

Title

**Analyses of Processed Commodities from Transgenic Event FG72
Soybeans for HPPDW336 and 2mEPSPS Proteins. USA 2009.**

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Test Guideline

None

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Study Identification

DQ09B008

Total Number of Pages 61



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STATEMENT OF NO DATA CONFIDENTIALITY CLAIMS

No claim of confidentiality is made for any information contained in this study on the basis of its falling within the scope of FIFRA §10(d)(1)(A), (B), or (C).

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GOOD LABORATORY PRACTICE COMPLIANCE STATEMENT

The undersigned hereby declare that the work to which this report refers was performed according to the procedures herein described and this report provides an accurate record of the results obtained. The study was conducted in accordance with the Good Laboratory Practice Standards as specified in 40 CFR 160 except for the following:

1. The seeds and processed fractions used in the study were not grown or produced under Good Laboratory Practice Standards.

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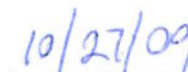


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QUALITY ASSURANCE STATEMENT OF INSPECTIONS

Study DQ09B008 was inspected by the Quality Assurance Unit for compliance with 40 CFR Part 160, Good Laboratory Practice Standards, according to Bayer CropScience Standard Operating Procedures. Following are the phases inspected, the dates inspections were completed and reported.

Dates Inspections Concluded	Phases Inspected	Dates Reported to Study Director	Dates Reported to Study Director Management
July 27, 2009	Protocol	July 27, 2009	July 27, 2009
August 26, 2009	ELISA	September 11, 2009	September 11, 2009
October 15, 2009	Data and Records	October 15, 2009	October 15, 2009
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APPROVALS PAGE

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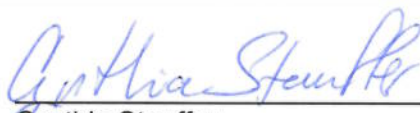


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TABLE OF CONTENTS

TITLE PAGE	1
STATEMENT OF <u>NO</u> DATA CONFIDENTIALITY CLAIMS	2
GOOD LABORATORY PRACTICE COMPLIANCE STATEMENT	3
QUALITY ASSURANCE STATEMENT OF INSPECTIONS	4
APPROVALS PAGE	5
TABLE OF CONTENTS	6
SUMMARY	8
STUDY IDENTIFICATION	9
ABBREVIATIONS, ACRONYMS AND SCIENTIFIC TERMS.....	10
1. INTRODUCTION	11
2. FIELD PHASE	11
3. ANALYTICAL PHASE	12
3.1. Reference Substances	12
3.2. Certificates of Analysis	13
3.3. Samples.....	13
3.4. Sample Preparation	13
3.5. Extraction.....	13
3.6. Immunoassay	14
3.7. Standards	14
3.8. Validation	14
3.9. Limit of Detection and Limit of Quantitation	20
3.10. Protein analyte content	21
3.11. Statistical analysis	22
4. RESULTS AND DISCUSSION	22
5. CONCLUSION.....	23
6. ARCHIVING.....	25
7. REFERENCES	26

TABLES

Table 1	Soybean Trial Site Identification from Study Number HT08SOY001	11
Table 2	Soybean Seed Collected from Study Number HT08SOY001	11
Table 3	Soybean Raw Agricultural Commodity (Seed) and Processed Fraction Samples Collected from Study Number DQ09B002.	12
Table 4	Reference Substances	13
Table 5	Validation of Sample Extraction with Fortified NT Whole Soybeans (BTID 1754A)	15
Table 6	Validation of Sample Extraction with Fortified NT Hull Material (BTID 2459B)	15
Table 7	Validation of Sample Extraction with Fortified NT Untoasted Meal (BTID 2459C).....	16
Table 8	Validation of Sample Extraction with Fortified NT Toasted Meal (BTID 2459D)	16

Table 9	Validation of Sample Extraction with Fortified NT Crude Oil (BTID 2459E)	17
Table 10	Validation of Sample Extraction with Fortified NT Crude Lecithin (BTID 2459F)	17
Table 11	Validation of Sample Extraction with Fortified NT Refined Oil (BTID 2459G)	18
Table 12	Validation of Sample Extraction with Fortified NT Refined Bleached Deodorized Oil (BTID 2459H)	18
Table 13	Validation of Sample Extraction with Fortified NT Protein Isolate (BTID 2459I).....	19
Table 14	Limits of Detection and Quantitation of 2mEPSPS Protein in Processed Fractions Derived from Non-Transgenic Whole Soybeans as Detected by ELISA.....	20
Table 15	Limits of Detection and Quantitation of HPPD Protein in Processed Fractions Derived from Non-Transgenic Whole Soybeans as Detected by ELISA.....	21
Table 16	Average 2mEPSPS Protein Content (Fresh Weight) in Whole Soybeans (RAC) and Processed Fractions as Detected by ELISA	22
Table 17	Average HPPD Protein Content (Fresh Weight) in Whole Soybeans (RAC) and Processed Fractions as Detected by ELISA	22
Table 18	2mEPSPS and HPPD Protein Content (Dry Weight) in Unsprayed and Sprayed FG72 Whole Soybeans and Processed Fractions	23
Table 19	2mEPSPS Processing Factors Generated from FG72 Whole Soybeans.....	24
Table 20	HPPD Processing Factors Generated from FG72 Whole Soybeans.....	25

APPENDICES

APPENDIX 1	Certificates of Analysis	27
APPENDIX 2	Supporting Data	32

The last page of this report is number 61

SUMMARY

Analyses of Processed Commodities from Transgenic Event FG72 Soybean for HPPDW336 and 2mEPSPS proteins. USA. 2009.

This study was carried out to determine the content of HPPDW336 and 2mEPSPS proteins in processed fractions from transgenic FG72 soybean. The *hppdpfw336* and *2mepsps* genes were genetically engineered into soybean as event FG72. When expressed, HPPDW336 (hydroxyl-phenyl-pyruvate-dioxygenase) confers tolerance to isoxaflutole herbicide and 2mEPSPS (5-enolpyruvylshikimate-3-phosphate synthase) confers tolerance to glyphosate herbicide.

The soybean seed raw agricultural commodity was produced in one trial site in Adel, Iowa. The plants were grown under conditions typical of production practices. One of the two transgenic event plots in the field trial was sprayed one time with the herbicides Isoxaflutole + Glyphosate (IFT + GLY). The other transgenic plot was untreated. The soybean grain (whole soybean seeds) was harvested and shipped to GLP Technologies, in Navasota, Texas for processing. The whole soybeans and the processed fraction samples obtained were stored frozen after production and shipped frozen on dry ice to Bayer Crop Science in Research Triangle Park, NC, for determination of the content of HPPD and 2mEPSPS proteins by ELISA.

The mean \pm standard deviation in ng/g for the protein analyte content in soybean grain and processed fractions samples on a fresh weight and dry weight basis are presented below.

Matrix	Regimen	2mEPSPS		HPPDW336	
		Fresh Weight (ng/g) \pm SD	Dry Weight (ng/g) \pm SD	Fresh Weight (ng/g) \pm SD	Dry Weight (ng/g) \pm SD
Whole Soybeans	Unsprayed	572 \pm 20	636 \pm 22	754 \pm 37	838 \pm 41
	Sprayed	740 \pm 66	819 \pm 74	917 \pm 58	1015 \pm 64
Hull Material	Unsprayed	552 \pm 56	624 \pm 63	941 \pm 64	1064 \pm 72
	Sprayed	501 \pm 16	563 \pm 17	957 \pm 42	1077 \pm 47
Protein Isolate	Unsprayed	483 \pm 31	493 \pm 32	627 \pm 50	640 \pm 51
	Sprayed	1020 \pm 41	1042 \pm 42	1078 \pm 17	1101 \pm 17
Untoasted Meal	Unsprayed	Not Detected		Not Detected	
	Sprayed	<LOQ		Not Detected	
Toasted Meal	Unsprayed	Not Detected		Not Detected	
	Sprayed	Not Detected		Not Detected	
Crude Oil	Unsprayed	Not Detected		Not Detected	
	Sprayed	Not Detected		Not Detected	
Crude Lecithin	Unsprayed	Not Detected		Not Detected	
	Sprayed	Not Detected		Not Detected	
Refined Oil	Unsprayed	Not Detected		Not Detected	
	Sprayed	Not Detected		Not Detected	
Refined Bleached Deodorized Oil	Unsprayed	Not Detected		Not Detected	
	Sprayed	Not Detected		Not Detected	

STUDY IDENTIFICATION

Study Initiated:	July 29, 2009
Experimental Start Date:	July 30, 2009
Experimental Termination Date:	August 26, 2009
Study Completion Date:	October 27, 2009
Sponsor Facility Address:	Bayer CropScience 2 T. W. Alexander Drive Research Triangle Park, NC 27709
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ABBREVIATIONS, ACRONYMS and SCIENTIFIC TERMS

2mEPSPS - Modified 5-enolpyruvyl-shikimate-3-phosphate synthase

BSA – Bovine Serum Albumin

COA – Certificate of Analysis

COAs – Certificates of Analysis

CV – Coefficient of Variation

d.w. – dry weight

ELISA – Enzyme Linked ImmunoSorbent Assay

f.w. – fresh weight

FRAC – Fractions of Raw Agricultural Commodity

g - gram

GLP – Good Laboratory Practice

GLPS – Good Laboratory Practice Standards

HPPD -- hydroxyl phenyl-pyruvate-dioxygenase

kDa – kilo Daltons

LOD – Limit of Detection

LOQ – Limit of Quantification

mL – milliLiter

mM – milliMoles (milliMolar)

NA – Not Applicable

ND – Not Detected

ng -- nanogram

NT – Non-transgenic

OD – Optical Density

PCR – Polymerase Chain Reaction

SD – Standard Deviation

USA – United States of America

1. INTRODUCTION

The *2mepsps* and *hppd* genes were genetically engineered into soybean as event FG72. When expressed, 2mEPSPS (5-enolpyruvylshikimate-3-phosphate synthase) confers tolerance to glyphosate herbicide, and HPPDW336 (hydroxyl-phenyl-pyruvate-dioxygenase) confers tolerance to isoxaflutole herbicide. Planting double-herbicide-tolerant soybean varieties containing transformation event FG72 provides growers with new options for weed control using IFT herbicide (registered in North America as Balance Pro®) in combination with glyphosate herbicide.

Soybean and soybean processed products are used for animal feed and human consumption. As a consequence, data are required on the amount of 2mEPSPS and HPPDW336 (also referred to as HPPD in this report) proteins in raw agricultural commodities to support the food and feed safety assessment of event FG72 soybean.

The purpose of this study was to determine the amounts of HPPD and 2mEPSPS proteins in processed fractions derived from soybean seed of transgenic event FG72. The test system was selected because the target crop, cultural practices, and application techniques, and processing procedures are all representative of the intended use pattern of the FG72 transgenic event soybean plants. The seed for all soybean grown, analyzed, and reported herein was supplied by MS Technologies LLC, Adel, Iowa.

2. FIELD PHASE

The transgenic soybean and its non-transgenic counterpart (control) were grown successfully at one trial site for Bayer CropScience in field study number HT08SOY001¹ in 2008 as outlined in the following table:

Table 1. Soybean Trial Site Identification from Study Number HT08SOY001

Trial Number	City	State	County	Principal Field Investigators
01	Adel	Iowa	Dallas	Justin Mason

The sample numbers for the harvested whole soybean seed is presented in the following table:

Table 2. Soybean Seed Collected from Study Number HT08SOY001

Regimen	Sample Number	Description
A	HT08SOY001-01-01	Non-transgenic Control
B	HT08SOY001-01-02	FG72: Unsprayed Transgenic
C	HT08SOY001-01-03	FG72: Sprayed Transgenic*

Regimen C received one foliar tank mix application of Balance® Pro (active ingredient: isoxaflutole) at 0.062 lb ai/A (70 g ai/ha), Roundup Original Max® (active ingredient: glyphosate) at 0.95 lb ai/A (1060 g ai/ha), and ammonium sulfate at 8 lb /100 gal (2850 g/ha) at post V4-V5 growth stage.

The soybean was harvested at normal maturity by mechanical means to obtain the required seed RAC. After harvest, the soybeans were shipped directly to GLP Technologies, in Navasota, Texas for processing under Bayer CropScience study number DQ09B002⁸. The processed samples obtained and assigned sample numbers are presented in Table 3.

Table 3. Soybean Raw Agricultural Commodity (Seed) and Processed Fraction Samples Collected from Study Number DQ09B002.

Description	Non-Transgenic Control*	FG72: Unsprayed Transgenic	FG72: Sprayed Transgenic
Parent Sample No.	HT08SOY001-01-01	HT08SOY001-01-02	HT08SOY001-01-03
	BTID No.	BTID No.	BTID No.
Whole Soybeans (RAC))	2459A	2460A	2461A
Hull Material (H)	2459B	2460B	2461B
Untoasted Soybean Meal (M)	2459C	2460C	2461C
Toasted Soybean Meal (T)	2459D	2460D	2461D
Crude Oil (C)	2459E	2460E	2461E
Crude Lecithin (L)	2459F	2460F	2461F
Refined Oil (R)	2459G	2460G	2461G
Refined Bleached Deodorized Oil (D)	2459H	2460H	2461H
Protein Isolate (P)	2459I	2460I	2461I

*Non-transgenic control samples were not analyzed for gene product content. However, they were used for background control and ELISA validation.

The samples were shipped on dry ice overnight via Federal Express to Bayer CropScience, RTP, NC. Upon receipt at Bayer CropScience, the samples were logged into the BioAnalytics laboratory and placed in a walk-in freezer. The samples were stored in the freezer set to maintain a temperature of -10 °C or lower, except when removed for analysis. The samples were returned to frozen storage following analysis.

A total of 27 samples of soybean seed and processed fractions were generated as described in study DQ09B002 and shipped to Bayer CropScience in Research Triangle Park, NC, for determination of the content of the HPPD and 2mEPSPS proteins. Non-transgenic control samples were not analyzed for gene product content. However, they were used for background control and ELISA validation

3. ANALYTICAL PHASE

3.1. Reference Substances

The reference substances used in this study are described in Table 4. 2mEPSPS and HPPD protein reference substances were used as standards and to fortify non-transgenic samples.

Table 4 Reference Substances

Reference Substance (protein)	Batch No./ COA No.	Chemical name	Molecular Weight
2mEPSPS	LEJ5838/ BBS06-009 ²	modified 5-enolpyruvyl-shikimate-3-phosphate synthase	47 kDa ⁴
HPPDW336	LB020309/ BBS09-001 ³	modified hydroxyl-phenyl-pyruvate-dioxygenase	40 kDa ⁵

3.2. Certificates of Analysis

Certificate of analysis (COA) BTS-0021/09 documents the identity of the processed soybean samples from study DQ09B002. Bayer CropScience in RTP analyzed the processed samples for the presence of DNA from event FG72. The COA is provided in Appendix 1.

Bayer CropScience in Gent, Belgium, produced reports serving as COAs for the 2mEPSPS and HPPDW336 proteins. Copies of the certificates of analysis are maintained with the study file.

3.3. Samples

The whole soybeans and processed samples were maintained at Bayer CropScience in Research Triangle Park, NC in a freezer at -10°C or lower until sample preparation. The amounts of 2mEPSPS and HPPD were determined at Bayer CropScience, NC. The critical dates for receipt, sample transfer to RTP, processing and analysis of the samples are given in Appendix 2, Tables A2-4.

3.4. Sample Preparation

An aliquot of the whole soybeans, hull material, untoasted meal, and toasted meal were ground in the presence of dry ice using a waring blender according to SOP 98034.00. Small amounts of dry ice were added to the blender periodically to ensure the samples remained frozen during preparation. A separate blender was used for each sample. The ground samples were stored in a freezer at approximately -20°C for overnight or longer to allow the dry ice to sublimate before extraction. Crude oil, crude lecithin, refined oil, refined bleached deodorized oil, and protein isolate samples were analyzed as received without any additional homogenization.

3.5. Extraction

Total protein was extracted from the whole soybeans and processed fractions according to SOP 98033.00, and was determined as a relative measure of extraction efficiency. PBST Extraction/Dilution Buffer, Agdia, Inc. Catalog Number ACC 00501A, was used. A representative fraction (approximately 0.1 g) of sample was mixed with either 2 mL or 4 mL of extraction buffer in a 50 mL polypropylene centrifuge tube, and then shaken for 30 minutes at ~ 4°C on a shaker (IKA-SCHÜTTLER MTS 4) at 250 rpm. The liquid extract was transferred to a clean centrifuge tube and centrifuged at approximately 18000 x g for 10 minutes at ~ 4°C.

The clear supernatant was then used for 2mEPSPS and HPPD analyses. Duplicate extracts were prepared for each sample.

3.6. Immunoassay

The levels of HPPD and 2mEPSPS proteins were determined by an Enzyme Linked ImmunoSorbent Assay (ELISA) using antibodies specific for each protein according to SOPs 98060 (Draft) and 98052. SOP 98052 was modified by changing the extraction/dilution buffer to PBST Extraction/Dilution Buffer, (Agdia, Inc. Catalog Number ACC 00501), and the sample to buffer ratio was modified for each matrix. All quantitative determinations of 2mEPSPS and HPPD proteins were conducted at Bayer CropScience, Research Triangle Park, NC.

3.7. Standards

Protein standards were included in duplicate on each 2mEPSPS ELISA plate at the following concentrations: 32, 16, 8, 4, 2, 1, 0.5 ng/mL. The standards were plated in duplicate at concentrations of 32, 16, 8, 4, 2, 1 ng/mL on the HPPD ELISA plate.

3.8. Validation

The ELISA procedures were validated according to SOP 98007 using a non-transgenic sample that was also produced in study DQ09B002. The critical dates for validation are listed in Appendix 2, Table A2-1 through A2-3. The non-transgenic samples were fortified at the concentrations listed in Tables 5 through 13. The standards were added to the extraction buffer at the indicated concentrations prior to extraction in five replicates. Each replicate was analyzed using duplicate wells. The protein analyte detected and its recovery were expressed as the average of 10 data points from duplicate extracts of 5 samples at each fortification level using non-transgenic matrix. A summary of the validation data for each analyte is shown in Tables 5 through 13. The complete data sets are given in Appendix 2, Tables A2-5 and A2-22.

