MRI

Determination of PCBs and PCDD/PCDF In Lobster

Data Report

For Therese Anderson
University of Maine

and Katherine Groves
University of Southern Maine

Proposal No. 0917-120
MRI Project No. 5120-A

July 6, 1998

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Data Report

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July 6, 1998

Preface

This report provides the results of the analyses of 8 lobster meat and 8 lobster tomalley samples for dioxins and furans and selected polychlorinated biphenyls. The samples were submitted by the University of Maine in cooperation with the University of Southern Maine. This work was conducted under Proposal No. 0917-120 (MRI Project No. 5120-A) with the University of Southern Maine.

The samples were analyzed using the Chemical Sciences SOP MRI-5201, and MRI 5405. Portions of these SOPs were modified to optimize the PCB recoveries. These SOPs are based on EPA Methods 8290, 1613B, and draft method 1668. The samples were prepared for analysis under the supervision of Ms. Janet Paper. HRGC/HRMS analysis and data reduction were conducted under the supervision of Mr. Mark Horrigan. Dr. Vincy Abraham supervised all project-related activities.

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July 6, 1998

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Executive Summary

Sixteen samples (lobster meat and lobster tomalley) were prepared and analyzed for polychlorinated dibenzofurans (PCDFs), polychlorinated dibenzo-*p*-dioxins (PCDDs) and polychlorinated biphenyls (PCBs). The overall results are summarized in Table 1 showing a range of selected analyte concentrations organized by matrix. The isomers presented are those with the highest international toxic equivalence factors.

In general, the lobster meat samples showed very few detected PCDD/PCDF isomers above the low standard based detection limits. PCB #77 was found in all of the lobster meat samples.

The lobster tomalley samples showed 2,3,7,8-TCDF and 2,3,7,8-TCDD in nearly all of the samples. In addition, some of the higher chlorinated PCDD/PCDF isomers were present, including OCDD. Most of the PCB congeners were found in each tomalley sample. Several congeners were routinely above the upper limit of the calibration range.

Overall, the IQS recoveries were within the acceptable range of 25 to 150% for the PCDD/PCDF and PCB labeled analogs.

Table 1. Analyte Range Summary

Matrix	Isomer	Whole weight (pg/g)		Lipid weight (pg/g)	
		Low	High	Low	High
Meat	2,3,7,8-TCDF	0.125	0.186	54.4	115
	2,3,7,8-TCDD	U	U	U	U
	2,3,4,7,8-PeCDF	U	U	U	U
	1,2,3,7,8-PeCDD	U	U	U	U
	77-TCB	1.64	3.66	856	3130
	126-PeCB	0.174	0.174	247	247
	169-HxCB	U	U	U	U
Tomalley	2,3,7,8-TCDF	16.2	29	88.6	200
	2,3,7,8-TCDD	1.93	2.37	8.26	18.8
	2,3,4,7,8-PeCDF	5.95	10.8	32.6	74.7
	1,2,3,7,8-PeCDD	4.03	7.37	20.7	50.8
	77-TCB	437	786	2490	5960
	126-PeCB	116	175	657	1300
	169-HxCB	18.2	35.8	122	181

U = undetected.

1. Introduction

The University of Southern Maine contracted with Midwest Research Institute (MRI) to determine PCDD, PCDF, and PCB concentrations in lobsters living in the Casco Bay Estuary.

This report describes the methods used to prepare and analyze the samples and presents the results of the analyses of 8 lobster meat, and 8 lobster tomalley samples that were provided in sample shipments to MRI.

2. Methodology

This section describes the methodology used to log-in and prepare the samples for analysis. The detailed sample preparation methodology used for this program is contained in MRI's Chemical Science Department SOP MRI-5201 which is based upon EPA Method 8290, 1613B. Additions and modifications to the SOP were made to incorporate the PCBs as specified below. HRGC/HRMS analytical parameters are given and data reduction and calculation procedures are discussed.

