDNTVRSFASSAAAFGAATAMVKMGNISPLTGTGQIRLICS 319

Query: 2170 RIN 2178

+N

Sbjct: 320 AVN 322

Score = 94.7 bits (234), Expect = 8e-17
Identities = 68/168 (40%), Positives = 85/168 (50%), Gaps = 1/168 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD SILL E+NA PN S RG++VID+IK+ +E VC VSCADIL +AARD

Sbjct: 79 GCDASILLAGN-----ERNAAPNF-SVRGYDVIDSIKTQIEAVCKQTVSCADILTVAARD 132

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W+V LGRR

Sbjct: 133 SV-----VALGGPSWSVPLGRR 149

Query: 1517 DARTASQSAANNGIPAP-TSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ A+ +A AP T +L QLIS +++ GLS DLVALSG I

Sbjct: 150 DSTGAATAAQVISSLAPSTDSLAQLISAYASKGLSATDLVALSGAHTI 197

Score = 67.8 bits (164), Expect = 1e-08
Identities = 39/70 (55%), Positives = 46/70 (65%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L L L+ +A A LS FY SCP S +KSTV +A++ E RMGASL

Sbjct: 1 MAS-ASSLGLLLMLAALV-STATAHLSPTFYDTSCPRAMSIKSTVTAAVNNEPRMGASL 58

Query: 751 LRLFFHDCFV 780

LRL FHDCFV

Sbjct: 59 LRLHFHDCFV 68

>gb|EEE56633.1| hypothetical protein OsJ_06032 [Oryza sativa Japonica Group]

Length = 303

Score = 159 bits (402), Expect = 3e-36
Identities = 74/123 (60%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C FR IYN+TN++ FA R++ CP SGSGD+NLAPLD T +FDN Y+++LV
Sbjct: 179 AQCQFFRGGHIYNDTNVDPLFAAERRRRCPAASGSGDSNLAPLDDMTALAFDNAYYRDLVG 238

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D V+ YST+P F+ DF AAMIKMG I PLTG+ G+IRKNCR
Sbjct: 239 RRGLLHSDQELFNGGSQDERVKKYSTDPDLFAGDFVAAMIKMGKICPLTGAAGQIRKNCR 298

Query: 2170 RIN 2178
+N
Sbjct: 299 VVN 301

Score = 95.9 bits (237), Expect = 3e-17
Identities = 48/70 (68%), Positives = 54/70 (77%), Gaps = 2/70 (2%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324
+QGCD SILLDD S F GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+
Sbjct: 80 VQGDASILLDDVPSKGFVGEKTAGPNTNSIRGYEVIDKIKANVEAACPGVVSCADILAL 139

Query: 1325 AARDSVQIVS 1354
AAR+ V +VS
Sbjct: 140 AAREGVNLVS 149

Score = 60.5 bits (145), Expect = 2e-06
Identities = 34/76 (44%), Positives = 47/76 (61%), Gaps = 7/76 (9%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANA-----QLSTNFYYHSCP NLFSSVKSTVQSAISKET 732
+S +R + LAL + + SA A ++ ++Y SCP L + V+ T+ SAI E
Sbjct: 5 SSTTTRFCLLLALVLPMISSAAAGDDALPLPMTPSYRKSCTLEAIVRGTMLSAIKAER 64

Query: 733 RMGASLLRLLFFHDCFV 780
RMGAS+LRLFFHDCFV
Sbjct: 65 RMGASILRLLFFHDCFV 80

>ref|XP_002281731.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 317

Score = 159 bits (402), Expect = 3e-36
Identities = 76/124 (61%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD++T FDN Y++NL+
Sbjct: 196 QAQCFTFRSRIYNDTIDPNFAATRRSTCP-VSG-GNSNLAPLDIRTMNRFDNIIYQNLN 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TRRGLLHSDQELFNGGSQDALVRTYNANNALFFRDFAAAMVKMSNISPLTGTNGEIRSNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RVVN 317

Score = 151 bits (381), Expect = 7e-34
Identities = 85/169 (50%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 129 RDGV-----VQLGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAANN IP+P ++L+ LIS F+A GL+ +D+ ALSG+ I
Sbjct: 146 RRDARTASQSAANNEIPSPLASLSALISGFAAKGLNARDMTALSGSHTI 194

Score = 71.6 bits (174), Expect = 7e-10
Identities = 35/71 (49%), Positives = 49/71 (69%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MASF + + ++ L+ S N QLS NFY +CPN+ + V+ ++ A+ +E RMGAS+
Sbjct: 1 MASFTNSFVV-FSII SLLACSLNQLSPNFYASTCPNVQNI VVRVAMRQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>gb|EAZ05136.1| hypothetical protein OsI_27329 [Oryza sativa Indica Group]
Length = 338

Score = 159 bits (402), Expect = 3e-36
Identities = 72/123 (58%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC FR R+YNETNI+ AFA + +CP T GSGD NLAPLD TPT+FDN Y++NL+
Sbjct: 215 ARCRGFRTRLYNETNIDAAFAAALKANCPATPGSGDGNLAPLDTTPTAFDNAYYRNLLS 274

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KGLLHSDQ+LF+ GSTD+ VR ++++ F + FA AM+KMG+ISPLTG+ G+IR C
Sbjct: 275 NKGLLHSDQELFSNGSTDNTVRSFASSAAAFGAATAMVKMGNISPLTGTQGGQIRLICS 334

Query: 2170 RIN 2178
+N
Sbjct: 335 AVN 337

Score = 96.7 bits (239), Expect = 2e-17
Identities = 69/169 (40%), Positives = 86/169 (50%), Gaps = 1/169 (0%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
QGCD SILL E+NA PN S RG++VID+IK+ +E VC VSCADIL +AAR
Sbjct: 93 QGCDA SILLAGN-----ERNAAPNF-SVRGYDVIDSIKTQIEAVCKQTVSCADILTVAAR 146

Query: 1334 DSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGP+W+V LGR
Sbjct: 147 DSV-----VALGGPSWSVPLGR 163

Query: 1514 RDARTASQSAANNGIPAP-TSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RD+ A+ +A AP T +L QLIS +++ GLS DLVALSG I
Sbjct: 164 RDSTGAATAAQVISSLAPSTDSLAQLISAYASKGLSATDLVALSGAHTI 212

Score = 69.3 bits (168), Expect = 3e-09
Identities = 45/93 (48%), Positives = 55/93 (59%), Gaps = 1/93 (1%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L L L+ +A A LS FY SCP S +KSTV +A++ E RMGASL
Sbjct: 1 MAS-ASSLGLLLMLALV-STATAHLSPTFYDTSCPRAMSIKSTVTA AVNNEPRMGASL 58

Query: 751 LRLFFHDCFVNV-IYLHLLPLTYKYAKLTYSSS 846

LRL FHDCFV +L P+ + Y L SS
Sbjct: 59 LRLHFHDCFVQARFHLTNHPVFFFYFDLMPKSS 91

>ref|NP_001046402.1| Os02g0240500 [Oryza sativa (japonica cultivar-group)]
dbj|BAD28874.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69270.1| TPA: class III peroxidase 28 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAF08316.1| Os02g0240500 [Oryza sativa Japonica Group]
Length = 334

Score = 159 bits (402), Expect = 3e-36
Identities = 74/123 (60%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C FR IYN+TN++ FA R++ CP SGSGD+NLAPLD T +FDN Y+++LV
Sbjct: 210 AQCQFFRGHIYNDTNVDPLFAAERRRRCPAASGSGDSNLAPLDDMTALAFDNAYYRDLVG 269

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D V+ YST+P F+ DF AAMIKMG I PLTG+ G+IRKNCR
Sbjct: 270 RRGLLHSDQELFNGGSQDERVKKYSTDPDLFAGDFVAAMIKMGKICPLTGAAGQIRKNCR 329

Query: 2170 RIN 2178
+N
Sbjct: 330 VVN 332

Score = 134 bits (336), Expect = 1e-28
Identities = 76/173 (43%), Positives = 96/173 (55%), Gaps = 2/173 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1324
+QGCD SILLDD S F GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+
Sbjct: 80 VQGCASILLDDVPSKGFVGEKTAGPNTNSIRGYEVIDKIKANVEAACPCGVVSCADILAL 139

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AAR+ V + LGGP+W V
Sbjct: 140 AAREGVNL-----LGGPSWEVP 156

Query: 1505 LRRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHISH 1663
LRRRD+ TAS+S A++ +P P+S+L L++ F GL+ +D+ ALSG I +
Sbjct: 157 LRRRDSTTASKSEADSDLPGSSSLADLVAAFGKKGLAPRDMTALSGAHTIGY 209

Score = 60.5 bits (145), Expect = 2e-06

Identities = 34/76 (44%), Positives = 47/76 (61%), Gaps = 7/76 (9%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANA-----QLSTNFYHSCPNLFSSVKSTVQSAISKET 732
+S +R + LAL + + SA A ++ ++Y SCP L + V+ T+ SAI E
Sbjct: 5 SSTTRFCLLLALVLPMISSAAAGDDALPLPMTPSYYRKSCPTLEAIVRGTMLSAIKAER 64

Query: 733 RMGASLLRRLFHDCFV 780
RMGAS+LRLFHDCFV
Sbjct: 65 RMGASILRRLFHDCFV 80

>ref|NP_001060630.1| Os07g0677400 [Oryza sativa (japonica cultivar-group)]
gb|AAC49820.1| peroxidase [Oryza sativa Indica Group]
dbj|BAC79530.1| peroxidase [Oryza sativa Japonica Group]
dbj|BAD30310.1| peroxidase [Oryza sativa Japonica Group]
tpe|CAH69355.1| TPA: class III peroxidase 113 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF22544.1| Os07g0677400 [Oryza sativa Japonica Group]
Length = 314

Score = 159 bits (402), Expect = 3e-36
Identities = 72/123 (58%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
ARC FR R+YNETNI+ AFA + +CP T GSGD NLAPLD TPT+FDN Y++NL+
Sbjct: 191 ARCRGFRTRLYNETNIDAAFAAALKANCPATPGSGDGNLAPLDTTPTAFDNAYRNLLS 250

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KGLLHSDQ+LF+ GSTD+ VR ++++ F + FA AM+KMG+ISPLTG+ G+IR C
Sbjct: 251 NKGLLHSDQELFNSGSTDNTVRSFASAAAFGAATAMVKMGNISPLTGTGQIRLICS 310

Query: 2170 RIN 2178
+N
Sbjct: 311 AVN 313

Score = 97.1 bits (240), Expect = 2e-17
Identities = 69/170 (40%), Positives = 87/170 (51%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGKKNANPNRNSARGFEVIDNIKSAVEKVC PGVSCADILAI AA 1330
+QGCD SILL E+NA PN S RG++VID+IK+ +E VC VSCADIL +AA
Sbjct: 68 VQGCDASILLAGN-----ERNAAPNF-SVRGYDVIDSIKTQIEAVCKQT VSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W+V LG

Sbjct: 122 RDSV-----VALGGPSWSVPLG 138

Query: 1511 RRDARTASQSAANNGIPAP-TSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+ +A AP T +L QLIS +++ GLS DLVALSG I

Sbjct: 139 RRDSTGAATAAQVISSLAPSTDSLAQLISAYASKGLSATDLVALSGAHTI 188

Score = 67.8 bits (164), Expect = 1e-08
Identities = 39/70 (55%), Positives = 46/70 (65%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L L L+ +A A LS FY SCP S +KSTV +A++ E RMGASL

Sbjct: 1 MAS-ASSLGLLLMLAALV-STATAHLSPTFYDTS CPRAMSIIKSTVTA AVNNEPRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV

Sbjct: 59 LRLHFHDCFV 68

>emb|CAA59487.1| peroxidase [Triticum aestivum]
gb|ACF08093.1| class III peroxidase [Triticum aestivum]
Length = 319

Score = 159 bits (401), Expect = 3e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+TAF A + + +CPR +GSGD++LAPLD TP +FDN Y++NL+

Sbjct: 196 QAQCQNFDRRLYNETNIDTAFATSLRANCPRPTGSGDSSLAPLDTTTPNAFDNAYYRNLM 255

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L N G T +VR YS+ F+ DF AAM+ MG+ISPLTG+ G++R +C

Sbjct: 256 SQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNDRDFRAAMVSMGNISPLTGTQQQVRLSC 315

Query: 2167 RRIN 2178
R+N

Sbjct: 316 SRVN 319

Score = 131 bits (329), Expect = 7e-28
Identities = 76/169 (44%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILL DT++FTGE+ A PN S RG VIDNIK+ VE VC VSCADILA+AA

Sbjct: 69 VQGCASILLSDTATFTGEQAGPNAGSIRGMNVIDNIKAQVEAVCTQTVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNLNL*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 129 RDSV-----VALGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P P+ ++ L + F+A GLS D+VALSG I

Sbjct: 146 RRDSTTASLSLANSDLPPPSFDVANLTANFAAKGLSVTDMVALSGAHTI 194

Score = 60.5 bits (145), Expect = 2e-06
Identities = 35/73 (47%), Positives = 44/73 (60%), Gaps = 1/73 (1%)
Frame = +1

Query: 565 LTMASFCs-RLTICLALFVLIWGSANAQLSTNFYHSCPFLFSSVKSTVQSAISKETRMG 741
+ MAS S L +CLA ++AQLS FY SCP + ++ V +A+ E RMG

Sbjct: 3 MAMASSLSVLLLLCLA-----APSSAQLSPRFYARSCPRAQAIIRRGVAAAVRSERRMG 56

Query: 742 ASLLRRLFHDCFV 780

ASLLRL FHDCFV

Sbjct: 57 ASLLRRLFHDCFV 69

>gb|AAB02554.1| cationic peroxidase [Stylosanthes humilis]
Length = 320

Score = 159 bits (401), Expect = 3e-36
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYNE+NI+ ++A++ Q +CP S GD+NL+P D+ TP FDN Y+ NL

Sbjct: 198 QARCTTFRTRIYNESNIDPSYAKSLQGNCP--SVGGDSNLSPFDVTPNKFNDAYYINLK 255

Query: 1987 QKKGLLHSDQQLFNGG-STDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
KKGLLH+DQQLFNGG STDS V YS N TF++DF AMIKMG++SPLTG++G+IR N

Sbjct: 256 NKKGLLHADQQLFNGGSTDSQVTAYSNNAATFNTDFGNAMIKMGNLSPLTGTSGQIRTN 315

Query: 2164 CRRIN 2178

CR+ N

Sbjct: 316 CRKTN 320

Score = 152 bits (384), Expect = 3e-34
Identities = 85/169 (50%), Positives = 103/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLDDTS+FTGEK A PN NSARGF+VID IKS VE +CPGVVSCADILA+AA
Sbjct: 71 VQGCDASVLLDDTSTFTGEKTAFPNVNSARGFDVIDTIKSQVESLCPGVVSCADILALAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+WNV+LG
Sbjct: 131 RDSV-----VALGGPSWNVQLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS ++AN+ +P P+ NL+ LIS FS G + K+LV LSG I
Sbjct: 148 RRDSTTASLNSANSDLPGPSFNLSGLISAFSKKGFTAKELVTLGAHTI 196

Score = 75.1 bits (183), Expect = 6e-11
Identities = 35/62 (56%), Positives = 45/62 (72%), Gaps = 1/62 (1%)
Frame = +1

Query: 598 ICLALFVLI-WGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDC 774
+C +F+ + G + QLS+NFY CPN S++KS V SA+SKE R+GASLLRL FHDC
Sbjct: 10 VCFIIFMCLNIGLGGQLSSNFYATKCPNALSTIKSAVNSAVSKEARLGASLLRHFHDC 69

Query: 775 FV 780
FV
Sbjct: 70 FV 71

>sp|P16147.2|PERX_LUPPO RecName: Full=Peroxidase
emb|CAA36066.1| peroxidase [Lupinus polyphyllus]
prf||1805332A peroxidase:ISOTYPE=basic isozyme
Length = 158

Score = 159 bits (401), Expect = 3e-36
Identities = 79/124 (63%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+ C F+ RIYN+TNI+T FA +RQ +CP ++G G+ NLAPLD TP FDN Y+K+LV
Sbjct: 36 QSECQFFKTRINNDTNIDTNFATSRQANCPFSAG-GETNLAPLDSLTPNRFDNYYKDLV 94

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+GLLHSDQ LFNGGS D++VR YSTN F SDFAAA++KM ISPLTG GEIRKNC
Sbjct: 95 SNRGLLHSDQVLFNGGSQDTLVRTYSTNNVFFSDFAAAIKMSKISPLTG IAGEIRKNC 154

Query: 2167 RRIN 2178
R IN
Sbjct: 155 RVIN 158

>dbj|BAA77389.1| peroxidase 3 [Scutellaria baicalensis]
Length = 318

Score = 159 bits (401), Expect = 3e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYN+TNI AFA + +CPR+ G DNNLAPLD +P F+N Y++NL+
Sbjct: 197 QARCTTFRGRIYNDTNINGAFATGLRANCPRSGG--DNNLAPLDNVSPARFNNDYYRNL 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+GLLHSDQ+LFN G+ D+ VR YSTN F +DFA AM+KM ++SPLTG+NG+IR+NC
Sbjct: 255 GLRGLLHSDQELFNNGTADAQVRAYSTNSAAFFNDFANAMVKMSNLSPLTGNGQIRRNC 314

Query: 2167 RRIN 2178
RR N
Sbjct: 315 RRTN 318

Score = 135 bits (341), Expect = 3e-29
Identities = 76/169 (44%), Positives = 94/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+ GCD S+LLDD + FTGEK A PN NS RGF+VIDNIK+ VE CP +VSC+DIL++AA
Sbjct: 70 VNGCDASVLLDDRTGFTGEKTAGPNANSLRGFDVIDNIKTLVEGSCPNIVSCSDILSVAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V V GGP+W V LG
Sbjct: 130 RDGVVAV-----GGPSWAVALG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS +AAN IP P NLN LI+ FS G + +++VALSG+ I
Sbjct: 147 RRDSTTASLNAANTQIPGPGLNLNALITSFSNKGFTAREMVALSGSHTI 195

Score = 87.4 bits (215), Expect = 1e-14
Identities = 42/71 (59%), Positives = 53/71 (74%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MASF S + L L +L+ G +NAQLS NFY +CPNL + +++ V SA+S +TRMGASL
Sbjct: 1 MASFVSEFSTRMLVLLLIGVSNAQLSANFYNTTCPNLLTIIRNAVNSAVSSDTRMGASL 60

Query: 751 LRLFFHDCFVN 783

LRL FHDCFVN
Sbjct: 61 LRLHFHDCFVN 71

>ref|XP_002461207.1| hypothetical protein SORBIDRAFT_02g042840 [Sorghum bicolor]
gb|EER97728.1| hypothetical protein SORBIDRAFT_02g042840 [Sorghum bicolor]
Length = 318

Score = 158 bits (400), Expect = 4e-36
Identities = 73/124 (58%), Positives = 93/124 (75%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++C NFRA IYN+TN+ AFA R+ SCP +G GD NL PLD T T+FDN Y+ NL+
Sbjct: 195 SQCKNFRAHIYNDTNVNAFATLRKVSPPAAAGDGDGNTPLDTATSTAFDNAYYTNLLS 254

Query: 1990 KKGLLHSDQQLFN-GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ GLLHSDQQLFN GG+TD +VR Y++ P F+ DF AAMI+MG+ISPLTG G+IR+ C
Sbjct: 255 RSGLLHSDQQLFNFGGGATDGLVRYASTPFRNRDFTAAMIRMGNISPLTGRQGQIRAC 314

Query: 2167 RRIN 2178
R+N
Sbjct: 315 SRVN 318

Score = 138 bits (347), Expect = 6e-30
Identities = 79/169 (46%), Positives = 98/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE VCPGVVSCADILA+AA
Sbjct: 67 VQGCDASVLLNDTATFTGEQTANPNVGSIRGFGVVDNIKAQVEAVCPGVVSCADILAVAA 126

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 127 RDSV-----VALGGPSWRVLLG 143

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +PAP+ +L L + F+ LS DLVALSG I
Sbjct: 144 RRDSTTASLALANSIDLPAISLDLANLTAFAKKRSLRDLVALSGAHTI 192

Score = 67.0 bits (162), Expect = 2e-08
Identities = 30/49 (61%), Positives = 38/49 (77%)
Frame = +1

Query: 634 ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780

A+AQLS FY SCP +++KS V +A+++E RMGASLLRL FHDCFV
Sbjct: 19 ASAQLSATFYRSRCPRALATIksAVTAAVAQEP RMGASLLRLHFHDCFV 67

>gb|EEC82684.1| hypothetical protein OsI_27330 [Oryza sativa Indica Group]
Length = 309

Score = 158 bits (400), Expect = 4e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+
Sbjct: 187 QAQCSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTNNL 244

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C
Sbjct: 245 SNKGLLHSDQVLFNGGSTDNTVRNFASNAAAFSSAFATAMVNMGNIAPKTG TNGQIRLSC 304

Query: 2167 RRIN 2178
++N
Sbjct: 305 SKVN 308

Score = 102 bits (254), Expect = 4e-19
Identities = 64/167 (38%), Positives = 85/167 (50%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AARD
Sbjct: 67 GCDASVLLSGN-----EQDAPPNKDSL RGYGVIDSIKAQIETVCNQT VSCADILTVAARD 121

Query: 1337 SVQIVSQGTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V LGRR
Sbjct: 122 SV-----VALGGPTWTVPLGRR 138

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ AS + A + +P T++L +L+ F+ GLS D+VALSG I
Sbjct: 139 DSTGASAALAI SDLPFTASLQELVDAFAKGLSVTDMVALSGAHTI 185

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/61 (54%), Positives = 43/61 (70%), Gaps = 2/61 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC

Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIKSAVTAAVNSEPRMGASLLRLHFHDC 65

Query: 775 F 777
F

Sbjct: 66 F 66

>gb|AAW52720.1| peroxidase 6 [Triticum monococcum]
Length = 322

Score = 158 bits (400), Expect = 4e-36
Identities = 73/123 (59%), Positives = 95/123 (77%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++C NFR IYN TNI+ AFA R+++CP + +GD NLAP D+QT FDN Y++NLV

Sbjct: 199 SQCLNFRDHIYNGTNIDPAFATLRKRTCPAQAPNGDKNLAPFDVQTQLLFDNAYYRNLVA 258

Query: 1990 KKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLL+SDQ LFNNGS D++VR Y NP F+SDF AMIKMG+I+PLTG+ G+IR+NCR

Sbjct: 259 KRGLLNSDQVLFNNGSQDALVRQYVANPALFASDFVTAMIKMGNINPLTGTAGQIRRNCR 318

Query: 2170 RIN 2178
+N

Sbjct: 319 VVN 321

Score = 131 bits (329), Expect = 7e-28
Identities = 76/169 (44%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCDGSILLDD SF GEK A PN +S RG+EVID IK VE +CPG+VSCADI A+AA

Sbjct: 71 VQGCDGSILLDDVGSFVGEKTAFPNVDSVRGYEVIDEIKKNVELLCPGIVSCADIAALAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD + LGGP+W+V LG

Sbjct: 131 RDGTFL-----LGGPSWSVPLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +PAP+ +L LI F LS +DL ALSG I

Sbjct: 148 RRDSTTASLTEANSDLPAPSLSLGLLIKAFDCKQLSPQDLTALSGAHTI 196

Score = 64.3 bits (155), Expect = 1e-07
Identities = 33/60 (55%), Positives = 39/60 (65%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNISSSVKSTVQSAISKETRMGASLLRRLFHDCFV 780
CL L+ SA QLS +FY SCP L V++T+ A+ E RMGASLLRL FHD CFV
Sbjct: 12 CLLALFLLSSSAYGQLSPSYAKSCPTLQLIVRATMIKALLAERRMGASLLRRLFHDCFV 71

>gb|AAQ55292.1| class III peroxidase GvPx2b [Vitis vinifera]
Length = 255

Score = 158 bits (400), Expect = 4e-36
Identities = 76/124 (61%), Positives = 100/124 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR IYN+T+I+ AFA ++Q+ CPR+ G D+NL+PLD T T FDN YF+ L
Sbjct: 135 KARCTFRNHIYNDTIDPFAASKQKICPRSGG--DDNLSPLD-GTTTVFDNVYFRGLE 191

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ L+NGGSTDS+V+ YS + TF +D A AM++MGDISPLTG+NG+IR NC
Sbjct: 192 EKKGLLHSDQVLYNGGSTDSLVTYSIDTATFFTDVANAMVRMGDISPLTGNGQIRTNC 251