Table 5 Validation of Sample Extraction with Fortified NT Whole Soybeans (BTID1754A) ^a

2mEPSPS ELISA Validation				HPPD ELISA Validation			
2mEPSPS fortified (ng/mL)	2mEPSPS detected (ng/mL) Mean \pm SD	% 2mEPSPS Recovery Mean \pm SD	2mEPSPS Recovery %CV	HPPD fortified (ng/mL)	HPPD detected (ng/mL) Mean \pm SD	% HPPD Recovery Mean \pm SD	HPPD Recovery %CV
100	82.5 \pm 2.7	82.5 \pm 2.7	3.32	100	123 \pm 4	123 \pm 4	3.01
32	23.0 \pm 0.5	71.7 \pm 1.6	2.21	32	31.4 \pm 1.3	98.2 \pm 3.9	4.01
16	10.4 \pm 0.3	64.8 \pm 1.6	2.45	16	18.0 \pm 0.9	112 \pm 6	5.26
8	5.14 \pm 0.20	64.2 \pm 2.6	3.98	8	8.34 \pm 0.54	104 \pm 7	6.47
4	2.59 \pm 0.19	64.8 \pm 4.7	7.23	4	3.51 \pm 0.24	87.8 \pm 6.0	6.78
2	1.21 \pm 0.07	60.4 \pm 3.5	5.74	2	1.43 \pm 0.26	71.6 \pm 13.1	18.2
1	0.615 \pm 0.097	61.5 \pm 9.7	15.7	1	0.430 \pm 0.192	43.0 \pm 19.2	44.6
0.5	0.447 \pm 0.116	89.5 \pm 23.2	26.0				

^a Non-Transgenic Whole Soybeans were validated in study DQ09B003

Table 6 Validation of Sample Extraction with Fortified NT Hull Material (BTID 2459B)

2mEPSPS ELISA Validation				HPPD ELISA Validation			
2mEPSPS fortified (ng/mL)	2mEPSPS detected (ng/mL) Mean \pm SD	% 2mEPSPS Recovery Mean \pm SD	2mEPSPS Recovery %CV	HPPD fortified (ng/mL)	HPPD detected (ng/mL) Mean \pm SD	% HPPD Recovery Mean \pm SD	HPPD Recovery %CV
100	115 \pm 4	115 \pm 4	3.08	100	95.8 \pm 3.4	95.8 \pm 3.4	3.54
32	26.9 \pm 0.7	84.2 \pm 2.3	2.73	32	24.8 \pm 0.9	77.6 \pm 2.9	3.78
16	12.3 \pm 0.3	77.0 \pm 1.6	2.05	16	13.9 \pm 0.4	86.8 \pm 2.7	3.10
8	6.11 \pm 0.20	76.4 \pm 2.5	3.23	8	7.40 \pm 0.22	92.5 \pm 2.7	2.97
4	3.04 \pm 0.22	75.9 \pm 5.5	7.18	4	3.79 \pm 0.62	94.7 \pm 15.6	16.4
2	1.32 \pm 0.16	65.9 \pm 8.1	12.3	2	1.66 \pm 0.20	82.8 \pm 10.2	12.3
1	0.86 \pm 0.18	85.9 \pm 18.1	21.0	1	0.65 \pm 0.12	64.9 \pm 11.6	17.9
0.5	0.29 \pm 0.12	58.6 \pm 23.2	39.5				

Table 7 Validation of Sample Extraction with Fortified NT Untoasted Meal (BTID 2459C)

2mEPSPS ELISA Validation				HPPD ELISA Validation			
2mEPSPS fortified (ng/mL)	2mEPSPS detected (ng/mL) Mean \pm SD	% 2mEPSPS Recovery Mean \pm SD	2mEPSPS Recovery %CV	HPPD fortified (ng/mL)	HPPD detected (ng/mL) Mean \pm SD	% HPPD Recovery Mean \pm SD	HPPD Recovery %CV
100	115 \pm 3	115 \pm 3	2.52	100	126 \pm 4	126 \pm 4	3.23
32	31.3 \pm 0.7	97.8 \pm 2.1	2.19	32	34.5 \pm 1.0	108 \pm 3	2.96
16	14.1 \pm 0.7	88.3 \pm 4.1	4.65	16	17.9 \pm 0.8	112 \pm 5	4.35
8	6.87 \pm 0.19	85.9 \pm 2.4	2.78	8	9.81 \pm 0.33	123 \pm 4	3.37
4	3.43 \pm 0.14	85.8 \pm 3.5	4.13	4	5.16 \pm 0.26	129 \pm 6	4.96
2	1.61 \pm 0.10	80.6 \pm 5.2	6.41	2	2.56 \pm 0.57	128 \pm 28	22.2
1	0.75 \pm 0.07	75.5 \pm 7.5	9.87	1	1.25 \pm 0.12	125 \pm 12	9.60
0.5	0.36 \pm 0.11	72.9 \pm 21.9	30.1				

Table 8 Validation of Sample Extraction with Fortified NT Toasted Meal (BTID 2459D)

2mEPSPS ELISA Validation				HPPD ELISA Validation			
2mEPSPS fortified (ng/mL)	2mEPSPS detected (ng/mL) Mean \pm SD	% 2mEPSPS Recovery Mean \pm SD	2mEPSPS Recovery %CV	HPPD fortified (ng/mL)	HPPD detected (ng/mL) Mean \pm SD	% HPPD Recovery Mean \pm SD	HPPD Recovery %CV
100	116 \pm 4	116 \pm 4	3.53	100	92.5 \pm 6.4	92.5 \pm 6.4	6.90
32	31.2 \pm 0.8	97.5 \pm 2.6	2.66	32	26.6 \pm 0.9	83.2 \pm 2.8	3.40
16	14.7 \pm 0.2	91.7 \pm 1.4	1.51	16	13.3 \pm 0.3	83.4 \pm 2.1	2.46
8	7.38 \pm 0.15	92.2 \pm 1.8	2.00	8	7.28 \pm 0.22	91.0 \pm 2.7	3.00
4	3.77 \pm 0.08	94.2 \pm 2.0	2.15	4	3.68 \pm 0.13	92.1 \pm 3.2	3.46
2	1.82 \pm 0.16	91.0 \pm 8.0	8.76	2	1.90 \pm 0.11	94.9 \pm 5.7	6.02
1	0.83 \pm 0.10	83.5 \pm 9.8	11.7	1	1.04 \pm 0.06	104 \pm 6	6.05
0.5	0.40 \pm 0.09	80.5 \pm 18.4	22.8				

Table 9 Validation of Sample Extraction with Fortified NT Crude Oil (BTID 2459E)

2mEPSPS ELISA Validation				HPPD ELISA Validation			
2mEPSPS fortified (ng/mL)	2mEPSPS detected (ng/mL) Mean \pm SD	% 2mEPSPS Recovery Mean \pm SD	2mEPSPS Recovery %CV	HPPD fortified (ng/mL)	HPPD detected (ng/mL) Mean \pm SD	% HPPD Recovery Mean \pm SD	HPPD Recovery %CV
100	110 \pm 10	110 \pm 10	8.68	100	105 \pm 5	105 \pm 5	4.46
32	29.1 \pm 1.7	90.9 \pm 5.4	5.97	32	21.4 \pm 1.0	66.8 \pm 3.0	4.53
16	13.9 \pm 0.3	86.8 \pm 2.1	2.43	16	11.7 \pm 1.7	73.3 \pm 10.8	14.7
8	6.87 \pm 0.16	85.9 \pm 2.0	2.32	8	5.60 \pm 0.26	70.0 \pm 3.2	4.58
4	3.49 \pm 0.21	87.3 \pm 5.2	5.91	4	2.47 \pm 0.13	61.8 \pm 3.2	5.17
2	1.83 \pm 0.19	91.6 \pm 9.5	10.3	2	1.43 \pm 0.15	71.4 \pm 7.4	10.4
1	0.80 \pm 0.14	80.4 \pm 14.3	17.8	1	0.59 \pm 0.14	59.1 \pm 13.7	23.3
0.5	0.33 \pm 0.09	66.3 \pm 18.3	27.6				

Table 10 Validation of Sample Extraction with Fortified NT Crude Lecithin (BTID 2459F)

2mEPSPS ELISA Validation				HPPD ELISA Validation			
2mEPSPS fortified (ng/mL)	2mEPSPS detected (ng/mL) Mean \pm SD	% 2mEPSPS Recovery Mean \pm SD	2mEPSPS Recovery %CV	HPPD fortified (ng/mL)	HPPD detected (ng/mL) Mean \pm SD	% HPPD Recovery Mean \pm SD	HPPD Recovery %CV
100	123 \pm 6	123 \pm 6	4.75	100	79.1 \pm 10.2	79.1 \pm 10.2	13.0
32	33.2 \pm 0.6	104 \pm 2	1.81	32	28.5 \pm 0.8	89.0 \pm 2.4	2.74
16	15.8 \pm 0.3	98.8 \pm 2.1	2.12	16	12.9 \pm 0.7	80.9 \pm 4.4	5.47
8	7.92 \pm 0.29	99.1 \pm 3.6	3.66	8	7.33 \pm 0.31	91.7 \pm 3.8	4.17
4	3.99 \pm 0.14	99.7 \pm 3.4	3.42	4	3.88 \pm 0.12	97.1 \pm 2.9	2.98
2	1.86 \pm 0.17	93.0 \pm 8.6	9.28	2	2.26 \pm 0.24	113 \pm 12	10.5
1	0.84 \pm 0.16	84.4 \pm 15.6	18.5	1	1.06 \pm 0.16	106 \pm 16	14.8
0.5	0.42 \pm 0.16	83.2 \pm 31.7	38.1				

Table 11 Validation of Sample Extraction with Fortified NT Refined Oil (BTID 2459G)

2mEPSPS ELISA Validation				HPPD ELISA Validation			
2mEPSPS fortified (ng/mL)	2mEPSPS detected (ng/mL) Mean \pm SD	% 2mEPSPS Recovery Mean \pm SD	2mEPSPS Recovery %CV	HPPD fortified (ng/mL)	HPPD detected (ng/mL) Mean \pm SD	% HPPD Recovery Mean \pm SD	HPPD Recovery %CV
100	112 \pm 2	112 \pm 2	2.09	100	77.2 \pm 1.9	77.2 \pm 1.9	2.43
32	33.9 \pm 1.9	106 \pm 6	5.55	32	30.4 \pm 0.7	95.0 \pm 2.2	2.30
16	15.7 \pm 0.5	97.9 \pm 2.9	2.96	16	13.6 \pm 0.2	85.0 \pm 1.4	1.62
8	7.73 \pm 0.28	96.7 \pm 3.5	3.65	8	7.37 \pm 0.48	92.2 \pm 6.0	6.53
4	3.95 \pm 0.11	98.7 \pm 2.8	2.80	4	4.20 \pm 0.17	105 \pm 4	4.05
2	1.76 \pm 0.08	88.2 \pm 4.1	4.61	2	2.23 \pm 0.22	111 \pm 11	10.1
1	0.84 \pm 0.17	83.7 \pm 16.7	20.0	1	0.89 \pm 0.18	89.2 \pm 18.4	20.6
0.5	0.32 \pm 0.11	64.8 \pm 21.7	33.5				

Table 12 Validation of Sample Extraction with Fortified NT Refined Bleached Deodorized Oil (BTID 2459H)

2mEPSPS ELISA Validation				HPPD ELISA Validation			
2mEPSPS fortified (ng/mL)	2mEPSPS detected (ng/mL) Mean \pm SD	% 2mEPSPS Recovery Mean \pm SD	2mEPSPS Recovery %CV	HPPD fortified (ng/mL)	HPPD detected (ng/mL) Mean \pm SD	% HPPD Recovery Mean \pm SD	HPPD Recovery %CV
100	123 \pm 6	123 \pm 6	4.80	100	103 \pm 3	103 \pm 3	2.48
32	36.8 \pm 2.2	115 \pm 7	5.85	32	28.4 \pm 0.6	88.8 \pm 1.9	2.08
16	16.5 \pm 0.5	103 \pm 3	3.05	16	13.8 \pm 0.3	86.5 \pm 1.7	1.92
8	7.51 \pm 0.47	93.9 \pm 5.9	6.31	8	7.71 \pm 0.13	96.4 \pm 1.6	1.66
4	3.43 \pm 0.30	85.8 \pm 7.5	8.69	4	3.32 \pm 0.25	83.0 \pm 6.3	7.60
2	1.82 \pm 0.13	91.2 \pm 6.5	7.13	2	2.12 \pm 0.17	106 \pm 9	8.13
1	0.85 \pm 0.09	85.3 \pm 8.8	10.3	1	1.23 \pm 0.20	123 \pm 20	15.9
0.5	0.37 \pm 0.12	74.8 \pm 23.1	30.9				

Table 13 Validation of Sample Extraction with Fortified NT Protein Isolate (BTID 2459I)

2mEPSPS ELISA Validation				HPPD ELISA Validation			
2mEPSPS fortified (ng/mL)	2mEPSPS detected (ng/mL) Mean ± SD	% 2mEPSPS Recovery Mean ± SD	2mEPSPS Recovery %CV	HPPD fortified (ng/mL)	HPPD detected (ng/mL) Mean ± SD	% HPPD Recovery Mean ± SD	HPPD Recovery %CV
100	79.2 ± 3.6	79.2 ± 3.6	4.57	100	87.3 ± 2.4	87.3 ± 2.4	2.75
32	22.2 ± 0.8	69.5 ± 2.5	3.58	32	25.4 ± 0.7	79.5 ± 2.3	2.86
16	12.9 ± 2.5	80.4 ± 15.8	19.7	16	11.5 ± 0.4	71.7 ± 2.3	3.14
8	5.29 ± 0.33	66.1 ± 4.1	6.22	8	6.30 ± 0.19	78.7 ± 2.4	3.00
4	2.59 ± 0.25	64.9 ± 6.3	9.67	4	3.34 ± 0.28	83.4 ± 6.9	8.26
2	1.22 ± 0.16	60.9 ± 8.0	13.1	2	1.61 ± 0.27	80.5 ± 13.3	16.5
1	1.15 ± 0.81	115 ± 81	70.4	1	0.75 ± 0.18	75.3 ± 18.2	24.2
0.5	0.69 ± 0.62	138 ± 123	89.1				

3.9. Limit of Detection and Limit of Quantitation

The limit of detection (LOD) is determined for the matrix using the average standard curve and the concentration derived from the background optical density (OD) of the negative control samples. The LOD is defined as the concentration corresponding to an OD value three standard deviations above the mean background OD.

The LOD is expressed in the unit of concentration (ng/mL) and the unit of weight ratio (ng/g matrix, i.e. ppb) calculated based on the extraction of an amount of the matrix with a known volume of extraction buffer, e.g., 0.1 g of matrix per 4 mL extraction buffer. The data used for these calculations are given in Appendix 2, Table A2-23 through A2-28 and are summarized in Tables 14 and 15 below. An absorbance reading giving rise to a protein analyte concentration above the LOD is assumed to be greater than the zero dose reading.

The limit of quantification (LOQ) is defined as the lowest concentration of the standard that meets the validity criteria for the LOQ. Validity criteria are a) analyte recoveries from fortified matrix samples are $\geq 60\%$ and $\leq 130\%$ and b) the coefficient of variance (relative standard deviation) is less than 25%. When a lower recovery is caused by the nature of a specific matrix or the effect of a process, the lowest concentration of the standard that gives a coefficient of variance equal to or less than 25% is used as the LOQ. Values below the LOD are reported as “not detected” and values below the LOQ but above the LOD are reported as “<LOQ”. In calculations, values below the LOD are treated as zero. Values below the LOQ but above the LOD are assumed to be at the LOQ. The LOQ values are determined by inspection from Tables 14 and 15. The LOD and LOQ of HPPD and 2mEPSPS proteins in whole soybeans and processed fractions are summarized and presented below in Tables 14 and 15.

Table 14. Limits of Detection and Quantitation of 2mEPSPS Protein in Processed Fractions Derived from Non-Transgenic Whole Soybeans as Detected by ELISA

Raw Agricultural Product	LOD		LOQ	
	ng/mL	ng/g	ng/mL	ng/g
Whole Soybeans ^a	0.258	10.3	1.00	40.0
Hull Material ^a	0.375	15.0	1.00	40.0
Untoasted Meal ^b	0.353	7.06	1.00	20.0
Toasted Meal ^b	0.291	5.82	0.50	10.0
Crude Oil ^b	0.357	7.14	1.00	20.0
Crude Lecithin ^b	0.393	7.86	1.00	20.0
Refined Oil ^b	0.256	5.12	1.00	20.0
Refined Bleached Deodorized Oil ^b	0.204	4.08	1.00	20.0
Protein Isolate ^a	0.706	28.2	2.00	80.0

^a Calculated based on the extraction of 0.1 g matrix per 4 mL of extraction buffer for whole soybeans, hull material, and protein isolate.

^b Calculated based on the extraction of 0.1 g matrix per 2 mL of extraction buffer for untoasted meal, toasted meal, crude lecithin, and all oil processed fractions.

Table 15. Limits of Detection and Quantitation of HPPD Protein in Processed Fractions Derived from Non-Transgenic Whole Soybeans as Detected by ELISA

Raw Agricultural Product	LOD		LOQ	
	ng/mL	ng/g	ng/mL	ng/g
Whole Soybeans ^a	0.521	20.8	2.00	80.0
Hull Material ^a	0.672	26.9	1.00	40.0
Untoasted Meal ^b	0.333	6.66	1.00	20.0
Toasted Meal ^b	0.308	6.16	1.00	20.0
Crude Oil ^b	0.639	12.8	2.00	40.0
Crude Lecithin ^b	0.358	7.16	1.00	20.0
Refined Oil ^b	0.641	12.8	1.00	20.0
Refined Bleached Deodorized Oil ^b	0.861	17.2	1.00	20.0
Protein Isolate ^a	0.697	27.9	1.00	40.0

^a Calculated based on the extraction of 0.1 g matrix per 4 mL of extraction buffer for whole soybeans, hull material, and protein isolate.

^b Calculated based on the extraction of 0.1 g matrix per 2 mL of extraction buffer for untoasted meal, toasted meal, crude lecithin, and all oil processed fractions.

3.10. Protein Analyte Content

SoftMax Pro™ software (Molecular Devices, Version 4.0) was used to derive the concentration of 2mEPSPS and HPPD proteins from the ELISA data. Absorbance units were adjusted for the buffer blank. A set of wells containing samples of the corresponding non-transgenic matrix was included on each plate for background subtraction. The appropriate background corrections for the transgenic samples were obtained from background values of a non-transgenic sample, which was diluted on the same plate and to the same extent as the transgenic sample. Thus the dilution of the non-transgenic sample used for background subtraction was the same as the dilution of the transgenic sample that was required in order to place the OD reading in the center portion of the standard curve. The absorbance readings corrected for both buffer blank and non-transgenic background were converted to the protein concentration using the standard curve. The analytical results from the ELISA data are presented in Appendix 2, Tables A2-29 through A2-30.

The absorbance assays give results in units of ng of analyte per milliliter of extract. Results are then converted into amount of analyte per gram of fresh sample. Percent moisture data for these samples were obtained from study DQ09B009⁶. The data are summarized in Table 18. Dry weight analyte content is obtained by dividing the fresh weight analyte content by the calculated percent dry matter and multiplying by 100. Percent dry matter is obtained by subtracting the percent moisture from 100. The following is the formula used.

$$\text{analyte dry weight content ng / g} = \left(\frac{\text{ng analyte / g}}{(100 - \% \text{ moisture})} \right) \times 100$$

3.11. Statistical Analysis

Descriptive statistics (mean, standard deviation, and coefficient of variance) were calculated for each sample matrix and treatment⁷. Bayer CropScience conducted all statistical analyses.

4. RESULTS AND DISCUSSION

Transgenic whole soybeans and processed fraction samples were analyzed to determine the amounts of 2mEPSPS protein and HPPD protein. Detailed fresh weight amounts of analyte measured are presented in Tables A2-29 through A2-30 in Appendix 2. The mean and standard deviations for the amount of 2mEPSPS and HPPD proteins are presented in Tables 16 and 17, respectively. Averages and standard deviations for the individual matrices were based on 4 measurements (2 sample extracts assayed in duplicate).