2.1 Sample Receipt

The lobster meat and tomalley samples were received on April 29, 1998. The sample labels were checked against the inventory sheet received with the shipment, and the condition of each sample was noted. Unique five-digit numbers were assigned to each sample using preprinted labels. This sample number was used to identify the sample throughout the entire sample preparation, analysis, and reporting procedure. All samples were stored frozen until thawed for grinding or extraction.

2.2 Sample Preparation Procedures

The samples were prepared in one analytical batch. A method blank and a laboratory control spike (LCS) were prepared with these samples. The matrix for the method blank and LCS was sodium sulfate. A matrix spike/matrix spike duplicate (MSD) pair was prepared for each sample type in this batch.

A 50-g sample of the ground meat tissue (10 g was used for the lobster tomalley samples) was mixed with 200 to 400 g of sodium sulfate and the mixture placed into a Soxhlet extractor, fortified with the internal quantitation standard cocktail (Table 2), and extracted 16 hr with 750 mL of 1:1 dichloromethane: hexane. After extraction, the solvent was evaporated, the percent lipid determined, the lipid redissolved in hexane, and the extract was then subjected to a 2-hr acid silica gel slurry step (40% H_2SO_4 on silica gel) to remove bulk lipids. The extract from the acid silica gel slurry of the fish extract was eluted through a 6-g/1-g acid/neutral silica gel column. The elutant was concentrated to 10 mL and split into two 5 mL portions. One portion, to be analyzed for PCBs was concentrated to ~ 500 µL spiked with 50 µL of Recovery Standards (RS) and evaporation continued to 50 µL final volume.

The other portion, to be analyzed for PCDD/PCDFs was prepared as follows. The eluent from the silica gel column was further cleaned by eluting through a neutral alumina column. The final fraction was eluted through a 0.34-g column of 18% Carbopak C/Celite 545®. The extract was then concentrated under prepurified nitrogen to approximately 100 µL. Then 10 µL of the recovery standard solution (Table 2) was

added and the evaporation was continued to a final volume of 10 μL. The extract was stored in a refrigerator until HRGC/HRMS analysis.

After initial analysis of selected dioxin samples, it was determined that an additional clean-up step would be needed to reduce and/or eliminate some persistent matrix interferences. The dioxin extracts were put through a second 0.34g column of AX-21/celite 545. These extracts were concentrated to ~ 100 mL and spiked with 10 μL (8 μL was used if the sample had already been analyzed) of tridecane. Evaporation continued until a final volume of 10 μL (8μL) was obtained.

Table 2. Internal Standard Spiking Solutions

Compound	Concentration (pg/µL)
Labeled dioxin and furan analog standard[a]	
^{13}C-2,3,7,8-TCDF	20
^{13}C-2,3,7,8-TCDD	20
^{13}C-1,2,3,7,8-PeCDF	20
^{13}C-2,3,4,7,8-PeCDF	20
^{13}C-1,2,3,7,8-PeCDD	20
^{13}C-1,2,3,4,7,8-HxCDF	20
^{13}C-1,2,3,6,7,8-HxCDF	20
^{13}C-1,2,3,7,8,9-HxCDF	20
^{13}C-2,3,4,6,7,8-HxCDF	20
^{13}C-1,2,3,4,7,8-HxCDD	20
^{13}C-1,2,3,6,7,8-HxCDD	20
^{13}C-1,2,3,4,6,7,8-HpCDF	20
^{13}C-1,2,3,4,7,8,9-HpCDF	20
^{13}C-1,2,3,4,6,7,8-HpCDD	20
^{13}C-OCDD	40
Labeled PCB standard[a]	
^{13}C-3,3′,4,4′-tetra PCB (B/Z #77)[c]	20
^{13}C-2,3′,4,4′,5-penta PCB (B/Z #118)	20
^{13}C-2,3,3′,4,4′-penta PCB (B/Z #105)	20
^{13}C-3,3′,4,4′,5-penta PCB (B/Z #126)	20
^{13}C-2,3,3′,4,4′,5-hexa PCB (B/Z #156)	20
^{13}C-3,3′,4,4′,5,5′-hexa PCB (B/Z #169)	20
^{13}C-2,2′,3,4,4′,5,5′-Hepta PCB (B/Z #180)	20
Internal recovery standard[b]	
^{13}C-1,2,3,4-TCDD	100
^{13}C-1,2,3,7,8,9-HxCDD	100