Query: 2167 RRIN 2178
R++N
Sbjct: 252 RKNV 255

Score = 147 bits (372), Expect = 8e-33
Identities = 83/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLD T++FTGEK A PN NS RG+EVID IKS V +CPGVVSCADI+A+AARD
Sbjct: 10 GCDASILLDGTATFTGEKTAGPNNNSVRGYEVIDTIKSQVGS LCPGVVSCADIVAVAARD 69

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV I+ GGPTW V+LGRR
Sbjct: 70 SVVIL-----GGPTWTVRLGRR 86

Query: 1517 DARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS SAA +P P +L+QLIS FS GL+TK++V LSGT I
Sbjct: 87 DSTTASFSAAGTDLPGPNLSLSQLISAFSKKGLTTKEMVVLSGTHTI 133

>gb|AAF65464.2|AF247700_1 peroxidase POC1 [Oryza sativa Indica Group]
Length = 311

Score = 158 bits (400), Expect = 4e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+

Sbjct: 189 QAQCSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTLL 246

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C

Sbjct: 247 SNKGLLHSDQVLFNNGSTDNTVRNFASNAAAFSSAFATAMVNMGNIAPKTGTTNGQIRLSC 306

Query: 2167 RRIN 2178

++N

Sbjct: 307 SKVN 310

Score = 104 bits (260), Expect = 7e-20

Identities = 65/169 (38%), Positives = 87/169 (51%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AA

Sbjct: 67 VQGCDASVLLSGN-----EQDAPPNKDSL RGYGVIDS IKAQIEAVCNQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG

Sbjct: 122 RDSV-----VALGGPTWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ AS + A + +P T++L +L+ F+ GLS D+VALSG I

Sbjct: 139 RRDSTGASAAALASDLPPFTASLQELVDAFAKKGLSVTDMVALSGAHTI 187

Score = 68.2 bits (165), Expect = 8e-09

Identities = 34/62 (54%), Positives = 44/62 (70%), Gaps = 2/62 (3%)

Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC

Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIIKSAVTA AVNSEPRMGASLLR LHFHDC 65

Query: 775 FV 780

FV

Sbjct: 66 FV 67

>ref|XP_002311022.1| predicted protein [Populus trichocarpa]

gb|EEE88389.1| predicted protein [Populus trichocarpa]

Length = 319

Score = 158 bits (399), Expect = 6e-36
Identities = 79/124 (63%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR + + LAPLDL TP SFDN YFKNL+
Sbjct: 197 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGSN--STLAPLDLVTPNSFDNYYFKNLM 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS G+IR+ C
Sbjct: 255 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPAPFKSDFGSAMIKMGDIGLLTGSAGQIRRIC 314

Query: 2167 RRIN 2178
+N
Sbjct: 315 SAVN 318

Score = 126 bits (316), Expect = 2e-26
Identities = 74/166 (44%), Positives = 94/166 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLD+T S EK A N NSARG+ VID K+ VEK+CPGVVSCADI+A+AA
Sbjct: 70 VQGCDA SILLDETLSIQSEKTALGNLNSARGYNVIDKAKTEVEKICPGVVSCADIIAVAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGPTWNVKLG 1510
RD+ S +GGP++ VKLG
Sbjct: 130 RDA-----SAYVGGPSYAVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS++ AN +PA +L LISRF GL+ +D+VALSG+
Sbjct: 147 RRDSTTASRTLANAELPAFFESLESISRFFQKKGLTARDMVALSGS 192

Score = 62.4 bits (150), Expect = 4e-07
Identities = 28/57 (49%), Positives = 40/57 (70%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCP NFLSSVKSTVQSAISKETRMGASLLRRLFHDFCV 780
+ L+ + AQLS FY SCPN S++++ ++SAI+ + RM ASL+RL FHDFCV
Sbjct: 14 MLFLLNTACQAQLSPAFYDSSCPNAISAIRTAIRSAIASDRRMAASLIRLHFHDFCV 70

>gb|EEE67819.1| hypothetical protein OsJ_25574 [Oryza sativa Japonica Group]
Length = 309

Score = 158 bits (399), Expect = 6e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+
Sbjct: 187 QACSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTNNL 244

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C
Sbjct: 245 SNKGLLHSDQVLFNNGSTDNTVRNFASNAAEFSSAFATAMVNMGNIAPKTGTNGQIRLSC 304

Query: 2167 RRIN 2178
++N
Sbjct: 305 SKVN 308

Score = 102 bits (254), Expect = 4e-19
Identities = 64/167 (38%), Positives = 85/167 (50%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCVGVVSCADILAI AARD 1336
GCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AARD
Sbjct: 67 GCDASVLLSGN-----EQDAPPNKDSL RGYGVIDSIKAQIEAVCNQTVSCADILTVAARD 121

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V LGRR
Sbjct: 122 SV-----VALGGPTWTVPLGRR 138

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ AS + A + +P T++L +L+ F+ GLS D+VALSG I
Sbjct: 139 DSTGASAALAI SDLPPTASLQELVDAFAKGLSVTDMVALSGAHTI 185

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/61 (54%), Positives = 43/61 (70%), Gaps = 2/61 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC
Sbjct: 6 CISLLVVVALATAASAQLSATFYDTS CPRAMSIKSAVTA AVNSEPRMGASLLR LHFHDC 65

Query: 775 F 777
F
Sbjct: 66 F 66

>ref|NP_001147216.1| LOC100280824 [Zea mays]
gb|ACG26145.1| peroxidase 52 precursor [Zea mays]
Length = 318

Score = 158 bits (399), Expect = 6e-36
Identities = 72/124 (58%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIY +T+I +FA RQQ+CPR+ G G NLAP+D+QTP FD YF NL+
Sbjct: 196 QARCTTFRGRIYGD TDINASFAALRQQTCPRSGGDG--NLAPIDVQTPVRFDTAYFTNLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++VR YS + F++DF AAMI+MG++ LTG+ G+IR+NC
Sbjct: 254 SRRGLFHSDQELFNGGSQDALVRQYSASASLNFADVAAMIRMGNVGVLGTAGQIRRNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RNVN 317

Score = 134 bits (338), Expect = 7e-29
Identities = 83/169 (49%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGKKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCDGSILLD GEK A PN NS RGFEVID IK VE CPGVVSCADILA+AA
Sbjct: 73 VQGCDGSILLDAG----GEKTAGPNLSVRGFEVIDT IKRNVEAACPGVVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD TNL LGGPTW+V LG
Sbjct: 129 RDG-----TNL-----LGGPTWSVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P PT++L LIS F GLS +D+ ALSG I
Sbjct: 146 RRDSTTASASLANSNLPPPTASLGTLISLFRQGLSPRDMTALSGAHTI 194

Score = 73.2 bits (178), Expect = 2e-10
Identities = 40/75 (53%), Positives = 49/75 (65%)
Frame = +1

Query: 556 LSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETR 735
+ +L MAS L CL + L+ A+AQLS FY SCPNL S V++ + A+ E R
Sbjct: 1 MQQLAMAS--PTLMQCLVVVSLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVGSEQR 58

Query: 736 MGASLLRRLFHDCFV 780
MGASLLRRLFHDCFV
Sbjct: 59 MGASLLRRLFHDCFV 73

>ref|NP_001060631.1| Os07g0677500 [Oryza sativa (japonica cultivar-group)]
dbj|BAC79531.1| peroxidase POC1 [Oryza sativa Japonica Group]
dbj|BAD30311.1| peroxidase POC1 [Oryza sativa Japonica Group]
tpe|CAH69356.1| TPA: class III peroxidase 114 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF22545.1| Os07g0677500 [Oryza sativa Japonica Group]
Length = 311

Score = 158 bits (399), Expect = 6e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+
Sbjct: 189 QAQCSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTNNL 246

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C
Sbjct: 247 SNKGLLHSDQVLFNNGSTDNVTRNFASNAEFSSAFATAMVMGNIAPKTG TNGQIRLSC 306

Query: 2167 RRIN 2178
++N
Sbjct: 307 SKVN 310

Score = 104 bits (260), Expect = 7e-20
Identities = 65/169 (38%), Positives = 87/169 (51%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AA
Sbjct: 67 VQGCDA SVLLSGN-----EQDAPPNKDSL RGYGVIDS IKAQIEAVCNQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNLNLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 122 RDSV-----VALGGPTWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ AS + A + +P T++L +L+ F+ GLS D+VALSG I
Sbjct: 139 RRDSTGASAA LAISDLPPFTASLQELVDAFAKKGLSVTDMVALSGAHTI 187

Score = 68.2 bits (165), Expect = 8e-09
Identities = 34/62 (54%), Positives = 44/62 (70%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC
Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIKSAVTAAVNSEPRMGASLLRRLFHDC 65

Query: 775 FV 780
FV
Sbjct: 66 FV 67

>pdb|1SCH|A Chain A, Peanut Peroxidase
pdb|1SCH|B Chain B, Peanut Peroxidase
Length = 294

Score = 158 bits (399), Expect = 6e-36
Identities = 76/124 (61%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CT FR RIYNE+NI+ +A++ Q +CP S GD NL+P D+ TP FDN Y+ NL
Sbjct: 173 QAQCTAFRTRIYNESNIDPTYAKSLQANCP--SVGGDTNLSPFDVTPNKFVNAYYINLR 230

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS V YS N TF++DF AMIKMG++SPLTG++G+IR NC
Sbjct: 231 NKKGLLHSDQQLFNGVSTDSQVTAYSNNAATFNTDFGNAMIKMGNLSPLTGTSGQIRTNC 290

Query: 2167 RRIN 2178
R+ N
Sbjct: 291 RKTN 294

Score = 152 bits (385), Expect = 2e-34
Identities = 87/169 (51%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDTS+FTGEK A PN NS RGFEVID IKS VE +CPGVVSCADILA+AA
Sbjct: 46 VQGCDASVLLDDTSNFTGEKTAGPNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVAA 105

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGG +WNV LG
Sbjct: 106 RDSV-----VALGGASWNVLLG 122

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S+AN+ +PAP NL+ LIS FS G +TK+LV LSG I

Sbjct: 123 RRDSTTASLSSANSDL PAPPFNLSGLISAFSNKGFTTKELVTLGAHTI 171

Score = 68.9 bits (167), Expect = 4e-09
Identities = 31/45 (68%), Positives = 36/45 (80%)
Frame = +1

Query: 646 LSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
LS+NFY CPN S++KS V SA++KE RMGASLLRL FHDCFV
Sbjct: 2 LSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLR LHFHDCFV 46

>sp|P22195.2|PER1_ARAHY RecName: Full=Cationic peroxidase 1; AltName: Full=PNPC1; Flags:
Precursor
gb|AAB06183.1| cationic peroxidase [Arachis hypogaea]
Length = 316

Score = 158 bits (399), Expect = 6e-36
Identities = 76/124 (61%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QA+CT FR RIYNE+NI+ +A++ Q +CP S GD NL+P D+ TP FDN Y+ NL
Sbjct: 195 QAQCTAFRTRIYNESNIDPTYAKSLQANCP--SVGGDTNLSFPDVTTPNKFDNAYYINLR 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS V YS N TF++DF AMIKMG++SPLTG++G+IR NC
Sbjct: 253 NKKGLLHSDQQLFNGVSTDSQVTAYSNNAATFNTDFGNAMIKMGNLSPLTGTSGQIRTNC 312

Query: 2167 RRIN 2178
R+ N
Sbjct: 313 RKTN 316

Score = 152 bits (385), Expect = 2e-34
Identities = 87/169 (51%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSTFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LLDDTS+FTGEK A PN NS RGFEVID IKS VE +CPGVVSCADILA+AA
Sbjct: 68 VQGCDASVLLDDTSNFTGEKTAGPNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGG +WNV LG
Sbjct: 128 RDSV-----VALGGASWNVLLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS S+AN+ +PAP NL+ LIS FS G +TK+LV LSG I
Sbjct: 145 RRDSTTASLSSANSDDLPAFFNLSGLISAFSNKGFTTKELVTLGAHTI 193

Score = 77.0 bits (188), Expect = 2e-11
Identities = 35/57 (61%), Positives = 44/57 (77%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
+F+ + G +AQLS+NFY CPN S++KS V SA++KE RMGASLLRL FHDCFV
Sbjct: 12 IFMCLIGLGS AQLSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLRLHFHDCFV 68

>gb|ACU22965.1| unknown [Glycine max]
Length = 322

Score = 157 bits (398), Expect = 7e-36
Identities = 78/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI+++FA + Q +CP S GD+NLAPLD T FDN YFK+L
Sbjct: 202 QAKCSTFRTRIYNETNIDSSFATSLQANCP--SVGGDSNLAPLDSNQNT-FDNAYFKDLQ 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLH+DQ LFNGGSTDS V GY+++P +F++DFA AM+KMG+ISPLTGS+GEIR NC
Sbjct: 259 SQKGLLHTDQVLFNGGSTDSQVNGYASDPSSFNTDFANAMVKMGNISPLTGSSGEIRTNC 318

Query: 2167 RRIN 2178
+ N
Sbjct: 319 WKTN 322

Score = 134 bits (338), Expect = 7e-29
Identities = 78/165 (47%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKS AVEKVC PGVVSCADILAIAA 1330
+QGCD S+LL+DTSSFTGE+ A N NS RGF VIDNIKS VE +CPGVVSCADIL +AA
Sbjct: 75 VQGCDASVLLNDTSSFTGEQTAAGNVNSIRFGVIDNIKSQVESLCPGVVSCADILTVAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 135 RDSV-----VALGGPSWTVQLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS S+AN+ +P +L QL F GL+T ++VALSG

Sbjct: 152 RRDSTTASLSSANSDLPRFDLSLQQLSDNFQNKGLTTAEMVALSG 196

Score = 76.6 bits (187), Expect = 2e-11
Identities = 40/75 (53%), Positives = 51/75 (68%), Gaps = 5/75 (6%)
Frame = +1

Query: 571 MASFC SRLT-----ICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETR 735
MAS C +T I LF+ G +++QLS++FY +CPN S++KS V SA+S E R
Sbjct: 1 MASSCF SMTPIFKIRFFLFLCFIGISSQLSSDFYSTTCPNALSTIKSAVDSAVSNEAR 60

Query: 736 MGASLLR LFFHDCFV 780
MGASLLRL FHDCFV
Sbjct: 61 MGASLLR LHFHDCFV 75

>ref|XP_002311955.1| predicted protein [Populus trichocarpa]
gb|EEE89322.1| predicted protein [Populus trichocarpa]
Length = 187

Score = 157 bits (398), Expect = 7e-36
Identities = 79/124 (63%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR + + LAPLDL TP SFDN YFKNL+
Sbjct: 65 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGSN--STLAPLDLVT PNSFDNYYFKNLM 122

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS G+IR+ C
Sbjct: 123 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPFRSDFGSAMIKMGDIGLLTGSAGQIRRIC 182

Query: 2167 RRIN 2178
+N
Sbjct: 183 SAVN 186

Score = 63.2 bits (152), Expect = 2e-07
Identities = 31/57 (54%), Positives = 43/57 (75%)
Frame = +2

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
+GGP++ VKLGRRD+ TAS++ AN +PA +L LISRF GL+ +D+VALSG+
Sbjct: 4 VGGPSYAVKLGRRDSTASRTLANAELPAFFESLESISR FQKKGLTARDMVALSGS 60

>gb|AAM61588.1| peroxidase [Arabidopsis thaliana]

Length = 316

Score = 157 bits (398), Expect = 7e-36
Identities = 76/124 (61%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYN +NI+T+FA +++++CP TSGSGDN A LD+++P FD+ ++K L+
Sbjct: 193 RAQCVTFRNRIYNASNIDTSFAISKRRNCPATSGSGDNKKANLDVRSPDRFDHGFYKQLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLL SDQ LFN G TDS+V YS N F DFA AMIKMGDISPLTGSNG+IR+NC
Sbjct: 253 SKKGLLTSQVLFNNGPTDSLVIAYSHNLNAFYRDFARAMIKMGDISPLTGSNGQIRQNC 312

Query: 2167 RRIN 2178
RR N
Sbjct: 313 RRPN 316

Score = 150 bits (378), Expect = 2e-33
Identities = 85/170 (50%), Positives = 103/170 (60%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDT SF GEK + P+ NS RGFEVID IK VEK+CPG+VSCADILAI A
Sbjct: 65 VNGCDGSLLLDDTSPFLGEKTSGPSNNSVRGFEVIDKIKFKVEKMCPGIVSCADILAITA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPWNVKLG 1510
RDSV + LGGP W+VKLG
Sbjct: 125 RDSVLL-----LGGPGWSVKLG 141

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA+ +AAN+G IP P + L+ LI+RF A GLST+D+VALSG+ I
Sbjct: 142 RRDSTTANFAAANSVIPPPIITLNLINRFKAQGLSTRDMVALSGSHTI 191

Score = 72.8 bits (177), Expect = 3e-10
Identities = 32/62 (51%), Positives = 46/62 (74%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777
+ L + +++ + AQL+ +FY SCP+LF V+ V+ A+++E RMGASLLRLLFFHDCF
Sbjct: 5 VLLMMIMMLASQSEAQLNRDFYKESCPSLFLVRRRVVKRAVAREPRMGASLLRLLFFHDCF 64

Query: 778 VN 783
VN
Sbjct: 65 VN 66

>ref|NP_200647.1| peroxidase, putative [Arabidopsis thaliana]
sp|Q9LVL2.1|PER67_ARATH RecName: Full=Peroxidase 67; Short=Atperox P67; AltName: Full=ATP44;
Flags: Precursor
dbj|BAA96930.1| peroxidase [Arabidopsis thaliana]
Length = 316

Score = 157 bits (398), Expect = 7e-36
Identities = 76/124 (61%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRSTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYN +NI+T+FA +++++CP TSGSGDN A LD+++P FD+ ++K L+
Sbjct: 193 RAQCVTFRNRIYNASNIDTSFAISKRRNCPATSGSGDNKKANLDVRSPDRFDHGFYKQLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLL SDQ LFN G TDS+V YS N F DFA AMIKMGDISPLTGSNG+IR+NC
Sbjct: 253 SKKGLLTSQVLFNNGPTDSLVIAYSHNLNAFYRDFARAMIKMGDISPLTGSNGQIRQNC 312

Query: 2167 RRIN 2178
RR N
Sbjct: 313 RRPN 316

Score = 149 bits (377), Expect = 2e-33
Identities = 85/170 (50%), Positives = 102/170 (60%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAIAA 1330
+ GCDGS+LLDDT SF GEK + P+ NS RGFEVID IK VEK+CPG+VSCADILAI A
Sbjct: 65 VNGCDGSLLDDTSPFLGEKTSGPSNNSVRGFEVIDKIKFKVEKMCPGIVSCADILAITA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W+VKLG
Sbjct: 125 RDSVLL-----LGGPGWSVKLG 141

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA+ +AAN+G IP P + L+ LI+RF A GLST+D+VALSG I
Sbjct: 142 RRDSTANFAAANSVIPPITTLNLRNRFKAQGLSTRDMVALSGAHTI 191

Score = 72.8 bits (177), Expect = 3e-10
Identities = 32/62 (51%), Positives = 46/62 (74%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCF 777

+ L + +++ + AQL+ +FY SCP+LF V+ V+ A+++E RMGASLLRLLFFHDCF
Sbjct: 5 VLLMMIMMLASQSEAQLNRDFYKESCPSLFLVRRVVKRAVAREPRMGASLLRLLFFHDCF 64

Query: 778 VN 783

VN

Sbjct: 65 VN 66

>ref|XP_002460939.1| hypothetical protein SORBIDRAFT_02g037840 [Sorghum bicolor]
gb|EER97460.1| hypothetical protein SORBIDRAFT_02g037840 [Sorghum bicolor]
Length = 325

Score = 157 bits (397), Expect = 1e-35
Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C N++ARIYN+ NI AFA + + CP G G N APLD TP +FDN Y+ +LV

Sbjct: 204 QAQCQNYQARIYNDANINAAFAASLRAGCPAGGGGGAN--APLDASTPNAFDNAYYGDLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGSTD +VR Y+ + FSSDFAAAM+KMG I +TGS+GE+R+NC

Sbjct: 262 AQQGLLHSDQELFNGGSTDGLVRSYAASSARFSSDFAAAMVKMGIGVITGSSGEVRRNC 321

Query: 2167 RRIN 2178

RR+N

Sbjct: 322 RRVN 325

Score = 139 bits (349), Expect = 4e-30
Identities = 76/165 (46%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+QGCD S+LLDDT +FTGEK+A PN S RGF VID IK+ +E +CP VSCADILA+AA

Sbjct: 77 VQGCDAVLLDDTGNFTGEKSAGPNAGSLRFGVIDTIKALLEALCPRTVSCADILAVAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG

Sbjct: 137 RDSV-----VALGGPSWTVQLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRD+ TAS S AN +P+P S+L+ L++ F+ GLS+ D+VALSG

Sbjct: 154 RRDSTTASLSTANTDLPSPASSLSTLLAAFARKGLSSTDMVALSG 198

Score = 64.7 bits (156), Expect = 8e-08

Identities = 30/65 (46%), Positives = 43/65 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S+L++ + + +A AQLS FY SCP ++K+ V++A+ + RMGASLLRL F
Sbjct: 13 SKLSVLILALATVVAARAQLSPTFYASSCPAALVTIKTAVRAALVLDRRMGASLLRLHF 72

Query: 766 HDCFV 780
HDCFV
Sbjct: 73 HDCFV 77

>ref|XP_002334018.1| predicted protein [Populus trichocarpa]
gb|EEE77880.1| predicted protein [Populus trichocarpa]
Length = 307

Score = 157 bits (397), Expect = 1e-35
Identities = 79/124 (63%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR + LAPLDL TP SFDN YFKNL+
Sbjct: 186 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGSNA--TLAPLDLVTPNSFDNYYFKNLM 243

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS G+IR+ C
Sbjct: 244 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPFRFRSDFGSAMIKMGDIGLLTGSAGQIRRIC 303

Query: 2167 RRIN 2178
+N
Sbjct: 304 SAVN 307

Score = 127 bits (319), Expect = 1e-26
Identities = 74/166 (44%), Positives = 95/166 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLD+T+S EK A N NSARG+ VID K+ VEK+CPGVVSCADI+A+AA
Sbjct: 59 VQGCDASILLDETTSIQSEKTALGNLNSARGYNVIDKAKTEVEKICPGVVSCADIIAVAA 118

Query: 1331 RDSVQIVSGQTTNKNLTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP++ VKLG
Sbjct: 119 RDA-----SAYVGGPSYAVKLG 135

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS++ AN +PA +L LISRF GL+ +D+VALSG+
Sbjct: 136 RRDSTTASRTLANAELPAFFESLESLSIRFQKKGLTARDMVALSGS 181

Score = 60.5 bits (145), Expect = 2e-06
Identities = 27/50 (54%), Positives = 36/50 (72%)
Frame = +1

Query: 631 SANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
+ AQLS FY SCPN S++ + ++SAI+ + RM ASL+RL FHDCFV
Sbjct: 10 ACQAQLSPAIFYDSSCPNLSAIGTAIRSAIASDRRMAASLIRLHFHDCFV 59

>gb|EAY85151.1| hypothetical protein OsI_06506 [Oryza sativa Indica Group]
Length = 335

Score = 157 bits (397), Expect = 1e-35
Identities = 73/123 (59%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C FR IYN+TN++ FA R++ CP SGSGD+NLAPLD T +FDN Y+++LV
Sbjct: 211 AQCQFFRGIHYNDTNVDPLFAAERRRRCPAASGSGDNLAPLDDMTALAFDNAYYRDLVG 270

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D V+ YST+P F+ DF AAMIKMG I PLTG+ G+IRKNCR
Sbjct: 271 RRGLLHSDQELFNGGSQDERVKKYSTDPDLFAGDFVAAMIKMGKICPLTGAAGQIRKNCR 330

Query: 2170 RIN 2178
++
Sbjct: 331 VVS 333

Score = 138 bits (347), Expect = 6e-30
Identities = 76/171 (44%), Positives = 95/171 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD F GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+AA
Sbjct: 83 VQGCDASILLDDVQGFVGEKTAGPNANSIRGYEVIDKIKANVEAACPGVVSCADILALAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
R+ V + LGGP+W V LG
Sbjct: 143 REGVNL-----LGGPSWEVPLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHISH 1663
RRD+ TAS+S A++ +P P+S+L LI+ F GL+ +D+ ALSG I +
Sbjct: 160 RRDSTTASKSEADSLPGPSSSLADLIAAFGKKGLAPRDMTALSGAHTIGY 210

Score = 58.2 bits (139), Expect = 8e-06
Identities = 26/45 (57%), Positives = 34/45 (75%)
Frame = +1