Table 16. Average 2mEPSPS Protein Content (Fresh Weight) in Whole Soybeans (RAC) and Processed Fractions as Detected by ELISA

Soybean Matrix	Average 2mEPSPS Content (ng/g fresh weight) \pm SD	
	FG72 Unsprayed Transgenic	FG72 Sprayed Transgenic
Whole Soybeans	572 \pm 20	740 \pm 66
Hull Material	552 \pm 56	501 \pm 16
Untoasted Meal	ND	<LOQ
Toasted Meal	ND	ND
Crude Oil	ND	ND
Crude Lecithin	ND	ND
Refined Oil	ND	ND
Refined Bleached Deodorized Oil	ND	ND
Protein Isolate	483 \pm 31	1020 \pm 41

Table 17. Average HPPD Protein Content (Fresh Weight) in Whole Soybeans (RAC) and Processed Fractions as Detected by ELISA

Soybean Matrix	Average HPPD Content (ng/g fresh weight) \pm SD	
	FG72 Unsprayed Transgenic	FG72 Sprayed Transgenic
Whole Soybeans	754 \pm 37	917 \pm 58
Hull Material	941 \pm 64	957 \pm 42
Untoasted Meal	ND	ND
Toasted Meal	ND	ND
Crude Oil	ND	ND
Crude Lecithin	ND	ND
Refined Oil	ND	ND
Refined Bleached Deodorized Oil	ND	ND
Protein Isolate	627 \pm 50	1078 \pm 17

Analyte levels, calculated on a dry weight and percent total protein basis using percent moisture and total protein values are summarized in Table 18.

Table 18. 2mEPSPS and HPPD Protein Content (Dry Weight) in Unsprayed & Sprayed FG72 Whole Soybeans & Processed Fractions

Treatment	BTID	Matrix	% Moisture	2mEPSPS Content		HPPD Content	
				fresh weight (ng/g) ± SD	dry weight (ng/g) ± SD	fresh weight (ng/g) ± SD	dry weight (ng/g) ± SD
Unsprayed	2460A	Whole Soybeans	10.0	572 ± 20	636 ± 22	754 ± 37	838 ± 41
Unsprayed	2460B	Hull Material	11.6	552 ± 56	624 ± 63	941 ± 63	1064 ± 72
Unsprayed	2460C	Untoasted Meal	8.83	ND	ND	ND	ND
Unsprayed	2460D	Toasted Meal	11.3	ND	ND	ND	ND
Unsprayed	2460I	Protein Isolate	1.92	483 ± 31	493 ± 32	627 ± 50	640 ± 51
Sprayed	2461A	Whole Soybeans	9.67	740 ± 66	819 ± 74	917 ± 58	1015 ± 64
Sprayed	2461B	Hull Material	11.1	501 ± 16	563 ± 17	957 ± 42	1077 ± 47
Sprayed	2461C	Untoasted Meal	9.51	<LOQ	<LOQ	ND	ND
Sprayed	2461D	Toasted Meal	11.0	ND	ND	ND	ND
Sprayed	2461I	Protein Isolate	2.10	1020 ± 41	1042 ± 42	1078 ± 17	1101 ± 17

ND

Not detected

NA

Not applicable, since recombinant proteins were not detected or below the LOQ

2mEPSPS protein was either not detected or was detected below the LOQ for untoasted meal, toasted meal, crude oil, crude lecithin, refined oil, and refined bleached deodorized oil matrices in both unsprayed and sprayed transgenic regimens.

HPPD protein was not detected for untoasted meal, toasted meal, crude oil, crude lecithin, refined oil, and refined bleached deodorized oil matrices in both unsprayed and sprayed transgenic regimens.

5. CONCLUSION

Processing factors were calculated to determine the extent the protein analytes concentrated in the processed fractions (Tables 19 and 20) according to the following formula:

$$\text{Processing factor} = \frac{\text{Average protein concentration in processed fraction}}{\text{Average protein concentration in whole soybeans}}$$

Following the production of FG72 transgenic whole soybeans and the subsequent processing of the soybeans into the processed commodities, 2mEPSPS concentrated only slightly (<2X) in protein isolate from the sprayed regimen. HPPD concentrated only slightly (<2X) in unsprayed hull material and sprayed protein isolate.

Table 19. 2mEPSPS Processing Factors Generated from FG72 Whole Soybeans.

RAC or Processed Fraction	Regimen	Average 2mEPSPS Content (ng/g)	Processing Factor^a
Whole Soybeans	Unsprayed	572	Not Applicable
Whole Soybeans	Sprayed	740	Not Applicable
Hull Material	Unsprayed	552	<1.0 (1.0 X)
Hull Material	Sprayed	501	<1.0 (0.7 X)
Untoasted Meal	Unsprayed	Not Detected	Not Applicable
Untoasted Meal	Sprayed	<LOQ	Not Applicable
Toasted Meal	Unsprayed	Not Detected	Not Applicable
Toasted Meal	Sprayed	Not Detected	Not Applicable
Crude Oil	Unsprayed	Not Detected	Not Applicable
Crude Oil	Sprayed	Not Detected	Not Applicable
Crude Lecithin	Unsprayed	Not Detected	Not Applicable
Crude Lecithin	Sprayed	Not Detected	Not Applicable
Refined Oil	Unsprayed	Not Detected	Not Applicable
Refined Oil	Sprayed	Not Detected	Not Applicable
Refined Bleached Deodorized Oil	Unsprayed	Not Detected	Not Applicable
Refined Bleached Deodorized Oil	Sprayed	Not Detected	Not Applicable
Protein Isolate	Unsprayed	483	<1.0 (0.8 X)
Protein Isolate	Sprayed	1020	1.4 X

^a Processing factor =
$$\frac{\text{Average 2mEPSPS in processed fraction}}{\text{Average 2mEPSPS in whole soybeans}}$$

Table 20. HPPD Processing Factors Generated from FG72 Whole Soybeans.

RAC or Processed Fraction	Regimen	Average HPPD Content (ng/g)	Processing Factor^a
Whole Soybeans	Unsprayed	754	Not Applicable
Whole Soybeans	Sprayed	917	Not Applicable
Hull Material	Unsprayed	941	1.2 X
Hull Material	Sprayed	957	1.0 X
Untoasted Meal	Unsprayed	Not Detected	Not Applicable
Untoasted Meal	Sprayed	Not Detected	Not Applicable
Toasted Meal	Unsprayed	Not Detected	Not Applicable
Toasted Meal	Sprayed	Not Detected	Not Applicable
Crude Oil	Unsprayed	Not Detected	Not Applicable
Crude Oil	Sprayed	Not Detected	Not Applicable
Crude Lecithin	Unsprayed	Not Detected	Not Applicable
Crude Lecithin	Sprayed	Not Detected	Not Applicable
Refined Oil	Unsprayed	Not Detected	Not Applicable
Refined Oil	Sprayed	Not Detected	Not Applicable
Refined Bleached Deodorized Oil	Unsprayed	Not Detected	Not Applicable
Refined Bleached Deodorized Oil	Sprayed	Not Detected	Not Applicable
Protein Isolate	Unsprayed	627	<1.0 (0.8 X)
Protein Isolate	Sprayed	1078	1.2 X

$$^a \text{ Processing factor} = \frac{\text{Average HPPD in processed fraction}}{\text{Average HPPD in whole soybeans}}$$

6. ARCHIVING

The final report, raw data, computer generated listings of raw data and supporting documentation are archived under study number DQ09B008 in the Archives of Bayer CropScience, 2 T.W. Alexander Drive, Research Triangle Park, NC 27709. Retained samples are stored at the same address.

7. REFERENCES

No.	Author(s). Year. Title. Source. Edition. Pages.
1	Kowite, William J. 2009. Production of Raw Agricultural Commodities (Grain) of Transgenic Event FG72 Soybeans from Single Field Trial, USA, 2008. Study Identification Number HT08SOY001.
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4	Lebrun, M., Sailland, A., Freyssinet, G., and Degryse, E. 1997. Mutated 5-enolpyruvylshikimate-3-phosphate synthase, gene encoding for said protein and transformed plants containing said gene. International patent publication WO 97/04103-A2. 06.02.97. 25 pages.
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7	Devore, J; Peck, R. (1986). Statistics. West Publishing Company, St. Paul
8	Kowite, William J. 2009. Production of Processed Commodities from Transgenic Event FG72 Soybeans and the Non-transgenic Counterpart (2009). Study Identification Number DQ09B002.

APPENDIX 1
Certificate of Analysis



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No. BTS-0021/09
Page 1 of 4

CERTIFICATE OF ANALYSIS NO. BTS-0021/09

General

This Certificate fulfills the requirement for the characterization of sample used in a study according to Good Laboratory Practice (GLP) regulations (40 CFR Part 160). It documents the identity of the sample.

Designation of the Certified Material:

Material: Soybean Processed Agricultural Commodities (FRAC) produced from soybeans containing event FG72 and a non-transgenic counterpart.

Study No.: DQ09B010

Sample Nos.: BTID 2459A-I: Regimen A, non-transgenic counterpart
BTID 2460A-I: Regimen B, unsprayed event FG72
BTID 2461A-I: Regimen C, sprayed event FG72

Additional information: The soybean RAC was produced by study HT08SOY001.
The processed fractions were generated by study DQ09B002, and analyzed for gene product content in study DQ09B008.

Origin of the Certified Material

Joseph Gibson
GLP Technologies
22723 State Highway 6 South
Navasota, TX 77868

Methods

The ☒ Identity
☐ Purity
☐ Content

of the material was established by use of the following method(s):

☒ Discriminating PCR (SOP98049.00, SOP98037.00, BAM/011/01, MDP0675_01)
☐ Southern Blotting
☐ ELISA
☐ Bradford Assay
☒ Real Time Discriminating PCR (PGS0475_01, MDP0678_01)



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No. BTS-0021/09
Page 2 of 4

Date(s) of Analysis

August 14, 2009 to October 3, 2009

Results

Four of the FRAC matrices required grinding before analysis: whole soybeans, hulls, meal, and toasted meal. They were ground according to SOP 98034.00 in a blender with dry ice. The meals were already coarsely ground; this grinding was done in order to reduce the particle size for more efficient extraction. Crude oil, crude lecithin, refined oil, RBD Oil, and protein isolate were not ground prior to DNA extraction.

DNA was extracted in duplicate from each sample using a silica gel based technology (SOP 98049.00). Real Time PCR was used to detect FG72 DNA sequence, as well as a soybean endogenous reference gene. When compared to the leaf DNA positive control, FG72 DNA was detected only in seed, hulls, meal, and toasted meal. Real time PCR results from all other matrices were inconclusive; therefore, discriminating PCR was carried out according to method BAM/011/01 and SOP 98037.00 using primers from method MDP0675_01 for event FG72. Event FG72 DNA was detected in all matrices except refined oil and RBD oil. Results are given in Tables 1-3.

Table 1: PCR results from BTID 2459A-I: Regimen A, Non-transgenic soybean

<i>BTID</i>	<i>Description</i>	<i>Sample Number</i>	<i>FG72 DPCR</i>
2459A	Whole Soybeans (RAC)	HT08SOY001-01-01	-
2459B	Hull Material	DQ09B002-AH	-
2459C	Meal	DQ09B002-AM	-
2459D	Toasted Meal	DQ09B002-AT	-
2459E	Crude Oil	DQ09B002-AC	-
2459F	Crude Lecithin	DQ09B002-AL	-
2459G	Refined Oil	DQ09B002-AR	-
2459H	Refined, Bleached, Deodorized Oil (RBD Oil)	DQ09B002-AD	-
2459I	Protein Isolate	DQ09B002-AP	-

Table 2: PCR results from BTID 2460A-I: Regimen B, Event FG72 soybean, Unsprayed

<i>BTID</i>	<i>Description</i>	<i>Sample Number</i>	<i>FG72 DPCR</i>
2460A	Whole Soybeans (RAC)	HT08SOY001-01-02	+
2460B	Hull Material	DQ09B002-BH	+
2460C	Meal	DQ09B002-BM	+
2460D	Toasted Meal	DQ09B002-BT	+
2460E	Crude Oil	DQ09B002-BC	+
2460F	Crude Lecithin	DQ09B002-BL	+
2460G	Refined Oil	DQ09B002-BR	ND
2460H	Refined, Bleached, Deodorized Oil (RBD Oil)	DQ09B002-BD	ND
2460I	Protein Isolate	DQ09B002-BP	+

ND=Not detected



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No. BTS-0021/09
Page 3 of 4

Table 3: PCR results from BTID 2461A-I: Regimen C, Event FG72 soybean, Sprayed

BTID	Whole Soybeans (RAC)	Sample Number	FG72 DPCR
2461A	Hull Material	HT08SOY001-01-03	+
2461B	Meal	DQ09B002-CH	+
2461C	Toasted Meal	DQ09B002-CM	+
2461D	Crude Oil	DQ09B002-CT	+
2461E	Crude Lecithin	DQ09B002-CC	+
2461F	Refined Oil	DQ09B002-CL	+
2461G	Refined, Bleached, Deodorized Oil (RBD Oil)	DQ09B002-CR	ND
2461H	Protein Isolate	DQ09B002-CD	ND
2461I	Whole Soybeans (RAC)	DQ09B002-CP	+

ND=Not detected

Since no PCR product was observed in refined oil or RBD oil, a spike and recovery experiment was done in order to estimate the LOD in those matrices. The LOD is defined as the minimum amount of DNA in a sample that can be reliably detected by PCR.

The non-transgenic sample of each of the two oils (BTID 2459G-H) was fortified in the matrix prior to extraction at 1, 0.1, and 0.01 ng/μL using DNA extracted from the FG72 whole soybean fraction (BTID 2461A). DNA extraction was performed according to SOP 98049.

Each extract was analyzed by discriminating PCR according to method MDP0675_01. PCR products were reliably detected at all fortification levels above 0.01ng/μL. PCR products were not detected from unfortified oil. Therefore, if any DNA is present in refined oil and RBD oil, its concentration is less than 0.1ng/μL. The LOD in these matrices is 0.1 ng genomic DNA/ μL (Table 4).

Table 4: LOD Determination in refined oil and RBD oil (BTID 2459G-H)

Fortified with FG72 DNA (ng/μL)	FG72 DPCR
1	+
0.1	+
0.01	-



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No. BTS-0021/09
Page 4 of 4

Testing Facility

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Report and raw data are archived at Bayer CropScience, RTP, NC

	Name (Typed)	Signature	Date
Responsible Scientist:	Martha R. Poe	<i>Martha R. Poe</i>	Oct. 27, 2009
Authorized by:	Sandra J. W. Mackie	<i>Sandra J. W. Mackie</i>	Oct. 27, 2009

APPENDIX 2

Supporting Data

Table A2-1 Critical Dates for Validation of 2mEPSPS and HPPD proteins for Non-transgenic Whole Soybeans^a

Sample ID:	Matrix	Sample Received	Sample Ground	Sample Extracted	2mEPSPS Assayed	HPPD Assayed
1754A	Grain	11/13/2008	4/3/2009	7/21/2009	7/21/2009	7/21/2009

^a Non-Transgenic Whole Soybeans was validated in study DQ09B003

Table A2-2 Critical Dates for Validation of 2mEPSPS proteins for Non-transgenic Processed Fractions

Sample ID:	Matrix	Sample Received	Sample Ground	Sample Extracted	2mEPSPS Assayed
2459B	Hull Material	7/15/2009	7/30/2009	8/11/2009, 8/17/2009	8/11/2009, 8/17/2009
2459C	Untoasted Meal	7/15/2009	7/30/2009	8/11/2009, 8/17/2009	8/11/2009, 8/17/2009
2459D	Toasted Meal	7/15/2009	7/30/2009	8/12/2009	8/12/2009
2459E	Crude Oil	7/15/2009	7/30/2009	8/12/2009	8/12/2009
2459F	Crude Lecithin	7/15/2009	7/30/2009	8/13/2009	8/13/2009
2459G	Refined Oil	7/15/2009	7/30/2009	8/13/2009, 8/17/2009	8/13/2009, 8/17/2009
2459H	Refined Bleached Deodorized Oil	7/15/2009	7/30/2009	8/19/2009	8/19/2009
2459I	Protein Isolate	7/15/2009	7/30/2009	8/19/2009, 8/24/2009	8/19/2009, 8/24/2009

Table A2-3 Critical Dates for Validation of HPPD proteins for Non-transgenic Processed Fractions

Sample ID:	Matrix	Sample Received	Sample Ground	Sample Extracted	HPPD Assayed
2459B	Hull Material	7/15/2009	7/30/2009	8/11/2009	8/11/2009
2459C	Untoasted Meal	7/15/2009	7/30/2009	8/11/2009, 8/17/2009	8/11/2009, 8/17/2009
2459D	Toasted Meal	7/15/2009	7/30/2009	8/12/2009	8/12/2009
2459E	Crude Oil	7/15/2009	7/30/2009	8/12/2009	8/12/2009
2459F	Crude Lecithin	7/15/2009	7/30/2009	8/13/2009	8/13/2009
2459G	Refined Oil	7/15/2009	7/30/2009	8/13/2009	8/13/2009
2459H	Refined Bleached Deodorized Oil	7/15/2009	7/30/2009	8/19/2009, 8/24/2009	8/19/2009, 8/24/2009
2459I	Protein Isolate	7/15/2009	7/30/2009	8/19/2009	8/19/2009

Table A2-4 Critical Dates for Whole Soybeans and Processed Fractions Analysis of 2mEPSPS and HPPD.