[a] Prepared in isooctane, 100 mL spiked for 10-mL final extract volume.
[b] Prepared in tridecane, 250 mL spiked for 50-mL final extract volume.
[c] Ballschmitter-Zell designation.

2.3 Sample Analysis Procedures

Analysis was performed using a VG70-250S high resolution mass spectrometer operating in the selected ion monitoring (SIM) mode at a mass resolution of 10,000 or greater. Samples were analyzed using a DB-5MS (60 meter, 0.25mm ID, 0.25 micron film thickness) fused silica column under conditions which were specific for 2,3,7,8-TCDD (parameters in Table 3). The analytical method criterion was primarily that specified in EPA Method 8290.

MRI has modified the mass ions used for identification of the pentachlorodibenzo-*p*-dioxins. The mass ion 353.8576 (M) is used along with mass ion 355.8546 (M + 2) for identification of this isomer. Similarly the mass ion 365.8979 (M) is used along with mass ion 367.8949 (M + 2) for identification of the ^{13}C-labeled analog. A theoretical ion ratio (M + 2/M) value of 1.64 ± 15% was used for identification of both the native and labeled compounds. Acquisition of these masses are necessary to avoid contribution from the HEXA-PCBs which were spiked into these samples.

A typical analysis day was initiated with the mass calibration of the mass spectrometer, followed by the analysis of a window-defining mix used to demonstrate 25% valley separation between 2,3,7,8-TCDD and all other TCDD isomers. Analysis of a mid-level standard (e.g., 10 pg TCDD/TCDF and 100 pg PCB) was next. Relative response factors (RRFs) were calculated based on this run and were compared to those RRFs established during the initial calibration. The dioxin/furan initial calibration curve consisted of a series of six standards ranging in concentrations from 0.25 to 200 pg/μL 2,3,7,8-TCDD. All other 2,3,7,8-substituted PCDDs and PCDFs are included in the calibration standards. The PCB initial calibration curve consisted of a series of five standards ranging in concentrations from 5 to 500 pg/μL. Tables 4 and 5 give the concentration ranges for each of the isomers in the calibration standards. For the initial calibration to be acceptable, the percent relative standard deviation of the average RRFs must be less than or equal to 20% for all native analytes and less than or equal to 30% for all labeled compounds.

Criteria for passing the beginning-of-the-day calibration dictate that the daily RRF for all analytes must be within ±20% deviation from the initial RRFs. End-of-the-day criteria for dioxins and furans are that the RRFs must be within ±25% for native isomers and ±35% for labeled isomers. Beginning and end of the day criteria for PCBs dictate that the RRFs must be within ±30% from the initial RRFs. Following the analysis of the mid-level standard, a solvent blank (tridecane) was analyzed, then the Method Blank and LCS followed by the field samples. This analysis sequence was repeated for the next 12-hr shift.

2.4 Data Reduction Procedures

Data reduction was conducted using a basic computer program which receives a specially formatted data file as input, and outputs an extract concentration. The sample

weight and other concentration or dilution factors were taken into account to arrive at a final sample concentration. Detection limits were determined for each 2,3,7,8-substituted isomer in each sample by either of the two following methods. First, if no interfering peak was observed, the sample concentration equivalent to the low calibration standard concentration was used as the method detection limit (MDL). Second, the concentration of a coeluting or interfering peak that did not match the qualitative ion ratio criteria for that isomer was reported when an interference was observed. The latter case was reported as an EMPC, the estimated maximum possible concentration for that isomer in that instance.