Query: 646 LSTNFYYHSCP NFLSSVKSTVQSAISKETRMGASLLRRLFHDCFV 780
++ ++Y SCP L + V+ T+ SAI E RMGAS+LRLFHDCFV
Sbjct: 39 MTPSYRKSQCPTLEAIVRGTMVSAIKAERRMGASILRRLFHDCFV 83

>emb|CAH10842.1| peroxidase [Picea abies]
Length = 320

Score = 157 bits (397), Expect = 1e-35
Identities = 77/124 (62%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYNE+NI AFA + + +CP S GDN L+PLD+ T FDN Y+ NL
Sbjct: 199 QSRCAFFRTRIYNESNINAAFATSVKANCP--SAGGDNTLSPLDVVTSIKFDNKYYGNLK 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQLFNGG TDS V YSTN +F +DFAAAM+KM +ISPLTG++G+IRKNC
Sbjct: 257 IQKGLLHSDQQLFNGGPTDSQVTAYSTNQNSFFTFDFAAAMVKMSNISPLTGTSGQIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKAN 320

Score = 151 bits (382), Expect = 5e-34
Identities = 88/169 (52%), Positives = 98/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDD ++FTGEK A PN NSARGF+VID IK+ VE C GVVSCADIL IAA
Sbjct: 72 VNGCDGSILLDDNATFTGEKTAGPNANSARGFDVIDTIKTQVEAACSGVVSCADILTIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GPTW V LG
Sbjct: 132 RDSV-----VELQGPTWTVMGL 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP+P S+L+ LIS F GLSTKDLVALSG I
Sbjct: 149 RRDSTTASLSDANNIPSPASSLSALISSFKGHGLSTKDLVALSGAHTI 197

Score = 65.5 bits (158), Expect = 5e-08
Identities = 34/70 (48%), Positives = 43/70 (61%), Gaps = 5/70 (7%)
Frame = +1

Query: 589 RLTICLALFVLIWGSAN-----AQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLL 753
R +C+ + + S N QLS+ FY SCP S VK V+ A++KE RMGASL+
Sbjct: 4 RTLLCIGVMAVFCVSININAVSGQLSSTFYDKSCPRAQSIVKRVVQAVAKEKRMGASLV 63

Query: 754 RLFFHDCFVN 783
RL FHDCFVN
Sbjct: 64 RLHFHDCFVN 73

>emb|CBI22007.1| unnamed protein product [Vitis vinifera]
Length = 425

Score = 157 bits (396), Expect = 1e-35
Identities = 75/121 (61%), Positives = 97/121 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD++T FDN Y++NL+
Sbjct: 196 QAQCFTFRSRIYNDTNIDPNFAATRRSTCP-VSG-GNSNLAPLDIRTMNRFDNIIYYQNL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TRRGLLHSDQELFNGGSQDALVRTYNANNALFFRDFAAAMVKMSNISPLTGTNGEIRSNC 313

Query: 2167 R 2169
R
Sbjct: 314 R 314

Score = 151 bits (381), Expect = 7e-34
Identities = 85/169 (50%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDT IKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 129 RDGV-----VQLGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAANN IP+P ++L+ LIS F+A GL+ +D+ ALSG+ I

Sbjct: 146 RRDARTASQSAANNEIPSPLASLSALISGFAAKGLNARDMTALSGSHTI 194

Score = 71.6 bits (174), Expect = 7e-10
Identities = 35/71 (49%), Positives = 49/71 (69%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNI FSSVKSTVQSAISKETRMGASL 750
MASF + + ++ L+ S N QLS NFY +CPN+ + V+ ++ A+ +E RMGAS+
Sbjct: 1 MASFTNSFVV-FSII SLLACSLNGQLSPNFYASTCPNVQNI VVRVAMRQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>ref|XP_002283995.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 316

Score = 157 bits (396), Expect = 1e-35
Identities = 76/124 (61%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYNETN++ AFA+++Q+ CP T G D NL+ LD +T T FD YFK+L+
Sbjct: 195 KAQCIKFRYRIYNETNVDAFAKSKQKICPWTGG--DENLSDLD-ETTTVFDTVYFKDLI 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YST+ TF +D A AM+KMG++SPLTG++GEIR NC
Sbjct: 252 EKKGLLHSDQQLYNGNSTDSMVETYSTDSTFFFTDVANAMVKMGNSPLTGTGDEIRTNC 311

Query: 2167 RRIN 2178
R+IN
Sbjct: 312 RKIN 315

Score = 148 bits (374), Expect = 4e-33
Identities = 82/167 (49%), Positives = 101/167 (60%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILLDDTANFTGEKTAGPNNNSLRGYDVIDTIK SQMESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V++GRR
Sbjct: 130 SV-----VALGGPTWTVQMGRR 146

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN +PAPTS+L+ L S FS G +T+++VALSGT I
Sbjct: 147 DSTTASLSTANADLPAPTSDDLVLTSLSFNKGFTTQEMVALSGHTI 193

Score = 74.3 bits (181), Expect = 1e-10
Identities = 38/70 (54%), Positives = 48/70 (68%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPFLSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS NFY SCP S++++ V +A++KE RMGASL
Sbjct: 1 MASLSLFSFFCMFSFLL--GMAHAQLSPNFYASSCPRALSTIRTAVNNAVAKERRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>emb|CAN81400.1| hypothetical protein [Vitis vinifera]
Length = 317

Score = 157 bits (396), Expect = 1e-35
Identities = 75/124 (60%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C F +RIYN+TNI+ FA TR+ +CP SG G++NLAPLD++T FDN Y++NL+
Sbjct: 196 QAQCFTFXSRIYNDTNIDPNFAATTRSTCP-VSG-GNSNLAPLDIRTMNRFDNIIYQNLN 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TRRGLLHSDQELFNGGSQDALVRTYNANNALFFRDFAAAMVKMSNISPLTGTNGEIRSNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RVVN 317

Score = 150 bits (380), Expect = 9e-34
Identities = 84/169 (49%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W + LG
Sbjct: 129 RDGV-----VQLGGPSWTIPLG 145

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAANN IP+P ++L+ LIS F+A GL+ +D+ ALSG+ I
Sbjct: 146 RRDARTASQSAANNEIPSPLASLSALISGFAAKGLNARDMTALSGSHTI 194

Score = 71.6 bits (174), Expect = 7e-10
Identities = 35/71 (49%), Positives = 49/71 (69%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MASF + + ++ L+ S N QLS NFY +CPN+ + V+ ++ A+ +E RMGAS+
Sbjct: 1 MASFTNSFVV-FSIISLLACSLNGQLSPNFYASTCPNVQNIWRVAMRQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>emb|CAN63655.1| hypothetical protein [Vitis vinifera]
Length = 272

Score = 157 bits (396), Expect = 1e-35
Identities = 76/124 (61%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYNETN++ AFA+++Q+ CP T G D NL+ LD +T T FD YFK+L+
Sbjct: 151 KAQCIKFRYRIYNETNVDAFAKSKQKICPWTGG--DENLSDLD-ETTTVFDTVYFKDLI 207

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQ+NG STDS+V YST+ TF +D A AM+KMG++SPLTG++GEIR NC
Sbjct: 208 EKKGLLHSDQQLYNGNSTDSMVETYSTDSTFFFTDVANAMVKGMLSPLTGTGDEIRTNC 267

Query: 2167 RRIN 2178
R+IN
Sbjct: 268 RKIN 271

Score = 150 bits (379), Expect = 1e-33
Identities = 83/168 (49%), Positives = 102/168 (60%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AAR 1333

Sbjct: 25 QGCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AAR
QGCDASILLDDTANFTGEKTAGPNNNSLRGYDVIDTIKSMESLCPGVVSCADIVAVAAAR 84

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGPTW V++GR

Sbjct: 85 DSV-----VALGGPTWTVQMGR 101

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RD+ TAS S AN +PAPTS+L+ L S FS G +T+++VALSGT I

Sbjct: 102 RDSTTASLSTANADLPAPTSDDLVLTSLFSNKGFTTQEMVALSGTHTI 149

>gb|AAA20472.1| peroxidase [Cenchrus ciliaris]
Length = 307

Score = 156 bits (395), Expect = 2e-35
Identities = 75/125 (60%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT FR RIY +TNI+ +FA +QQ+CPR+ G G NLAP+D QTP FDN Y+ NLV

Sbjct: 188 QARCTTFRGRIYGD TNIDASFAALQQQTCPRSGGDG--NLAPIDAQTPARFDNAYYTNLV 245

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSN-GEIRKN 2163
++GL HSDQ+LFNGGS D++VR YS++P F+SDF AAMIKMG+I G+N G++R+N

Sbjct: 246 SRRGLFHSDQELFNGGSQDALVRQYSSSPSQFNSDFVAAMIKMGNI----GANAGQVRRN 301

Query: 2164 CRRIN 2178
CR +N

Sbjct: 302 CRVVN 306

Score = 108 bits (271), Expect = 4e-21
Identities = 71/168 (42%), Positives = 83/168 (49%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SIL S GEK+A PN NS RG+EVID IK VE CPGVVSCA I+ +AA

Sbjct: 68 VQGCDASIL----SRSGGEKSAGPNANSVRGYEVIDTIKKNVEAACPGVVSCATIVPLAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
R ++ G PTWNV LG

Sbjct: 124 RPGPNLLGG-----PTWNVPLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKH 1654
RRD+ TA S AN +P PTS L LIS F LS +D++ALSG H

Sbjct: 141 RRDSTTAMLSLANQLPPPTS-LGTLISLFGG-RLSARDMIALSGAHH 186

Score = 73.6 bits (179), Expect = 2e-10
Identities = 35/60 (58%), Positives = 44/60 (73%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNI FSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
CL L+ +A+ AQLST FY SCPNL + V++ + A+S E RMGAS+LRLFFHDCFV
Sbjct: 9 CLLAISLLSFTAHAQLSTTFYASSCPNLQTVVRAAMTQAVSSEPRMGASILRFFHDCFV 68

>gb|ACF08096.1| class III peroxidase [Triticum aestivum]
Length = 313

Score = 156 bits (394), Expect = 2e-35
Identities = 72/126 (57%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI + FA + + +CP+ +GSGD NLA LD+ TP SFDN Y+ NL
Sbjct: 188 QAQCQNFRDRLYNETNINSGFATSLKANCPQPTGSGDRNLANDVSTPYSFDNAYYSNLK 247

Query: 1987 QKKGLLHSDQQLF--NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+KGLLHSDQ LF GG TD+ V +++NP FSS FA+AM+KMG++SPLTGS G++R
Sbjct: 248 SQKGLLHSDQVLFVTGTGGTDNTVNNFASNPAAFSSAFASAMVKMGNSPLTGSQQQVRL 307

Query: 2161 NCRRIN 2178
+C ++N
Sbjct: 308 SCSKVN 313

Score = 101 bits (252), Expect = 6e-19
Identities = 64/169 (37%), Positives = 83/169 (49%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGFVID+IK+ +E +C VSCADIL +AA
Sbjct: 66 VQGCDAVLLSGM-----EQNAFPNVMSLRGFVIDSIKAKLETMCKQTVSCADILTVAA 120

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 121 RDSV-----VALGGPSWTVPLG 137

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P P +L L F G + D+VALSG I
Sbjct: 138 RRDSTNANEAVANSDLPPFFDLVNLTSFGDKGFTVTDMLVALSGAHTI 186

Score = 72.4 bits (176), Expect = 4e-10
Identities = 36/72 (50%), Positives = 50/72 (69%)
Frame = +1

Query: 565 LTMASFC SRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGA 744
+ +S + L +CLA+ +A+AQLS FY +CPN +++KS V +A++KE RMGA
Sbjct: 1 MASSSLSAVLLLCLAV-----AASAQLSPTFYDTTCPNALATI KSAVTA AVNKENRMGA 54

Query: 745 SLLR LFFHDCFV 780
SLLRL FHDCFV
Sbjct: 55 SLLR LHFHDCFV 66

>ref|XP_002461211.1| hypothetical protein SORBIDRAFT_02g042870 [Sorghum bicolor]
gb|EER97732.1| hypothetical protein SORBIDRAFT_02g042870 [Sorghum bicolor]
Length = 321

Score = 156 bits (394), Expect = 2e-35
Identities = 74/125 (59%), Positives = 95/125 (76%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR-TSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR IYN+TNI +AFA + Q +CPR +GSGD+ LAPLD +PT+FDN YF NL
Sbjct: 196 QAQCRFFRDHIYNDTNINS AFAASLQANCP RPANGSGDSTLAPLDAASPTAFDNAYFSNL 255

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMI KMGDISPLTGSNGEIRKN 2163
+ KGLLHSDQQLFNGGSTDS VR ++++ FS+ FA AM+ MG+I+P TGS G+IR
Sbjct: 256 MSHKGLLHSDQQLFNGGSTDSTVRSFASSASAFSNAFATAMVNMGN IAPKTGSQQGIRVT 315

Query: 2164 CRRIN 2178
C ++N
Sbjct: 316 CSKVN 320

Score = 121 bits (303), Expect = 8e-25
Identities = 71/165 (43%), Positives = 88/165 (53%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTG EKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD S+LL DT SFTGE+ A PN+NS RGF VID+IK+ VE VC VSCADILA+AA
Sbjct: 69 VDGCDASVLLADTGSFTGEQGAIPNKNSLRGFSVIDSIKTQVEAVCNQTVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V +G
Sbjct: 129 RDSV-----VALGGPSWTVLVG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRD+ TAS+ A +P P+ +L L F+ LS D+VALSG
Sbjct: 146 RRDSTTASKDNAERDLPPPSFDLANLTRSFANKNLSVTDMVALSG 190

Score = 71.2 bits (173), Expect = 9e-10
Identities = 33/66 (50%), Positives = 47/66 (71%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
SRL++ + + + +A AQLS+ FY SCP +++KS V +A++ E RMGASLLRL F
Sbjct: 5 SRLSLLVAILALATAATAQLSSTFYDTSCP KALATI KSAVTA AVNNEARMGASLLRLHF 64

Query: 766 HDCFVN 783
HDCFV+
Sbjct: 65 HDCFVD 70

>sp|Q02200.1|PERX_NICSY RecName: Full=Lignin-forming anionic peroxidase; Flags: Precursor
gb|AAA34050.1| anionic peroxidase [Nicotiana glauca]
Length = 322

Score = 156 bits (394), Expect = 2e-35
Identities = 82/125 (65%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIY N T+I+ FA TR++ CP+ +G NLAPLDL TP FDN YFKNL
Sbjct: 200 QAQCFLFRDRIYSNGTDIDAGFASTRRRQCPQEGENG--NLAPLDLVTPNQFDNYYFKNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LFNGGSTD+IV YS + FSSDFAAAMIKMGDISPL+G NG IRK
Sbjct: 258 IQKKGLLQSDQVLFNGGSTDNIVSEYSNSARAFSSDFAAAMIKMGDISPLSGQNGIIRKV 317

Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CGSVN 322

Score = 134 bits (337), Expect = 9e-29
Identities = 76/169 (44%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLD+T S EK A PN SARGF +I++ K VEK+CPGVVSCADIL +AA
Sbjct: 73 VQGCDASILLDETPSIESEKTALPNLGSARGFGIIEDAKREVEKICPGVVSCADILTVAA 132

Query: 1331 RDSVQIVSGQTTNKNLTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

Sbjct: 133 RD+ S +GGP+W VKLG
RDA-----SAAVGGPSWTVKLG 149

Query: 1511 RRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ A +P P LN+LIS F++ GLST+D+VALSG I
Sbjct: 150 RRDSTTASKTLAETDLPFPDPLNRLISSFASKGLSTRDMVALSGAHTI 198

Score = 64.7 bits (156), Expect = 8e-08
Identities = 32/68 (47%), Positives = 47/68 (69%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR 756
SF ++ I +L +L +AQLS FY ++CPN ++++++V+ AIS E RM ASL+R
Sbjct: 7 SFRAKAAI-FSLLLLSCMQCHAQLSATFYDNTCPNALNTIRTSVRQAISSERRMAASLIR 65

Query: 757 LFFHDCFV 780
L FHDCFV
Sbjct: 66 LHFHDCFV 73

>ref|XP_002437129.1| hypothetical protein SORBIDRAFT_10g021620 [Sorghum bicolor]
gb|EER88496.1| hypothetical protein SORBIDRAFT_10g021620 [Sorghum bicolor]
Length = 313

Score = 155 bits (393), Expect = 3e-35
Identities = 73/124 (58%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR+RIY +TNI +FA RQQ+CP++ G G NLA +D QTPT FD Y+ NL+
Sbjct: 191 QARCTTFRSRIYGD TNINASFAALRQQTCPQSGGDG--NLASIDEQTPTRFDTDYYTNLM 248

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++VR YS + F+SDF AAMIKMG++ LTG+ G+IR+NC
Sbjct: 249 LQRGLFHSDQELFNGGSQDALVRQYSASSSLFNSDFVAAMIKMGVGLTGTAGQIRRNC 308

Query: 2167 RRIN 2178
R +N
Sbjct: 309 RVVN 312

Score = 128 bits (322), Expect = 5e-27
Identities = 76/169 (44%), Positives = 90/169 (53%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330

+QGCDGSILLD GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+AA
Sbjct: 68 VQGCDGSILLDAG----GEKTAGPNANSVRGYEVIDTIKTNVEAACPGVVSCADILALAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGP TWNVKLG 1510
R+ ++ G PTWNV LG

Sbjct: 124 REGTNLLGG-----PTWNVPLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P T++L LIS F GLS +D+ ALSG I

Sbjct: 141 RRDSTTASASLANSLPPATASLGTLISLFRQGLSARDMTALSGAHSI 189

Score = 69.7 bits (169), Expect = 3e-09
Identities = 35/60 (58%), Positives = 41/60 (68%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFV 780
CL L+ A+ AQLST FY SCP L S V+ + A+S + RMGASLLRRLFHDCFV

Sbjct: 9 CLVAISLLSCVAHAQLSTTFYASSCPKLSIVRKAMIQALSNDQRMGASLLRRLFHDCFV 68

>gb|AAW52718.1| peroxidase 4 [Triticum monococcum]
Length = 313

Score = 155 bits (393), Expect = 3e-35
Identities = 72/126 (57%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI + FA + + +CP+ +GSGD NLA LD+ TP SFDN Y+ NL

Sbjct: 188 QAQCQNFDRRLYNETNINSGFATSLKANCPQPTGSGDRNLANLDVSTPYSFDNAYYSNLK 247

Query: 1987 QKKGLLHSDQQLF--NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+KGLLHSDQ LF GG TD+ V +++NP FSS FA+AM+KMG++SPLTGS G++R

Sbjct: 248 SQKGLLHSDQVLFVTGTGGTDNTVNNFASNPAAFSSAFASAMVKGMLSPLTGSQQQVRI 307

Query: 2161 NCRRIN 2178
+C ++N

Sbjct: 308 SCSKVN 313

Score = 104 bits (260), Expect = 7e-20
Identities = 66/169 (39%), Positives = 84/169 (49%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGFEVID+IK+ +E +C VSCADIL +AA

Sbjct: 66 VQGCDAVLLSGM-----EQNAIPNVMSLRGFEVIDSIKAQLETMCKQTVSCADILTVAA 120

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 121 RDSV-----VALGGPSWTVPLG 137

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+++AANN +P P +L L F G + D+VALSG I

Sbjct: 138 RRDSTNANEEAANNEPFPFDLVNLTQSFQDKGFTVTDMAVALSGAHTI 186

Score = 72.4 bits (176), Expect = 4e-10
Identities = 36/72 (50%), Positives = 50/72 (69%)
Frame = +1

Query: 565 LTMASFCRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
+ +S + L +CLA+ +A+AQLS FY +CPN +++KS V +A++KE RMGA

Sbjct: 1 MASSSLSAVLLLCLAV-----AASAQLSPTFYDTTCPNALATIKAHTAANVKNRMGA 54

Query: 745 SLLRLLFFHDCFV 780

SLLRL FHDCFV

Sbjct: 55 SLLRLHFHDCFV 66

>gb|ACI03401.1| peroxidase 1 [Litchi chinensis]
Length = 318

Score = 155 bits (392), Expect = 4e-35
Identities = 87/169 (51%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTS+F GEK A PN S RGF V+D IK+ +EK CPGVVSCAD+LAIAA

Sbjct: 69 VNGCDGSLLDDTSTFVGEKTAVPNNISVRGFNVVDQIKAKLEKACPGVVSCADLLAIAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG

Sbjct: 129 RDSV-----VHLGGPSWKVRLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ AN IP PTSNL+ LIS FSA GLS KDLVALSG+ I

Sbjct: 146 RRDSTTASRALANTSIPPPTSNSALISSFSAQGLSLKDLVALSGSHTI 194

Score = 150 bits (379), Expect = 1e-33
Identities = 70/123 (56%), Positives = 91/123 (73%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCT+FR +YN+TNI+++FA++ ++ CPR+ DN LA LD QTP FD Y+ NL++
Sbjct: 197 ARCTSFRGHVYNDTNIDSSFAQSLRRKCPRSGN--DNVLANLDRQTPFCFDKLYDNLLK 254

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KKGLLHSDQQLF GGS D V+ Y+ N F DFA AM+KMG+I PLTG G+IR NCR
Sbjct: 255 KKGLLHSDQQLFKGGSADPFVKKYANNTSAFFKDFAGAMVKMGNIKPLTGRAGQIRINCR 314

Query: 2170 RIN 2178
++N
Sbjct: 315 KVN 317

Score = 63.9 bits (154), Expect = 1e-07
Identities = 31/50 (62%), Positives = 34/50 (68%)
Frame = +1

Query: 634 ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
AN QL NFY +CP S V V +AI ETR+GASLLRL FHDCFVN
Sbjct: 21 ANGQLCPNFYESTCPQALSIVHKGVAIAIKNETRIGASLLRLLFHDCFVN 70

>ref|XP_002284007.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 316

Score = 155 bits (392), Expect = 4e-35
Identities = 76/124 (61%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C+ FR RIYNETNI+ FA ++Q CP S GD NL+ LD +T T FDN YF NL+
Sbjct: 195 KAQCSKFRDRIYNETNIDATFATSKQAICP--SSGDENLSDLD-ETTTVFDNVYFTNLI 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YS + TF +D A+AM+KMG++SPLTG++GEIR NC
Sbjct: 252 EKKGLLHSDQQLYNGNSTDSMVETYSNDSTTFFTDVASAMVKMGNLSPLTGTGDEIRTNC 311

Query: 2167 RRIN 2178
R IN
Sbjct: 312 RAIN 315

Score = 151 bits (381), Expect = 7e-34
Identities = 83/167 (49%), Positives = 102/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
 GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD
 Sbjct: 70 GCDASILLDDTANFTGEKTAGPNNNSVRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
 SV + LGGPTW V+LGRR
 Sbjct: 130 SV-----VALGGPTWTVQLGRR 146

Query: 1517 DARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
 D+ TAS S AN+ +PAPTS+L+ LIS FS G +T+++V LSGT I
 Sbjct: 147 DSTTASFSTANS DLPAPTS DLDALISLFSNKGFTTQEMVVLSGHTI 193

Score = 70.9 bits (172), Expect = 1e-09
 Identities = 35/70 (50%), Positives = 50/70 (71%)
 Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASL 750
 MAS C+ F+L G A+AQLS+++Y SCP+ S++++ V +A++ E+RMGASL
 Sbjct: 1 MASLSLFS LFCMFSFLL--GMAHAQLSSDYSSSCPSALSTIQ TAVNNAVADES RMGASL 58

Query: 751 LRLFFHDCFV 780
 LRL FHDCFV
 Sbjct: 59 LRLHFHDCFV 68

>ref|XP_002323054.1| predicted protein [Populus trichocarpa]
 gb|EEF04815.1| predicted protein [Populus trichocarpa]
 Length = 317

Score = 155 bits (392), Expect = 4e-35
 Identities = 74/124 (59%), Positives = 94/124 (75%)
 Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
 QARCT F RI NETNI+++F + Q C T NN PLD+ +PTSFD+ Y++NL+
 Sbjct: 199 QARCTTFLTRINNETNIDSSFKTSTQAQCQNT-----NNFVPLDVTSPSFD SAYSRRNLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
 +KGLLHSDQQLF+GGSTD+ VR YS+N F +DFA AMIKMG++SPLTG+NG+IR NC
 Sbjct: 254 NQKGLLHSDQQLFSGGSTDAQVRAYSSNQAAFRTDFANAMIKMGNLSPLTG TNGQIRTNC 313