Sample Number	BTID ID	Matrix	Regimen	Description	Sample received	Sample ground	Sample extracted	2mEPSPS and HPPD assayed
HT08SOY001-01-02	2460A	Whole Soybeans	B	Unsprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-BH	2460B	Hull Material	B	Unsprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-BM	2460C	Untoasted Meal	B	Unsprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-BT	2460D	Toasted Meal	B	Unsprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-BC	2460E	Crude Oil	B	Unsprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-BL	2460F	Crude Lecithin	B	Unsprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-BR	2460G	Refined Oil	B	Unsprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-BD	2460H	Refined Bleached Deodorized Oil	B	Unsprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-BP	2460I	Protein Isolate	B	Unsprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
HT08SOY001-01-03	2461A	Whole Soybeans	C	Sprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-CH	2461B	Hull Material	C	Sprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-CM	2461C	Untoasted Meal	C	Sprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-CT	2461D	Toasted Meal	C	Sprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-CC	2461E	Crude Oil	C	Sprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-CL	2461F	Crude Lecithin	C	Sprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-CR	2461G	Refined Oil	C	Sprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-CD	2461H	Refined Bleached Deodorized Oil	C	Sprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009
DQ09B002-CP	2461I	Protein Isolate	C	Sprayed	7/15/2009	7/30/2009	8/26/2009	8/26/2009

Table A2-5 Validation of 2mEPSPS ELISA for Whole Soybeans using Sample ID 1754A.

ng 2mEPSPS/ mL spiked	Sample I Weight (g/ 4 mL extraction buffer)	Sample II Weight (g/ 4 mL extraction buffer)	Sample III Weight (g/ 4 mL extraction buffer)	Sample IV Weight (g/ 4 mL extraction buffer)	Sample V Weight (g/ 4 mL extraction buffer)
100	0.11	0.11	0.11	0.10	0.11
32	0.11	0.10	0.10	0.11	0.10
16	0.11	0.11	0.11	0.11	0.10
8	0.10	0.10	0.10	0.11	0.10
4	0.10	0.10	0.10	0.10	0.11
2	0.11	0.11	0.11	0.10	0.10
1	0.10	0.11	0.11	0.11	0.10
0.5	0.10	0.11	0.10	0.11	0.10
0	0.10	0.11	0.10	0.10	0.10

ng 2mEPSPS/ mL spiked	Sample I 2mEPSPS 1 (ng/mL)	Sample I 2mEPSPS 2 (ng/mL)	Sample II 2mEPSPS 1 (ng/mL)	Sample II 2mEPSPS 2 (ng/mL)	Sample III 2mEPSPS 1 (ng/mL)	Sample III 2mEPSPS 2 (ng/mL)	Sample IV 2mEPSPS 1 (ng/mL)	Sample IV 2mEPSPS 2 (ng/mL)	Sample V 2mEPSPS 1 (ng/mL)	Sample V 2mEPSPS 2 (ng/mL)	2mEPSPS (ng/mL) Average	2mEPSPS (ng/mL) SD	2mEPSPS (ng/mL) %CV
100	80.3	80.6	82.8	83.7	82.5	77.3	87.0	84.0	85.3	81.9	82.5	2.74	3.32
32	22.3	22.4	22.7	22.8	22.4	23.3	23.1	23.3	23.8	23.5	23.0	0.51	2.21
16	10.4	10.1	10.3	10.5	10.8	10.6	9.91	10.2	10.5	10.4	10.4	0.25	2.45
8	5.27	5.56	5.08	5.26	5.07	5.29	5.02	4.96	4.97	4.88	5.14	0.20	3.98
4	2.56	2.29	2.60	2.62	3.01	2.71	2.45	2.47	2.58	2.62	2.59	0.19	7.23
2	1.07	1.25	1.31	1.27	1.20	1.26	1.13	1.22	1.19	1.20	1.21	0.07	5.74
1	0.47	0.49	0.61	0.75	0.59	0.66	0.56	0.73	0.59	0.71	0.62	0.10	15.7
0.5	0.35	0.76	0.45	0.47	0.44	0.39	0.43	0.44	0.40	0.35	0.45	0.12	26.0
0	0.03	-0.01	0.10	0.22	0.11	0.20	0.09	0.13	0.08	0.11	0.11	0.07	64.2

ng 2mEPSPS/ mL spiked	% 2mEPSPS Recovery 1	% 2mEPSPS Recovery 2	% 2mEPSPS Recovery 3	% 2mEPSPS Recovery 4	% 2mEPSPS Recovery 5	% 2mEPSPS Recovery 6	% 2mEPSPS Recovery 7	% 2mEPSPS Recovery 8	% 2mEPSPS Recovery 9	% 2mEPSPS Recovery 10	% 2mEPSPS Recovery Average	% 2mEPSPS Recovery SD	% 2mEPSPS Recovery %CV
100	80.3	80.6	82.8	83.7	82.5	77.3	87.0	84.0	85.3	81.9	82.5	2.74	3.32
32	69.7	70.0	70.8	71.2	70.0	72.7	72.3	72.9	74.3	73.3	71.7	1.59	2.21
16	64.8	63.1	64.5	65.8	67.3	66.5	61.9	64.0	65.4	64.8	64.8	1.59	2.45
8	65.8	69.5	63.5	65.8	63.3	66.1	62.8	62.0	62.2	61.0	64.2	2.56	3.98
4	64.0	57.3	65.0	65.4	75.3	67.7	61.3	61.7	64.5	65.6	64.8	4.68	7.23
2	53.6	62.7	65.4	63.3	59.9	62.9	56.4	61.0	59.5	60.0	60.4	3.47	5.74
1	47.3	48.6	61.1	75.1	59.0	65.6	56.0	73.2	58.6	70.9	61.5	9.66	15.7
0.5	69.0	151.2	89.6	93.6	88.4	78.8	85.2	88.8	80.2	69.8	89.5	23.2	26.0

^a Non-Transgenic Whole Soybeans were validated in study DQ09B003

Table A2-6 Validation of 2mEPSPS ELISA for Hull Material using Sample ID 2459B.

ng 2mEPSPS/ mL spiked	Sample I Weight (g/ 4 mL extraction buffer)	Sample II Weight (g/ 4 mL extraction buffer)	Sample III Weight (g/ 4 mL extraction buffer)	Sample IV Weight (g/ 4 mL extraction buffer)	Sample V Weight (g/ 4 mL extraction buffer)
100	0.10	0.10	0.10	0.11	0.10
32	0.11	0.10	0.11	0.11	0.11
16	0.10	0.10	0.10	0.10	0.10
8	0.10	0.10	0.10	0.10	0.10
4	0.10	0.10	0.10	0.10	0.10
2	0.10	0.10	0.10	0.11	0.10
1	0.10	0.10	0.10	0.10	0.10
0.5	0.10	0.11	0.10	0.11	0.10
0	0.11	0.11	0.1	0.11	0.10

ng 2mEPSPS/ mL spiked	Sample I 2mEPSPS 1 (ng/mL)	Sample I 2mEPSPS 2 (ng/mL)	Sample II 2mEPSPS 1 (ng/mL)	Sample II 2mEPSPS 2 (ng/mL)	Sample III 2mEPSPS 1 (ng/mL)	Sample III 2mEPSPS 2 (ng/mL)	Sample IV 2mEPSPS 1 (ng/mL)	Sample IV 2mEPSPS 2 (ng/mL)	Sample V 2mEPSPS 1 (ng/mL)	Sample V 2mEPSPS 2 (ng/mL)	2mEPSPS (ng/mL) Average	2mEPSPS (ng/mL) SD	2mEPSPS (ng/mL) %CV
100	116	111	111	113	120	118	115	110	119	114	115	3.53	3.08
32	26.7	26.1	26.3	25.8	27.5	27.6	27.0	27.2	26.9	28.2	26.9	0.74	2.73
16	12.1	12.3	12.3	12.1	12.2	12.9	12.10	12.5	12.2	12.5	12.3	0.25	2.05
8	5.67	5.95	6.12	6.10	6.30	6.18	6.07	6.15	6.17	6.40	6.11	0.20	3.23
4	3.45	2.74	2.96	2.82	3.17	3.07	2.97	3.17	3.19	2.81	3.04	0.22	7.18
2	1.13	1.15	1.55	1.24	1.48	1.07	1.41	1.33	1.44	1.37	1.32	0.16	12.3
1	0.54	0.81	0.67	0.91	0.88	1.01	0.94	1.18	0.75	0.91	0.86	0.18	21.0
0.5	0.06	0.14	0.31	0.29	0.33	0.40	0.27	0.42	0.32	0.40	0.29	0.12	39.5
0	-0.06	0.07	0.04	0.00	0.02	0.12	-0.21	-0.14	-0.02	0.14	-0.01	0.11	-1973

ng 2mEPSPS/ mL spiked	% 2mEPSPS Recovery 1	% 2mEPSPS Recovery 2	% 2mEPSPS Recovery 3	% 2mEPSPS Recovery 4	% 2mEPSPS Recovery 5	% 2mEPSPS Recovery 6	% 2mEPSPS Recovery 7	% 2mEPSPS Recovery 8	% 2mEPSPS Recovery 9	% 2mEPSPS Recovery 10	% 2mEPSPS Recovery Average	% 2mEPSPS Recovery SD	% 2mEPSPS Recovery %CV
100	116	111	111	113	120	118	115	110	119	114	115	3.53	3.08
32	83.4	81.6	82.2	80.6	85.9	86.3	84.4	85.0	84.1	88.1	84.2	2.30	2.73
16	75.6	76.9	76.9	75.6	76.3	80.6	75.6	78.1	76.3	78.1	77.0	1.58	2.05
8	70.9	74.4	76.5	76.3	78.8	77.3	75.9	76.9	77.1	80.0	76.4	2.47	3.23
4	86.3	68.5	74.0	70.5	79.3	76.8	74.3	79.3	79.8	70.3	75.9	5.45	7.18
2	56.5	57.5	77.5	62.0	74.0	53.5	70.5	66.5	72.0	68.5	65.9	8.12	12.3
1	53.5	80.7	67.2	91.2	88.3	101	93.5	118	75.0	90.5	85.9	18.1	21.0
0.5	11.6	27.6	61.6	58.2	65.2	79.8	54.4	83.8	63.4	80.6	58.6	23.2	39.5

Table A2-7 Validation of 2mEPSPS ELISA for Untoasted Meal using Sample ID 2459C.

ng 2mEPSPS/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.10	0.10	0.10	0.10
32	0.10	0.10	0.10	0.10	0.10
16	0.10	0.10	0.11	0.11	0.10
8	0.11	0.10	0.10	0.10	0.11
4	0.10	0.11	0.11	0.11	0.10
2	0.10	0.10	0.10	0.10	0.11
1	0.10	0.10	0.10	0.10	0.11
0.5	0.10	0.11	0.11	0.10	0.10
0	0.10	0.11	0.10	0.10	0.11

ng 2mEPSPS/ mL spiked	Sample I 2mEPSPS 1 (ng/mL)	Sample I 2mEPSPS 2 (ng/mL)	Sample II 2mEPSPS 1 (ng/mL)	Sample II 2mEPSPS 2 (ng/mL)	Sample III 2mEPSPS 1 (ng/mL)	Sample III 2mEPSPS 2 (ng/mL)	Sample IV 2mEPSPS 1 (ng/mL)	Sample IV 2mEPSPS 2 (ng/mL)	Sample V 2mEPSPS 1 (ng/mL)	Sample V 2mEPSPS 2 (ng/mL)	2mEPSPS (ng/mL) Average	2mEPSPS (ng/mL) SD	2mEPSPS (ng/mL) %CV
100	115	113	111	120	115	111	118	116	115	116	115	2.89	2.52
32	31.3	30.7	31.5	32.5	31.5	31.2	30.7	30.3	32.2	30.9	31.3	0.68	2.19
16	13.8	13.5	14.2	14.0	13.1	14.1	15.60	14.3	14.3	14.4	14.1	0.66	4.65
8	6.55	6.56	6.89	6.87	6.98	7.04	6.90	6.76	7.07	7.06	6.87	0.19	2.78
4	3.27	3.13	3.47	3.37	3.57	3.45	3.54	3.50	3.58	3.42	3.43	0.14	4.13
2	1.44	1.56	1.59	1.63	1.61	1.47	1.63	1.73	1.75	1.71	1.61	0.10	6.41
1	0.62	0.68	0.76	0.73	0.73	0.86	0.77	0.84	0.75	0.82	0.75	0.07	9.87
0.5	0.29	0.15	0.34	0.28	0.46	0.53	0.36	0.47	0.40	0.37	0.36	0.11	30.1
0	-0.13	0.11	-0.05	0.15	0.09	0.03	0.13	0.06	0.23	0.14	0.08	0.10	136

ng 2mEPSPS/ mL spiked	% 2mEPSPS Recovery 1	% 2mEPSPS Recovery 2	% 2mEPSPS Recovery 3	% 2mEPSPS Recovery 4	% 2mEPSPS Recovery 5	% 2mEPSPS Recovery 6	% 2mEPSPS Recovery 7	% 2mEPSPS Recovery 8	% 2mEPSPS Recovery 9	% 2mEPSPS Recovery 10	% 2mEPSPS Recovery Average	% 2mEPSPS Recovery SD	% 2mEPSPS Recovery %CV
100	115	113	111	120	115	111	118	116	115	116	115	2.89	2.52
32	97.8	95.9	98.4	102	98.4	97.5	95.9	94.7	101	96.6	97.8	2.14	2.19
16	86.3	84.4	88.8	87.5	81.9	88.1	97.5	89.4	89.4	90.0	88.3	4.10	4.65
8	81.9	82.0	86.1	85.9	87.3	88.0	86.3	84.5	88.4	88.3	85.9	2.39	2.78
4	81.8	78.3	86.8	84.3	89.3	86.3	88.5	87.5	89.5	85.5	85.8	3.54	4.13
2	72.0	78.0	79.5	81.5	80.5	73.5	81.5	86.5	87.5	85.5	80.6	5.17	6.41
1	61.5	67.7	75.7	72.6	73.0	85.5	76.5	84.4	75.2	82.4	75.5	7.45	9.87
0.5	57.0	30.2	67.6	56.2	92.6	105.0	71.6	94.8	79.8	74.6	72.9	21.9	30.1

Table A2-8 Validation of 2mEPSPS ELISA for Toasted Meal using Sample ID 2459D.

ng 2mEPSPS/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.11	0.11	0.10	0.10
32	0.11	0.10	0.10	0.10	0.10
16	0.11	0.10	0.10	0.10	0.10
8	0.10	0.10	0.10	0.10	0.10
4	0.10	0.11	0.11	0.10	0.10
2	0.10	0.11	0.10	0.10	0.10
1	0.10	0.11	0.10	0.11	0.10
0.5	0.11	0.10	0.10	0.10	0.10
0	0.10	0.10	0.10	0.10	0.10

ng 2mEPSPS/ mL spiked	Sample I 2mEPSPS 1 (ng/mL)	Sample I 2mEPSPS 2 (ng/mL)	Sample II 2mEPSPS 1 (ng/mL)	Sample II 2mEPSPS 2 (ng/mL)	Sample III 2mEPSPS 1 (ng/mL)	Sample III 2mEPSPS 2 (ng/mL)	Sample IV 2mEPSPS 1 (ng/mL)	Sample IV 2mEPSPS 2 (ng/mL)	Sample V 2mEPSPS 1 (ng/mL)	Sample V 2mEPSPS 2 (ng/mL)	2mEPSPS (ng/mL) Average	2mEPSPS (ng/mL) SD	2mEPSPS (ng/mL) %CV
100	116	115	118	115	115	115	127	114	113	113	116	4.09	3.53
32	31.2	31.1	31.8	31.6	29.1	31.3	31.6	30.7	31.4	32.1	31.2	0.83	2.66
16	14.6	14.6	14.8	14.2	14.9	14.9	14.50	14.9	14.6	14.7	14.7	0.22	1.51
8	7.28	7.18	7.59	7.51	7.52	7.51	7.30	7.37	7.34	7.18	7.38	0.15	2.00
4	3.74	3.56	3.82	3.74	3.77	3.76	3.82	3.82	3.80	3.84	3.77	0.08	2.15
2	1.61	1.52	1.77	1.93	2.04	1.97	1.77	1.85	1.84	1.89	1.82	0.16	8.76
1	0.70	0.73	0.72	0.80	0.90	1.00	0.93	0.83	0.84	0.91	0.83	0.10	11.7
0.5	0.18	0.40	0.42	0.51	0.42	0.47	0.35	0.39	0.44	0.47	0.40	0.09	22.8
0	-0.14	-0.20	-0.08	-0.12	0.07	0.06	-0.02	0.14	0.06	0.03	-0.02	0.11	-543

ng 2mEPSPS/ mL spiked	% 2mEPSPS Recovery 1	% 2mEPSPS Recovery 2	% 2mEPSPS Recovery 3	% 2mEPSPS Recovery 4	% 2mEPSPS Recovery 5	% 2mEPSPS Recovery 6	% 2mEPSPS Recovery 7	% 2mEPSPS Recovery 8	% 2mEPSPS Recovery 9	% 2mEPSPS Recovery 10	% 2mEPSPS Recovery Average	% 2mEPSPS Recovery SD	% 2mEPSPS Recovery %CV
100	116	115	118	115	115	115	127	114	113	113	116	4.09	3.53
32	97.5	97.2	99.4	98.8	90.9	97.8	98.8	95.9	98.1	100	97.5	2.60	2.66
16	91.3	91.3	92.5	88.8	93.1	93.1	90.6	93.1	91.3	91.9	91.7	1.38	1.51
8	91.0	89.8	94.9	93.9	94.0	93.9	91.3	92.1	91.8	89.8	92.2	1.84	2.00
4	93.5	89.0	95.5	93.5	94.3	94.0	95.5	95.5	95.0	96.0	94.2	2.03	2.15
2	80.5	76.0	88.5	96.5	102	98.5	88.5	92.5	92.0	94.5	91.0	7.96	8.76
1	70.1	73.1	71.9	80.2	89.8	99.6	92.6	83.1	83.9	90.5	83.5	9.80	11.7
0.5	35.2	79.6	83.0	101	83.6	94.6	69.6	77.6	87.0	94.0	80.5	18.4	22.8

Table A2-9 Validation of 2mEPSPS ELISA for Crude Oil using Sample ID 2459E.

ng 2mEPSPS/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.10	0.11	0.10	0.10
32	0.11	0.10	0.11	0.11	0.10
16	0.10	0.10	0.10	0.10	0.10
8	0.11	0.10	0.10	0.11	0.10
4	0.10	0.10	0.10	0.10	0.10
2	0.11	0.11	0.10	0.11	0.10
1	0.10	0.10	0.10	0.10	0.10
0.5	0.11	0.10	0.11	0.10	0.11
0	0.11	0.11	0.10	0.10	0.10

ng 2mEPSPS/ mL spiked	Sample I 2mEPSPS 1 (ng/mL)	Sample I 2mEPSPS 2 (ng/mL)	Sample II 2mEPSPS 1 (ng/mL)	Sample II 2mEPSPS 2 (ng/mL)	Sample III 2mEPSPS 1 (ng/mL)	Sample III 2mEPSPS 2 (ng/mL)	Sample IV 2mEPSPS 1 (ng/mL)	Sample IV 2mEPSPS 2 (ng/mL)	Sample V 2mEPSPS 1 (ng/mL)	Sample V 2mEPSPS 2 (ng/mL)	2mEPSPS (ng/mL) Average	2mEPSPS (ng/mL) SD	2mEPSPS (ng/mL) %CV
100	99.8	95.4	115	123	112	121	103	104	119	106	110	9.53	8.68
32	28.7	25.9	33.0	29.4	28.7	28.5	29.1	28.5	29.8	29.3	29.1	1.74	5.97
16	14.2	13.8	14.4	13.5	13.8	13.7	13.7	13.4	14.2	14.2	13.9	0.34	2.43
8	7.08	7.11	6.81	6.63	6.90	6.82	6.95	6.69	6.97	6.75	6.87	0.16	2.32
4	3.40	3.31	3.49	3.52	3.61	3.21	3.55	3.97	3.37	3.47	3.49	0.21	5.91
2	1.71	1.47	1.98	1.79	2.16	1.81	1.80	1.70	1.93	1.96	1.83	0.19	10.3
1	0.59	0.65	1.09	0.86	0.74	0.87	0.90	0.71	0.85	0.79	0.80	0.14	17.8
0.5	0.22	0.20	0.25	0.45	0.30	0.45	0.34	0.31	0.43	0.38	0.33	0.09	27.6
0	0.02	0.20	0.23	0.10	0.37	0.11	-0.03	0.16	0.04	0.02	0.12	0.12	99.2

ng 2mEPSPS/ mL spiked	% 2mEPSPS Recovery 1	% 2mEPSPS Recovery 2	% 2mEPSPS Recovery 3	% 2mEPSPS Recovery 4	% 2mEPSPS Recovery 5	% 2mEPSPS Recovery 6	% 2mEPSPS Recovery 7	% 2mEPSPS Recovery 8	% 2mEPSPS Recovery 9	% 2mEPSPS Recovery 10	% 2mEPSPS Recovery Average	% 2mEPSPS Recovery SD	% 2mEPSPS Recovery %CV
100	99.8	95.4	115	123	112	121	103	104	119	106	110	9.53	8.68
32	89.7	80.9	103	91.9	89.7	89.1	90.9	89.1	93.1	91.6	90.9	5.42	5.97
16	88.8	86.3	90.0	84.4	86.3	85.6	85.6	83.8	88.8	88.8	86.8	2.11	2.43
8	88.5	88.9	85.1	82.9	86.3	85.3	86.9	83.6	87.1	84.4	85.9	2.00	2.32
4	85.0	82.8	87.3	88.0	90.3	80.3	88.8	99.3	84.3	86.8	87.3	5.16	5.91
2	85.5	73.5	99.0	89.5	108	90.5	90.0	85.0	96.5	98.0	91.6	9.46	10.3
1	59.2	64.5	109	86.4	73.6	87.2	89.7	71.2	84.5	78.7	80.4	14.3	17.8
0.5	43.6	39.8	50.4	89.0	60.8	89.2	67.4	62.0	85.2	76.0	66.3	18.3	27.6