Table 3. HRGC/HRMS Operating Conditions for PCDD/PCDF Analysis

Mass Spectrometer	
Accelerating voltage:	8,000 V
Trap current:	500 µA
Electron energy:	35 eV
Photo-multiplier voltage:	350 V
Source temperature:	280°C
Resolution:	≥ 10,000 (10% valley definition)
Overall SIM cycle time:	1 sec
Gas Chromatograph	
Column coating:	DB-5MS
Film thickness:	0.25 µm
Column dimensions:	60 m × 0.25 mm i.d.
He linear velocity:	~ 25 cm/sec
He head pressure:	25 psi
Injection type:	Splitless, 45 sec
Split flow:	30 mL/min
Purge flow:	3 mL/min
Injector temperature:	290°C
Interface temperature:	280°C
Injection size:	1 µL
Initial temperature:	180°C
Initial time:	2 min
Temperature program:	180° to 220°C at 5°C/min
Second hold time:	16 min
Second temperature ramp:	220° to 235°C at 5°C/min
Third hold time:	7 min
Third temperature ramp:	235° to 330°C at 5°C/min
Final hold time:	4 min

Table 4. Dioxin/Furan Calibration Standard Concentrations (pg/μL)

COMPOUND	CS.25	CS1	CS2	CS3	CS4	CS5
2,3,7,8-TCDF	0.25	0.5	2	10	40	200
2,3,7,8-TCDD	0.25	0.5	2	10	40	200
1,2,3,7,8-PeCDF	1.25	2.5	10	50	200	1000
2,3,4,7,8-PeCDF	1.25	2.5	10	50	200	1000
1,2,3,7,8-PeCDD	1.25	2.5	10	50	200	1000
1,2,3,4,7,8-HxCDF	1.25	2.5	10	50	200	1000
1,2,3,6,7,8-HxCDF	1.25	2.5	10	50	200	1000
2,3,4,6,7,8-HxCDF	1.25	2.5	10	50	200	1000
1,2,3,7,8,9-HxCDF	1.25	2.5	10	50	200	1000
1,2,3,4,7,8-HxCDD	1.25	2.5	10	50	200	1000
1,2,3,6,7,8-HxCDD	1.25	2.5	10	50	200	1000
1,2,3,7,8,9-HxCDD	1.25	2.5	10	50	200	1000
1,2,3,4,6,7,8-HpCDF	1.25	2.5	10	50	200	1000
1,2,3,4,7,8,9-HpCDF	1.25	2.5	10	50	200	1000
1,2,3,4,6,7,8-HpCDD	1.25	2.5	10	50	200	1000
OCDF	2.5	5	20	100	400	2000
OCDD	2.5	5	20	100	400	2000
Labeled Analog						
13C-2,3,7,8-TCDF	100	100	100	100	100	100
13C-2,3,7,8-TCDD	100	100	100	100	100	100
13C-1,2,3,7,8-PeCDF	100	100	100	100	100	100
13C-1,2,3,7,8-PeCDD	100	100	100	100	100	100
13C-1,2,3,4,7,8-HxCDF	100	100	100	100	100	100
13C-1,2,3,6,7,8-HxCDD	100	100	100	100	100	100
13C-1,2,3,4,6,7,8-HpCDF	100	100	100	100	100	100
13C-1,2,3,4,6,7,8-HpCDD	100	100	100	100	100	100
13C-OCDD	200	200	200	200	200	200
Recovery Standard						
13C-1,2,3,4-TCDD	100	100	100	100	100	100
13C-1,2,3,7,8,9-HxCDD	100	100	100	100	100	100

Table 5. PCB Calibration Standard Concentrations (pg/µL)