Query: 2167 RRIN 2178
 R+ N
 Sbjct: 314 RKAN 317

Score = 119 bits (297), Expect = 4e-24
Identities = 73/170 (42%), Positives = 93/170 (54%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+ GCD S+LLD GEK A N NS RGFEVID+IK+ +E CPGVVSCADIL++AA
Sbjct: 76 VNGCDASVLLDG-----GEKTAPANTNSLRGFEVIDSIKTQLESSCPGVVSCADILSVAA 130

Query: 1331 RDSVQIVSGQTTNKNLNLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 131 RDSV-----VALGGPSWVQVQLG 147

Query: 1511 RRDARTA-SQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA S S NN +P+P +++ LIS FS G + K++VALSG+ I
Sbjct: 148 RRDSATAGSVSDVNNNVPSPALSVSGLISAFSNGFTAKEMVALSGSHTI 197

Score = 79.0 bits (193), Expect = 4e-12
Identities = 37/57 (64%), Positives = 46/57 (80%)
Frame = +1

Query: 613 FVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783
F+L+ G A+AQL++NFY SCP++ S +KS V SA+S E RMGASLLRL FHFDCFVN
Sbjct: 21 FLLLVGVASAQLASNFYGTSCPSVLSVIKSAVDSAVSNEARMGASLLRRLFHDCFVN 77

>gb|EEC82681.1| hypothetical protein OsI_27325 [Oryza sativa Indica Group]
Length = 313

Score = 155 bits (392), Expect = 4e-35
Identities = 70/124 (56%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFD Y+ NL+
Sbjct: 190 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTPYSFDTAYYSNLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PL GS G+IR +C
Sbjct: 250 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLIGSQGQIRLSC 309

Query: 2167 RRIN 2178
++N
Sbjct: 310 SKVN 313

Score = 129 bits (325), Expect = 2e-27

Identities = 73/167 (43%), Positives = 91/167 (54%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C VSCADILA+AARD

Sbjct: 65 GCDASVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQTVSCADILAVAARD 124

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR

Sbjct: 125 SV-----VALGGPSWTVGLGRR 141

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ TAS +ANN +P P +L LI F G S D+VALSG I

Sbjct: 142 DSTTASMDSANNDLPPPFDFLENLIKAFGDKGFSVTDMVALSGAHTI 188

Score = 65.5 bits (158), Expect = 5e-08
Identities = 30/61 (49%), Positives = 43/61 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC

Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTCPRALATI KSAVTA AVNNEPRMGASLLR LHFHDC 63

Query: 775 F 777

F

Sbjct: 64 F 64

>gb|EAZ01280.1| hypothetical protein OsI_23303 [Oryza sativa Indica Group]
Length = 327

Score = 155 bits (392), Expect = 4e-35
Identities = 73/124 (58%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA +Q+CP+ SG GD NLAP D QTP +FDN YFKNLV

Sbjct: 205 RARCLMFRGRIYGEANINATFAAALRQTCPQ-SGGGDGNLAPFDDQTPDAFDNAYFKNLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNP GTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N G F+ DFA AM+KMG + P G+ E+R NC

Sbjct: 264 AQRGLLHSDQELFNGGSQDALVRKYAGNAGMFAGDFAKAMVKMGGLMPAAGTPTEVRLNC 323

Query: 2167 RRIN 2178

R++N

Sbjct: 324 RKNV 327

Score = 135 bits (339), Expect = 5e-29
Identities = 74/165 (44%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IKS VE C GVVSCADI+A+A+
Sbjct: 78 VNGCDASILLDDTPTFTGEKNAGANINSVRGYEVIDAIKSQVEAACKGVVSCADIVALAS 137

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 138 RDAVNLLGG-----PTWNVQLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
R+D+RTAS +AAN +P P S+ L++ F+ GLS +++ ALSG
Sbjct: 155 RKDSRTASGTAANANLPGPASSGASLVAAFAGKGLSAREMTALSG 199

Score = 67.0 bits (162), Expect = 2e-08
Identities = 30/51 (58%), Positives = 39/51 (76%)
Frame = +1

Query: 631 SANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFVN 783
+A A LST FY +CP + + V+S V A++KE RMGAS++RLFFHDCFVN
Sbjct: 29 AAKAGLSTKIFYAKTC PGVDTIVRSVVAQAVAKEPRMGASII RLFFHDCFVN 79

>gb|AA Y89058.1| class III peroxidase [Phelipanche ramosa]
Length = 325

Score = 155 bits (392), Expect = 4e-35
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
Q+RC FR+RIY N T+I+ FA TR++ CP+T G DNNLAPLDL TP SFDN YF+NL
Sbjct: 203 QSRCFLFRSRIYSNGTDIDPNFASTRRRRQCPQTGG--DNNLAPLDLVT P NSFDNYYFRNL 260

Query: 1984 VQKKGLLHSDQQLFN GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFN GGST+++V YS NP F++DFA+AM++M +I PL GSNG IR+
Sbjct: 261 IQRKGLLES DQVLFN GGSTNALVTSYSNNPRLFATDFASAMVRMSEIQPLLGSNGI IRRV 320

Query: 2164 CRRIN 2178
C IN
Sbjct: 321 CNVIN 325

Score = 124 bits (311), Expect = 9e-26
Identities = 70/169 (41%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD+ + EK+A PN NS RG++VI+ K VE +CP VSCADI+A+AA
Sbjct: 76 VQGCDASILLDDSPTIQSEKSAGPNVNSVRGYDVIETAKREVESICPRNVSCADIVALAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW VKLG
Sbjct: 136 RDA-----SVAVGGPTWTVKLG 152

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA+ + AN +P+P ++L LI+ F GLS D+VALSG+ I
Sbjct: 153 RRDSTTANPNEANTDLPSPFASLQTLITAFDDKGLSETDMVALSGSHTI 201

Score = 61.2 bits (147), Expect = 9e-07
Identities = 31/71 (43%), Positives = 46/71 (64%), Gaps = 3/71 (4%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGS---ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGAS 747
S S LT+ ++ +L+ S AQLS FY CPN S++++++ A++ E RM AS
Sbjct: 6 SINSLLTLTISSLILLSITPCQAQLSPTFYDSICPNALSTIRTSIRRAVAEERRMAAS 65

Query: 748 LLRLFFHDCFV 780
L+RL FHDCFV
Sbjct: 66 LIRLHFHDCFV 76

>gb|AAW52719.1| peroxidase 5 [Triticum monococcum]
Length = 259

Score = 155 bits (392), Expect = 4e-35
Identities = 72/126 (57%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI + FA + + +CP+ +GSGD NLA LD+ TP SFDN Y+ NL
Sbjct: 134 QAQCLNFRDRLYNETNINSGFATSLKANCPQPTGSGDRNLANLDVLTYPYFDNAYYSNLK 193

Query: 1987 QKKGLLHSDQQLF--NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+KGLLHSDQ LF GG TD+ V +++NP FSS FA+AM+KMG++SPLTGS G++R
Sbjct: 194 SQKGLLHSDQVLFVTGTGGTDNTVNNFASNPAAFSSAFASAMVKMGNLSPLTGSQQQVRL 253

Query: 2161 NCRRIN 2178
+C ++N

Sbjct: 254 SCSKVN 259

Score = 101 bits (252), Expect = 6e-19
Identities = 64/169 (37%), Positives = 83/169 (49%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LL E+NA PN S RGFVID+IK+ +E +C VSCADIL +AA
Sbjct: 12 VQGCDA SVLLSGM-----EQNAFPNVMSLRGFVIDSIKAKLETMCKQTVSCADILTVAA 66

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 67 RDSV-----VALGGPSWTVPLG 83

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P P +L L F G + D+VALSG I
Sbjct: 84 RRSTNANEAVANS DLPPFFDLVNLQSF GDKGFTV TDMVALSGAHTI 132

>gb|AAC49819.1| peroxidase [Oryza sativa Indica Group]
Length = 315

Score = 155 bits (392), Expect = 4e-35
Identities = 70/124 (56%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFD Y+ NL+
Sbjct: 192 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALD TTPYSFD TAYYSNLL 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PL GS G+IR +C
Sbjct: 252 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLIGSQGQIRLSC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 132 bits (331), Expect = 4e-28
Identities = 74/169 (43%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C VSCADILA+AA
Sbjct: 65 VQGCDA SVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQTVSCADILAVAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 125 RDSV-----VALGGPSWTVGLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS +ANN +P P +L LI F G S D+VALSG I
Sbjct: 142 RRDSTTASMDSANNDLPPPFDFLENLIKAFGDKGFSVTDMVALSGAHTI 190

Score = 67.0 bits (162), Expect = 2e-08
Identities = 31/62 (50%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSATSKETRMGASLLRRLFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC
Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTA AVNNEPRMGASLLRRLFHDC 63

Query: 775 FV 780
FV
Sbjct: 64 FV 65

>dbj|BAD97435.1| peroxidase [Pisum sativum]
Length = 318

Score = 155 bits (392), Expect = 4e-35
Identities = 80/125 (64%), Positives = 91/125 (72%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q C FR RIYNETNI+T FA R+ +CP S GD NLAPLD TPT+FDN Y+ +L+
Sbjct: 196 QTECQFFRNRIYNETNIDTNFATLRKSNCP--SSGGDTNLAPLDSVTPTTFDNYYNDLI 253

Query: 1987 QKKGLLHSDQQLFNG-GSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
KGLLHSDQ LFNG GS S+VR YS N F DFAAAMIK+ ISPLTG+NGEIRKN
Sbjct: 254 ANKGLLHSDQALFNGVGSQVSLVRTYSRNTVAFKRDFAAAMIKLSRISPLTGTNGEIRKN 313

Query: 2164 CRRIN 2178
CR +N
Sbjct: 314 CRLVN 318

Score = 141 bits (355), Expect = 7e-31
Identities = 82/169 (48%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDT++FTGEK+A PN NSARGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDGSILLDDTATFTGEKSAGPNINSARGFEVIDTIKTNVEASCNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD + ++ GGPTW V LG
Sbjct: 129 RDGIFLL-----GGPTWMVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAAN+ IP P+S+L L + F GL+ DL LSG I
Sbjct: 146 RRDARTASQSAANSQIPGPSSDLATLTTMFRNKGLTLNDLTVLSGAHTI 194

Score = 73.9 bits (180), Expect = 1e-10
Identities = 38/71 (53%), Positives = 52/71 (73%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+F +L + L++ L+ S NAQL NFY +CP+L + V++T+ SAI E R+GAS+
Sbjct: 1 MATFI-KLFVLSIISLLACSTNAQLINNFYATTCPSLQTIVRNTMISAIKTEARIGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>ref|NP_001057821.1| Os06g0547100 [Oryza sativa (japonica cultivar-group)]
dbj|BAD54117.1| putative bacterial-induced peroxidase precursor [Oryza sativa
Japonica Group]
tpe|CAH69329.1| TPA: class III peroxidase 87 precursor [Oryza sativa (japonica
cultivar-group)]
gb|EAZ37289.1| hypothetical protein OsJ_21627 [Oryza sativa Japonica Group]
Length = 327

Score = 155 bits (392), Expect = 4e-35
Identities = 73/124 (58%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA +Q+CP+ SG GD NLAP D QTP +FDN YFKNLV
Sbjct: 205 RARCLMFRGRIYGEANINATFAAALRQTC PQ-SGGGDGNLAPFDDQTPDAFDNAYFKNLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N G F+ DFA AM+KMG + P G+ E+R NC
Sbjct: 264 AQRGLLHSDQELFNGGSQDALVRKYAGNAGMFAGDFAKAMVKMGLMPAAGTPTEVRLNC 323

Query: 2167 RRIN 2178
R++N

Sbjct: 324 RKVN 327

Score = 134 bits (338), Expect = 7e-29
Identities = 74/165 (44%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IKS VE C GVVSCADI+A+A+
Sbjct: 78 VNGCDASILLDDTLTFTGEKNAGANINSVRGYEVIDAIKSQVEAACKGVVSCADIVALAS 137

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 138 RDAVNLLGG-----PTWNVQLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
R+D+RTAS +AAN +P P S+ L++ F+ GLS +++ ALSG
Sbjct: 155 RKDSRTASGTAANLPGPASSGASLVAAFAGKLSAREMTALSG 199

Score = 64.7 bits (156), Expect = 8e-08
Identities = 29/51 (56%), Positives = 38/51 (74%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPFLSSVKSTVQSAISKETRMGASLLRRLFHDFVFN 783
+A A LS FY +CP + + V+S V A++KE RMGAS++RRLFHDFVFN
Sbjct: 29 AAKAGLSIKFYAKTCPGVDTIVRSVVAQAVAKEPRMGASIRRLFHDFVFN 79

>emb|CBI19220.1| unnamed protein product [Vitis vinifera]
Length = 373

Score = 155 bits (391), Expect = 5e-35
Identities = 85/167 (50%), Positives = 103/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1336
GCD SILLDDT+SFTGEK A PN++S RG+EVID IKS VE +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILLDDTASFTGEKTAGPNKDSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW ++LGRR
Sbjct: 130 SV-----VALGGPTWTLQLGRR 146

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN+ +P P S+L+ LISRFS G +TK++VALSGT I
Sbjct: 147 DSTTASLSTANSDLPGPASDLSTLISRFSNKGFTTKEMVALSGTHTI 193

Score = 128 bits (321), Expect = 6e-27
Identities = 64/95 (67%), Positives = 76/95 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR+RIYNETNI+ AFA ++Q+ CP T G DNNL+ LD +T T FDN YF+NL
Sbjct: 195 KARCTSFRRSRIYNETNIDAAFATSKQKICPSTGG--DNNLSLDL-ETTTVFDNVYFRNLK 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSD 2091
KKGLLHSDQQL+NGGSTDSIV YSTN TF +D
Sbjct: 252 AKKGLLHSDQQLYNGGSTDSIVETYSTNSATFFTD 286

Score = 75.1 bits (183), Expect = 6e-11
Identities = 38/70 (54%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCP NFLSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+NFY SCP S++++ V +A++KE RMGASL
Sbjct: 1 MASLSLFSLFCVFSFLL--GMAHAQLSSNFYASSCPKALSTIRAAVNNAVAKERRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>gb|ACN30737.1| unknown [Zea mays]
Length = 260

Score = 155 bits (391), Expect = 5e-35
Identities = 73/127 (57%), Positives = 97/127 (76%), Gaps = 3/127 (2%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF NL+
Sbjct: 134 RAQCKNCRARIYNDTDIDASFAASLRASCPAQAGAGDGALEPLDGSTPDAFDNAYFGNLL 193

Query: 1987 QKKGLLHSDQQLF---NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIR 2157
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GEIR
Sbjct: 194 SQRGLLHSDQALFGGGGGATDGLVSAAYASNAGQWADFAAAMVKMGSISPLTGTGEIR 253

Query: 2158 KNCRIN 2178
NCRIN
Sbjct: 254 VNCRRVN 260

Score = 145 bits (365), Expect = 5e-32
Identities = 82/164 (50%), Positives = 96/164 (58%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILA+AAR
Sbjct: 8 QGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAV AAR 67

Query: 1334 DSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV LGGP+W V LGR
Sbjct: 68 DSVAQ-----LGGPSWAVPLGR 84

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 85 RDATTASASLANS DLPGPTSSLNGLLNAFSNKGLSSTD MVALSG 128

>gb|ACG40622.1| peroxidase 2 precursor [Zea mays]
Length = 342

Score = 155 bits (391), Expect = 5e-35
Identities = 73/127 (57%), Positives = 97/127 (76%), Gaps = 3/127 (2%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF NL+
Sbjct: 216 RAQCKNCRARIYNDTDIDASFAASLRASCPAQAGAGDGALEPLDGSTPD AFDNAYFGNLL 275

Query: 1987 QKKGLLHSDQQLF---NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIR 2157
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GEIR
Sbjct: 276 SQRGLLHSDQALFGGGGGGATDGLVSAAYASNAGQWGFADFAAAMVKMGSISPLTGT DGEIR 335

Query: 2158 KNCRRIN 2178
NCRN+N
Sbjct: 336 VNCRRVN 342

Score = 145 bits (366), Expect = 4e-32
Identities = 82/165 (49%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI A 1330
+QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILA+AA
Sbjct: 89 VQGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAV AA 148

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL G 1510

Sbjct: 149 RDSV-----LGGP+W V LG
RDSVAQ-----LGGPSWAVPLG 165

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG

Sbjct: 166 RRDATTASASLANSDLPGPTSSLNGLLNAFNSNKGLSSTDMVALSG 210

Score = 57.8 bits (138), Expect = 1e-05
Identities = 32/67 (47%), Positives = 41/67 (61%), Gaps = 1/67 (1%)
Frame = +1

Query: 583 CSRLTICLALFVLIWGSANAQLSTNFYH-SCPNLFSSVKSTVQSAISKETRMGASLLRL 759
C L + LAL +AQLS+ YY SCP ++++ V +A+ E RMGASLLRL
Sbjct: 24 CGLLVLALALATTA-AVGSAQLSSESYYDASCPAALLTIRTAVSTAVLLEPRMGASLLRL 82

Query: 760 FFHDCFV 780
FFHDCFV
Sbjct: 83 HFHDCFV 89

>emb|CAN83972.1| hypothetical protein [Vitis vinifera]
Length = 290

Score = 154 bits (390), Expect = 6e-35
Identities = 76/124 (61%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C+ FR RIYNETNI+ FA ++Q CP S GD NL+ LD T T FDN YF NL+
Sbjct: 169 KAQCSKFRDRIYNETNIDATFATSKQAICP--SSGGDENLSDLXTT-TXFDNVYFTNLI 225

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YS + TF +D A+AM+KMG++SPLTG++GEIR NC
Sbjct: 226 EKKGLLHSDQQLYNGNSTDSMVETYSNDSTFFFTDVASAMVKMGNLSPLTGTGDEIRTNC 285

Query: 2167 RRIN 2178
R IN
Sbjct: 286 RAIN 289

Score = 135 bits (340), Expect = 4e-29
Identities = 81/186 (43%), Positives = 101/186 (54%), Gaps = 18/186 (9%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGKKNANPNRNSARGFE-----VIDNIKSAVE 1279
QGCD SILLDDT++FTGEK A PN NS RG++ + IKS +E

Sbjct: 25 QGCDASILLDDTANFTGEKTAGPNNNSXRGYDSSNCGSDWYPLCIRVVTCTENTIKSQME 84
Query: 1280 KVCPGVVSCADILAI AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC 1459
+CPGVVSCADI+A+AARDSV
Sbjct: 85 SLCPGVVSCADIVAVAARDSV----- 105
Query: 1460 *F*SI*LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVAL 1639
+ LGGPTW V+LGRRD+ TAS S AN+ +PAPTS+L+ LIS FS G +T+++V L
Sbjct: 106 ----VALGGPTWTVQLGRRDSTASFSTANS DLPAPTS DLDALISLFSNKGF TQEMVVL 161
Query: 1640 SGT KHI 1657
SGT I
Sbjct: 162 SGT HTI 167

>ref|XP_002509737.1| Lignin-forming anionic peroxidase precursor, putative [Ricin
communis]
gb|EEF51124.1| Lignin-forming anionic peroxidase precursor, putative [Ricin
communis]
Length = 322

Score = 154 bits (389), Expect = 8e-35
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIYN ++I+ FA TR+ +CP+T G+G NLAPLDL TP +FDN Y+ NL
Sbjct: 200 QAQCVTFRDRIYNNASDIDPDFAATRRGNCPQTGGNG--NLAPLDLVTPNNFDNNYYSNL 257
Query: 1984 VQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ K+GLL SDQ LF+GGSTDSIV YST+ +F SDFAAAM+KMG+ISPLTG+ GEIR+
Sbjct: 258 IAKRGLLASDQILFSGGSTDSIVNEYSTDSSSFSDFAAAMVKGNI SPLTGTQGEIRRI 317
Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CSAVN 322

Score = 131 bits (330), Expect = 6e-28
Identities = 75/169 (44%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI A 1330
+QGCDGS+LL DT +FTGEK+A N NS RG VID+ K+ VE +CPG+VSCADILA+AA
Sbjct: 73 VQGCDGSVLLVDTPFTGEKSARNNANSIRGENVIDDAKAQVESICPGIVSCADILAVAA 132
Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ GGP+W V LG

Sbjct: 133 RDA-----SVAAGGPSWTVNLG 149

Query: 1511 RRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P + LN+LIS FS GL+ +D+VALSG I

Sbjct: 150 RRDSTTASLAQANSDLPGFSDPLNRLISLFSKGLNERDMVALSGAHTI 198

Score = 68.9 bits (167), Expect = 4e-09
Identities = 36/73 (49%), Positives = 49/73 (67%), Gaps = 3/73 (4%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGS---NAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMG 741
MAS S + L +F +I S+ AQLS+NFY ++CPN +++KS + +AI E RM

Sbjct: 1 MASRLSFACMILTIFFIINYSSLPCQAQLSSNFYDNTCPNALTTIKSAIDAAIESEQRMA 60

Query: 742 ASLLRRLFHDCFV 780
ASL+RL FHDCFV

Sbjct: 61 ASLIRLHFHDCFV 73

>ref|XP_002268412.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 318

Score = 154 bits (389), Expect = 8e-35
Identities = 75/123 (60%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C F+ RIYNE+NI+ AFAR RQ +CP GD LAPLD T FD YF NLV+

Sbjct: 199 AQCFFKNRIYNESNIDPAFARARQSTCP--PNGGDTKLAPLD-PTAARFDTGYFTNLVK 255

Query: 1990 KKGLLHSDQQLFNGGSTDIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGSTD++V+ YSTN G FS+DFA +M+KMG+I PLTG G+IR NCR

Sbjct: 256 RRGLLHSDQALFNGGSTDTLVKTYSTNFGAFSADFAKSMVKMGNIKPLTGKKGQIRVNCR 315

Query: 2170 RIN 2178
++N

Sbjct: 316 KVN 318

Score = 136 bits (343), Expect = 2e-29
Identities = 82/166 (49%), Positives = 97/166 (58%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC-PGVVSCADILAI 1327
+ GCD SILLD TS+ EKNA N NSARGF V+D+IKS V+KVC VVSCADILA+A

Sbjct: 70 VNGCDASILLDATSTIDSEKNAGANANSARGFNVDIKSQVDKVCGRPVVSCADILAVA 129

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGP+W V+L
Sbjct: 130 ARDSV-----VALGGPSWTVQL 146

Query: 1508 GRRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRD+ TAS++ ANN IP+P +L LI+RFS GL TKDLVALSG
Sbjct: 147 GRRDSTTASRTDANNIPSPFMDLPALITRFSNQLDTKDLVALSG 192

Score = 66.6 bits (161), Expect = 2e-08
Identities = 35/69 (50%), Positives = 42/69 (60%), Gaps = 3/69 (4%)
Frame = +1

Query: 586 SRLTICLALFVLI---WGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR 756
SR +CL FVL +A LS FY CP ++K V++A+ KE RMGASLLR
Sbjct: 3 SRSLLCLYAFVLFSLATADFSAAALSPYFYNKVCPKALPTIKRVVEAAVQKEKRMGASLLR 62

Query: 757 LFFHDCFVN 783
L FHDCFVN
Sbjct: 63 LHFHDCFVN 71

>dbj|BAD36900.1| peroxidase [Lotus japonicus]
Length = 143

Score = 154 bits (389), Expect = 8e-35
Identities = 73/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC+ FR+RIY+E NI+ A+AR+ Q CPRTSG GD+NL+P+D TP FD+ Y++NL+
Sbjct: 21 QSRCSLFRSRIYSEQNIDPAYARSLQGQCPRTSVGVGDSNLSPIDT-TPNFFDSTYYRNL 79

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GL HSDQQLFNGGSTDS V Y++NP F DFA AM+KMG++ LTG+ G+IRK C
Sbjct: 80 NKRGLFHSDQQLFNGGSTDSKVSQYASNPLFRIDFANAMVKGMLGTLTGTTGQIRKVC 139

Query: 2167 RRIN 2178
+N
Sbjct: 140 SSVN 143

>gb|ACN26131.1| unknown [Zea mays]
Length = 323

Score = 154 bits (388), Expect = 1e-34
Identities = 71/124 (57%), Positives = 93/124 (75%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR RIYN+ NI FA RQQ+CP G D LAP+D+QTP +FDN Y+KNL+

Sbjct: 202 QARCATFRNRIYNDGNINATFASLRQQTCPLAGG--DAALAPIDVQTPEAFDNAYYKNLM 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++V+ YS N F++DFA AM++MG ISPLT + GE+R +C