Table A2-10 Validation of 2mEPSPS ELISA for Crude Lecithin using Sample ID 2459F.

ng 2mEPSPS/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.10	0.10	0.10	0.11
32	0.10	0.11	0.10	0.11	0.10
16	0.11	0.10	0.10	0.11	0.11
8	0.11	0.10	0.10	0.10	0.10
4	0.11	0.10	0.11	0.10	0.11
2	0.11	0.10	0.10	0.10	0.10
1	0.10	0.11	0.10	0.10	0.10
0.5	0.11	0.10	0.10	0.11	0.10
0	0.11	0.10	0.10	0.10	0.10

ng 2mEPSPS/ mL spiked	Sample I 2mEPSPS 1 (ng/mL)	Sample I 2mEPSPS 2 (ng/mL)	Sample II 2mEPSPS 1 (ng/mL)	Sample II 2mEPSPS 2 (ng/mL)	Sample III 2mEPSPS 1 (ng/mL)	Sample III 2mEPSPS 2 (ng/mL)	Sample IV 2mEPSPS 1 (ng/mL)	Sample IV 2mEPSPS 2 (ng/mL)	Sample V 2mEPSPS 1 (ng/mL)	Sample V 2mEPSPS 2 (ng/mL)	2mEPSPS (ng/mL) Average	2mEPSPS (ng/mL) SD	2mEPSPS (ng/mL) %CV
100	134	118	119	124	131	117	127	118	121	124	123	5.85	4.75
32	33.0	33.5	33.2	33.6	33.6	33.6	31.7	32.9	33.6	33.6	33.2	0.60	1.81
16	15.7	15.4	15.8	16.0	15.5	16.0	15.40	15.7	16.3	16.3	15.8	0.33	2.12
8	7.66	7.29	7.72	8.10	8.14	7.93	8.04	8.28	8.04	8.04	7.92	0.29	3.66
4	3.92	3.70	4.02	4.04	4.18	3.93	4.10	4.07	4.04	3.87	3.99	0.14	3.42
2	1.72	1.50	1.96	1.67	1.90	2.01	1.94	1.97	1.89	2.03	1.86	0.17	9.28
1	0.65	0.58	1.01	0.89	0.92	0.68	0.97	0.94	0.99	0.82	0.84	0.16	18.5
0.5	0.18	0.12	0.55	0.52	0.63	0.39	0.43	0.47	0.49	0.40	0.42	0.16	38.1
0	-0.21	-0.13	-0.01	0.23	0.00	0.06	0.13	0.19	-0.08	0.09	0.03	0.14	516

ng 2mEPSPS/ mL spiked	% 2mEPSPS Recovery 1	% 2mEPSPS Recovery 2	% 2mEPSPS Recovery 3	% 2mEPSPS Recovery 4	% 2mEPSPS Recovery 5	% 2mEPSPS Recovery 6	% 2mEPSPS Recovery 7	% 2mEPSPS Recovery 8	% 2mEPSPS Recovery 9	% 2mEPSPS Recovery 10	% 2mEPSPS Recovery Average	% 2mEPSPS Recovery SD	% 2mEPSPS Recovery %CV
100	134	118	119	124	131	117	127	118	121	124	123	5.85	4.75
32	103	105	104	105	105	105	99.1	103	105	105	104	1.88	1.81
16	98.1	96.3	98.8	100	96.9	100	96.3	98.1	102	102	98.8	2.09	2.12
8	95.8	91.1	96.5	101	102	99.1	101	104	101	101	99.1	3.63	3.66
4	98.0	92.5	101	101	105	98.3	103	102	101	96.8	99.7	3.41	3.42
2	86.0	75.0	98.0	83.5	95.0	101	97.0	98.5	94.5	102	93.0	8.62	9.28
1	64.5	57.6	101	89.0	91.7	68.1	96.8	94.0	98.7	82.2	84.4	15.6	18.5
0.5	36.0	23.8	109	105	125	77.4	85.2	93.0	98.4	79.2	83.2	31.7	38.1

Table A2-11 Validation of 2mEPSPS ELISA for Refined Oil using Sample ID 2459G.

ng 2mEPSPS/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.10	0.10	0.11	0.11
32	0.10	0.11	0.10	0.10	0.10
16	0.11	0.10	0.11	0.11	0.10
8	0.11	0.11	0.11	0.11	0.10
4	0.10	0.10	0.11	0.10	0.10
2	0.11	0.10	0.10	0.10	0.10
1	0.10	0.11	0.11	0.10	0.11
0.5	0.11	0.11	0.10	0.11	0.10
0	0.11	0.10	0.10	0.10	0.11

ng 2mEPSPS/ mL spiked	Sample I 2mEPSPS 1 (ng/mL)	Sample I 2mEPSPS 2 (ng/mL)	Sample II 2mEPSPS 1 (ng/mL)	Sample II 2mEPSPS 2 (ng/mL)	Sample III 2mEPSPS 1 (ng/mL)	Sample III 2mEPSPS 2 (ng/mL)	Sample IV 2mEPSPS 1 (ng/mL)	Sample IV 2mEPSPS 2 (ng/mL)	Sample V 2mEPSPS 1 (ng/mL)	Sample V 2mEPSPS 2 (ng/mL)	2mEPSPS (ng/mL) Average	2mEPSPS (ng/mL) SD	2mEPSPS (ng/mL) %CV
100	113	115	113	111	109	116	112	110	109	112	112	2.34	2.09
32	32.6	33.6	33.5	33.0	33.5	33.8	32.9	39.1	33.5	33.1	33.9	1.88	5.55
16	15.6	15.4	15.3	16.2	16.2	14.8	15.9	15.7	15.4	16.2	15.7	0.46	2.96
8	7.92	7.35	7.91	7.68	7.43	8.09	7.73	7.41	7.67	8.15	7.73	0.28	3.65
4	3.98	3.88	3.94	3.82	4.14	3.83	3.95	3.84	4.02	4.09	3.95	0.11	2.80
2	1.64	1.63	1.89	1.78	1.81	1.77	1.85	1.77	1.74	1.76	1.76	0.08	4.61
1	0.67	0.56	0.73	0.88	0.96	0.99	0.92	0.94	1.05	0.66	0.84	0.17	20.0
0.5	0.13	0.15	0.40	0.38	0.33	0.38	0.32	0.44	0.30	0.43	0.32	0.11	33.5
0	-0.23	-0.08	-0.07	-0.08	-0.10	0.09	-0.05	0.27	0.02	-0.04	-0.03	0.13	-496

ng 2mEPSPS/ mL spiked	% 2mEPSPS Recovery 1	% 2mEPSPS Recovery 2	% 2mEPSPS Recovery 3	% 2mEPSPS Recovery 4	% 2mEPSPS Recovery 5	% 2mEPSPS Recovery 6	% 2mEPSPS Recovery 7	% 2mEPSPS Recovery 8	% 2mEPSPS Recovery 9	% 2mEPSPS Recovery 10	% 2mEPSPS Recovery Average	% 2mEPSPS Recovery SD	% 2mEPSPS Recovery %CV
100	113	115	113	111	109	116	112	110	109	112	112	2.34	2.09
32	102	105	105	103	105	106	103	122	104	103	106	5.88	5.56
16	97.5	96.3	95.6	101	101	92.5	99.4	98.1	96.3	101	97.9	2.90	2.96
8	99.0	91.9	98.9	96.0	92.9	101	96.6	92.6	95.9	102	96.7	3.53	3.65
4	99.5	97.0	98.5	95.5	104	95.8	98.8	96.0	101	102	98.7	2.76	2.80
2	82.0	81.5	94.5	89.0	90.5	88.5	92.5	88.5	87.0	88.0	88.2	4.07	4.61
1	67.3	56.1	72.9	88.2	96.4	98.8	92.4	94.0	105	65.7	83.7	16.7	20.0
0.5	25.2	29.2	79.0	75.4	65.8	76.4	64.4	87.0	59.8	85.8	64.8	21.7	33.5

Table A2-12 Validation of 2mEPSPS ELISA for Refined Bleached Deodorized Oil using Sample ID 2459H.

ng 2mEPSPS/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.10	0.10	0.11	0.11
32	0.10	0.11	0.11	0.10	0.11
16	0.11	0.10	0.11	0.11	0.11
8	0.11	0.11	0.11	0.11	0.10
4	0.11	0.10	0.11	0.11	0.10
2	0.11	0.10	0.10	0.11	0.11
1	0.10	0.10	0.10	0.11	0.11
0.5	0.11	0.11	0.10	0.11	0.11
0	0.11	0.10	0.11	0.10	0.10

ng 2mEPSPS/ mL spiked	Sample I 2mEPSPS 1 (ng/mL)	Sample I 2mEPSPS 2 (ng/mL)	Sample II 2mEPSPS 1 (ng/mL)	Sample II 2mEPSPS 2 (ng/mL)	Sample III 2mEPSPS 1 (ng/mL)	Sample III 2mEPSPS 2 (ng/mL)	Sample IV 2mEPSPS 1 (ng/mL)	Sample IV 2mEPSPS 2 (ng/mL)	Sample V 2mEPSPS 1 (ng/mL)	Sample V 2mEPSPS 2 (ng/mL)	2mEPSPS (ng/mL) Average	2mEPSPS (ng/mL) SD	2mEPSPS (ng/mL) %CV
100	121	124	119	115	118	122	118	123	130	134	123	5.88	4.80
32	37.6	35.1	36.0	41.5	38.3	37.8	37.7	35.5	34.3	34.7	36.8	2.15	5.85
16	16.7	16.6	16.2	16.8	17.1	17.4	16.0	16.3	15.9	16.1	16.5	0.50	3.05
8	6.87	7.04	8.20	8.19	7.44	7.26	8.04	7.50	7.32	7.24	7.51	0.47	6.31
4	3.24	3.09	3.09	3.25	3.23	3.38	3.72	3.70	3.79	3.84	3.43	0.30	8.69
2	1.72	1.77	1.97	2.07	1.72	1.90	1.88	1.83	1.71	1.67	1.82	0.13	7.13
1	0.67	0.73	0.84	0.85	0.94	0.87	0.88	0.94	0.89	0.92	0.85	0.09	10.3
0.5	0.17	0.20	0.39	0.30	0.44	0.42	0.39	0.44	0.46	0.52	0.37	0.12	30.9
0	0.18	0.08	0.10	-0.01	-0.07	0.02	-0.03	-0.10	-0.02	0.12	0.03	0.09	319

ng 2mEPSPS/ mL spiked	% 2mEPSPS Recovery 1	% 2mEPSPS Recovery 2	% 2mEPSPS Recovery 3	% 2mEPSPS Recovery 4	% 2mEPSPS Recovery 5	% 2mEPSPS Recovery 6	% 2mEPSPS Recovery 7	% 2mEPSPS Recovery 8	% 2mEPSPS Recovery 9	% 2mEPSPS Recovery 10	% 2mEPSPS Recovery Average	% 2mEPSPS Recovery SD	% 2mEPSPS Recovery %CV
100	121	124	119	115	118	122	118	123	130	134	123	5.88	4.80
32	117	110	113	130	120	118	118	111	107	109	115	6.73	5.85
16	104	104	101	105	107	109	100	102	99.3	100	103	3.14	3.05
8	85.9	88.0	102	102	93.0	90.7	100	93.7	91.5	90.5	93.9	5.92	6.31
4	81.0	77.2	77.3	81.2	80.8	84.5	93.0	92.6	94.7	96.0	85.8	7.46	8.69
2	86.1	88.5	98.4	104	86.1	94.9	94.0	91.6	85.4	83.6	91.2	6.50	7.13
1	67.3	73.3	83.8	84.8	94.2	86.8	88.2	94.1	88.9	91.6	85.3	8.76	10.3
0.5	33.8	39.6	78.6	59.6	88.8	83.8	78.4	88.4	92.4	104	74.8	23.1	30.9

Table A2-13 Validation of 2mEPSPS ELISA for Protein Isolate using Sample ID 2459I.

ng 2mEPSPS/ mL spiked	Sample I Weight (g/ 4 mL extraction buffer)	Sample II Weight (g/ 4 mL extraction buffer)	Sample III Weight (g/ 4 mL extraction buffer)	Sample IV Weight (g/ 4 mL extraction buffer)	Sample V Weight (g/ 4 mL extraction buffer)
100	0.10	0.11	0.10	0.11	0.10
32	0.10	0.10	0.10	0.10	0.10
16	0.10	0.11	0.10	0.10	0.10
8	0.10	0.10	0.10	0.10	0.11
4	0.10	0.10	0.10	0.10	0.10
2	0.10	0.10	0.10	0.10	0.10
1	0.11	0.10	0.10	0.10	0.10
0.5	0.11	0.10	0.11	0.11	0.10
0	0.10	0.10	0.10	0.10	0.11

ng 2mEPSPS/ mL spiked	Sample I 2mEPSPS 1 (ng/mL)	Sample I 2mEPSPS 2 (ng/mL)	Sample II 2mEPSPS 1 (ng/mL)	Sample II 2mEPSPS 2 (ng/mL)	Sample III 2mEPSPS 1 (ng/mL)	Sample III 2mEPSPS 2 (ng/mL)	Sample IV 2mEPSPS 1 (ng/mL)	Sample IV 2mEPSPS 2 (ng/mL)	Sample V 2mEPSPS 1 (ng/mL)	Sample V 2mEPSPS 2 (ng/mL)	2mEPSPS (ng/mL) Average	2mEPSPS (ng/mL) SD	2mEPSPS (ng/mL) %CV
100	77.2	75.2	83.7	81.0	82.6	79.8	80.5	71.7	81.3	78.6	79.2	3.62	4.57
32	21.5	20.7	22.1	21.7	22.4	23.3	21.9	22.8	22.7	23.2	22.2	0.80	3.58
16	11.3	14.2	11.1	19.5	12.5	11.2	12.7	11.4	12.8	12.1	12.9	2.53	19.7
8	4.50	5.24	5.70	5.35	5.40	5.09	5.50	5.18	5.54	5.38	5.29	0.33	6.22
4	2.48	2.31	2.52	2.50	3.08	2.60	2.97	2.43	2.68	2.38	2.59	0.25	9.67
2	1.00	1.12	1.10	1.31	1.02	1.42	1.15	1.40	1.27	1.39	1.22	0.16	13.1
1	2.09	2.89	1.73	0.56	0.75	0.74	0.82	0.70	0.47	0.74	1.15	0.81	70.4
0.5	0.10	0.70	0.16	1.36	0.13	1.39	0.19	0.92	0.27	1.71	0.69	0.62	89.1
0	-0.23	-0.09	-0.09	0.50	0.06	0.52	-0.06	0.16	0.13	0.56	0.15	0.29	194

ng 2mEPSPS/ mL spiked	% 2mEPSPS Recovery 1	% 2mEPSPS Recovery 2	% 2mEPSPS Recovery 3	% 2mEPSPS Recovery 4	% 2mEPSPS Recovery 5	% 2mEPSPS Recovery 6	% 2mEPSPS Recovery 7	% 2mEPSPS Recovery 8	% 2mEPSPS Recovery 9	% 2mEPSPS Recovery 10	% 2mEPSPS Recovery Average	% 2mEPSPS Recovery SD	% 2mEPSPS Recovery %CV
100	77.2	75.2	83.7	81.0	82.6	79.8	80.5	71.7	81.3	78.6	79.2	3.62	4.57
32	67.2	64.8	69.1	67.9	69.9	72.7	68.5	71.3	70.8	72.5	69.5	2.49	3.58
16	70.5	88.6	69.4	122	78.0	69.8	79.3	71.1	79.9	75.6	80.4	15.8	19.7
8	56.3	65.5	71.2	66.8	67.5	63.6	68.8	64.8	69.3	67.3	66.1	4.11	6.22
4	62.0	57.7	63.1	62.6	77.0	64.9	74.2	60.7	67.0	59.5	64.9	6.27	9.67
2	50.1	56.0	55.2	65.5	51.1	71.0	57.3	70.2	63.6	69.7	60.9	8.00	13.1
1	209	289	173	56.4	74.7	73.6	81.8	70.0	46.5	74.1	115	80.8	70.4
0.5	19.0	139.6	31.0	272	26.6	277.4	37.4	184	53.2	342	138	123	89.1

Table A2-14 Validation of HPPD ELISA for Whole Soybeans using Sample ID 1754A.