COMPOUND	CS1	CS2	CS3	CS4	CS5
77-TCB	5	20	100	250	500
123-PeCB	5	20	100	250	500
118-PeCB	5	20	100	250	500
114-PeCB	5	20	100	250	500
105-PeCB	5	20	100	250	500
126-PeCB	5	20	100	250	500
167-HxCB	5	20	100	250	500
156-HxCB	5	20	100	250	500
157-HxCB	5	20	100	250	500
169-HxCB	5	20	100	250	500
180-HpCB	5	20	100	250	500
170-HpCB	5	20	100	250	500
189-HpCB	5	20	100	250	500
Labeled Analog					
13C 77-TPCB	100	100	100	100	100
13C 118-PeCB	100	100	100	100	100
13C 105-PeCB	100	100	100	100	100
13C 126-PeCB	100	100	100	100	100
13C 156-HxCB	100	100	100	100	100
13C 169-HxCB	100	100	100	100	100
13C 180-HpCB	100	100	100	100	100
Recovery Standard					
13C-1,2,3,4-TCDD	100	100	100	100	100
13C-1,2,3,7,8,9-HxCDD	100	100	100	100	100

2.5 Calculation Theory

During the initial calibration, a series of standards is analyzed, and relative response factors (RRFs) are determined for each native analyte relative to the corresponding ^{13}C-labeled internal quantitation standard (IQS) and for each IQS relative to the recovery standards (RS). The average of the RRFs from all the standards is used in all succeeding calculations to determine sample amounts for a specific isomer.

As previously indicated, known amounts of IQS are added to the sample before extraction. In the data calculations, the response of the IQS, its known concentration, the response of the native, and the average RRF are used to calculate the concentration of the native isomers in the extract. Since the IQSs are affected by the sample matrix and the overall extraction procedure, the calculation procedure adjusts for recovery from the sample matrix.

$$\text{Concentration} = \frac{(\text{Summed Area of Native})\,(\text{Amount of IQS in Total pg})}{(\text{Summed Area of IQS})\,(\text{Sample Size in g})\,(\text{RRF}_{ave})}$$

The recovery standards, added to the extract just prior to HRGC/HRMS analysis, are used to determine the absolute recovery of the IQS. The delivery of these two RS compounds in a high boiling solvent also ensures the integrity of the volume of the final extract.

The Internal Quantitation Standards, (IQS) were quantitated relative to the Recovery Standards (RS). The PCB IQS were quantitated relative to the ^{13}C-TCDD recovery standard. The native results were quantitated relative to the appropriate IQS, per method 8290 for PCDD/PCDF. The PCB natives were quantitated relative to the closest eluting IQS.

The International Toxicity Equivalents (I-TEs) for each sample were calculated using the factors given in Table 6. The detection limits were used for undetected analytes to calculate the maximum I-TE value, zero was used for undetected analytes to calculate the minimum I-TE value.

Table 6. International Toxic Equivalents

PCDD/F	Factor(a)	PCB	Factor(b)
2378TCDF	0.1	77-TCB	0.0005
2378TCDD	1	123-PeCB	0.0001
12378PECDF	0.05	118-PeCB	0.0001
23478PECDF	0.5	114-PeCB	0.0005
12378PECDD	0.5	105-PeCB	0.0001
123478HXCDF	0.1	126-PeCB	0.1
123678HXCDF	0.1	167-HxCB	0.00001
234678HXCDF	0.1	156-HxCB	0.0005
123789HXCDF	0.1	157-HxCB	0.0005
123478HXCDD	0.1	169-HxCB	0.01
123678HXCDD	0.1	180-HpCB	0.00001
123789HXCDD	0.1	170-HpCB	0.0001
1234678HPCDF	0.01	189-HpCB	0.0001
1234789HPCDF	0.01		
1234678HPCDD	0.01		
12346789OCDF	0.001		
12346789OCDD	0.001		

(a)- Source: Chemosphere,20(7-9):751-757 (1990)).
(b)- Source: Chemosphere,28(6):1049-1067 (1994)).

3. Results and Discussion

The following section discusses the results of the analyses of the field samples and the quality control samples.