Sbjct: 260 ARQGLFHSDQELFNGGSQDALVKKYSNAAMFTADFAKAMVRMGAIISPLTATQGEVRLDC 319

Query: 2167 RRIN 2178

R++N

Sbjct: 320 RKNV 323

Score = 140 bits (353), Expect = 1e-30

Identities = 79/165 (47%), Positives = 94/165 (56%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA

Sbjct: 75 VNGCDASILLDDTATFTGEKNAGPNANSVRGYEVIDAIKARVEASCNATVSCADILALAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + LGGP+W V LG

Sbjct: 135 RDAVNL-----LGGPSWTVYLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRDARTASQS AN +P P S+L L++ F GLS +D+ ALSG

Sbjct: 152 RRDARTASQSDANANLPGPGSSLATLVTMFGNKLSARDMTALSG 196

Score = 67.8 bits (164), Expect = 1e-08

Identities = 36/73 (49%), Positives = 47/73 (64%), Gaps = 4/73 (5%)

Frame = +1

Query: 577 SFCSRLTICLALF----VLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
S S + CL L VL +A LST+FY CP++ S V++ V SA++ E RMGA

Sbjct: 4 SAASSVVRCLQLLTVA AVLAGAAAGGLSTSFYSKCPDVQSIVRAGVASAVAAEKRMGA 63

Query: 745 SLLRLLFFHDCFVN 783

S+LR+FFHDCFVN

Sbjct: 64 SILRMFFHDCFVN 76

>gb|ACF08094.1| class III peroxidase [Triticum aestivum]

Length = 321

Score = 153 bits (387), Expect = 1e-34
Identities = 70/124 (56%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR+R+YNETNI+ AFA + + +CPRT+ SG+++LAPLD TP FDN Y+ NL+
Sbjct: 198 QSQCRRFFRSRLYNETNIDAAFATSLKANCPRRTSSGNSSLAPLDTTTPNGFDNAYYSNLM 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L N G T +VR YS+ F+ DFAAAM++MG+ISPLTG+ G+IR +C
Sbjct: 258 SQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNRFDAAMVRMGNISPLTGAQQGIRLSC 317

Query: 2167 RRIN 2178
R+N
Sbjct: 318 SRVN 321

Score = 132 bits (332), Expect = 3e-28
Identities = 76/165 (46%), Positives = 93/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL DT++FTGE+ A PN S RG VIDNIK+ VE VC VSCADILA+AA
Sbjct: 71 VQGCDASVLLSDTATFTGEQGAAPNARSIRGMNVIDNIKAQVEAVCRQTVSCADILAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 131 RDSV-----VALGGPSWTVPLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS S AN+ +PAP+ +L L + F+A GLS D+VALSG
Sbjct: 148 RRDSTTASLSLANSDLPAFDFLANLTANFAAKGLSVTDMVALSG 192

Score = 65.5 bits (158), Expect = 5e-08
Identities = 32/63 (50%), Positives = 41/63 (65%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L++ L L + SA+ LS FY SCP +++KS V +A+ E RMGASLLRL FHD
Sbjct: 9 LSVLLLLCLAAAASAPPLSPQFYAKSCPRALATIKSAVTA AVRSEPRMGASLLRLHFHD 68

Query: 772 CFV 780
CFV
Sbjct: 69 CFV 71

>ref|XP_002509733.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus communis]
gb|EEF51120.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus communis]
Length = 321

Score = 153 bits (387), Expect = 1e-34
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIYN ++I+ FA TR+ +CP+T G+G NLAPLDL TP +FDN Y+ NL
Sbjct: 199 QAQCVTFRDRIYNNASDIDPDFAAATRRGNCPQTGGNG--NLAPLDLVTNNFDNNYYSNL 256

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ K+G LL SDQ LF+GGSTDSIV YST+ +F SDFAAAM+KMG+ISPLTG+ GEIR+
Sbjct: 257 MAKRGLLASDQILFSGGSTDSIVNEYSTDSSSFSDFAAAMVKGNISPLTGTQGEIRRL 316

Query: 2164 CRRIN 2178
C +N
Sbjct: 317 CSAVN 321

Score = 131 bits (330), Expect = 6e-28
Identities = 75/169 (44%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCDGS+LL DT +FTGEK+A N NS RG VID+ K+ VE +CPG+VSCADILA+AA
Sbjct: 72 VQGCDGSVLLVDTPFTFTGEKSARNNANSIRGENVIDDAKAQVESICPGIVSCADILAVAA 131

Query: 1331 RDSVQIVSGQTTNKNLTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ GGP+W V LG
Sbjct: 132 RDA-----SVAAGGPSWTVNLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P + LN+LIS FS GL+ +D+VALSG I
Sbjct: 149 RRDSTTASLAQANSDLPGFSDPLNRLISLFSKGLNERDMVALSGAHTI 197

Score = 67.4 bits (163), Expect = 1e-08
Identities = 35/72 (48%), Positives = 48/72 (66%), Gaps = 2/72 (2%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSA--NAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
MAS S + L +F + S+ AQLS+NFY ++CPN +++KS + +AI E RM A

Sbjct: 1 MASHLSFACMILTIFIPNYSSLQQAQLSSNFYDNTCPNALTTIKSAIDAAIESEQRMAA 60

Query: 745 SLLRLLFFHDCFV 780
SL+RL FHDCFV

Sbjct: 61 SLIRLHFHDCFV 72

>ref|XP_002319407.1| predicted protein [Populus trichocarpa]
gb|EEE95330.1| predicted protein [Populus trichocarpa]
Length = 302

Score = 153 bits (387), Expect = 1e-34
Identities = 72/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YNET++++ A + + +CP T D++L+ LD TP +FDN YFKNL

Sbjct: 181 QARCLLFRNRVYNETSLLDSTLATSLSKSNCPNTGS--DDSLSSLDATTPVTFDINSYFKNLA 238

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLF+GG+TDS V+ YS N TF +DFA+AM+KMG ISPLTGS+G+IR NC

Sbjct: 239 NNKGLLHSDQQLFSGGTTDSQVKTYINSATFYADFASAMVKMGSISPLTGSDDGQIRTNC 298

Query: 2167 RRIN 2178
++N

Sbjct: 299 AKVN 302

Score = 147 bits (372), Expect = 8e-33
Identities = 83/180 (46%), Positives = 105/180 (58%)
Frame = +2

Query: 1118 AS*ILSKH*QMCGCDGSILLDDTSSFTGKKNANPNRNSARGFEVIDNIKSAVEKVC PGV 1297
AS + + H QGCD S+LLDDTSSFTGK A PN NS RG++VID IKS +E +CPGV

Sbjct: 43 ASLLRLLHFHDCFQGCDA SVLLDDTSSFTGKTAGPNANSLRGYDVIDTIKSLQLESICPGV 102

Query: 1298 VSCADILAI AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI* 1477
VSCADILA+AARDSV +

Sbjct: 103 VSCADILAVAARDSV-----VA 119

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
L GP+W V+LGRRD+ TAS AAN+ +P+P +L+ LI+ FS G + K++VALSG+ I

Sbjct: 120 LSGPSWTVQLGRRDSTTASLGAANS DLP SPLMDLSDLITSFSNKGFTAKEMVALSGSHTI 179

Score = 65.5 bits (158), Expect = 5e-08
Identities = 30/54 (55%), Positives = 39/54 (72%)

Frame = +1

Query: 616 VLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCF 777
+L+ G +AQLST FY +CP S++++ V A+ KE RMGASLLRL FHDCF
Sbjct: 1 MLLGLVHAQLSTTFYATTCPKALSTIRTAVLKAVVKEHRMGASLLRRLFHDCF 54

>dbj|BAA77388.1| peroxidase 2 [Scutellaria baicalensis]
Length = 325

Score = 153 bits (387), Expect = 1e-34
Identities = 78/126 (61%), Positives = 97/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
Q++C NFRARIY N ++IE FA TR++ CP+ GSGD+NLAPLDL TP SFDN Y++NL
Sbjct: 201 QSQCGNFRARIYSNGSDIEANFASTRRRQCPQ-DGSGDSNLAPLDLVTPNSFDNYYRNL 259

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAIKMGDISPL-TGSNGEIRK 2160
V ++GLL SDQ L +GG TD+IV YS+NP TF+SDF A MIKMG+I PL G NG IR+
Sbjct: 260 VARRGLLQSDQVLLSGGETDAIVTSYSSNPATFASDFANAMIKMGEIQPLQLGQNGIIRR 319

Query: 2161 NCRRIN 2178
C +N
Sbjct: 320 TCGAVN 325

Score = 140 bits (353), Expect = 1e-30
Identities = 75/165 (45%), Positives = 98/165 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLD+TS+ EK A PN S RGF+VID K+AVE++CPGVVSCADIL +AA
Sbjct: 74 VQGCDASILLDETSTIQSEKTAGPNAGSVRGFQVIDAAKTAVERLCPGVVSCADILTAA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W V+LG
Sbjct: 134 RDA-----SVAVGGPSWTVRLG 150

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TA+++ AN +P PTS L QLI+RF A GL+ +++VALSG
Sbjct: 151 RRDSTTANRAQANTDLPGPSTLTQLITRFDAKGLNAREMVALSG 195

Score = 63.9 bits (154), Expect = 1e-07
Identities = 30/68 (44%), Positives = 44/68 (64%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR 756
SF +I +L + AQLS FY +CPN S+++++ A+S E RM ASL+R
Sbjct: 7 SFRPIFSIAALVLLLTLPSEAQLSATFYDSTCPNAVSTIRTSIRQAVSAERRMAASLIR 66

Query: 757 LFFHDCFV 780
L FHDCFV
Sbjct: 67 LHFHDCFV 74

>gb|ACF08095.1| class III peroxidase [Triticum aestivum]
Length = 321

Score = 153 bits (386), Expect = 2e-34
Identities = 69/124 (55%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR+R+YNETNI+ AFA + + +CPR++GSG+++LAPLD TP FDN Y+ NL+
Sbjct: 198 QSQCRFFRSRLYNETNIDAAFAASLKANCPSTGSGNSSLAPLDTNTPNGFDNAYYSNLM 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L N G T +VR YS+ F+ DFA AM++MG+ISPLTG+ G+IR +C
Sbjct: 258 SQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNRDFAVAMVRMGNISPLTGAQQGIRLSC 317

Query: 2167 RRIN 2178
R+N
Sbjct: 318 SRVN 321

Score = 132 bits (332), Expect = 3e-28
Identities = 76/165 (46%), Positives = 93/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAIAA 1330
+QGCD S+LL DT++FTGE+ A PN S RG VIDNIK+ VE VC VSCADILA+AA
Sbjct: 71 VQGCDAVLLSDTATFTGEQGAAPNARSIRGMNVIDNIKAQVEAVCRQTVSCADILAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 131 RDSV-----VALGGPSWTVPLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS S AN+ +PAP+ +L L + F+A GLS D+VALSG
Sbjct: 148 RRDSTTASLSLANSIDLPAFDFLANLTANFAAKGLSVTDMVALSG 192

Score = 67.8 bits (164), Expect = 1e-08
Identities = 33/63 (52%), Positives = 42/63 (66%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L++ L L + SA+ QLS FY SCP +++KS V +A+ E RMGASLLRL FHD
Sbjct: 9 LSVLLLLCLAAAASASPQLSPQFYAKSCPRALATIKSAVTA AVRSEPRMGASLLRRLFHD 68

Query: 772 CFV 780
CFV
Sbjct: 69 CFV 71

>gb|EAZ01279.1| hypothetical protein OsI_23302 [Oryza sativa Indica Group]
Length = 318

Score = 153 bits (386), Expect = 2e-34
Identities = 68/124 (54%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RI+ + N++ AFA RQQ+CP++ G D+ LAP+D+QTP +FDN Y+ NLV
Sbjct: 197 QARCATFRSRIFGDGNVDAFAALRQQACPQSGG--DSTLAPIDVQTPDAFDNAYYANLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+K+GL HSDQ+LFNGGS D++VR Y+ N G F++DFA AM++MG + P G+ E+R NC
Sbjct: 255 KKQGLFHSDQELFNGGSQDALVRKYAGNAGMFAADFAKAMVRMGALLPAAGTPTEVRLNC 314

Query: 2167 RRIN 2178
R++N
Sbjct: 315 RKNV 318

Score = 140 bits (354), Expect = 9e-31
Identities = 78/165 (47%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCVGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 70 VNGCDASILLDDTANFTGEKNAGPNANSVRGYEVIDAIKTQVEASCNATVSCADILALAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNV 1510
RD+V ++ GGPTW ++LG
Sbjct: 130 RDAVNLL-----GGPTWTMQLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRDA TASQSAAN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 147 RRDALTASQSAANGNLPGPSDLATLVTMFGNKGLSPRDMTALSG 191

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/71 (43%), Positives = 46/71 (64%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ + + + + G+A QLST +Y CPN+ S V++ + A++ E RMGAS+
Sbjct: 1 MATQWVLVVVAVMAVLFAGGAAGGQLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRMGASI 60

Query: 751 LRLFFHDCFVN 783
LR+FFHDCFVN
Sbjct: 61 LRMFFHDCFVN 71

>ref|NP_001046392.1| Os02g0236600 [Oryza sativa (japonica cultivar-group)]
dbj|BAD27598.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69269.1| TPA: class III peroxidase 27 precursor [Oryza sativa (japonica cultivar-group)]
gb|EAY85140.1| hypothetical protein OsI_06495 [Oryza sativa Indica Group]
gb|EAZ22363.1| hypothetical protein OsJ_06021 [Oryza sativa Japonica Group]
dbj|BAH01530.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 321

Score = 152 bits (385), Expect = 2e-34
Identities = 82/169 (48%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+ GCD S+LLDD+S+ TGEKNA PN NS RGFEVID+IKS VE CPG VSCADILA+AA
Sbjct: 73 VNGCDASVLLDDSSSTITGEKNAGPNANSLRGFEVIDSIKSQVEAACPGTVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++ GGPTW V+LG
Sbjct: 133 RDGVNLL-----GGPTWAVQLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD RTASQSAAN+ +P+P+S+ L+S F++ GL ++D+VALSG I
Sbjct: 150 RRDTRTASQSAANSLPSPSSAAALVSAFASKGLDSRDMVALSGAHTI 198

Score = 151 bits (382), Expect = 5e-34
Identities = 72/123 (58%), Positives = 89/123 (72%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989

ARC FRAR+YN+TNI FA R+Q CP + GD NLAPLD + FDN YF+NL+
Sbjct: 201 ARCATFRARVYNDTNISPGFAVRRRQVCP--ASGGDGNLAPLDALSSVRFDNGYFRNLMG 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
+ GLLHSDQ+LFNGG DSI + Y+ N FS DF A++KMG+ISPLTGS+GE+R NCR

Sbjct: 259 RFGLLHSDQELFNGGPVDSIAQQYAANGAAFSRDFVTAVVKMGNISPLTGSSGEVRSNCR 318

Query: 2170 RIN 2178
+ N

Sbjct: 319 KPN 321

Score = 68.2 bits (165), Expect = 8e-09
Identities = 33/66 (50%), Positives = 47/66 (71%), Gaps = 1/66 (1%)
Frame = +1

Query: 589 RLTICLALFVLIW-GSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRRLF 765
R+ + +A+ L+ G AQL+ +Y SCP+L S V+S + +A+ +E RMGAS+LRLFF

Sbjct: 9 RMVVVVAIAALVAPGEVAAQLTPTYDGCPSLQSIVRSAMAAVQQEPRMGASILRRLF 68

Query: 766 HDCFVN 783
HDCFVN

Sbjct: 69 HDCFVN 74

>gb|EAZ37287.1| hypothetical protein OsJ_21626 [Oryza sativa Japonica Group]
Length = 309

Score = 152 bits (385), Expect = 2e-34
Identities = 68/124 (54%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RI+ + N++ AFA RQQ+CP++ G D LAP+D+QTP +FDN Y+ NLV

Sbjct: 188 QARCATFRSRIFGDGNVDAAFALRQQACPQSGG--DTLAPIDVQTPDAFDNAYYANLV 245

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+K+GL HSDQ+LFNGGS D++VR Y+ N G F++DFA AM++MG + P G+ E+R NC

Sbjct: 246 KKQGLFHSDQELFNGGSQDALVRKYAGNAGMFAADFAKAMVRMGALLPAAGTPTEVRLNC 305

Query: 2167 RRIN 2178
R++N

Sbjct: 306 RKNV 309

Score = 122 bits (307), Expect = 3e-25
Identities = 73/165 (44%), Positives = 87/165 (52%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA

Sbjct: 70 VNGCDASILLDDTANFTGEKNAGPNANSVRGYEVIDAIKTQVEASCNATVSCADILALAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + LG

Sbjct: 130 RDAVNL-----LG 137

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRDA TASQSAAN +P P S+L L++ F GLS +D+ ALSG

Sbjct: 138 RRDALTASQSAANGNLPGPSDLATLVMTFGNKGLSPRDMTALSG 182

Score = 66.6 bits (161), Expect = 2e-08

Identities = 31/71 (43%), Positives = 46/71 (64%)

Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750

MA+ + + + G+A QLST +Y CPN+ S V++ + A++ E RMGAS+

Sbjct: 1 MATQWVLVVAVMAVLFAGGAAGQLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRMGASI 60

Query: 751 LRLFFHDCFVN 783

LR+FFHDCFVN

Sbjct: 61 LRMFFHDCFVN 71

>gb|ABD47726.1| peroxidase [Eucalyptus globulus subsp. globulus]

Length = 258

Score = 152 bits (385), Expect = 2e-34

Identities = 73/123 (59%), Positives = 92/123 (74%)

Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989

ARCT+FR RIYN++NI+T+FA Q CP+ D+ L LD+QTPT FDN Y+ NL+Q

Sbjct: 138 ARCTSFRGRIYNDNSNIDTSFAHKLQNICPKIGN--DSVLQRLDIQTPTFFDNLYYHLLQ 195

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169

KKGLLHSDQ+LFNG S DS+V+ Y+ + G F DFA AMIKM I P GS+G+IRKNCR

Sbjct: 196 KKGLLHSDQELFNGSSVDSL VKKYACDTGKFFRDFAKAMIKMSKIKPPKGSSGQIRKNCR 255

Query: 2170 RIN 2178

++N

Sbjct: 256 KVN 258

Score = 152 bits (383), Expect = 4e-34
Identities = 85/169 (50%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD SILLDDT SF GEK A PN NS RGFEVID IK+++EK CPGVVSCADI+A+AA
Sbjct: 10 VNGCDASILLDDTPSFVGEKTAAPNNNSVRGFEVIDRIKASLEKECPGVVSCADIVALAA 69

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 70 RDSV-----VHLGGPSWTVSLG 86

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
R+D+ TAS+S AN IP PTSNL+ LI+ F+A GLS K++VALSG+ I
Sbjct: 87 RKDSITASRSLANTSIPPPTSNSLALITSFAAQGLSVKNMVALSGSHTI 135

>ref|NP_001057820.1| Os06g0546500 [Oryza sativa (japonica cultivar-group)]
dbj|BAD54114.1| putative bacterial-induced peroxidase precursor [Oryza sativa
Japonica Group]
tpe|CAH69330.1| TPA: class III peroxidase 88 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF19734.1| Os06g0546500 [Oryza sativa Japonica Group]
dbj|BAG93666.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 318

Score = 152 bits (385), Expect = 2e-34
Identities = 68/124 (54%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RI+ + N++ AFA RQQ+CP++ G D LAP+D+QTP +FDN Y+ NLV
Sbjct: 197 QARCATFRSRIFGDGNVDAFAALRQQACPQSGG--DTTLAPIDVQTPDAFDNAYYANLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+K+GL HSDQ+LFNGGS D++VR Y+ N G F++DFA AM++MG + P G+ E+R NC
Sbjct: 255 KKQLFHSDQELFNGGSQDALVRKYAGNAGMFAADFAKAMVRMGALLPAAGTPTEVRLNC 314

Query: 2167 RRIN 2178
R++N
Sbjct: 315 RKNV 318

Score = 142 bits (357), Expect = 4e-31
Identities = 79/165 (47%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVSCADILAI AA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 70 VNGCDASILLDDTANFTGEKNAGPNANSVRGYEVIDAIKTQEASCNATVSCADILALAA 129

Query: 1331 RDSVQIVSQGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ GGPTW V+LG
Sbjct: 130 RDAVNLL-----GGPTWTVQLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRDA TASQSAAN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 147 RRDALTASQSAANGNLPGPSDLATLVMTFGNKGLSPRDMTALSG 191

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/71 (43%), Positives = 46/71 (64%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ + + + + G+A QLST +Y CPN+ S V++ + A++ E RMGAS+
Sbjct: 1 MATQWVLVVAVMAVLFAGGAAGGQLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRMGASI 60

Query: 751 LRLFFHDCFVN 783
LR+FFHDCFVN
Sbjct: 61 LRMFFHDCFVN 71

>ref|XP_002438534.1| hypothetical protein SORBIDRAFT_10g021650 [Sorghum bicolor]
gb|EER89901.1| hypothetical protein SORBIDRAFT_10g021650 [Sorghum bicolor]
Length = 325

Score = 152 bits (384), Expect = 3e-34
Identities = 71/124 (57%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+++C FR+RIY E+NI +FA RQ++CPR+ G D LAP D+QTP FDN Y++NLV
Sbjct: 204 RSQCQFFRSRIYTESNINASFALRQKTCPRSGG--DATLAPFDVQTPDGF DNAYYQNLV 261

Query: 1987 QKKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNNGS D++VR YSTN FS+DF +AMIKMG++ P +G+ E+R NC
Sbjct: 262 AQKGLLHSDQELFNNGSQDALVRQYSTNANQFSADFVSAMIKMGNLMPSSGTPTEVRLNC 321

Query: 2167 RRIN 2178
R+ N
Sbjct: 322 RKTN 325

Score = 143 bits (360), Expect = 2e-31
Identities = 81/169 (47%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+ GCDGSILLDDTS+FTGEK A PN NS RGFEVID IK+ VE C VSCADILA+AA

Sbjct: 77 VNGCDGSILLDDTSTFTGEKGAGPNANSVRGFEVIDAIKTKVEASCKATVSCADILALAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++ GGPTW+V LG

Sbjct: 137 RDGVNLL-----GGPTWSVPLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

R+D+RTASQS AN+ +P P S+L LI F GLS +D+ ALSG I

Sbjct: 154 RKDSRTASQSLANSNLPGPGSSLATLIRMFNGQLSARDMTALSGAHTI 202

Score = 68.9 bits (167), Expect = 4e-09
Identities = 39/78 (50%), Positives = 54/78 (69%), Gaps = 7/78 (8%)
Frame = +1

Query: 571 MASFCR----LTICLALFV--LIWGSANAQ--LSTNFYHSCP NLFSSVKSTVQS AISKE 729
MA+F R L++ A+ V L G+A+AQ LS NFY +CPN+ + V+ + SA++ E

Sbjct: 1 MATFTCRSM AFLSLAAAVLVALLTAGAADAQKLSPNFYSKTCPNVATIVRQQMASAVAAE 60

Query: 730 TRMGASLLRLFFHDCFVN 783

RMGAS+LR+FFHDCFVN

Sbjct: 61 KRMGASILRMFFHDCFVN 78

>ref|NP_001140437.1| hypothetical protein LOC100272496 [Zea mays]
gb|ACF83840.1| unknown [Zea mays]
Length = 263

Score = 152 bits (384), Expect = 3e-34
Identities = 72/129 (55%), Positives = 97/129 (75%), Gaps = 5/129 (3%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF +L+

Sbjct: 135 RAQCKNCRARIYNDTIDASFAASLRASCPAQAGAGDGALEPLDGSTPDAFDNAYFGDLL 194

Query: 1987 QKKGLLHSDQQLF-----NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGE 2151
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GE

Sbjct: 195 SQRGLLHSDQALFGGGGGGGGATDGLVSAYASNAGQWGADFAAAMVKMGSISPLTGTGDE 254

Query: 2152 IRKNCRRIN 2178

IR NCRR+N

Sbjct: 255 IRVNCRRVN 263

Score = 145 bits (366), Expect = 4e-32
Identities = 83/164 (50%), Positives = 96/164 (58%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILAI AAR
Sbjct: 9 QGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAI AAR 68

Query: 1334 DSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV LGGP+W V LGR
Sbjct: 69 DSVAQ-----LGGPSWAVPLGR 85

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 86 RDATTASASLANSDLPGPTSSLNGLLNAFSNKGLSSTDMVALSG 129

>gb|ACF82414.1| unknown [Zea mays]
Length = 349

Score = 152 bits (384), Expect = 3e-34
Identities = 72/129 (55%), Positives = 97/129 (75%), Gaps = 5/129 (3%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF +L+
Sbjct: 221 RAQCKNCRARIYNDTIDASFAASLRASCPAQAGAGDGALEPLDGSTPDAFDNAYFGDLL 280