ng HPPD/ mL spiked	Sample I Weight (g/ 4 mL extraction buffer)	Sample II Weight (g/ 4 mL extraction buffer)	Sample III Weight (g/ 4 mL extraction buffer)	Sample IV Weight (g/ 4 mL extraction buffer)	Sample V Weight (g/ 4 mL extraction buffer)
100	0.11	0.11	0.11	0.10	0.11
32	0.11	0.10	0.10	0.11	0.10
16	0.11	0.11	0.11	0.11	0.10
8	0.10	0.10	0.10	0.11	0.10
4	0.10	0.10	0.10	0.10	0.11
2	0.11	0.11	0.11	0.10	0.10
1	0.10	0.11	0.11	0.11	0.10
0	0.10	0.11	0.10	0.10	0.10

ng HPPD/ mL spiked	Sample I HPPD 1 (ng/mL)	Sample I HPPD 2 (ng/mL)	Sample II HPPD 1 (ng/mL)	Sample II HPPD 2 (ng/mL)	Sample III HPPD 1 (ng/mL)	Sample III HPPD 2 (ng/mL)	Sample IV HPPD 1 (ng/mL)	Sample IV HPPD 2 (ng/mL)	Sample V HPPD 1 (ng/mL)	Sample V HPPD 2 (ng/mL)	HPPD (ng/mL) Average	HPPD (ng/mL) SD	HPPD (ng/mL) %CV
100	116	124	120	127	124	130	122	122	124	123	123	3.70	3.01
32	32.8	30.6	32.6	30.9	32.4	32.1	30.8	28.6	31.8	31.6	31.4	1.26	4.01
16	18.9	19.5	18.1	18.9	17.4	17.1	16.6	17.0	18.5	17.8	18.0	0.94	5.26
8	8.09	7.23	9.17	8.83	8.65	8.23	8.77	8.13	8.22	8.11	8.34	0.54	6.47
4	3.15	3.14	3.55	3.71	3.65	3.53	3.75	3.28	3.78	3.58	3.51	0.24	6.78
2	0.94	0.97	1.42	1.51	1.53	1.70	1.55	1.56	1.53	1.61	1.43	0.26	18.2
1	0.09	0.13	0.38	0.48	0.44	0.69	0.50	0.61	0.42	0.56	0.43	0.19	44.6
0	-0.67	-0.52	-0.01	-0.15	-0.28	-0.08	-0.33	-0.23	-0.25	0.28	-0.22	0.27	-119

ng HPPD/ mL spiked	% HPPD Recovery 1	% HPPD Recovery 2	% HPPD Recovery 3	% HPPD Recovery 4	% HPPD Recovery 5	% HPPD Recovery 6	% HPPD Recovery 7	% HPPD Recovery 8	% HPPD Recovery 9	% HPPD Recovery 10	% HPPD Recovery Average	% HPPD Recovery SD	%HPPD Recovery %CV
100	116	124	120	127	124	130	122	122	124	123	123	3.70	3.01
32	102	95.6	102	96.6	101	100	96.3	89.3	99.5	98.9	98.2	3.94	4.01
16	118	122	113	118	109	107	104	106	116	111	112	5.91	5.26
8	101	90.4	115	110	108	103	110	102	103	101	104	6.75	6.47
4	78.7	78.6	88.9	92.7	91.2	88.3	93.7	82.1	94.5	89.6	87.8	5.95	6.78
2	47.2	48.4	71.0	75.3	76.6	85.2	77.3	77.8	76.7	80.6	71.6	13.1	18.2
1	9.40	12.5	38.3	48.4	44.2	68.6	49.5	61.0	41.7	56.1	43.0	19.2	44.6

^a Non-Transgenic Whole Soybeans was validated in study DQ09B003

Table A2-15 Validation of HPPD ELISA for Hull Material using Sample ID 2459B.

ng HPPD/ mL spiked	Sample I Weight (g/ 4 mL extraction buffer)	Sample II Weight (g/ 4 mL extraction buffer)	Sample III Weight (g/ 4 mL extraction buffer)	Sample IV Weight (g/ 4 mL extraction buffer)	Sample V Weight (g/ 4 mL extraction buffer)
100	0.10	0.10	0.10	0.11	0.10
32	0.11	0.10	0.11	0.11	0.11
16	0.10	0.10	0.10	0.10	0.10
8	0.10	0.10	0.10	0.10	0.10
4	0.10	0.10	0.10	0.10	0.10
2	0.10	0.10	0.10	0.11	0.10
1	0.10	0.10	0.10	0.10	0.10
0	0.11	0.11	0.10	0.11	0.10

ng HPPD/ mL spiked	Sample I HPPD 1 (ng/mL)	Sample I HPPD 2 (ng/mL)	Sample II HPPD 1 (ng/mL)	Sample II HPPD 2 (ng/mL)	Sample III HPPD 1 (ng/mL)	Sample III HPPD 2 (ng/mL)	Sample IV HPPD 1 (ng/mL)	Sample IV HPPD 2 (ng/mL)	Sample V HPPD 1 (ng/mL)	Sample V HPPD 2 (ng/mL)	HPPD (ng/mL) Average	HPPD (ng/mL) SD	HPPD (ng/mL) %CV
100	101	96.5	91.3	95.4	96.3	89.3	97.3	97.9	94.8	97.7	95.8	3.39	3.54
32	23.2	24.5	25.0	23.9	25.0	24.5	25.3	24.5	26.3	26.2	24.8	0.94	3.78
16	14.4	14.8	14.0	13.5	13.8	13.9	13.5	13.7	13.7	13.6	13.9	0.43	3.10
8	7.70	7.35	7.68	7.70	7.23	7.39	7.18	7.22	7.14	7.45	7.40	0.22	2.97
4	2.27	3.81	3.39	4.47	4.03	3.86	3.72	4.31	3.80	4.25	3.79	0.62	16.4
2	1.30	1.35	1.67	1.87	1.68	1.61	1.64	1.77	1.72	1.95	1.66	0.20	12.3
1	0.60	0.50	0.76	0.67	0.65	0.79	0.42	0.71	0.72	0.66	0.65	0.12	17.9
0	-0.92	-0.38	-0.22	-0.33	-0.25	-0.26	-0.53	-0.54	-0.32	-0.32	-0.41	0.21	-52.1

ng HPPD/ mL spiked	% HPPD Recovery 1	% HPPD Recovery 2	% HPPD Recovery 3	% HPPD Recovery 4	% HPPD Recovery 5	% HPPD Recovery 6	% HPPD Recovery 7	% HPPD Recovery 8	% HPPD Recovery 9	% HPPD Recovery 10	% HPPD Recovery Average	% HPPD Recovery SD	%HPPD Recovery %CV
100	101	96.5	91.3	95.4	96.3	89.3	97.3	97.9	94.8	97.7	95.8	3.39	3.54
32	72.6	76.5	78.1	74.6	78.1	76.7	79.0	76.5	82.2	81.7	77.6	2.93	3.78
16	90.0	92.7	87.2	84.3	86.5	86.7	84.3	85.9	85.3	84.7	86.8	2.69	3.10
8	96.2	91.9	96.0	96.2	90.4	92.3	89.8	90.3	89.3	93.1	92.5	2.74	2.97
4	56.7	95.3	84.8	112	101	96.4	92.9	108	95.1	106	94.7	15.6	16.4
2	65.0	67.3	83.6	93.7	84.2	80.4	81.8	88.5	86.1	97.3	82.8	10.2	12.3
1	60.3	50.3	75.8	66.8	65.3	79.3	41.5	71.1	72.4	66.2	64.9	11.6	17.9

Table A2-16 Validation of HPPD ELISA for Untoasted Meal using Sample ID 2459C.

ng HPPD/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.10	0.10	0.10	0.11
32	0.10	0.10	0.10	0.10	0.10
16	0.10	0.10	0.11	0.11	0.10
8	0.11	0.10	0.10	0.10	0.11
4	0.10	0.11	0.11	0.11	0.10
2	0.10	0.10	0.10	0.10	0.11
1	0.10	0.10	0.10	0.10	0.10
0	0.10	0.11	0.10	0.10	0.11

ng HPPD/ mL spiked	Sample I HPPD 1 (ng/mL)	Sample I HPPD 2 (ng/mL)	Sample II HPPD 1 (ng/mL)	Sample II HPPD 2 (ng/mL)	Sample III HPPD 1 (ng/mL)	Sample III HPPD 2 (ng/mL)	Sample IV HPPD 1 (ng/mL)	Sample IV HPPD 2 (ng/mL)	Sample V HPPD 1 (ng/mL)	Sample V HPPD 2 (ng/mL)	HPPD (ng/mL) Average	HPPD (ng/mL) SD	HPPD (ng/mL) %CV
100	131	129	129	128	124	124	126	121	118	126	126	4.06	3.23
32	36.2	36.2	34.9	34.7	34.2	33.6	34.0	34.1	33.9	33.2	34.5	1.02	2.96
16	19.2	18.2	18.5	18.1	18.0	18.3	18.2	16.9	17.6	16.5	17.9	0.78	4.35
8	9.89	9.47	10.1	9.97	9.74	9.50	9.86	9.33	9.78	10.5	9.81	0.33	3.37
4	4.81	4.92	5.52	5.49	5.11	5.42	4.86	5.12	5.20	5.15	5.16	0.26	4.96
2	2.37	2.20	2.50	2.36	2.33	4.15	2.32	2.63	2.34	2.44	2.56	0.57	22.2
1	1.14	1.11	1.28	1.23	1.17	1.19	1.40	1.16	1.42	1.41	1.25	0.12	9.60
0	-0.75	-0.67	-0.27	-0.14	-0.19	-0.08	-0.29	-0.17	-0.24	-0.12	-0.29	0.23	-78.9

ng HPPD/ mL spiked	% HPPD Recovery 1	% HPPD Recovery 2	% HPPD Recovery 3	% HPPD Recovery 4	% HPPD Recovery 5	% HPPD Recovery 6	% HPPD Recovery 7	% HPPD Recovery 8	% HPPD Recovery 9	% HPPD Recovery 10	% HPPD Recovery Average	% HPPD Recovery SD	%HPPD Recovery %CV
100	131	129	129	128	124	124	126	121	118	126	126	4.06	3.23
32	113	113	109	108	107	105	106	107	106	104	108	3.20	2.96
16	120	114	116	113	112	115	114	105	110	103	112	4.87	4.35
8	124	118	126	125	122	119	123	117	122	131	123	4.13	3.37
4	120	123	138	137	128	136	121	128	130	129	129	6.40	4.96
2	118	110	125	118	117	207	116	132	117	122	128	28.4	22.2
1	114	111	128	123	117	119	140	116	142	141	125	12.0	9.60

Table A2-17 Validation of HPPD ELISA for Toasted Meal using Sample ID 2459D.

ng HPPD/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.11	0.11	0.10	0.10
32	0.11	0.10	0.10	0.10	0.10
16	0.11	0.10	0.10	0.10	0.10
8	0.10	0.10	0.10	0.10	0.10
4	0.10	0.11	0.11	0.10	0.10
2	0.10	0.11	0.10	0.10	0.10
1	0.10	0.11	0.10	0.11	0.10
0	0.10	0.10	0.10	0.10	0.10

ng HPPD/ mL spiked	Sample I HPPD 1 (ng/mL)	Sample I HPPD 2 (ng/mL)	Sample II HPPD 1 (ng/mL)	Sample II HPPD 2 (ng/mL)	Sample III HPPD 1 (ng/mL)	Sample III HPPD 2 (ng/mL)	Sample IV HPPD 1 (ng/mL)	Sample IV HPPD 2 (ng/mL)	Sample V HPPD 1 (ng/mL)	Sample V HPPD 2 (ng/mL)	HPPD (ng/mL) Average	HPPD (ng/mL) SD	HPPD (ng/mL) %CV
100	92.3	79.6	91.2	88.0	94.2	90.2	100	101	90.4	98.3	92.5	6.38	6.90
32	26.5	27.1	25.3	25.8	25.9	28.2	26.3	27.9	26.9	26.5	26.6	0.91	3.40
16	13.9	13.7	13.4	13.1	13.4	13.5	13.4	13.1	12.9	13.0	13.3	0.33	2.46
8	7.81	7.28	7.48	7.23	7.19	7.09	7.29	7.18	7.21	7.05	7.28	0.22	3.00
4	3.55	3.57	3.54	3.66	3.64	3.82	3.64	3.95	3.71	3.74	3.68	0.13	3.46
2	1.85	1.61	1.92	1.90	1.97	1.88	1.90	1.97	1.99	2.00	1.90	0.11	6.02
1	0.95	0.92	1.07	1.12	1.04	1.02	1.06	1.10	1.07	1.06	1.04	0.06	6.05
0	-0.12	-0.20	0.02	0.12	0.05	0.06	0.02	0.08	0.00	0.06	0.01	0.10	1085

ng HPPD/ mL spiked	% HPPD Recovery 1	% HPPD Recovery 2	% HPPD Recovery 3	% HPPD Recovery 4	% HPPD Recovery 5	% HPPD Recovery 6	% HPPD Recovery 7	% HPPD Recovery 8	% HPPD Recovery 9	% HPPD Recovery 10	% HPPD Recovery Average	% HPPD Recovery SD	%HPPD Recovery %CV
100	92.3	79.6	91.2	88.0	94.2	90.2	100	101	90.4	98.3	92.5	6.38	6.90
32	82.8	84.6	79.0	80.6	80.9	88.0	82.2	87.1	84.0	82.8	83.2	2.83	3.40
16	87.0	85.4	83.5	81.8	83.8	84.5	84.0	81.6	80.4	81.4	83.4	2.05	2.46
8	97.6	91.0	93.5	90.4	89.9	88.7	91.2	89.8	90.1	88.1	91.0	2.73	3.00
4	88.8	89.4	88.6	91.6	91.1	95.5	91.0	98.7	92.8	93.5	92.1	3.19	3.46
2	92.7	80.3	95.8	94.8	98.7	94.0	94.9	98.3	99.6	99.9	94.9	5.71	6.02
1	94.9	91.9	107	112	104	102	106	110	107	106	104	6.30	6.05

Table A2-18 Validation of HPPD ELISA for Crude Oil using Sample ID 2459E.

ng HPPD/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.10	0.11	0.10	0.10
32	0.11	0.10	0.11	0.11	0.10
16	0.10	0.10	0.10	0.10	0.10
8	0.11	0.10	0.10	0.11	0.10
4	0.10	0.10	0.10	0.10	0.10
2	0.11	0.11	0.10	0.11	0.10
1	0.10	0.10	0.10	0.10	0.10
0	0.11	0.11	0.10	0.10	0.10

ng HPPD/ mL spiked	Sample I HPPD 1 (ng/mL)	Sample I HPPD 2 (ng/mL)	Sample II HPPD 1 (ng/mL)	Sample II HPPD 2 (ng/mL)	Sample III HPPD 1 (ng/mL)	Sample III HPPD 2 (ng/mL)	Sample IV HPPD 1 (ng/mL)	Sample IV HPPD 2 (ng/mL)	Sample V HPPD 1 (ng/mL)	Sample V HPPD 2 (ng/mL)	HPPD (ng/mL) Average	HPPD (ng/mL) SD	HPPD (ng/mL) %CV
100	113	112	103	108	104	102	104	102	98.5	102	105	4.68	4.46
32	22.7	22.3	20.9	20.8	22.7	22.2	20.6	20.4	20.9	20.3	21.4	0.97	4.53
16	8.44	12.2	8.87	13.0	12.5	13.5	12.0	13.1	11.4	12.2	11.7	1.73	14.7
8	5.75	5.84	5.75	5.59	5.70	5.39	5.79	4.97	5.59	5.67	5.60	0.26	4.58
4	2.27	2.29	2.54	2.63	2.62	2.50	2.40	2.55	2.38	2.54	2.47	0.13	5.17
2	1.28	1.11	1.44	1.41	1.39	1.49	1.55	1.44	1.51	1.66	1.43	0.15	10.4
1	0.52	0.35	0.69	0.65	0.75	0.38	0.72	0.58	0.61	0.67	0.59	0.14	23.3
0	-0.45	-0.80	-0.28	-0.36	-0.31	-0.28	-0.29	-0.28	-0.22	-0.17	-0.34	0.18	-51.6

ng HPPD/ mL spiked	% HPPD Recovery 1	% HPPD Recovery 2	% HPPD Recovery 3	% HPPD Recovery 4	% HPPD Recovery 5	% HPPD Recovery 6	% HPPD Recovery 7	% HPPD Recovery 8	% HPPD Recovery 9	% HPPD Recovery 10	% HPPD Recovery Average	% HPPD Recovery SD	%HPPD Recovery %CV
100	113	112	103	108	104	102	104	102	98.5	102	105	4.68	4.46
32	70.9	69.8	65.3	65.1	70.9	69.4	64.4	63.8	65.2	63.4	66.8	3.03	4.53
16	52.8	76.3	55.4	81.3	78.1	84.4	75.0	81.9	71.3	76.3	73.3	10.8	14.7
8	71.8	73.0	71.9	69.9	71.3	67.4	72.3	62.1	69.8	70.9	70.0	3.21	4.58
4	56.9	57.3	63.4	65.7	65.6	62.4	60.1	63.7	59.4	63.5	61.8	3.20	5.17
2	64.2	55.7	71.9	70.5	69.5	74.4	77.6	71.9	75.4	82.9	71.4	7.44	10.4
1	51.5	34.9	68.9	64.8	74.8	37.6	71.5	58.2	61.4	66.9	59.1	13.7	23.3

Table A2-19 Validation of HPPD ELISA for Crude Lecithin using Sample ID 2459F.

ng HPPD/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.10	0.10	0.10	0.11
32	0.10	0.11	0.10	0.11	0.10
16	0.11	0.10	0.10	0.11	0.11
8	0.11	0.10	0.10	0.10	0.10
4	0.11	0.10	0.11	0.10	0.11
2	0.11	0.10	0.10	0.10	0.10
1	0.10	0.11	0.10	0.10	0.10
0	0.11	0.10	0.10	0.10	0.10

ng HPPD/ mL spiked	Sample I HPPD 1 (ng/mL)	Sample I HPPD 2 (ng/mL)	Sample II HPPD 1 (ng/mL)	Sample II HPPD 2 (ng/mL)	Sample III HPPD 1 (ng/mL)	Sample III HPPD 2 (ng/mL)	Sample IV HPPD 1 (ng/mL)	Sample IV HPPD 2 (ng/mL)	Sample V HPPD 1 (ng/mL)	Sample V HPPD 2 (ng/mL)	HPPD (ng/mL) Average	HPPD (ng/mL) SD	HPPD (ng/mL) %CV
100	51.7	84.3	77.7	84.5	77.6	83.0	77.7	81.5	85.7	87.1	79.1	10.2	13.0
32	29.0	28.9	27.2	27.8	27.8	27.8	28.6	28.7	29.3	29.6	28.5	0.78	2.74
16	13.0	12.9	12.7	12.3	14.5	13.7	12.5	12.1	13.1	12.7	12.9	0.71	5.47
8	7.06	6.95	7.39	7.13	7.54	7.41	7.95	7.60	7.15	7.15	7.33	0.31	4.17
4	3.89	3.81	3.92	4.00	3.72	3.87	4.08	3.93	3.90	3.71	3.88	0.12	2.98
2	1.84	1.88	2.50	2.50	2.40	2.47	2.19	2.26	2.30	2.29	2.26	0.24	10.5
1	0.83	0.86	1.35	1.27	1.07	1.06	0.99	1.03	1.06	1.05	1.06	0.16	14.8
0	-0.23	-0.22	0.10	0.08	-0.01	-0.03	-0.12	-0.18	-0.01	0.21	-0.04	0.15	-356

ng HPPD/ mL spiked	% HPPD Recovery 1	% HPPD Recovery 2	% HPPD Recovery 3	% HPPD Recovery 4	% HPPD Recovery 5	% HPPD Recovery 6	% HPPD Recovery 7	% HPPD Recovery 8	% HPPD Recovery 9	% HPPD Recovery 10	% HPPD Recovery Average	% HPPD Recovery SD	%HPPD Recovery %CV
100	51.7	84.3	77.7	84.5	77.6	83.0	77.7	81.5	85.7	87.1	79.1	10.2	13.0
32	90.6	90.3	85.1	86.9	86.8	86.8	89.2	89.7	91.5	92.7	89.0	2.44	2.74
16	81.2	80.7	79.2	76.7	90.6	85.8	78.1	75.8	81.6	79.3	80.9	4.43	5.47
8	88.3	86.9	92.4	89.1	94.3	92.7	99.4	95.1	89.4	89.3	91.7	3.82	4.17
4	97.2	95.3	98.1	100.1	93.0	96.7	102	98.3	97.4	92.6	97.1	2.90	2.98
2	91.9	94.2	125	125	120	124	109	113	115	114	113	11.9	10.5
1	83.1	86.1	135	127	107	106	99.4	103	106	105	106	15.7	14.8