3.1 Sample Results and Discussion

3.1.1 PCDD/F Introduction

Sample results for dioxins and furans are in Table 7 through 10. The method blank results are presented before the sample results for each matrix type. The percent lipid value given for the method blank represents the average for that matrix type. Results for 2,3,7,8-TCDF are to be considered as maximum possible concentrations since the DB5-MS column does not have full resolution of this isomer from one other TCDF isomer. Determination of 2,3,7,8-TCDF by a confirmation column was not part of the scope of this project. International toxic equivalents (I-TE) are also given in each table. These values were calculated using the published toxic equivalency factors as discussed in Section 2.5 of this report. The I-TEs given are for PCDD/F only, and do not include the PCB values.

3.1.2 PCDD/F Results

A summary of the lobster meat PCDD/F sample results are given in Tables 7 and 8. Results are reported as pg/g on a whole weight and percent lipid basis, respectively. The samples were prepared in one laboratory batch.

Most of the samples showed no PCDD/F isomers detected above the level of the low calibration standard. Low levels of 2,3,7,8-TCDF and OCDD, were detected in a few of the samples.

A summary of the lobster tomalley PCDD/F sample results are given in Tables 9 and 10. Results are reported as pg/g on a whole weight and percent lipid basis, respectively. The samples were prepared in the same batch as the lobster meat samples.

The tomalley samples showed the presence of 2,3,7,8-TCDF and 2,3,7,8-TCDD in nearly every sample. Field ID "T-Jewel-1" contained detected levels of most of the 2,3,7,8 substituted isomers, this sample also had the highest I-TE (min) value.

3.1.3 PCB Introduction

Sample results for PCBs are in Tables 11 through 14. The method blank results are presented before the sample results for each matrix. Most of the tomalley samples showed values that were above the upper concentration limit of the calibration range with PCB No. 118 often saturating the mass spectrometer detector. These difficulties are flagged accordingly in the tables and the values should be considered as estimated levels. International toxic equivalents (I-TE) are also given in each table. These values were calculated using the published toxic equivalency factors as discussed in Section 2.5 of this report. The I-TEs given are for PCBs only, and do not include the PCDD/F values. These I-TEs should be considered estimates due to the difficulties with detector saturation and results above the calibration range.

3.1.4 PCB Results

A summary of the lobster meat PCB sample results are given in Tables 11 and 12. Results are reported as pg/g on a whole weight and percent lipid basis, respectively. All of the samples contained 77-TCB at concentrations above the level of the low calibration standard. PCB No. 118 and No. 180 were consistently the isomers with the greatest concentrations found.

A summary of the lobster tomalley PCB sample results are given in Tables 13 and 14. Results are reported as pg/g on a whole weight and percent lipid basis, respectively. The lobster tomalley samples showed detectable levels for all PCB isomers. Several isomers were routinely found at levels that exceeded the upper limit of the calibration range. In addition, PCB No. 118 often gave a saturated peak response. Values above the calibration range and those with a saturated peak response should be considered as estimated levels.

3.2 Quality Control Results and Discussion

3.2.1 Internal Quantitation Standard Recoveries

Recoveries of the PCDD/F internal quantitation standard recoveries (IQS) are given in Tables 15 and 16. Recoveries of the PCB IQS are given in Tables 17 and 18. The last two columns in each table show the overall average and standard deviation. These results are presented to give an estimate of the absolute overall efficiency of the extraction and cleanup process. The recommended acceptable range of recovery for these labeled compounds is from 25 to 150%, based on MRI's 5405 and guidance from EPA Method 1613.

All of the PCDD/PCDF IQS recoveries were acceptable in these samples. The PCB recoveries were acceptable in the majority of the samples. High PCB recoveries were

observed for ^{13}C-169HxCB in two samples (L-Jewel-1 and L-Jewel-4) and for ^{13}C-180-HpCB in the L-Jewel-4 sample. The unusually high values were due to matrix intereferences observed in the corresponding PFK reference mass (lock mass) used to monitor drift of the mass spectrometer.