Query: 1987 QKKGLLHSDQQLF-----NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGE 2151
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GE
Sbjct: 281 SQRGLLHSDQALFGGGGGGGATDGLVSAYASNAGQWGADFAAAMVKMGDISPLTGTGDGE 340

Query: 2152 IRKNCRRIN 2178
IR NCRR+N
Sbjct: 341 IRVNCRRVN 349

Score = 145 bits (367), Expect = 3e-32
Identities = 83/165 (50%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILAI AA
Sbjct: 94 VQGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAI AA 153

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV LGGP+W V LG
Sbjct: 154 RDSVAQ-----LGGPSWAVPLG 170

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 171 RRDATTASASLANSDLPGPTSSLNGLLNAFNSKGLSSTDMVALSG 215

Score = 57.4 bits (137), Expect = 1e-05
Identities = 36/92 (39%), Positives = 51/92 (55%), Gaps = 1/92 (1%)
Frame = +1

Query: 508 TPFQSNNT*STKLVCLSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYH-SCPNL 684
TP + + +++ LS+ C L + LAL +AQLS+ YY SCP
Sbjct: 4 TPLECDMAPAASRNKHLRSWPLPRCGLLVLVLALAATA-AVGSAQLSSEDYYDASCPAA 62

Query: 685 FSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
++++ V +A+ E RMGASLLRL FHDCFV
Sbjct: 63 LLTIRTAVSTAVLLEPRMGASLLRHFHDCFV 94

>dbj|BAF19735.2| Os06g0547100 [Oryza sativa Japonica Group]
Length = 353

Score = 152 bits (383), Expect = 4e-34
Identities = 72/122 (59%), Positives = 89/122 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA +Q+CP+ SG GD NLAP D QTP +FDN YFKNLV
Sbjct: 205 RARCLMFRGRIYGEANINATFAAALRQTCPQ-SGGGDGNLAPFDDQTPDAFDNAYFKNLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N G F+ DFA AM+KMG + P G+ E+R NC
Sbjct: 264 AQRGLLHSDQELFNGGSQDALVRKYAGNAGMFAGDFAKAMVKMGGLMPAAGTPTEVRLNC 323

Query: 2167 RR 2172
R+
Sbjct: 324 RK 325

Score = 134 bits (338), Expect = 7e-29
Identities = 74/165 (44%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IKS VE C GVVSCADI+A+A+
Sbjct: 78 VNGCDASILLDDTLTFTGEKNAGANINSVRGYEVIDAIKSQVEAACKGVVSCADIVALAS 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 138 RDAVNLLGG-----PTWNVQLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
R+D+RTAS +AAN +P P S+ L++ F+ GLS +++ ALSG
Sbjct: 155 RKDSRTASGTAANANLPGPASSGASLVAFAAGKLSAREMTALSG 199

Score = 64.7 bits (156), Expect = 8e-08
Identities = 29/51 (56%), Positives = 38/51 (74%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
+A A LS FY +CP + + V+S V A++KE RMGAS++RLFFHDCFVN
Sbjct: 29 AAKAGLSIKFYAKTCPGVDTIVRSVVAQAVAKEPRMGASII RLFFHDCFVN 79

>ref|XP_002438533.1| hypothetical protein SORBIDRAFT_10g021640 [Sorghum bicolor]
gb|EER89900.1| hypothetical protein SORBIDRAFT_10g021640 [Sorghum bicolor]
Length = 318

Score = 151 bits (382), Expect = 5e-34
Identities = 71/124 (57%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA RQQ+CP+T G G NLAP D QTP +FDN Y+ NLV
Sbjct: 197 RARCVRFRGRIYGEPNINATFAAVRQQTCPQTGGDG--NLAPFDDQTPDAFDNAYYANLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGG+ D++VR YS N F++DFA AM+KMG ++P G+ E+R NC
Sbjct: 255 ARRGLLHSDQELFNGGTQDALVRKYSNGRMFANFAKAMVKMGLLAPAAGTPTEVRLNC 314

Query: 2167 RRIN 2178
R++N
Sbjct: 315 RKNV 318

Score = 136 bits (342), Expect = 2e-29
Identities = 75/165 (45%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI AA 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IK+ VE C VSCADI+A+A+
Sbjct: 70 VNGCDASILLDDTPTFTGEKNAGANVNSVRGYEVIDAIKTQVEAACKATVSCADIVALAS 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 130 RDAVNLLGG-----PTWNVQLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
R D+RTASQSAAN +P P S+ L++ F+A GLS +D+ ALSG
Sbjct: 147 RTDSRTASQSAANANLPGPGSSAASLVAAFAAKGLSARDMTALSG 191

Score = 66.2 bits (160), Expect = 3e-08
Identities = 29/63 (46%), Positives = 43/63 (68%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDC 774
++ L + + + +LST FY SCP + + V+S A++KE RMGAS++RLFFHDC
Sbjct: 9 SVALLTLLCLLLTCHGKLS TKFYAKSCP GVA AIVRSVTAQAVAKEPRMGAS IIRLFFHDC 68

Query: 775 FVN 783
FVN
Sbjct: 69 FVN 71

>gb|ACE00594.1| lignin biosynthetic peroxidase [Leucaena leucocephala]
Length = 316

Score = 151 bits (382), Expect = 5e-34
Identities = 76/124 (61%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q +C FR RIYNE NI+ +FA TR+ +CPRT G NLAPLD TP FDN Y+K+LV
Sbjct: 196 QGQC NFRNRRIYENNIIDPSFAATRRATCPRTGGG--INLAPLDF-TPNRFDNYYKDLV 252

Query: 1987 QKKG LLSHQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ FNGGS D+IVR YSTN F DFA AM+KM I+PLTGS GEIRK+C
Sbjct: 253 NRRGLFHS DQVFFNGGSQDAIVRAYSTNSVLFFGDFAFAMVKMSSITPLTGSQGEIRKDC 312

Query: 2167 RRIN 2178
R +N
Sbjct: 313 RVVN 316

Score = 126 bits (317), Expect = 2e-26

Identities = 77/169 (45%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD ILLDDT+SFTGEKNA PN+ SARG+EVID IK+ VE C G VSCADILA+AA

Sbjct: 70 VNGCDAGILLDDTASFTGEKNAGPNQ-SARGYEVIDAIKTNVEAACRGTVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
++ V LGGP L

Sbjct: 129 QEGVTQ-----LGGPHGQYHLA 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDARTASQS AN+ IP P+S L+ LIS F+A GL+ +++ LSG I

Sbjct: 146 RRDARTASQSKANSEIPGPSSSELSTLISMFAAKGLNAREMTVLSGAHSI 194

Score = 80.1 bits (196), Expect = 2e-12
Identities = 37/71 (52%), Positives = 52/71 (73%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS + L++ L S+NAQLS NFY SCPN+ + V++T++ A+++E R+GAS+

Sbjct: 1 MASLTHFFLLALSVL SLFASSNAQLSPNFYARSCPNVRAIVRNTMRQALAREARLGASI 60

Query: 751 LRLFFHDCFVN 783

LRLFFHDCFVN

Sbjct: 61 LRLFFHDCFVN 71

>emb|CBI19221.1| unnamed protein product [Vitis vinifera]
Length = 441

Score = 151 bits (381), Expect = 7e-34
Identities = 83/167 (49%), Positives = 102/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD

Sbjct: 68 GCDASILLDDTANFTGEKTAGPNNNSVRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 127

Query: 1337 SVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V+LGRR

Sbjct: 128 SV-----VALGGPTWTVQLGRR 144

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ TAS S AN+ +PAPTS+L+ LIS FS G +T+++V LSGT I

Sbjct: 145 DSTTASFSTANS DLPAPTSDDLALISLFSNKGFTTQEMVVLSGHTI 191

Score = 83.2 bits (204), Expect = 2e-13
Identities = 45/84 (53%), Positives = 55/84 (65%)
Frame = +1

Query: 1867 FARTRQQSCPRTSGSDNNLAPLDLQTPTSFDNYYFKNLVQKKGLLHSDQQLFNGGSTDS 2046
F RT+ + R GD+NL+PLD +T T F YF++L +KKGLLHSDQQL+N GSTDS
Sbjct: 357 FFRTKGITVIRIESGGDDNLSPLD-KTTTVFYAYFRDLKEKKGLLHSDQQLYNDGSTDS 415

Query: 2047 IVRGYSTNPGTFSSDFAAAMIKMG 2118
IV YS N TF D AM+ G
Sbjct: 416 IVESYSINSATFFRDVTNAMVLDG 439

Score = 69.3 bits (168), Expect = 3e-09
Identities = 34/69 (49%), Positives = 49/69 (71%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCP NFLSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+++Y SCP+ S++++ V +A++ E+RMGASL
Sbjct: 1 MASLSLFSLFCMFSFLL--GMAHAQLSSDYSSSCPSALSTIQTAVNNAVADES RMGASL 58

Query: 751 LRLFFHDCF 777
LRL FHDCF
Sbjct: 59 LRLHFHDCF 67

Score = 42.7 bits (99), Expect = 0.35
Identities = 17/30 (56%), Positives = 23/30 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCP 1896
+A+C+ FR RIYNETNI+ FA ++Q CP
Sbjct: 193 KAQCSKFRDRIYNETNIDATFATSKQAICP 222

Score = 38.1 bits (87), Expect = 8.5
Identities = 17/30 (56%), Positives = 22/30 (73%)
Frame = +2

Query: 1556 IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
+P PT NL+QL+S FS G +TK+ V LSG
Sbjct: 302 LPGPTLNLSQLVSAFNSKGF TTKETVVLSG 331

>ref|XP_002451846.1| hypothetical protein SORBIDRAFT_04g008590 [Sorghum bicolor]
gb|EES04822.1| hypothetical protein SORBIDRAFT_04g008590 [Sorghum bicolor]
Length = 325

Score = 151 bits (381), Expect = 7e-34
Identities = 83/169 (49%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDD+++ TGEKNA PN NS RGFEVID IKS VE CPG VSCADILA+AA
Sbjct: 75 VQGCDA SVLLDD SATLTGEKNAAPNANSLRGFEVIDAIKSQVEAACPGTVSCADILALAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++S GPTW V+LG
Sbjct: 135 RDGVNLLS-----GPTWAVQLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD RTASQSAAN+ +P+P+S+ L+S F++ GL ++DLVALSG I
Sbjct: 152 RRDRTRTASQAANSNLPSPSSAAALVSAFASKGLDSRDLVALSGAHTI 200

Score = 147 bits (372), Expect = 8e-33
Identities = 70/123 (56%), Positives = 87/123 (70%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
ARC +FR+RIYN++NI FA R+Q C SG D NLAPLD + FDN YF++LV
Sbjct: 203 ARCASFRRSRIYNDNINAGFAAKRKQICGPGSGGTDGNLAPLDAMSSVKFDNGYFRDLVS 262

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
+ GLLHSDQ+LF G DS+ Y+ N FSSDF A++KMG+ISPLTGS+GEIR NCR
Sbjct: 263 QFGLLHSDQELFGAGVVDSVTARYARNGAAFSSDFVTAIVKMGNISPLTGSSGEIRANCR 322

Query: 2170 RIN 2178
+ N
Sbjct: 323 KPN 325

Score = 66.6 bits (161), Expect = 2e-08
Identities = 34/62 (54%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDC 774
T+ +A V + G+ QLS FY SCPNL S V+S + +A+ +E RMGAS+LRLFFHDC
Sbjct: 15 TVAVACVVAL-GAMAQQLSPTFYDASCPNLQSI VRSGMAAAVQQEPRMGASILRLLFFHDC 73

Query: 775 FV 780

FV
Sbjct: 74 FV 75

>emb|CAL25299.1| properoxidase [Picea abies]
Length = 341

Score = 151 bits (381), Expect = 7e-34
Identities = 86/169 (50%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
++GCDGSILLDDTSSFTGEK ANPNRNS RGF V+D IKS +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTGEKTANPNRNSVRGFGVVDQIKSELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F GL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNIPGPNSTHTLETKFKRQGLNVVDLVALSQAHTI 208

Score = 122 bits (305), Expect = 4e-25
Identities = 65/132 (49%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFARLYNQTVNGKSDPTLDTTYLKHLRAVCPQT-GTDDNQTTPLDPVTPIKFDID 269

Query: 1969 YFKNLVQKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142
Y+ N+V KGLL SDQ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNNVAGKGLLASDQILYSTKGSRTVGLVESYSTSMHAFFKQFAASMIKMGINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N
Sbjct: 330 HGEIRKNCRRMN 341

Score = 62.4 bits (150), Expect = 4e-07
Identities = 37/71 (52%), Positives = 45/71 (63%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ----LSTNFYHSCPFLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE RM AS

Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPKAQAIKSVVEDAVRKEARMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV

Sbjct: 73 LLRLHFHDCFV 83

>emb|CBI15847.1| unnamed protein product [Vitis vinifera]
Length = 263

Score = 150 bits (380), Expect = 9e-34
Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986
Q+RC FR RIYN+ NI+++FA + + +CP T G D+NL+ LD +P FDN YFKNLV

Sbjct: 142 QSRCLVFRDRIYNDNIDSSFAESLKSNCPTDG--DDNLSALDDTSPVIFDNGYFKNLV 199

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFN GSTDS V Y+++ +F DF AAM+KMG+ISPLTG+ G+IR NC

Sbjct: 200 DNKGLLHSDQELFNGGSTDSQVSSYASSATSFYKDFTAAMVKMGNISPLTGTKGQIRVNC 259

Query: 2167 RRIN 2178
R+IN

Sbjct: 260 RKIN 263

Score = 150 bits (378), Expect = 2e-33
Identities = 85/169 (50%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDT++FTGEK A PN +S RGFEVID+IKS VE VCPGVV+CADILA+AA

Sbjct: 15 VNGCDGSILLDDTANFTGEKTAGPNADSVRGFEVIDDIKSRVESVCPGVVTCADILAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V+LG

Sbjct: 75 RDSV-----VALGGPTWTVQLG 91

Query: 1511 RRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S A IP+P +L+ LIS FS G S K++VALSG+ I

Sbjct: 92 RRDSTTASISDAETDIPSPALDLDLISAFSDKGFSAKEMVALSGSHTI 140

>ref|XP_002451850.1| hypothetical protein SORBIDRAFT_04g008650 [Sorghum bicolor]
gb|EES04826.1| hypothetical protein SORBIDRAFT_04g008650 [Sorghum bicolor]
Length = 323

Score = 150 bits (380), Expect = 9e-34
Identities = 73/124 (58%), Positives = 92/124 (74%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRMSG-SGDNNLAPLDLQTPTSFDNYYFKNLV 1986
A+C +R+RIY++ NI FA T + +C T G S D NLA LD+QT FDN YF NL+

Sbjct: 200 AQCKTYRSRIYSDANINKQFANTLKGNCSTQGGSTDTNLAGLDVQTQVVFNDNAYFGNLM 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ+LFNGGS D++V+ Y +PG F+S F AMIKMG+ISPLTGS G+IR NC

Sbjct: 260 KKGLLHSDQELFNGGSQDALVQQYDADPGLFASHFVTAMIKMGNISPLTGSQGGIRANC 319

Query: 2167 RRIN 2178
R+N

Sbjct: 320 GRVN 323

Score = 139 bits (350), Expect = 3e-30
Identities = 77/166 (46%), Positives = 99/166 (59%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDT-SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIA 1327
+QGCD SILLDD +F GEKNA PN NS G++VI+NIK+AVE CPGVVSCADI+A+A

Sbjct: 71 VQGC DASILLDDVPGTFVGEKNAGPNANSVLGYDVINNIKTAVEANCPGVVSCADIVALA 130

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD V ++ GGPTW+V L

Sbjct: 131 ARDGVNLL-----GGPTWSVSL 147

Query: 1508 GRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRD+ TASQS AN+ +P+P S+L+ LI+ F++ GL+ D+ ALSG

Sbjct: 148 GRRDSTTASQSQANS DLPSPASSLSTLIAAFASKGLNATDMTALSG 193

Score = 64.3 bits (155), Expect = 1e-07
Identities = 33/56 (58%), Positives = 41/56 (73%), Gaps = 1/56 (1%)
Frame = +1

Query: 616 VLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISK-ETRMGASLLRLLFFHDCFV 780
+L+ +A QLST+FY SCP+L S+V+S V I+ RMGASLLRLLFFHDCFV

Sbjct: 16 ILLSSAAYGQLSTSFYDTSCPSLESTVRSVSVGVINNGNRRRMGASLLRLLFFHDCFV 71

>ref|XP_002276796.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 1225

Score = 150 bits (380), Expect = 9e-34

Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYN+ NI+++FA + + +CP T G D+NL+ LD +P FDN YFKNLV

Sbjct: 1104 QSRCLVFRDRIYNDNIDSSFAESLKSNCPTDG--DDNLSALDDTSPVIFDNGYFKNLV 1161

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFN GSTDS V Y+++ +F DF AAM+KMG+ISPLTG+ G+IR NC

Sbjct: 1162 DNKGLLHSDQELFNGGSTDSQVSSYASSATSFYKDFTAAMVKMGNISPLTGTKGQIRVNC 1221

Query: 2167 RRIN 2178

R+IN

Sbjct: 1222 RKIN 1225

Score = 150 bits (378), Expect = 2e-33
Identities = 85/169 (50%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDT++FTGEK A PN +S RGFEVID+IKS VE VCPGVV+CADILA+AA

Sbjct: 977 VNGCDGSILLDDTANFTGEKTAGPNADSVRGFEVIDDIKSRVESVCPGVVTCADILAVAA 1036

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V+LG

Sbjct: 1037 RDSV-----VALGGPTWTVQLG 1053

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS S A IP+P +L+ LIS FS G S K++VALSG+ I

Sbjct: 1054 RRDSTTASISDAETDIPSPALDLDLISAFSDKGFSAKEMVALSGSHTI 1102

Score = 62.8 bits (151), Expect = 3e-07
Identities = 27/52 (51%), Positives = 37/52 (71%)
Frame = +1

Query: 628 GSANAQLSTNFYYHSCP NFLS SVKSTVQSAISKETRMGASLLR LFFHDCFVN 783

G ++ LS+ FY CP S++++ V +A++ E RMGASLLRL FHDCFVN

Sbjct: 927 GVVSSGLSSTFYSAKCPKALSTIRTAVNTAVANENRMGASLLR LHFHDCFVN 978

>gb|EAZ22364.1| hypothetical protein OsJ_06022 [Oryza sativa Japonica Group]
Length = 282

Score = 150 bits (380), Expect = 9e-34
Identities = 71/124 (57%), Positives = 92/124 (74%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV

Sbjct: 160 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDLTPDAFDNGYYRNLV 217

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC

Sbjct: 218 AGAGLLHSDQELFNNGPVDSVVQLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 277

Query: 2167 RRIN 2178

R++N

Sbjct: 278 RKVN 281

Score = 78.6 bits (192), Expect = 6e-12

Identities = 38/65 (58%), Positives = 46/65 (70%), Gaps = 1/65 (1%)

Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNR-NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333

GCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAI AAR

Sbjct: 78 GCDASVLLDDTPAAPGEKGVGPNAVSTTVFDLVDTIKAQVEAVCPATVSCADVLAIAAR 137

Query: 1334 DSVQI 1348

DSV +

Sbjct: 138 DSVNL 142

Score = 61.2 bits (147), Expect = 9e-07

Identities = 28/63 (44%), Positives = 40/63 (63%)

Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHD 771

L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD

Sbjct: 14 LLLLLAVALAALARARAQLSPGFYSASCP TVHGVVRQVMSQAVMNDTRAGAAVLRRLFYHD 73

Query: 772 CFV 780

CFV

Sbjct: 74 CFV 76

>gb|EAY85141.1| hypothetical protein OsI_06496 [Oryza sativa Indica Group]

Length = 326

Score = 150 bits (380), Expect = 9e-34

Identities = 71/124 (57%), Positives = 92/124 (74%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV
Sbjct: 204 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC
Sbjct: 262 AGAGLLHSDQELFNNGPVDSVQVLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 119 bits (298), Expect = 3e-24
Identities = 68/164 (41%), Positives = 89/164 (54%), Gaps = 1/164 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNR-NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
GCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAI AAR
Sbjct: 78 GCDASVLLDDTPAAPGEKGVGPNAIGSTTVFDLVDTIKAQVEAVCPATVSCADVLAIAAR 137

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGP+W V LGR
Sbjct: 138 DSVNL-----LGGPSWAVPLGR 154

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RDA + S+SA + +P P ++++ L+S F+A GLS++DL ALSG
Sbjct: 155 RDALSPSRSAVSTDLPGPEADISALVSFAAAGLSSRDLAALSG 198

Score = 61.2 bits (147), Expect = 9e-07
Identities = 28/63 (44%), Positives = 40/63 (63%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD
Sbjct: 14 LLLLLAVALALAAARARAQLSPGFYSASCPTVHGVVRQVMSQAVMNDTRAGAAVLRRLFYHD 73

Query: 772 CFV 780
CFV
Sbjct: 74 CFV 76

>tpe|CAH69268.1| TPA: class III peroxidase 26 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 326

Score = 150 bits (380), Expect = 9e-34
Identities = 71/124 (57%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV
Sbjct: 204 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC
Sbjct: 262 AGAGLLHSDQELFNNGPVDSVVQLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 112 bits (281), Expect = 3e-22
Identities = 65/166 (39%), Positives = 88/166 (53%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNR--NSARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+QGCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAIA
Sbjct: 76 VQGCDASVLLDDTPAAPGEKGVGPNVAVGSTTVFDLVDTIKAQVEAVCPATVSCADVLAIA 135

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
R + + LGGP+W V L
Sbjct: 136 GRR-----RVQLGGPSWAVPL 152

Query: 1508 GRRDARTASQAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRDA + S+SA + +P P ++++ L+S F+A GLS++DL ALSG
Sbjct: 153 GRRDALSPRSVSTDLPGPEADISALVSAFAAKGLSSRDLAALSG 198

Score = 61.2 bits (147), Expect = 9e-07
Identities = 28/63 (44%), Positives = 40/63 (63%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD
Sbjct: 14 LLLLLAVALAARARAQLSPGFYSASCTVHGVVVRQVMSQAVMNDTRAGAVALRRLFYHD 73

Query: 772 CFV 780
CFV
Sbjct: 74 CFV 76

>ref|NP_001046393.1| Os02g0236800 [Oryza sativa (japonica cultivar-group)]
dbj|BAD27599.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
dbj|BAD29072.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
dbj|BAF08307.1| Os02g0236800 [Oryza sativa Japonica Group]
dbj|BAG91008.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG94336.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG96877.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 326

Score = 150 bits (380), Expect = 9e-34
Identities = 71/124 (57%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV
Sbjct: 204 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC
Sbjct: 262 AGALLHSDQELFNNGPVDSVVQLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKVN 325

Score = 119 bits (298), Expect = 3e-24
Identities = 68/164 (41%), Positives = 89/164 (54%), Gaps = 1/164 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNR-NSARGFEVIDNIKSAVEKVCVPGVVSCADILAI AAR 1333
GCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAI AAR
Sbjct: 78 GCDASVLLDDTPAAPGEKGVGPNAVSTTVFDLVDTIKAQVEAVCPATVSCADVLAIAAR 137

Query: 1334 DSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGP+W V LGR
Sbjct: 138 DSVNL-----LGGPSWAVPLGR 154

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RDA + S+SA + +P P ++++ L+S F+A GLS++DL ALSG
Sbjct: 155 RDALSPRSRAVSTDLPGPEADISALVSFAAKGLSSRDLAALSG 198

Score = 61.2 bits (147), Expect = 9e-07

Identities = 28/63 (44%), Positives = 40/63 (63%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD
Sbjct: 14 LLLLLAVALALAAARARAQLSPGFYSASCPTVHGVVRQVMSQAVMNDTRAGAAVLRRLFYHD 73

Query: 772 CFV 780
CFV
Sbjct: 74 CFV 76

>gb|ABK22680.1| unknown [Picea sitchensis]
Length = 341

Score = 150 bits (379), Expect = 1e-33
Identities = 85/169 (50%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
++GCDGSILLDDTSSFTGEK ANPN+NS RGF V+D IK +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTGEKTANPNKNSVRGFGVVDQIKCELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F LGL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGNSTHQ TLETKFKRLGLNVVDLVALSGAHTI 208

Score = 122 bits (305), Expect = 4e-25
Identities = 64/132 (48%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFARLYNQTVNGNHDP TLDTTYLKQLRAVCPQT-GTDDNQTTPLDPVTPIKFDIN 269