Table A2-20 Validation of HPPD ELISA for Refined Oil using Sample ID 2459G.

ng HPPD/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.10	0.11	0.10	0.10
32	0.10	0.11	0.10	0.10	0.10
16	0.11	0.10	0.10	0.11	0.10
8	0.11	0.11	0.11	0.11	0.10
4	0.10	0.10	0.11	0.10	0.10
2	0.11	0.10	0.10	0.10	0.10
1	0.10	0.11	0.11	0.10	0.11
0	0.11	0.10	0.10	0.10	0.11

ng HPPD/ mL spiked	Sample I HPPD 1 (ng/mL)	Sample I HPPD 2 (ng/mL)	Sample II HPPD 1 (ng/mL)	Sample II HPPD 2 (ng/mL)	Sample III HPPD 1 (ng/mL)	Sample III HPPD 2 (ng/mL)	Sample IV HPPD 1 (ng/mL)	Sample IV HPPD 2 (ng/mL)	Sample V HPPD 1 (ng/mL)	Sample V HPPD 2 (ng/mL)	HPPD (ng/mL) Average	HPPD (ng/mL) SD	HPPD (ng/mL) %CV
100	78.1	80.5	78.0	79.3	76.0	76.2	74.9	74.8	76.4	77.9	77.2	1.88	2.43
32	31.6	31.0	30.3	30.9	30.9	29.7	30.6	29.4	29.9	29.8	30.4	0.70	2.30
16	13.5	13.2	13.6	13.9	13.7	13.5	13.3	13.8	13.7	13.8	13.6	0.22	1.62
8	6.19	8.02	7.61	7.73	7.40	7.28	7.39	7.22	7.33	7.58	7.37	0.48	6.53
4	4.01	3.87	4.26	4.41	4.29	4.14	4.35	4.17	4.36	4.11	4.20	0.17	4.05
2	2.09	1.73	2.35	2.54	2.13	2.34	2.42	2.24	2.32	2.14	2.23	0.22	10.1
1	0.53	0.65	0.95	0.96	0.94	1.09	0.90	0.92	0.85	1.14	0.89	0.18	20.6
0	-0.54	-0.49	-0.03	0.28	-0.07	-0.03	-0.08	-0.06	0.00	-0.06	-0.11	0.24	-224

ng HPPD/ mL spiked	% HPPD Recovery 1	% HPPD Recovery 2	% HPPD Recovery 3	% HPPD Recovery 4	% HPPD Recovery 5	% HPPD Recovery 6	% HPPD Recovery 7	% HPPD Recovery 8	% HPPD Recovery 9	% HPPD Recovery 10	% HPPD Recovery Average	% HPPD Recovery SD	%HPPD Recovery %CV
100	78.1	80.5	78.0	79.3	76.0	76.2	74.9	74.8	76.4	77.9	77.2	1.88	2.43
32	98.7	96.9	94.7	96.4	96.6	92.7	95.6	91.8	93.6	93.2	95.0	2.18	2.30
16	84.4	82.5	85.0	86.7	85.7	84.3	83.2	86.3	85.9	86.0	85.0	1.38	1.62
8	77.3	100	95.1	96.6	92.4	91.0	92.4	90.3	91.7	94.8	92.2	6.02	6.53
4	100	96.8	107	110	107	103	109	104	109	103	105	4.25	4.05
2	105	86.3	118	127	107	117	121	112	116	107	111	11.2	10.1
1	52.6	64.8	95.1	95.9	93.5	109	90.3	91.9	85.4	114	89.2	18.4	20.6

Table A2-21 Validation of HPPD ELISA for Refined Bleached Deodorized Oil using Sample ID 2459H.

ng HPPD/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.10	0.10	0.11	0.11
32	0.10	0.11	0.11	0.10	0.11
16	0.11	0.10	0.11	0.11	0.11
8	0.11	0.11	0.11	0.11	0.10
4	0.10	0.10	0.10	0.11	0.11
2	0.11	0.10	0.10	0.11	0.11
1	0.10	0.10	0.10	0.11	0.11
0	0.11	0.10	0.11	0.10	0.10

ng HPPD/ mL spiked	Sample I HPPD 1 (ng/mL)	Sample I HPPD 2 (ng/mL)	Sample II HPPD 1 (ng/mL)	Sample II HPPD 2 (ng/mL)	Sample III HPPD 1 (ng/mL)	Sample III HPPD 2 (ng/mL)	Sample IV HPPD 1 (ng/mL)	Sample IV HPPD 2 (ng/mL)	Sample V HPPD 1 (ng/mL)	Sample V HPPD 2 (ng/mL)	HPPD (ng/mL) Average	HPPD (ng/mL) SD	HPPD (ng/mL) %CV
100	105	104	108	105	102	103	100	100	102	99.9	103	2.55	2.48
32	29.3	28.9	28.3	29.2	28.7	28.3	28.2	27.4	27.9	28.1	28.4	0.59	2.08
16	14.3	13.5	14.0	13.7	14.1	14.0	13.6	13.9	13.5	13.7	13.8	0.27	1.92
8	7.63	7.87	7.82	7.80	7.51	7.89	7.66	7.57	7.71	7.67	7.71	0.13	1.66
4	3.08	2.75	3.35	3.22	3.41	3.49	3.42	3.32	3.59	3.56	3.32	0.25	7.60
2	1.86	1.82	2.22	2.16	2.31	2.22	2.32	2.02	2.15	2.10	2.12	0.17	8.13
1	0.92	0.97	1.22	1.38	1.28	1.37	1.21	1.55	1.09	1.32	1.23	0.20	15.9
0	-0.38	-0.24	0.17	0.08	0.10	0.09	0.06	0.13	0.06	0.09	0.02	0.18	1182

ng HPPD/ mL spiked	% HPPD Recovery 1	% HPPD Recovery 2	% HPPD Recovery 3	% HPPD Recovery 4	% HPPD Recovery 5	% HPPD Recovery 6	% HPPD Recovery 7	% HPPD Recovery 8	% HPPD Recovery 9	% HPPD Recovery 10	% HPPD Recovery Average	% HPPD Recovery SD	%HPPD Recovery %CV
100	105	104	108	105	102	103	100	100	102	99.9	103	2.55	2.48
32	91.5	90.2	88.3	91.3	89.7	88.3	88.2	85.6	87.2	87.9	88.8	1.85	2.08
16	89.3	84.5	87.5	85.8	88.2	87.4	85.1	87.2	84.4	85.5	86.5	1.66	1.92
8	95.3	98.4	97.8	97.5	93.9	98.6	95.7	94.7	96.4	95.8	96.4	1.60	1.66
4	76.9	68.8	83.7	80.5	85.2	87.3	85.5	83.0	89.7	89.1	83.0	6.30	7.60
2	92.8	91.1	111	108	116	111	116	101	107	105	106	8.61	8.13
1	91.8	96.7	122	138	128	137	121	155	109	132	123	19.6	15.9

Table A2-22 Validation of HPPD ELISA for Protein Isolate using Sample ID 2459I.

ng HPPD/ mL spiked	Sample I Weight (g/ 2 mL extraction buffer)	Sample II Weight (g/ 2 mL extraction buffer)	Sample III Weight (g/ 2 mL extraction buffer)	Sample IV Weight (g/ 2 mL extraction buffer)	Sample V Weight (g/ 2 mL extraction buffer)
100	0.10	0.11	0.10	0.10	0.10
32	0.11	0.10	0.11	0.11	0.10
16	0.11	0.11	0.10	0.10	0.10
8	0.10	0.10	0.11	0.11	0.10
4	0.10	0.10	0.11	0.10	0.11
2	0.11	0.11	0.10	0.10	0.11
1	0.10	0.10	0.10	0.10	0.10
0	0.10	0.10	0.10	0.11	0.10

ng HPPD/ mL spiked	Sample I HPPD 1 (ng/mL)	Sample I HPPD 2 (ng/mL)	Sample II HPPD 1 (ng/mL)	Sample II HPPD 2 (ng/mL)	Sample III HPPD 1 (ng/mL)	Sample III HPPD 2 (ng/mL)	Sample IV HPPD 1 (ng/mL)	Sample IV HPPD 2 (ng/mL)	Sample V HPPD 1 (ng/mL)	Sample V HPPD 2 (ng/mL)	HPPD (ng/mL) Average	HPPD (ng/mL) SD	HPPD (ng/mL) %CV
100	87.7	87.2	86.2	89.4	85.0	91.1	90.0	83.1	86.7	86.3	87.3	2.40	2.75
32	26.3	26.3	25.0	25.4	24.5	26.2	24.2	25.9	25.3	25.3	25.4	0.73	2.86
16	11.2	11.7	11.1	11.5	11.5	11.8	11.0	11.1	11.9	12.0	11.5	0.36	3.14
8	6.45	6.13	6.34	6.01	6.40	6.25	6.18	6.35	6.68	6.19	6.30	0.19	3.00
4	3.10	2.98	3.22	3.65	3.26	3.68	3.37	2.97	3.47	3.66	3.34	0.28	8.26
2	1.07	1.32	1.45	1.80	1.86	1.75	1.49	1.76	1.87	1.71	1.61	0.27	16.5
1	0.51	0.40	0.61	0.87	0.82	0.93	0.87	0.90	0.87	0.75	0.75	0.18	24.2
0	-0.46	-0.52	0.17	0.04	0.20	0.04	0.03	-0.09	0.09	0.01	-0.05	0.25	-499

ng HPPD/ mL spiked	% HPPD Recovery 1	% HPPD Recovery 2	% HPPD Recovery 3	% HPPD Recovery 4	% HPPD Recovery 5	% HPPD Recovery 6	% HPPD Recovery 7	% HPPD Recovery 8	% HPPD Recovery 9	% HPPD Recovery 10	% HPPD Recovery Average	% HPPD Recovery SD	%HPPD Recovery %CV
100	87.7	87.2	86.2	89.4	85.0	91.1	90.0	83.1	86.7	86.3	87.3	2.40	2.75
32	82.1	82.3	78.2	79.2	76.6	81.8	75.7	80.8	78.9	79.1	79.5	2.27	2.86
16	70.1	72.9	69.4	71.7	71.9	73.9	68.5	69.6	74.3	74.9	71.7	2.25	3.14
8	80.6	76.6	79.2	75.1	80.0	78.1	77.2	79.4	83.5	77.4	78.7	2.36	3.00
4	77.6	74.4	80.5	91.3	81.4	92.1	84.2	74.3	86.8	91.6	83.4	6.89	8.26
2	53.7	65.9	72.7	90.0	93.2	87.5	74.7	88.0	93.7	85.4	80.5	13.3	16.5
1	51.2	40.3	60.6	86.9	81.5	92.9	87.1	89.8	87.1	75.3	75.3	18.2	24.2

Table A2-23 Determination of the LOD for 2mEPSPS Protein in Non-transgenic Whole Soybeans ^e, Hull Material, and Untoasted Meal

Matrix (BTID)	ng EPSPS/ mL spiked ^c	Sample I (OD value)		Sample II (OD value)		Sample III (OD value)		Sample IV (OD value)		Sample V (OD value)		Average	SD	3x SD	3x SD + avg ^d	LOD ^d ng/mL	LOD ^d ng/g
		1	2	1	2	1	2	1	2	1	2						
Grain ^a	0	0.010	0.003	0.022	0.043	0.024	0.041	0.020	0.028	0.019	0.024	0.023	0.012	0.037	0.060		
(1754A)	neg. ctrl.	0.013	0.011	0.031	0.000	0.009	0.006	0.028	0.007	0.018	0.027	0.015	0.010	0.031	0.046		
	both											0.019	0.012	0.036	0.055		
Grain ^b	0	-0.009	-0.016	0.003	0.024	0.004	0.022	0.001	0.009	-0.001	0.005	0.004	0.012	0.037	0.041		
(1754A)	neg. ctrl.	-0.006	-0.008	0.012	-0.019	-0.010	-0.013	0.009	-0.012	-0.001	0.008	-0.004	0.010	0.031	0.027		
	both											0.000	0.012	0.036	0.036	0.258	10.32
Hull ^a	0	0.058	0.071	0.068	0.064	0.066	0.076	0.044	0.051	0.062	0.077	0.064	0.011	0.032	0.095		
Material	neg. ctrl.	0.038	0.049	0.064	0.075	0.068	0.083					0.063	0.017	0.050	0.113		
(2459B)	both											0.063	0.013	0.038	0.101		
Hull ^b	0	-0.005	0.007	0.005	0.001	0.003	0.013	-0.020	-0.012	-0.001	0.014	0.000	0.011	0.032	0.032		
Material	neg. ctrl.	-0.025	-0.015	0.000	0.011	0.005	0.020					-0.001	0.017	0.050	0.050		
(2459B)	both											0.000	0.013	0.038	0.038	0.375	15.0
Untoasted Meal ^a	0	-0.008	0.015	0.000	0.019	0.012	0.007	0.016	0.010	0.026	0.017	0.011	0.010	0.030	0.041		
(2459C)	neg. ctrl.	-0.004	-0.006	0.025	-0.002	0.007	-0.001	0.000	0.009	0.005	0.024	0.006	0.011	0.033	0.039		
	both											0.009	0.011	0.032	0.040		
Untoasted Meal ^b	0	-0.017	0.006	-0.009	0.010	0.004	-0.002	0.007	0.002	0.018	0.009	0.003	0.010	0.030	0.033		
(2459C)	neg. ctrl.	-0.012	-0.014	0.016	-0.011	-0.001	-0.010	-0.008	0.000	-0.004	0.016	-0.003	0.011	0.033	0.030		
	both											0.000	0.011	0.032	0.032	0.353	7.06

^a OD values were subtracted with the plate background.

^b OD values were subtracted with both the plate background and the average 2mEPSPS OD value for the measurements calculated from both the 0 ng/mL spike and the negative control.

^c "0" identifies the data for the 0 ng/mL spike. "Neg. ctrl." identifies the data for the negative control on the same plate as the 0 ng/mL spike. "Both" identifies the data obtained by averaging the data from the 0 ng/mL spike and the negative control.

^d The value of 0 ng/g + 3 x SD was entered into the formula for the standard curve on the plate containing the 0 ng/mL spike and the negative control. The result is the LOD in ng/mL which is multiplied by the dilution during extraction (ratio of mL of extraction buffer / grams of matrix extracted) to convert to ng/g.

^e LOD for Whole Soybeans was retrieved from study DQ09B003

Table A2-24 Determination of the LOD for 2mEPSPS Protein in Non-Transgenic Toasted Meal, Crude Oil, and Crude Lecithin

Matrix (BTID)	ng EPSPS/ mL spiked ^c	Sample I (OD value)		Sample II (OD value)		Sample III (OD value)		Sample IV (OD value)		Sample V (OD value)		Average	SD	3x SD	3x SD + avg ^d	LOD ^d ng/mL	LOD ^d ng/g
		1	2	1	2	1	2	1	2	1	2						
Toasted	0	-0.018	-0.024	-0.011	-0.016	0.005	0.003	-0.006	0.012	0.003	0.001	-0.005	0.012	0.035	0.030		
Meal ^a	neg. ctrl.	0.004	-0.013	0.007	-0.004	-0.001	-0.005	-0.015	-0.003	0.006	0.007	-0.002	0.008	0.024	0.022		
(2459D)	both											-0.003	0.010	0.030	0.026		
Toasted	0	-0.015	-0.021	-0.008	-0.012	0.008	0.007	-0.002	0.015	0.006	0.004	-0.002	0.012	0.035	0.033		
Meal ^b	neg. ctrl.	0.007	-0.010	0.010	-0.001	0.002	-0.002	-0.011	0.000	0.010	0.011	0.002	0.008	0.024	0.026		
(2459D)	both											0.000	0.010	0.030	0.030	0.291	5.82
Crude	0	0.012	0.031	0.034	0.020	0.049	0.021	0.007	0.026	0.014	0.011	0.023	0.013	0.038	0.061		
Oil ^a	neg. ctrl.	0.019	0.011	0.007	-0.004	0.026	0.013	0.015	0.006	0.001	0.012	0.011	0.009	0.026	0.036		
(2459E)	both											0.017	0.012	0.037	0.053		
Crude	0	-0.004	0.015	0.017	0.004	0.032	0.005	-0.010	0.010	-0.003	-0.005	0.006	0.013	0.038	0.044		
Oil ^b	neg. ctrl.	0.002	-0.006	-0.010	-0.020	0.009	-0.004	-0.002	-0.010	-0.016	-0.004	-0.006	0.009	0.026	0.020		
(2459E)	both											0.000	0.012	0.037	0.037	0.357	7.14
Crude	0	-0.024	-0.015	-0.003	0.021	-0.002	0.004	0.011	0.018	-0.010	0.007	0.001	0.014	0.043	0.044		
Lecithin ^a	neg. ctrl.	-0.011	-0.012	0.003	-0.007	0.012	-0.007	-0.017	0.012	0.000	0.019	-0.001	0.012	0.036	0.035		
(2459F)	both											0.000	0.013	0.039	0.039		
Crude	0	-0.024	-0.015	-0.003	0.021	-0.002	0.004	0.011	0.018	-0.010	0.007	0.001	0.014	0.043	0.044		
Lecithin ^a	neg. ctrl.	-0.011	-0.012	0.003	-0.007	0.012	-0.007	-0.017	0.012	0.000	0.019	-0.001	0.012	0.036	0.035		
(2459F)	both											0.000	0.013	0.039	0.039	0.393	7.86

^a OD values were subtracted with the plate background.

^b OD values were subtracted with both the plate background and the average 2mEPSPS OD value for the measurements calculated from both the 0 ng/mL spike and the negative control.

^c "0" identifies the data for the 0 ng/mL spike. "Neg. ctrl." identifies the data for the negative control on the same plate as the 0 ng/mL spike. "Both" identifies the data obtained by averaging the data from the 0 ng/mL spike and the negative control.

^d The value of 0 ng/g + 3 x SD was entered into the formula for the standard curve on the plate containing the 0 ng/mL spike and the negative control. The result is the LOD in ng/mL which is multiplied by the dilution during extraction (ratio of mL of extraction buffer / grams of matrix extracted) to convert to ng/g.