3.2.2 Initial and Daily Calibration

Initial calibration curves were conducted on May 18, 1998 (PCBs), and June 17, 1998 (PCDD/PCDF). The relative standard deviation of all analytes were within the criteria as specified in Section 2.3 of this report. The daily calibrations passed the criteria as specified in MRI's SOP 5405.

3.2.3 Method Blanks

One method blank was prepared and analyzed with these samples. The results of the method blank are presented twice using the average size and percent lipid for each matrix type. The method blank is presented first in the tables followed by the sample results. The method blank is treated identically to the samples and serves as a measure of the laboratory background for these samples. The method blank showed only OCDD above the level of the low standard. The method blank showed most PCB isomers above the level of the low standard, however the amounts found were insignificant in comparison to the concentrations in the samples. PCB laboratory background levels are typically higher than dioxin/furan levels.

3.2.4 Fortified Sample Results

A matrix spike/matrix spike duplicate (MS/MSD) pair was prepared from each sample matrix associated with this batch. L-Jewel-1 was chosen for the meat MS/MSD and TNM-3 was chosen for the tomalley MS/MSD. The results of the MS/MSD are presented in Tables 19 and 20. The MS/MSD were spiked with known amounts of PCDD/F and PCB in order to demonstrate the accuracy and precision of the analytical method. The data quality objective for these spiked samples is to exhibit recoveries between 75% and 125% and a relative percent difference (RPD) between duplicates of 20% or less.

The PCDD/F MS/MSD results met the objectives for the lobster meat and tomalley samples. The amount of native PCB added to the lobster tomalley MS/MSD was low in comparison to the amount already present in the sample for most isomers. Due to the high levels found in all samples, the MS/MSD results presented in the tables only represent some of the PCB isomers.

3.2.5 Laboratory Control Spike (LCS)

A laboratory control spike (LCS) was prepared and the results are presented in Table 21. The matrix used for the LCS was sodium sulfate. The LCS was spiked with native PCDD/F and PCB as a measure of precision and accuracy of the overall method. The percent recovery was based upon the known amount spiked divided by the amount found. The LCS results for PCDD/F on this project showed acceptable recoveries between 85.1% and 124%. The recoveries were within the MRI objective of 75% to 125%.

The LCS results for most of the PCBs on this project showed acceptable recoveries between 77.8% and 105%. Three isomers were slightly outside the criteria, but within 70% to 130%. These objectives were met for the PCBs in the meat sample with the exception of 189-HpCB(% RPD=39.3%).

Table 7. Lobster Meat Native Results Summary (pg/g whole weight)