Query: 1969 YFKNLVQKKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142
Y+ N+V KGLL SD+ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDEILYSTKGSRTVGLVESYSTSTHAFKQFAASMIKMGINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N
Sbjct: 330 HGEIRKNCRRMN 341

Score = 62.4 bits (150), Expect = 4e-07
Identities = 37/71 (52%), Positives = 45/71 (63%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ---LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE RM AS
Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPKAQAIKSVVEDAVRKEARMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV
Sbjct: 73 LLRLHFHDCFV 83

>emb|CAN61440.1| hypothetical protein [Vitis vinifera]
Length = 262

Score = 150 bits (379), Expect = 1e-33
Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYN+ NI+++FA + + +CP T G D+NL+ LD +P FDN YFKNLV
Sbjct: 141 QSRLVFRDRIYNDNIDSSFAESLKSNCPTDG--DDNLSALDDTSPVIFDNGYFKNLV 198

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQ+LFN GSTDS V Y+++ +F DF AAM+KMG+ISPLTG+ G+IR NC
Sbjct: 199 DNKGLLHSDQELFNGGSTDSQVSSYASSATSFYKDFXAAMVKMGNISPLTGTKGQIRVNC 258

Query: 2167 RRIN 2178
R+IN
Sbjct: 259 RKIN 262

Score = 150 bits (378), Expect = 2e-33
Identities = 85/168 (50%), Positives = 101/168 (60%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
+GCDGSILLDDT++FTGEK A PN +S RGFEVID+IKS VE VCPGVV+CADILA+AAR
Sbjct: 15 KGCDSILLDDTANFTGEKTAGPNADSVRGFEVIDDIKSRVESVCPGVVTCADILAVAAR 74

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGPTW V+LGR
Sbjct: 75 DSV-----VALGGPTWTVQLGR 91

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RD+ TAS S A IP+P +L+ LIS FS G S K++VALSG+ I
Sbjct: 92 RDSTTASISDAETDIPSPALDLDLISAFSDKGFSKEMVALSGSHTI 139

>gb|AAC31550.1| peroxidase PXC2 precursor [Avena sativa]
Length = 313

Score = 150 bits (379), Expect = 1e-33
Identities = 71/126 (56%), Positives = 97/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPR-TSGSGDNNLAPLDLQTPTSFDNYYFKN 1980
QA+C NFR+RIY +TNI AFA + Q +CP+ T GSGD++LAPLD +TP +FDN Y+ N
Sbjct: 187 QAQCKNFRSRIYGGDTNINAAFATSLQANCPQATGGSGDSSLAPLDTKTPNAFDNSYNN 246

Query: 1981 LVQKKLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRK 2160
L+ +KLLHSDQ LFN G+TD+ VR ++++ F+ F AMIKMG+ISPLTG+ G+IR
Sbjct: 247 LLSQKLLHSDQVLFNNGTDTNVRNFASSASAFTGAFTTAMIKMGNISPLTGTGQGI 306

Query: 2161 NCRRIN 2178
+C ++N
Sbjct: 307 SCSKVN 312

Score = 105 bits (261), Expect = 6e-20
Identities = 69/167 (41%), Positives = 84/167 (50%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDNIK+ VE VC VSC DILA+AARD
Sbjct: 69 GCDASVLLSGN-----EQNAAPNAGSLRGFSVIDNIKTQVEAVCKQTVSCDDILAVAARD 123

Query: 1337 SVQIVSQGTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 124 SV-----VALGGPSWTVPLGRR 140

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ +A+ + + +PAPTS+L QL + FS L T D+VALSG I
Sbjct: 141 DSTSATGNTGD--LPAPTS SLAQLQA AFSKKNLDTTDMVALSGAHTI 185

Score = 65.5 bits (158), Expect = 5e-08
Identities = 32/64 (50%), Positives = 45/64 (70%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S +++ + L L +A+AQLS+ FY SCP +++KS V +A+S + RMGASLLRL F

Sbjct: 5 SCISLRVMLVALAATAASAQLSSTFYDTSCKALATIKSGVAAVSSDRRMGASLLRLHF 64

Query: 766 HDCF 777
HDCF

Sbjct: 65 HDCF 68

>gb|AAC31551.1| peroxidase PXC6 precursor [Avena sativa]
Length = 314

Score = 150 bits (379), Expect = 1e-33
Identities = 71/126 (56%), Positives = 97/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPR-TSGSGDNNLAPLDLQTPTSFDNYYFKN 1980
QA+C NFR+RIY +TNI AFA + Q +CP+ T GSGD++LAPLD +TP +FDN Y+ N
Sbjct: 188 QAQCKNFRSRIYGGDTNINAAFATSLQANCPQATGGSGDSSLAPLDTKTPNAFDNSYNN 247

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ +KLLHSDQ LFN G+TD+ VR ++++ F+ F AMIKMG+ISPLTG+ G+IR
Sbjct: 248 LLSQKKGLLHSDQVLFNNGTTDNTVRNFASSASAFTGAFTTAMIKMGNISPLTGTQQGQIRL 307

Query: 2161 NCRIN 2178
+C ++N

Sbjct: 308 SCSKVN 313

Score = 94.0 bits (232), Expect = 1e-16
Identities = 68/168 (40%), Positives = 82/168 (48%), Gaps = 1/168 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCVGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDNIK+ VE VC VSCADILA+AARD
Sbjct: 69 GCDASVLLSGN-----EQNAAPNAGSLRGSVIDNIKTQVEAVCKQTVSCADILAVAARD 123

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGP-TWNVKLGR 1513
SV + LGGP V LGR
Sbjct: 124 SV-----VALGGPFLEQVPLGR 140

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RD+ +A+ + + +PAPTS+L QL + FS L T +VALSG I
Sbjct: 141 RDSTSATGNTGD--LPAPTSSLAQLQAAFSCKKNLDTTGMVALSGAHTI 186

Score = 65.5 bits (158), Expect = 5e-08
Identities = 32/64 (50%), Positives = 45/64 (70%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S +++ + L L +A+AQLS+ FY SCP +++KS V +A+S + RMGASLLRL F
Sbjct: 5 SCISLRVMLVALAATAASAQLSSTFYDTSCKALATIKSGVAAAVSSDRRMGASLLRLHF 64

Query: 766 HDCF 777
HDCF
Sbjct: 65 HDCF 68

>emb|CAA71492.1| peroxidase [Spinacia oleracea]
Length = 315

Score = 149 bits (375), Expect = 3e-33
Identities = 81/165 (49%), Positives = 101/165 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDTS+F GEK A PN+NS RGF+ +D+IK+++EK CPGVVSCADILAIA+
Sbjct: 66 VNGCDGSILLDDTSTFRGEKTAIPKNNSVRGFKAVDSIKASLEKACPGVVSCADILAIA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + GGPTW V+LG
Sbjct: 126 RDAV-----VQYGGPTWQVRLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TA++SAAN IPAP+ NL L S F+ +GLS KD+V LSG
Sbjct: 143 RRDSL TANRSAANAFIPAPSFNLRNLTSSFTTVGLSFKDMVVLSG 187

Score = 133 bits (335), Expect = 1e-28
Identities = 66/124 (53%), Positives = 93/124 (75%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
ARCT+FR I+N+TNI AFA++ Q+ CP+ SG+G L PLD QT FD+ Y++NL+
Sbjct: 194 ARCTSFRPHIHNDTNINAFAKSLQKKCPQ-SGNG-KVLQPLDYQTKFRFDDKYYQNLV 251

Query: 1990 KKGLLHSDQQLFNGGST-DSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQL++G + D+ VR Y++ G F +F +MI+MG+I PLTG++G+IR+NC
Sbjct: 252 KKGLLHSDQQLYSGNNNADAYVRKYASKQGEFFQEFGNSMIRMGNIKPLTGTHGQIRRNC 311

Query: 2167 RRIN 2178
R+ N
Sbjct: 312 RKS N 315

Score = 64.3 bits (155), Expect = 1e-07
Identities = 29/51 (56%), Positives = 34/51 (66%)
Frame = +1

Query: 631 SANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
+ N QLS NFY +CPN VK + I KE R+GAS+LRL FHDCFVN
Sbjct: 17 TVNGQLSPNFYSSTCPNALRIVKQGIAKRIKKEARVGASILRLLHFHDCFVN 67

>ref|NP_001054096.1| Os04g0651000 [Oryza sativa (japonica cultivar-group)]
emb|CAE04507.2| OSJNBb0059K02.17 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69299.1| TPA: class III peroxidase 57 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF16010.1| Os04g0651000 [Oryza sativa Japonica Group]
dbj|BAG98582.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 319

Score = 149 bits (375), Expect = 3e-33
Identities = 82/169 (48%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGS+LLDDT++ TGEKNA PN+NS RGF EV+D+IKS +E C VVSCADILA+AA
Sbjct: 70 VNGCDGSVLLDDTAAITGEKNAKPNKNSLRGF EVVDDIKSQLEDACEQV VSCADILAVAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW+V+LG
Sbjct: 130 RDSV-----VALGGPTWDVELG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 147 RRDGTTASLDAANNDLPPPTSDLADLIKFSDFKGLTASDMIALSGAHTI 195

Score = 148 bits (373), Expect = 6e-33
Identities = 68/124 (54%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 197 QARCTNFRGRLYNETNL DATLATS LKPSCPNPTG-GDDNTAPLDPATSYVFDNFYRNLL 255

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G++R NC
Sbjct: 256 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQVRVNC 315

Query: 2167 RRIN 2178
R++N

Sbjct: 316 RKNV 319

Score = 74.7 bits (182), Expect = 8e-11
Identities = 34/70 (48%), Positives = 52/70 (74%), Gaps = 1/70 (1%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLL 753
++ ++ +C A+ L++ + +AQLST+FY +CP+ ++S V+ A+SKE+RMGASLL
Sbjct: 2 AYSRQIFVCSAMAALLFSAVVSAQLSTDFYDETCPDALDIIESAVRDAVSKESRMGASLL 61

Query: 754 RLFFHDCFVN 783
RL FHDCFVN
Sbjct: 62 RLHFHDCFVN 71

>ref|XP_002308244.1| predicted protein [Populus trichocarpa]
gb|EEE91767.1| predicted protein [Populus trichocarpa]
Length = 321

Score = 149 bits (375), Expect = 3e-33
Identities = 71/123 (57%), Positives = 95/123 (77%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
A+C F+ RIYNETNI+ FAR R+ +CPRT G D+NLAPL+ TP+ FD Y+ +L++
Sbjct: 202 AQCFTEKDRYNETNIDPKFARERKLTCPRTGG--DSNLAPLN-PTPSYFDARYYNDLLK 258

Query: 1990 KKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GL HSDQ LFNNGSTDS+V+ YS+N F +DFA +M+KMG+I+PLTG G+ R NCR
Sbjct: 259 KRGLFHSDQALFNNGSTDSLKAYSSNAKAFWTFANSMVKMGNINPLTGKQGQTRLNCR 318

Query: 2170 RIN 2178
++N
Sbjct: 319 KVN 321

Score = 135 bits (339), Expect = 5e-29
Identities = 82/166 (49%), Positives = 93/166 (56%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC-PGVVSCADILAIA 1327
+ GCD SILLD TS+F EKNANPN NS RGFEVID IK V+K C VVSCADILA+A
Sbjct: 73 VNGCDASILLDDTSAFDSEKNANPNINSIRGFEVIDRIKLEVDKACGRPVVSCADILAVA 132

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGPTW V+L

Sbjct: 133 ARDSV-----VALGGPTWAVQL 149

Query: 1508 GRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRD+ TAS++ ANN IPAP +L LI F GL+ KDLV LSG

Sbjct: 150 GRRDSTTASKTTANNDIPAPFMDLPDLIINFKKHGLNKKDLVVLVLSG 195

Score = 64.3 bits (155), Expect = 1e-07
Identities = 34/76 (44%), Positives = 47/76 (61%)
Frame = +1

Query: 556 LSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETR 735
++ L + S S L + LAL S++ LS N+Y + CP ++K V++A+ E R

Sbjct: 1 MASLGIFSLISTLFLVLALATT--ASSSKGLSPNYDYVCPKALPTIKRVVEAAVYNERR 58

Query: 736 MGASLLRRLFHDCFVN 783
MGASLLRL FHDCFVN

Sbjct: 59 MGASLLRLHFHDCFVN 74

>emb|CBI19222.1| unnamed protein product [Vitis vinifera]
Length = 255

Score = 148 bits (374), Expect = 4e-33
Identities = 82/167 (49%), Positives = 101/167 (60%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD

Sbjct: 17 GCDASILLDDTANFTGEKTAGPNNNSLRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 76

Query: 1337 SVQIVSQGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V++GRR

Sbjct: 77 SV-----VALGGPTWTVMGRR 93

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN +PAPTS+L+ L S FS G +T+++VALSGT I

Sbjct: 94 DSTTASLSTANADLPAPTSDDLVLTSLSFNKGFTTQEMVALSGTHTI 140

Score = 126 bits (317), Expect = 2e-26
Identities = 62/106 (58%), Positives = 82/106 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYNETN++ AFA+++Q+ CP T G D NL+ LD +T T FD YFK+L+

Sbjct: 142 KAQCIFRYRIYNETNVDAFAKSKQKICPWTGG--DENLSDLD-ETTTVFDTVYFKDLI 198

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDI 2124
+KKGLLHSDQQL+NG STDS+V YST+ TF +D A AM+KMG++
Sbjct: 199 EKKGLLHSDQQLYNGNSTDSMVETYSTDSTFFFTDVANAMVKMGNL 244

>ref|XP_002467656.1| hypothetical protein SORBIDRAFT_01g031740 [Sorghum bicolor]
gb|EER94654.1| hypothetical protein SORBIDRAFT_01g031740 [Sorghum bicolor]
Length = 344

Score = 148 bits (374), Expect = 4e-33
Identities = 83/165 (50%), Positives = 98/165 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILA+AA
Sbjct: 92 VQGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAVAA 151

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV LGGP+W+V LG
Sbjct: 152 RDSVAQ-----LGGPSWSVPLG 168

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDA TAS S AN+ +P PTSNLN L++ FS GLS+ D+VALSG
Sbjct: 169 RRDATTASASLANSDLPGPTSNLNGLLNAFNSKGLSSTDMVALSG 213

Score = 143 bits (361), Expect = 1e-31
Identities = 69/126 (54%), Positives = 95/126 (75%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCP-RTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
+A+C N R+RIYN+T+I+ +A + + SCP + G+ D L PLD TP +FDN YF NL
Sbjct: 219 RAQCKNIRSRIYNDTIDATYAASLRASCPAQAGGASDGALEPLDDATPDAFDNAYFGNL 278

Query: 1984 VQKKGLLHSDQQLFNGG-STDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+ ++GLLHSDQ LF GG +TD +V Y+++ + SDFAAAM+KMG+ISPLTG++GEIR
Sbjct: 279 LSQRGLLHSDQALFGGGGATDGLVSTYASSADQWGSDFAAAMVKMGNISPLTGTGDGEIRV 338

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 339 NCRRVN 344

Score = 55.5 bits (132), Expect = 5e-05
Identities = 29/65 (44%), Positives = 42/65 (64%), Gaps = 5/65 (7%)
Frame = +1

Query: 601 CLALFVLIWGS-----NAQLSTNFYYH-SCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
CL + ++ +A +AQLS+ YY SCP +++++ V +A+ + RMGASLLRL F
Sbjct: 28 CLLILIVALAAAAVASAQLSSEDYYDASCPAALFTIRTAVSTAVLLDRRMGASLLRLHF 87

Query: 766 HDCFV 780
HDCFV
Sbjct: 88 HDCFV 92

>gb|EEE61812.1| hypothetical protein OsJ_16433 [Oryza sativa Japonica Group]
Length = 1129

Score = 148 bits (374), Expect = 4e-33
Identities = 82/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCDGS+LLDDT++ TGEKNA PN+NS RGF EV+D+IKS +E C VVSCADILA+AARD
Sbjct: 78 GCDGSVLLDDTAAITGEKNAKPNKNSLRGF EVVDDIKS QLEDACEQVVSCADILAVAARD 137

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW+V+LGRR
Sbjct: 138 SV-----VALGGPTWDVELGRR 154

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 155 DGTASLDAANNDLPPPTS LADLIKFSFKGLTASDMIALSGAHTI 201

Score = 134 bits (336), Expect = 1e-28
Identities = 63/115 (54%), Positives = 82/115 (71%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 203 QARCTNFRGRLYNETNLDATLATS LKPCPNPTG-GDDNTAPLDPATSYVFDNFYRNLL 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGE 2151
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G+
Sbjct: 262 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQ 316

Score = 69.7 bits (169), Expect = 3e-09
Identities = 31/49 (63%), Positives = 40/49 (81%)
Frame = +1

Query: 637 NAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783
+AQLST+FY +CP+ ++S V+ A+SKE+RMGASLLRL FHDCFVN
Sbjct: 11 SAQLSTDFYDETCPDALDIIESAVRDAVSKESRMGASLLRRLFHDCFVN 59

>gb|EEC78144.1| hypothetical protein OsI_17703 [Oryza sativa Indica Group]
Length = 325

Score = 148 bits (374), Expect = 4e-33
Identities = 82/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCVGVVSCADILAI AARD 1336
GCDGS+LLDDT++ TGEKNA PN+NS RGFEV+D+IKS +E C VVSCADILA+AARD
Sbjct: 78 GCDGSVLLDDTAAITGEKNAKPNKNSLRGFEVVDDIKSQLEDACEQVSCADILAVAARD 137

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW+V+LGRR
Sbjct: 138 SV-----VALGGPTWDVELGRR 154

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 155 DGTASLDAANNDLPPTS LADLIKSFSDKGLTASDMIALSGAHTI 201

Score = 148 bits (373), Expect = 6e-33
Identities = 68/124 (54%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 203 QARCTNFRGRLYNETNL DATLATS LKPCPNPTG-GDDNTAPLDPATSYVFDNFYRNL 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G++R NC
Sbjct: 262 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGGIGVVTGSGGQVRVNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 70.1 bits (170), Expect = 2e-09
Identities = 31/49 (63%), Positives = 41/49 (83%)
Frame = +1

Query: 637 NAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783

+AQLST+FY +CP+ ++S V++A+SKE+RMGASLLRL FHDCFVN
Sbjct: 11 SAQLSTDFYDETCPDALDIIESAVRAAVSKESRMGASLLRLHFDCFVN 59

>emb|CAJ86184.1| H0212B02.16 [Oryza sativa (indica cultivar-group)]
emb|CAJ86323.1| OSIGBa0113E10.6 [Oryza sativa (indica cultivar-group)]
Length = 337

Score = 148 bits (374), Expect = 4e-33
Identities = 82/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCVGVVSCADILAI AARD 1336
GCDGS+LLDDT++ TGEKNA PN+NS RGFEV+D+IKS +E C VVSCADILA+AARD
Sbjct: 90 GCDGSVLLDDTAAITGEKNAKPNKNSLRGFEVVDDIKSQLEDACEQVSCADILAVAARD 149

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW+V+LGRR
Sbjct: 150 SV-----VALGGPTWDVELGRR 166

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 167 DGTASLDAANNDLPPTS LADLIKSFSDKGLTASDMIALSGAHTI 213

Score = 148 bits (373), Expect = 6e-33
Identities = 68/124 (54%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 215 QARCTNFRGRLYNETNL DATLATS LKPCPNPTG-GDDNTAPLDPATSYVFDNFYRNL 273

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G++R NC
Sbjct: 274 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQVRVNC 333

Query: 2167 RRIN 2178
R++N
Sbjct: 334 RKNV 337

Score = 75.1 bits (183), Expect = 6e-11
Identities = 34/70 (48%), Positives = 53/70 (75%), Gaps = 1/70 (1%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSA-NAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753

++ ++ +C A+ L++ + +AQLST+FY +CP+ ++S V++A+SKE+RMGASLL
Sbjct: 2 AYSRQIFVCSAMAALLFSAVVSAQLSTDFYDETCPDALDIIESAVRAAVSKESRMGASLL 61

Query: 754 RLFFHDCFVN 783
RL FHDCFVN

Sbjct: 62 RLHFHDCFVN 71

>gb|EAZ22372.1| hypothetical protein OsJ_06030 [Oryza sativa Japonica Group]
Length = 257

Score = 148 bits (374), Expect = 4e-33
Identities = 69/123 (56%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A CTNFRA IYN+ NI+ +FA R+++CP + +GD NLAPLD+QT +FDN Y+ NL+
Sbjct: 135 ALCTNFRAHIYNDANIDPSFAALRRRACPAAPNGDTNLAPLDVQTQNAFDNAYYGNTLV 194

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGS D++VR Y+ NP F++DFA AM+KMG+I S+GE+R +CR
Sbjct: 195 RRGLLHSDQVLFNGGSQDALVRQYAANPALFAADFAKAMVKMGNIG--QPSDGEVRCDCR 252

Query: 2170 RIN 2178
+N
Sbjct: 253 VVN 255

Score = 93.6 bits (231), Expect = 2e-16
Identities = 46/68 (67%), Positives = 53/68 (77%), Gaps = 2/68 (2%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD SILLDD + F GEK A PN NS RG+EVID IK+ VE VCPGVVSCADI+A+
Sbjct: 69 VQGCDASILLDDVPATGFVGEKTAAPNNSVRGYEVIDQIKANVEDVCPGVVSCADIVAL 128

Query: 1325 AARDSVQI 1348
AARDS +
Sbjct: 129 AARDSTAL 136

Score = 70.1 bits (170), Expect = 2e-09
Identities = 34/59 (57%), Positives = 43/59 (72%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
L +F L+ A+ QLST++Y SCP++ V +TV SAI E RMGASL+RLFFHDCFV

Sbjct: 11 LLVFFLLSDDASGQLSTSYYADSCPSVEKVVHATVASAIQAERRMGASLIRLFFHDCFV 69

>ref|NP_001046401.1| Os02g0240300 [Oryza sativa (japonica cultivar-group)]
dbj|BAD28871.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69271.1| TPA: class III peroxidase 29 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAF08315.1| Os02g0240300 [Oryza sativa Japonica Group]
dbj|BAG90221.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG96858.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 321

Score = 148 bits (374), Expect = 4e-33
Identities = 68/123 (55%), Positives = 95/123 (77%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++CTNFRA IYN+ NI+ +FA R+++CP + +GD NLAPLD+QT +FDN Y+ NL+
Sbjct: 199 SQCTNFRAHIYNDANIDPSFAALRRRACPAAPNGDTNLAPLDVQTQNAFDNAYYGNNLV 258

Query: 1990 KKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNNGS D++VR Y+ NP F++DFA AM+KMG+I S+GE+R +CR
Sbjct: 259 RRGLLHSDQVLFNNGSQDALVRQYAANPALFAADFAKAMVKMGNIG--QPSDGEVRCDCR 316

Query: 2170 RIN 2178
+N
Sbjct: 317 VVN 319

Score = 137 bits (344), Expect = 1e-29
Identities = 79/168 (47%), Positives = 95/168 (56%), Gaps = 2/168 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1324
+QGCD SILLDD + F GEK A PN NS RG+EVID IK+ VE VCPGVVSCADI+A+
Sbjct: 69 VQGCASILLDDVPATGFVGEKTAAPNNSVRGYEVIDQIKANVEDVCPGVVSCADIVAL 128

Query: 1325 AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 129 AARDSTAL-----LGGPSWAVP 145

Query: 1505 LGRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
LGR D+ TAS+S AN+ +P P SNL LI+RF GLS +D+ ALSG+
Sbjct: 146 LGRCDSTTASRSEANSDLPGPSNLTMLIARFGNKGLSPRDMTALSGS 193

Score = 70.1 bits (170), Expect = 2e-09
Identities = 34/59 (57%), Positives = 43/59 (72%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
L +F L+ A+ QLST++Y SCP++ V +TV SAI E RMGASL+RLFFHDCFV
Sbjct: 11 LLVFFLLSDDASGQLSTSYADSCPSVEKVVHATVASAIQAERRMGASLIRLFFHDCFV 69

>gb|ABK21983.1| unknown [Picea sitchensis]
Length = 341

Score = 148 bits (373), Expect = 6e-33
Identities = 84/169 (49%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
++GCDGSILLDDTSSFTGEK ANPN+NS RGF V+D IK +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTGEKTANPNKNSVRGFGVVDQIKCELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNLTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F GL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGPNSTHQ TLETKFKRQGLNVVDLVALSGAHTI 208

Score = 121 bits (304), Expect = 6e-25
Identities = 64/132 (48%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTP TSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFKARLYNQTVNGKPDPTLDTTYLKQLRAVCPQT-GTDDNQTP LDPVTPIKFDID 269