Table A2-25 Determination of the LOD for 2mEPSPS Protein in Non-Transgenic Refined Oil, Refined Bleached Deodorized Oil (RBD Oil), and Protein Isolate

Matrix (BTID)	ng EPSPS/ mL spiked ^c	Sample I (OD value)		Sample II (OD value)		Sample III (OD value)		Sample I V (OD value)		Sample V (OD value)		Average	SD	3x SD	3x SD + avg ^d	LOD ^d ng/mL	LOD ^d ng/g
		1	2	1	2	1	2	1	2	1	2						
Refined Oil ^a (2459G)	0	-0.012	0.004	0.005	0.004	0.002	0.021	0.008	0.041	0.014	0.008	0.010	0.014	0.042	0.052		
	neg. ctrl.	0.014	-0.008	0.011	0.004	0.000	0.001	0.004	0.002	0.008	0.021	0.006	0.008	0.025	0.031		
	both											0.008	0.011	0.034	0.042		
Refined Oil ^a (2459G)	0	-0.019	-0.004	-0.003	-0.003	-0.006	0.014	0.000	0.034	0.006	0.001	0.002	0.014	0.042	0.044		
	neg. ctrl.	0.007	-0.016	0.004	-0.004	-0.007	-0.006	-0.004	-0.006	0.000	0.013	-0.002	0.008	0.025	0.023		
	both											0.000	0.011	0.034	0.034	0.256	5.12
RBD Oil ^a (2459H)	0	-0.016	0.005	-0.012	0.000	-0.004	-0.014	-0.007	0.008	0.003	-0.008	-0.005	0.008	0.024	0.020		
	neg. ctrl.	0.025	0.009	0.012	-0.004	-0.013	0.001	-0.008	-0.018	-0.006	0.017	0.002	0.014	0.041	0.043		
	both											-0.002	0.011	0.034	0.033		
RBD Oil ^a (2459H)	0	-0.014	0.006	-0.011	0.001	-0.002	-0.012	-0.006	0.009	0.004	-0.007	-0.003	0.008	0.024	0.021		
	neg. ctrl.	0.027	0.011	0.014	-0.002	-0.012	0.002	-0.006	-0.016	-0.004	0.018	0.003	0.014	0.041	0.044		
	both											0.000	0.011	0.034	0.034	0.204	4.08
Protein Isolate ^a (2459I)	0	-0.004	0.018	0.016	0.107	0.040	0.109	0.022	0.055	0.051	0.115	0.053	0.043	0.130	0.183		
	neg. ctrl.	0.031	0.031	0.014	0.005			0.029	0.051			0.027	0.016	0.048	0.075		
	both											0.043	0.037	0.111	0.155		
Protein Isolate ^a (2459I)	0	-0.047	-0.026	-0.027	0.064	-0.003	0.066	-0.021	0.012	0.008	0.072	0.010	0.043	0.130	0.140		
	neg. ctrl.	-0.012	-0.012	-0.029	-0.038			-0.014	0.008			-0.016	0.016	0.048	0.031		
	both											0.000	0.037	0.111	0.111	0.706	28.2

^a OD values were subtracted with the plate background.

^b OD values were subtracted with both the plate background and the average 2mEPSPS OD value for the measurements calculated from both the 0 ng/mL spike and the negative control.

^c "0" identifies the data for the 0 ng/mL spike. "Neg. ctrl." identifies the data for the negative control on the same plate as the 0 ng/mL spike. "Both" identifies the data obtained by averaging the data from the 0 ng/mL spike and the negative control.

^d The value of 0 ng/g + 3 x SD was entered into the formula for the standard curve on the plate containing the 0 ng/mL spike and the negative control. The result is the LOD in ng/mL which is multiplied by the dilution during extraction (ratio of mL of extraction buffer / grams of matrix extracted) to convert to ng/g.

Table A2-26 Determination of the LOD for HPPD Protein in Non-transgenic Whole Soybeans ^e, Hull Material, and Untoasted Meal

Matrix (BTID)	ng HPPD/ mL spiked ^c	Sample I (OD value)		Sample II (OD value)		Sample III (OD value)		Sample IV (OD value)		Sample V (OD value)		Average	SD	3x SD	3x SD + avg ^d	LOD ^d ng/mL	LOD ^d ng/g
		1	2	1	2	1	2	1	2	1	2						
Grain ^a	0	-0.035	-0.027	-0.002	-0.009	-0.015	-0.005	-0.018	-0.013	-0.014	0.012	-0.013	0.013	0.039	0.026		
(1754A)	neg. ctrl.	-0.001	-0.005	-0.019	-0.017	-0.009	-0.008	-0.015	-0.005	0.000	0.000	-0.008	0.007	0.021	0.013		
	both											-0.010	0.010	0.031	0.021		
Grain ^b	0	-0.024	-0.017	0.008	0.001	-0.005	0.005	-0.008	-0.002	-0.004	0.022	-0.002	0.013	0.039	0.036		
(1754A)	neg. ctrl.	0.009	0.005	-0.009	-0.006	0.001	0.002	-0.005	0.005	0.011	0.010	0.002	0.007	0.021	0.024		
	both											0.000	0.010	0.031	0.031	0.521	20.8
Hull ^a	0	-0.018	0.012	0.021	0.015	0.019	0.018	0.004	0.003	0.015	0.015	0.010	0.012	0.035	0.045		
Material	neg. ctrl.	0.035	0.016	0.024	0.035	0.024	0.040	0.002	0.021	0.037	0.034	0.027	0.012	0.035	0.062		
(2459B)	both											0.019	0.014	0.042	0.061		
Hull ^b	0	-0.037	-0.007	0.002	-0.004	0.001	0.000	-0.015	-0.016	-0.003	-0.004	-0.008	0.012	0.035	0.027		
Material	neg. ctrl.	0.017	-0.003	0.005	0.017	0.005	0.021	-0.016	0.002	0.018	0.016	0.008	0.012	0.035	0.043		
(2459B)	both											0.000	0.014	0.042	0.042	0.672	26.9
Untoasted Meal ^a	0	-0.025	-0.020	0.001	0.008	0.005	0.011	0.000	0.006	0.003	0.009	0.000	0.012	0.037	0.036		
(2459C)	neg. ctrl.	0.003	0.005	0.010	0.007	0.000	0.005	-0.003	0.006	0.000	0.011	0.004	0.005	0.014	0.018		
	both											0.002	0.009	0.028	0.030		
Untoasted Meal ^b	0	-0.027	-0.022	-0.001	0.006	0.003	0.009	-0.002	0.004	0.001	0.007	-0.002	0.012	0.037	0.034		
(2459C)	neg. ctrl.	0.001	0.003	0.008	0.005	-0.002	0.003	-0.005	0.004	-0.002	0.009	0.002	0.005	0.014	0.016		
	both											0.000	0.009	0.028	0.028	0.333	6.66

^a OD values were subtracted with the plate background.

^b OD values were subtracted with both the plate background and the average 2mEPSPS OD value for the measurements calculated from both the 0 ng/mL spike and the negative control.

^c "0" identifies the data for the 0 ng/mL spike. "Neg. ctrl." identifies the data for the negative control on the same plate as the 0 ng/mL spike. "Both" identifies the data obtained by averaging the data from the 0 ng/mL spike and the negative control.

^d The value of 0 ng/g + 3 x SD was entered into the formula for the standard curve on the plate containing the 0 ng/mL spike and the negative control. The result is the LOD in ng/mL which is multiplied by the dilution during extraction (ratio of mL of extraction buffer / grams of matrix extracted) to convert to ng/g.

^e LOD for Whole Soybeans was retrieved from study DQ09B003

Table A2-27 Determination of the LOD for HPPD Protein in Non-Transgenic Toasted Meal, Crude Oil, and Crude Lecithin

Matrix (BTID)	ng HPPD/ mL spiked ^c	Sample I (OD value)		Sample II (OD value)		Sample III (OD value)		Sample I V (OD value)		Sample V (OD value)		Average	SD	3x SD	3x SD + avg ^d	LOD ^d ng/mL	LOD ^d ng/g
		1	2	1	2	1	2	1	2	1	2						
Toasted	0	-0.005	-0.012	0.008	0.017	0.011	0.012	0.009	0.014	0.007	0.012	0.007	0.009	0.027	0.034		
Meal ^a	neg. ctrl.	0.004	0.010	0.004	0.013	0.011	0.019	0.012	0.019	0.013	0.017	0.012	0.005	0.016	0.028		
(2459D)	both											0.010	0.007	0.022	0.032		
Toasted	0	-0.014	-0.021	-0.002	0.008	0.002	0.002	-0.001	0.004	-0.003	0.002	-0.002	0.009	0.027	0.024		
Meal ^b	neg. ctrl.	-0.005	0.000	-0.005	0.003	0.001	0.009	0.002	0.009	0.003	0.007	0.002	0.005	0.016	0.018		
(2459D)	both											0.000	0.007	0.022	0.022	0.308	6.16
Crude	0	-0.024	-0.049	-0.012	-0.018	-0.014	-0.012	-0.013	-0.012	-0.008	-0.005	-0.017	0.012	0.037	0.020		
Oil ^a	neg. ctrl.	0.002	0.003	-0.007	0.005	0.004	0.010	0.004	0.009	0.016	0.008	0.005	0.006	0.018	0.023		
(2459E)	both											-0.006	0.015	0.044	0.039		
Crude	0	-0.018	-0.043	-0.007	-0.012	-0.009	-0.006	-0.007	-0.006	-0.003	0.001	-0.011	0.012	0.037	0.026		
Oil ^b	neg. ctrl.	0.008	0.009	-0.002	0.010	0.010	0.015	0.010	0.015	0.021	0.014	0.011	0.006	0.018	0.029		
(2459E)	both											0.000	0.015	0.044	0.044	0.639	12.8
Crude	0	-0.007	-0.007	0.013	0.012	0.006	0.005	-0.001	-0.004	0.006	0.020	0.004	0.009	0.027	0.031		
Lecithin ^a	neg. ctrl.	0.008	0.009	0.009	0.008	0.007	0.005	-0.004	-0.001	0.010	0.014	0.007	0.005	0.016	0.022		
(2459F)	both											0.005	0.007	0.022	0.027		
Crude	0	-0.013	-0.012	0.007	0.007	0.001	0.000	-0.006	-0.009	0.001	0.014	-0.001	0.009	0.027	0.026		
Lecithin ^a	neg. ctrl.	0.002	0.004	0.004	0.002	0.002	0.000	-0.010	-0.006	0.005	0.009	0.001	0.005	0.016	0.017		
(2459F)	both											0.000	0.007	0.022	0.022	0.358	7.16

^a OD values were subtracted with the plate background.

^b OD values were subtracted with both the plate background and the average 2mEPSPS OD value for the measurements calculated from both the 0 ng/mL spike and the negative control.

^c "0" identifies the data for the 0 ng/mL spike. "Neg. ctrl." identifies the data for the negative control on the same plate as the 0 ng/mL spike. "Both" identifies the data obtained by averaging the data from the 0 ng/mL spike and the negative control.

^d The value of 0 ng/g + 3 x SD was entered into the formula for the standard curve on the plate containing the 0 ng/mL spike and the negative control. The result is the LOD in ng/mL which is multiplied by the dilution during extraction (ratio of mL of extraction buffer / grams of matrix extracted) to convert to ng/g.

Table A2-28 Determination of the LOD for HPPD Protein in Non-Transgenic Refined Oil, Refined Bleached Deodorized Oil (RBD Oil), and Protein Isolate

Matrix (BTID)	ng HPPD/ mL spiked ^c	Sample I (OD value)		Sample II (OD value)		Sample III (OD value)		Sample I V (OD value)		Sample V (OD value)		Average	SD	3x SD	3x SD + avg ^d	LOD ^d ng/mL	LOD ^d ng/g
		1	2	1	2	1	2	1	2	1	2						
Refined	0	-0.023	-0.021	0.003	0.019	0.001	0.003	0.001	0.002	0.005	0.002	-0.001	0.013	0.038	0.037		
Oil ^a	neg. ctrl.	-0.001	0.003	0.001	0.009	0.006	0.011	0.001	0.009	0.012	0.017	0.007	0.006	0.017	0.024		
(2459G)	both											0.003	0.010	0.031	0.034		
Refined	0	-0.027	-0.024	0.000	0.016	-0.002	0.000	-0.002	-0.001	0.002	-0.001	-0.004	0.013	0.038	0.034		
Oil ^a	neg. ctrl.	-0.004	0.000	-0.002	0.006	0.003	0.007	-0.002	0.006	0.009	0.014	0.004	0.006	0.017	0.021		
(2459G)	both											0.000	0.010	0.031	0.031	0.641	12.8
RBD Oil ^a	0	-0.020	-0.012	0.011	0.006	0.008	0.007	0.005	0.009	0.005	0.007	0.003	0.010	0.030	0.033		
(2459H)	neg. ctrl.	-0.002	0.003	0.003	0.018	0.011	0.019	0.006	0.018	-0.031	-0.046	0.000	0.022	0.065	0.065		
	both											0.001	0.017	0.050	0.051		
RBD Oil ^a	0	-0.021	-0.013	0.010	0.005	0.006	0.005	0.004	0.008	0.004	0.005	0.001	0.010	0.030	0.032		
(2459H)	neg. ctrl.	-0.003	0.002	0.002	0.016	0.009	0.018	0.005	0.017	-0.032	-0.047	-0.001	0.022	0.065	0.064		
	both											0.000	0.017	0.050	0.050	0.861	17.2
Protein	0	0.012	0.009	0.043	0.037	0.044	0.036	0.036	0.030	0.039	0.035	0.032	0.012	0.037	0.069		
Isolate ^a	neg. ctrl.	0.033	0.041	0.039	0.042	0.027	0.035	0.036	0.047	0.039	0.048	0.039	0.006	0.019	0.058		
(2459I)	both											0.035	0.010	0.030	0.065		
Protein	0	-0.024	-0.027	0.007	0.001	0.009	0.001	0.001	-0.005	0.004	0.000	-0.003	0.012	0.037	0.033		
Isolate ^a	neg. ctrl.	-0.002	0.005	0.004	0.006	-0.008	-0.001	0.000	0.012	0.004	0.012	0.003	0.006	0.019	0.022		
(2459I)	both											0.000	0.010	0.030	0.030	0.697	27.9

^a OD values were subtracted with the plate background.

^b OD values were subtracted with both the plate background and the average 2mEPSPS OD value for the measurements calculated from both the 0 ng/mL spike and the negative control.

^c "0" identifies the data for the 0 ng/mL spike. "Neg. ctrl." identifies the data for the negative control on the same plate as the 0 ng/mL spike. "Both" identifies the data obtained by averaging the data from the 0 ng/mL spike and the negative control.

^d The value of 0 ng/g + 3 x SD was entered into the formula for the standard curve on the plate containing the 0 ng/mL spike and the negative control. The result is the LOD in ng/mL which is multiplied by the dilution during extraction (ratio of mL of extraction buffer / grams of matrix extracted) to convert to ng/g.

Table A2-29 Analytical Results for 2mEPSPS Protein Content in Whole Soybeans and Processed Fractions

Description	Sample ID	Matrix	Regimen	Sample I a (ng/g)	Sample I b (ng/g)	Sample II a (ng/g)	Sample II b (ng/g)	Average (ng/g)	SD (ng/g)	%CV (ng/g)
Unsprayed	2460A	Whole Soybeans	B	543	576	585	584	572	19.5	3.41
Unsprayed	2460B	Hull Material	B	524	491	577	616	552	55.8	10.1
Unsprayed	2460C	Untoasted Meal	B	1.53	1.78	4.24	4.55	3.02	1.59	52.5
Unsprayed	2460D	Toasted Meal	B	-2.74	-3.64	-1.86	-1.26	-2.38	1.04	43.8
Unsprayed	2460E	Crude Oil	B	-2.60	-3.22	-2.28	-1.20	-2.33	0.85	36.4
Unsprayed	2460F	Crude Lecithin	B	-3.58	-4.04	-1.94	-0.50	-2.51	1.62	64.3
Unsprayed	2460G	Refined Oil	B	-6.04	-4.04	-5.25	-3.27	-4.65	1.23	26.5
Unsprayed	2460H	Refined Bleached Deodorized Oil	B	-7.58	-7.68	-5.40	-7.25	-6.98	1.07	15.3
Unsprayed	2460I	Protein Isolate	B	437	492	501	503	483	31.0	6.42
Sprayed	2461A	Whole Soybeans	C	701	668	780	810	740	66.4	8.97
Sprayed	2461B	Hull Material	C	523	493	490	497	501	15.5	3.09
Sprayed	2461C	Untoasted Meal	C	5.33	4.62	9.55	9.20	7.17	2.56	35.7
Sprayed	2461D	Toasted Meal	C	-0.56	-1.68	-0.29	-1.78	-1.08	0.76	70.7
Sprayed	2461E	Crude Oil	C	-2.86	-1.88	-2.08	-1.54	-2.09	0.56	26.8
Sprayed	2461F	Crude Lecithin	C	-9.38	-4.44	-2.76	-4.80	-5.35	2.83	53.0
Sprayed	2461G	Refined Oil	C	-6.02	-6.69	-7.28	-7.36	-6.84	0.62	9.10
Sprayed	2461H	Refined Bleached Deodorized Oil	C	-9.62	-10.4	-9.62	-8.56	-9.56	0.77	8.06
Sprayed	2461I	Protein Isolate	C	1060	1051	987	983	1020	40.9	4.01

Table A2-30 Analytical Results for HPPD Protein Content in Whole Soybeans and Processed Fractions

Description	Sample ID	Matrix	Regimen	Sample I a (ng/g)	Sample I b (ng/g)	Sample II a (ng/g)	Sample II b (ng/g)	Average (ng/g)	SD (ng/g)	%CV (ng/g)
Unsprayed	2460A	Whole Soybeans	B	792	733	778	714	754	36.8	4.88
Unsprayed	2460B	Hull Material	B	931	865	1019	947	941	63.5	6.75
Unsprayed	2460C	Untoasted Meal	B	-7.44	-8.95	-4.65	-5.20	-6.56	1.99	30.4
Unsprayed	2460D	Toasted Meal	B	-0.80	-0.78	-2.26	-2.74	-1.65	1.01	61.2
Unsprayed	2460E	Crude Oil	B	-5.68	-4.72	-5.68	-5.54	-5.41	0.46	8.54
Unsprayed	2460F	Crude Lecithin	B	-6.38	-20.7	-1.80	-2.46	-7.83	8.81	112
Unsprayed	2460G	Refined Oil	B	-4.80	-3.10	-3.31	-5.09	-4.08	1.02	24.9
Unsprayed	2460H	Refined Bleached Deodorized Oil	B	-5.04	-3.04	-3.11	-3.40	-3.65	0.94	25.8
Unsprayed	2460I	Protein Isolate	B	659	565	675	611	627	49.8	7.93
Sprayed	2461A	Whole Soybeans	C	870	865	952	980	917	57.8	6.30
Sprayed	2461B	Hull Material	C	921	923	983	1004	957	42.1	4.39
Sprayed	2461C	Untoasted Meal	C	-7.22	-6.60	0.27	0.07	-3.37	4.10	122
Sprayed	2461D	Toasted Meal	C	-0.60	0.56	2.02	3.33	1.33	1.71	129
Sprayed	2461E	Crude Oil	C	-4.26	-5.06	-4.32	-4.88	-4.63	0.40	8.64
Sprayed	2461F	Crude Lecithin	C	-8.94	-5.26	-1.90	1.52	-3.65	4.49	123
Sprayed	2461G	Refined Oil	C	0.25	-2.47	-5.16	-2.58	-2.49	2.21	88.8
Sprayed	2461H	Refined Bleached Deodorized Oil	C	-1.62	1.64	-0.18	-0.66	-0.21	1.37	667
Sprayed	2461I	Protein Isolate	C	1056	1096	1079	1080	1078	16.5	1.53