Query: 1969 YFKNLVQKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142
Y+ N+V KGLL SD+ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDEILYSTKGSRTVGLVESYSTSTHAFFKQFAASMIKMG NINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N
Sbjct: 330 HGEIRKNCRRMN 341

Score = 62.4 bits (150), Expect = 4e-07

Identities = 37/71 (52%), Positives = 45/71 (63%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ----LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE RM AS
Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPQAIIKSVVEDAVRKEARMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV
Sbjct: 73 LLRLHFHDCFV 83

>ref|XP_002461210.1| hypothetical protein SORBIDRAFT_02g042860 [Sorghum bicolor]
gb|EER97731.1| hypothetical protein SORBIDRAFT_02g042860 [Sorghum bicolor]
Length = 313

Score = 148 bits (373), Expect = 6e-33
Identities = 70/124 (56%), Positives = 93/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+NF IYN+TNI+ AFA + Q +CP SG +LAPLD TPT+FDN Y+ NL+
Sbjct: 191 QAQCSNFNDHIYNDTNIDAAFATSLQANCP---ASGSTSLAPLDTMPTTFDNDYYTNLM 247

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFN GSTDS V ++++ F+S F AAM+KMG++SPLTG++GEIR C
Sbjct: 248 SQKGLLHSDQELFNGGSTDSTVSNFASSASAFTSAFTAAMVKMGNLSPLTGTGEIRLAC 307

Query: 2167 RRIN 2178
+N
Sbjct: 308 GIVN 311

Score = 123 bits (309), Expect = 2e-25
Identities = 76/169 (44%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGS+LL+DTS GE+++ PN+ S R F+VID+IK+ VE VCPGVVSCADILA+AA
Sbjct: 68 VHGCDGSVLLNDTS---GEQSSPPNKGSLRRFDVIDSIKAQVEAVCPGVVSCADILAVAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 125 RDSV-----VALGGPSWTVLLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + +PAPTS+L QL+S FS L D+VALSG I
Sbjct: 142 RRDS-TASFPSETDLPAPTSLLQLLSLFSNKNLDATDMVALS GAHTI 189

Score = 68.2 bits (165), Expect = 8e-09
Identities = 34/63 (53%), Positives = 44/63 (69%), Gaps = 2/63 (3%)
Frame = +1

Query: 601 CLALFVL--IWGSANAQLSTNFYYHSCPNI FSSVKSTVQSAISKETRMGASLLRLFFHDC 774
CLA V + A+AQLS+ FY SCPN S++KS V +A+ +E R GASLLR+ FHDC
Sbjct: 7 CLAFLVAAAVASVASAQLSSTFYDTSCPINALSTIKSGVDAAVMQEARTGASLLRMHFHDC 66

Query: 775 FVN 783
FV+
Sbjct: 67 FVH 69

>emb|CBI18065.1| unnamed protein product [Vitis vinifera]
Length = 413

Score = 147 bits (372), Expect = 8e-33
Identities = 83/169 (49%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGKGNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDTS+FTGEK A PN NS RG+EV+D IKS +E CPGVVSCADILA+AA
Sbjct: 15 VNGCDASILLDDTSNFTGEKTAGPNANSVRGYEVVDTIKSQLEASCPGVVSCADILAVAA 74

Query: 1331 RDSVQIVSGQT TNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GP+W V+LG
Sbjct: 75 RDSV-----VALRGPSWVRLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ IPAPT NL+ LIS F+ G + +++VALSG+ I
Sbjct: 92 RRDSTTASLSAANSNIPAPTLNLSGLISAFTNKGFNAREMVALSGSHTI 140

Score = 136 bits (343), Expect = 2e-29
Identities = 66/101 (65%), Positives = 77/101 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT FR RIYNE NI+ +F + Q +CP S GDN L+PLD QTPT+FDN Y+ NLV
Sbjct: 142 QARCTTFRTRIYNEANIDASFKTSLQANCP--SSGGDNTLSPLDTQTPTTFDNAYYTNLV 199

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMI 2109
KKGLLHSDQQLFNGGST++V YST TF +DFA AM+
Sbjct: 200 NKKGLLHSDQQLFNGGSTDAVVNTYSTRSTTFFTFDFANAMM 240

Score = 106 bits (265), Expect = 2e-20
Identities = 64/139 (46%), Positives = 77/139 (55%), Gaps = 1/139 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC-PGVVSCADILAIA 1327
+ GCD SILLD TS+ EKNA N NSARGF V+D+IKS V+KVC VVSCADILA+A
Sbjct: 309 VNGCDASILLDATSTIDSEKNAGANANSARGFNVVDDIKSQVDKVCGRPVVSCADILAVA 368

Query: 1328 ARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGP+W V+L
Sbjct: 369 ARDSV-----VALGGPSWTVQL 385

Query: 1508 GRRDARTASQSAANNNGIPA 1564
GRRD+ TAS++ ANN IP+
Sbjct: 386 GRRDSTTASRTDANNNIPS 404

Score = 68.2 bits (165), Expect = 8e-09
Identities = 40/89 (44%), Positives = 49/89 (55%), Gaps = 4/89 (4%)
Frame = +1

Query: 529 NT*STKLVCL-SKLTMASFCSRLTICLALFVLI---WGSANAQLSTNFYHSCPNLFSSV 696
NT ST+ + A SR +CL FVL +A LS FY CP ++
Sbjct: 222 NTYSTRSTTFFTFDFANAMMASRLLCLYAFVLFSLATADFSAAALSPYFYNKVCPKALPTI 281

Query: 697 KSTVQSAISKETRMGASLLRRLFHDFVN 783
K V++A+ KE RMGASLLRL FHDFVN
Sbjct: 282 KRVVEAAVQKEKRMGASLLRRLFHDFVN 310

>gb|ACF08091.1| class III peroxidase [Triticum aestivum]
Length = 316

Score = 147 bits (372), Expect = 8e-33
Identities = 69/125 (55%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSVSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD TP +FDN Y+ NL
Sbjct: 191 QAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTPNAFDNAYYTNL 250

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAIKMGDISPLTGSNGEIRKN 2163
+ ++GLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +
Sbjct: 251 MSQRGLLHSDQVLFNNDTTDNTVRNFASNPAAFSSAFTTAMIKMGNIAPKTGTGGQIRLS 310

Query: 2164 CRRIN 2178

C R+N
Sbjct: 311 CSRVN 315

Score = 94.4 bits (233), Expect = 1e-16
Identities = 63/170 (37%), Positives = 85/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGKNNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILATAIA 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 68 VQGCDAVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICNQTVSCADILTVAA 122

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 123 RDSV-----VALGGPSWTVPLG 139

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSAL-GLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P S+ ++L + F GL+T D+VA SG I
Sbjct: 140 RRDSIDANEAEANSDLPGFNSSRSELEAAFLRKGLNTVDMVAPSGAHTI 189

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/62 (53%), Positives = 44/62 (70%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDC 774
C++L VL+ +A+ QLS FY SCP +++KS V +A+S + RMGASLLRL FHDC
Sbjct: 7 CISLVVLVALATAASGQLSPTFYDTSCPRALATIKSGVMAAVSSDPRMGASLLRRLFHDC 66

Query: 775 FV 780
FV
Sbjct: 67 FV 68

>gb|EAY85149.1| hypothetical protein OsI_06504 [Oryza sativa Indica Group]
Length = 135

Score = 147 bits (372), Expect = 8e-33
Identities = 69/123 (56%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++CTNFRA IYN+ NI+ +FA R+++CP + +GD NLAPLD+QT FDN Y+ NL+
Sbjct: 13 SQCTNFRAHIYNDANIDPSFAALRRRACPAAPNGDTNLAPLDVQTQNLFDNAYYG NLLV 72

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNNGS D++VR Y+ NP F++DFA AM+KMG+I S+GE+R +CR

Sbjct: 73 RRGLLHSDQVLFNGGSQDALVRQYAANPALFAADFAKAMVKMGNIG--QPSDGEVRCDCR 130

Query: 2170 RIN 2178
IN

Sbjct: 131 FIN 133

>gb|AAW52716.1| peroxidase 2 [Triticum monococcum]
Length = 316

Score = 147 bits (372), Expect = 8e-33
Identities = 69/125 (55%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD TP +FDN Y+ NL

Sbjct: 191 QAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTPNAFDNAYYTNL 250

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAAMIKMGDISPLTGSNGEIRKN 2163
+ ++GLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +

Sbjct: 251 MSQRGLLHSDQVLFNNDTTDNTVRNFASNPAAFSSAFTTAMIKMGNIAPKTGTQQGIRLS 310

Query: 2164 CRRIN 2178
C R+N

Sbjct: 311 CSRVN 315

Score = 97.1 bits (240), Expect = 2e-17
Identities = 64/170 (37%), Positives = 86/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA

Sbjct: 68 VQGCDA SVLLSGM-----EQNAIPNAGSLRGGFVIDSIKTQIEAICNQTVSCADILTVAA 122

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 123 RDSV-----VALGGPSWTVPLG 139

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSAL-GLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P S+ ++L + F GL+T D+VALSG I

Sbjct: 140 RRDSIDANEAEANSDLPGFNSSRSELEAAFLRKGLNTVDMVALSGAHTI 189

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/62 (53%), Positives = 44/62 (70%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDC 774
C++L VL+ +A+ QLS FY SCP +++KS V +A+S + RMGASLLRL FHDC
Sbjct: 7 CISLVVLVALATAASGQLSPTFYDTSCPRALATIKSGVMAAVSSDPRMGASLLRLLHFHDC 66

Query: 775 FV 780
FV
Sbjct: 67 FV 68

>gb|AAA32972.1| peroxidase [Hordeum vulgare]
Length = 315

Score = 147 bits (372), Expect = 8e-33
Identities = 70/125 (56%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI TA+A + + +CP+T GSGD +LA LD T +FDN Y+ NL
Sbjct: 190 QAQCSTFRARIYGGDTNINTAYAASLRANCPQTVGSGDGLANLDTTTANTFDNAYYTNL 249

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ +KGLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +
Sbjct: 250 MSQKGLLHSDQVLFNDDTTDNTVRNFASNPAAFSSAFTTAMIKMGNIAPKTGTQQGIRLS 309

Query: 2164 CRRIN 2178
C R+N
Sbjct: 310 CSRVN 314

Score = 95.9 bits (237), Expect = 3e-17
Identities = 64/170 (37%), Positives = 84/170 (49%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 67 VQGCDAVLLSGM-----EQNAIPNAGSLRGGVIDSIKTQIEAICKQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 122 RDSV-----VALGGPSWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRF-SALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN +P S+ +L + F GL+T D+VALSG I
Sbjct: 139 RRDSIDANENEANTDLPGFNSSRAEAAFLKKGGLNTVDMVALSGAHTI 188

Score = 65.5 bits (158), Expect = 5e-08
Identities = 31/59 (52%), Positives = 42/59 (71%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
L + V + +A+AQLS FY SCP +++KS V +A++ + RMGASLLRL FHDCFV
Sbjct: 9 LLVLVALVTAASAQLSPTFYDTSCPRALATIKSGVMAAVTSDPRMGASLLRLHFHDCFV 67

>emb|CBI22008.1| unnamed protein product [Vitis vinifera]
Length = 154

Score = 147 bits (371), Expect = 1e-32
Identities = 82/163 (50%), Positives = 97/163 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 25 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACKATVSCADILALAA 84

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 85 RDGVVL-----LGGPSWTVPLG 101

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVAL 1639
RRDARTA+QSAANN +PAP +NL+ LIS F+A GL+ D+ AL
Sbjct: 102 RRDARTANQSAANNLPPFANLSALISGFAAKGLNADDMTAL 144

Score = 43.5 bits (101), Expect = 0.20
Identities = 18/23 (78%), Positives = 21/23 (91%)
Frame = +1

Query: 715 AISKETRMGASLLR LFFHDCFVN 783
A+ +E RMGAS+LRLFFHDCFVN
Sbjct: 4 AVIREPRMGASILR LFFHDCFVN 26

>gb|ACD70388.1| class III peroxidase [Triticum aestivum]
Length = 316

Score = 147 bits (371), Expect = 1e-32
Identities = 70/124 (56%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR RIYNETNI+TAF A + + +CPR+ G DN+LAPLD TP FDN Y+ NL+
Sbjct: 194 QSQCRRFFRDRIYNETNIDTAFATSLRANCPRSGG--DNSLAPLDGTGPNGF DNAYYTNLM 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ LFNGG D+ VR +S++ TF+S F AMI MG+I+P TG+ G+IR C
Sbjct: 252 SQKGLLHSDQVLFNGGGADNTVRSFSSAATFNSAFTTAMINMGNIAPKTGTGGQIRLVC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 127 bits (320), Expect = 8e-27
Identities = 76/169 (44%), Positives = 89/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGKKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGS+LL DT SF GE+ A PN NS RG VIDNIK+ VE VC VSCADILA+AA
Sbjct: 67 VDGCDGSVLLADTGSFIGEQGAAPNNNSIRGMNVIDNIKTQVEAVCKQTVSCADILAVAA 126

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 127 RDSV-----VALGGPTWTVLLG 143

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ A N +P PT +L L + F LS D+VALSG I
Sbjct: 144 RRDSTTASKTNAENDLPPPTFDLQNLTTFLGKQLSMTDMVALSGAHTI 192

Score = 70.1 bits (170), Expect = 2e-09
Identities = 34/63 (53%), Positives = 46/63 (73%), Gaps = 2/63 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDC 774
CL L VL+ +A+AQLS+ FY SCPN +++K+ V +A+ E RMGASL+RL FHDC
Sbjct: 6 CLGLVVLVAMASAASAQLSSTFYDTSCPNALATIKAGVTA AVQNEARMGASLVRLHFHDC 65

Query: 775 FVN 783
FV+
Sbjct: 66 FVD 68

>gb|ABF48527.1| cell wall peroxidase [Capsicum annuum]
gb|ABG73021.1| cell wall peroxidase [Capsicum annuum]
Length = 322

Score = 147 bits (370), Expect = 1e-32
Identities = 79/125 (63%), Positives = 91/125 (72%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIY N T+I+ FA TR++ CP+ +G NLAPLDL TP DN YFKNL
Sbjct: 200 QAQCFLFRDRIYSNGTDIDAGFASTRRRRCPEQNG--NLAPLDLVTPNQLDNNYFKNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAAMIKMGDISPLTGSNGEIRKN 2163
Q+KGLL SDQ L +GGSTD IV YS +P F+SDFAAAMI+MGDISPLTGSNG IR
Sbjct: 258 RQRKGLLQSDQVLLSGGSTDDIVLEYSNSPRAFASDFAAAMIRMGDISPLTGSNGIIRTV 317

Query: 2164 CRRIN 2178
C IN
Sbjct: 318 CGAIN 322

Score = 127 bits (320), Expect = 8e-27
Identities = 71/169 (42%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLD+T + EK A PN S RG+ +I++ K +EK CPG+VSCADILA+AA
Sbjct: 73 VQGCDASILLDETPTIVSEKTALPNLGSVRGYIIEDAKRELEKTC PGIVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ +V GGP+W VKLG
Sbjct: 133 RDASTLV-----GGPSWTVKLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + A +P P L +LIS F+ GLST+D+VALSG+ I
Sbjct: 150 RRDSTTASHTLAETDLPGPFDP LTRLISGFAKKGLSTRDMVALSGSHSI 198

Score = 62.8 bits (151), Expect = 3e-07
Identities = 28/58 (48%), Positives = 41/58 (70%)
Frame = +1

Query: 607 ALFVLIWGSANAQLSTNFYHSCPNLFSVVKSTVQSAISKETRMGASLLRFFHDCFV 780
+L +L +AQLS+ FY +CPN +++++ +V+ A+S E RM ASL+RL FHDCFV
Sbjct: 16 SLVLLCSMQCHAQLSSTFYDRACP NALNTIRKSVRQAVSAERRMAASLIRLHFHDCFV 73

>gb|ACF08092.1| class III peroxidase [Triticum aestivum]
Length = 316

Score = 146 bits (369), Expect = 2e-32
Identities = 68/125 (54%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD TP +FDN Y+ NL
Sbjct: 191 QAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTPNAFDNAYYTNL 250

Query: 1984 VQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ ++GLLHSDQ LFN +TD+ VR +++NP FS+ F AMIKMG+I+P TG+ G+IR +
Sbjct: 251 MSQRGLLHSDQVLFNNDTTDNTVRNFASNPAAFSNAFTTAMIKMGNIAPKTGTQQGIRLS 310

Query: 2164 CRRIN 2178
C R+N
Sbjct: 311 CSRVN 315

Score = 97.1 bits (240), Expect = 2e-17
Identities = 64/170 (37%), Positives = 86/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 68 VQGCDAVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICNQTVSCADILTVAA 122

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 123 RDSV-----VALGGPSWTVPLG 139

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSAL-GLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P S+ ++L + F GL+T D+VALSG I
Sbjct: 140 RRDSIDANEAEANSDLPGFNSSRSELEAAFLRKGLNTVDMVALSGAHTI 189

Score = 65.5 bits (158), Expect = 5e-08
Identities = 33/62 (53%), Positives = 43/62 (69%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYHSCPFLSSVKSTVQSAISKETRMGASLLRLLFFHDC 774
C++L VL+ +A QLS FY SCP +++KS V +A+S + RMGASLLRL FHDC
Sbjct: 7 CISLVVLVALATAAAGQLSPTFYDTSCPRALATIKSGVMAAVSSDPRMGASLLRLLHFHDC 66

Query: 775 FV 780
FV
Sbjct: 67 FV 68

>gb|ACN37032.1| unknown [Zea mays]
Length = 314

Score = 146 bits (369), Expect = 2e-32

Identities = 68/124 (54%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C +F IYN+TNI AFA + + +CP SG ++LAPLD TPT+FDN Y+ NL+

Sbjct: 193 QAQCLSFNDHIYNDTNINPAFAMSLRTNCP---ASGSSSLAPLDAMTPTAFDNAYYTLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFN GS DS V ++ N F+S FA AM+KMG++SPLTGS G++R NC

Sbjct: 250 SQRGLLHSDQELFNNGSADSTVSSFAANAAFTSAFATAMVKMGNLSPLTGSQGGVVRINC 309

Query: 2167 RRIN 2178

R+N

Sbjct: 310 WRVN 313

Score = 115 bits (287), Expect = 5e-23
Identities = 72/170 (42%), Positives = 93/170 (54%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRN-SARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+QGCD S+LL+DTS GE+N PN+ + RGF+V D+IK+ VE VCPG+VSCADILA+A

Sbjct: 69 VQGCDASVLLNDTS---GEQNQIPNQTLNPRGFDVFDSIKAQVEAVCPGIVSCADILAVA 125

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD V + LGGP+W V L

Sbjct: 126 ARDGV-----VALGGPSWTVAL 142

Query: 1508 GRRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

GRRD+ TAS A + +P PTS+L QL+ +S L+ D+VALSG I

Sbjct: 143 GRRDS-TASFPAQTSDLPPPTSSLQQLLRAYSCKNLNQTDMVALSGAHTI 191

Score = 66.6 bits (161), Expect = 2e-08
Identities = 35/70 (50%), Positives = 50/70 (71%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ S L + L + V++ A+AQLS+ FY SCP+ S++ S V +A+++E R+GASL

Sbjct: 1 MAASASCL-LSLLVVVLAALASAQLSSTFYDTSCPSALSTISSGVTAAVAQEARVGASL 59

Query: 751 LRLFFHDCFV 780

LRL FHDCFV

Sbjct: 60 LRLHFHDCFV 69

>sp|P27337.1|PER1_HORVU RecName: Full=Peroxidase 1; Flags: Precursor

emb|CAA41294.1| peroxidase [Hordeum vulgare]
Length = 315

Score = 146 bits (369), Expect = 2e-32
Identities = 69/125 (55%), Positives = 93/125 (74%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD T +FDN Y+ NL
Sbjct: 190 QAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTANTFDNAYYTNL 249

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ +KGLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +
Sbjct: 250 MSQKGLLHSDQVLFNDDTTDNTVRNFASNPAAFSSSFTTAMIKMGNIAPKTGTQQGIRLS 309

Query: 2164 CRRIN 2178
C R+N
Sbjct: 310 CSRVN 314

Score = 95.9 bits (237), Expect = 3e-17
Identities = 64/170 (37%), Positives = 84/170 (49%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVWSCADILAI AA 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 67 VQGCDASVLLSGM-----EQNAIPNAGSLRGGFVIDSIKTQIEAICKQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 122 RDSV-----VALGGPSWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRF-SALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN +P S+ +L + F GL+T D+VALSG I
Sbjct: 139 RRDSIDANENEANTDLPGFNSRAELEAAFLKKGGLNTVDMVALSGAHTI 188

Score = 65.5 bits (158), Expect = 5e-08
Identities = 31/59 (52%), Positives = 42/59 (71%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
L + V + +A+AQLS FY SCP +++KS V +A++ + RMGASLLRL FHDCFV
Sbjct: 9 LLVLVALVTAASAQLSPTFYDTSCPRALATIKSGVMAAVTSDPRMGASLLR LHFHDCFV 67

>gb|ABV24961.1| peroxidase [Catharanthus roseus]

Length = 135

Score = 146 bits (368), Expect = 2e-32
Identities = 82/170 (48%), Positives = 98/170 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDTSSFTGEKNA PN+ S RGFEVID IKS +E +CPGVVSCADILA+AA
Sbjct: 8 VNGCDGSVLLDDTSSFTGEKNARPNKGLRGFEVIDTIKSQLETICPGVVSCADILAVAA 67

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W V+LG
Sbjct: 68 RDSV-----VALGGPAWIVELG 84

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHIS 1660
RRD+ TAS S A IP P +L +++ FS G S K++VALSG I+
Sbjct: 85 RRDSTTASLSDAEANIPFPRMDLTDILTAFSNKGFSKEMVALSGAHTIT 134

>emb|CAL25298.1| properoxidase [Picea abies]
Length = 341

Score = 146 bits (368), Expect = 2e-32
Identities = 84/169 (49%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
++GCDGSILLDDTSSFT EK ANPNRNS RGF V+D IK +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTREKTANPNRNSVRGFGVVDQIKCELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F GL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGPNSTHTQLETKFKRQGLNVVDLVALSGAHTI 208

Score = 121 bits (303), Expect = 8e-25
Identities = 64/132 (48%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFKARLYNQTVNGKPDPTLDTTYLKLHRAVCPQT-GTDDNQTTPLDPVTPIRFDIN 269

Query: 1969 YFKNLVQKKLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142

Y+ N+V KGLL SD+ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDEILYSTKGSRTVGLVESYSTSTHAFFKQFAASMIKMGINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N

Sbjct: 330 HGEIRKNCRRMN 341

Score = 59.7 bits (143), Expect = 3e-06
Identities = 36/71 (50%), Positives = 44/71 (61%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ----LSTNFYHSCPNLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE M AS
Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPKAQAIKSVVEDAVRKEAGMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV
Sbjct: 73 LLRLHFHDCFV 83

>gb|ACF08089.1| class III peroxidase [Triticum aestivum]
Length = 149

Score = 146 bits (368), Expect = 2e-32
Identities = 70/124 (56%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR RIYNETNI TAFa + + +CPR+ G DN+LAPLD TPT+FDN Y+ NL+
Sbjct: 27 QSQCRFFRDRIYNETNIGTAFATSLRANCPRSGG--DNSLAPLDGTPTAFDNAYYTNLM 84

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ LFNGG D+ V ++++ TF+S F AMI MG+I+P TG+ G+IR C
Sbjct: 85 SKKGLLHSDQVLFNGGGADNTVMSFASSAATFNSAFTTAMINMGNIAPKTGTQQQIRLVC 144

Query: 2167 RRIN 2178
++N
Sbjct: 145 SKVN 148

Database: /usr/local/blast/db/blastlibs/nr
Posted date: Feb 13, 2010 7:16 AM
Number of letters in database: 3,559,509,877
Number of sequences in database: 10,432,217

Lambda K H
0.318 0.134 0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 10432217

Number of Hits to DB: 20,370,324,626

Number of extensions: 397276250

Number of successful extensions: 861113

Number of sequences better than 10.0: 1949

Number of HSP's gapped: 858181

Number of HSP's successfully gapped: 6554

Length of query: 1289

Length of database: 3,559,509,877

Length adjustment: 149

Effective length of query: 1140

Effective length of database: 2,005,109,544

Effective search space: 2285824880160

Effective search space used: 2285824880160

Neighboring words threshold: 12

Window for multiple hits: 40

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 33 (17.3 bits)