Isomer	Field ID Extract ID MS Filename Sample Weight(g)	LNM 2 39767 F17V19.RPT 50.03	LNM 3 39768 F22V11.RPT 50.8	LNM 4 39769 F22V12.RPT 51.33	L-Jewel 1 39778 (MS) F18VQ48.RPT 25.54	L-Jewel 1 39779 (MSD) F18VQ49.RPT 25.18
2,3,7,8-TCDF(a)		U(.118 EMPC)	U(.116 EMPC)	U(.123 EMPC)	9.1	9.33
2,3,7,8-TCDD		U(.0999)	U(.118)	U(.0978)	8.44	9.26
1,2,3,7,8-PeCDF		U(.5)	U(.492)	U(.487)	42.7	41.5
2,3,4,7,8-PeCDF		U(.5)	U(.492)	U(.487)	40.2	38.3
1,2,3,7,8-PeCDD		U(.5)	U(.492)	U(.487)	54.3	57
1,2,3,4,7,8-HxCDF		U(.5)	U(.492)	U(.487)	41	38.4
1,2,3,6,7,8-HxCDF		U(.5)	U(.492)	U(.487)	38.9	38.3
2,3,4,6,7,8-HxCDF		U(.5)	U(.492)	U(.487)	34.5	33
1,2,3,7,8,9-HxCDF		U(.5)	U(.492)	U(.487)	34.3	33.3
1,2,3,4,7,8-HxCDD		U(.5)	U(.492)	U(.487)	48.7	49.1
1,2,3,6,7,8-HxCDD		U(.5)	U(.492)	U(.487)	42.4	43.2
1,2,3,7,8,9-HxCDD		U(.5)	U(.492)	U(.487)	46.4	47.6
1,2,3,4,6,7,8-HpCDF		U(.5)	U(.492)	U(.487)	45	42.7
1,2,3,4,7,8,9-HpCDF		U(.5)	U(.492)	U(.487)	37.4	35.8
1,2,3,4,6,7,8-HpCDD		U(.5)	U(.492)	U(.487)	35.5	35.2
OCDF		U(.999)	U(.984)	U(.974)	78.9	79.8
OCDD		U(.999)	1.0400	2.1900	96.3	98.4
Total TCDF		U(.0999)	U(.0984)	U(.0974)	9.1	9.86
Total TCDD		U(.0999)	U(.118)	U(.0978)	8.44	9.26
Total PeCDF		U(.5)	U(.492)	U(.487)	86.7	82.7
Total PeCDD		U(.5)	U(.492)	U(.487)	54.3	57
Total HxCDF		U(.5)	U(.492)	U(.487)	149	143
Total HxCDD		U(.5)	U(.492)	U(.487)	135	138
Total HpCDF		U(.5)	U(.492)	U(.487)	83.2	79.2
Total HpCDD		U(.5)	U(.492)	U(.487)	35.5	35.2
ITE-min		0	0.00104	0.00219	88.7	89.5
ITE-max		1.00	1.01	1.86	88.7	89.5
% Lipid		0.11	0.19	0.071	0.17	0.12

Table 7 (Continued)

Isomer	Field ID Extract ID MS Filename Sample Weight(g)	Method Blank 39783 F17V11.RPT 50.9	L-Jewel 1 39762 F17V14.RPT 51.77	L-Jewel 2 39763 F17V15.RPT 51.06	L-Jewel 3 39764 F17V16.RPT 50.63	L-Jewel 4 39765 F17V17.RPT 50.8	LNM 1 39766 F17V18.RPT 50.76
2,3,7,8-TCDF(a)		U(.0982)	0.125	U(.0979 EMPC	U(.0988)	0.186	U(.115 EMPC)
2,3,7,8-TCDD		U(.0982)	U(.194 EMPC)	U(.0979)	U(.0988)	U(.0984)	U(.0985)
1,2,3,7,8-PeCDF		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
2,3,4,7,8-PeCDF		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
1,2,3,7,8-PeCDD		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
1,2,3,4,7,8-HxCDF		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
1,2,3,6,7,8-HxCDF		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
2,3,4,6,7,8-HxCDF		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
1,2,3,7,8,9-HxCDF		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
1,2,3,4,7,8-HxCDD		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
1,2,3,6,7,8-HxCDD		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
1,2,3,7,8,9-HxCDD		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
1,2,3,4,6,7,8-HpCDF		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
1,2,3,4,7,8,9-HpCDF		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
1,2,3,4,6,7,8-HpCDD		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
OCDF		U(.982)	U(.966)	U(.979)	U(.988)	U(.984)	U(.985)
OCDD		1.7400	1.7800	U(.979)	U(.988)	U(1.32 EMPC)	U(.985)
Total TCDF		U(.0982)	0.125	U(.0979)	U(.0988)	0.186	U(.0985)
Total TCDD		U(.0982)	0.207	U(.0979)	U(.0988)	U(.0984)	U(.0985)
Total PeCDF		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
Total PeCDD		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
Total HxCDF		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
Total HxCDD		U(.491)	U(.483)	U(.49)	U(.494)	1.04	U(.493)
Total HpCDF		U(.491)	U(.483)	U(.49)	U(.494)	U(.492)	U(.493)
Total HpCDD		U(.491)	U(.483)	U(.49)	U(.494)	0.685	U(.493)
ITE-min		0.00174	0.01428	0	0	0.0186	0
ITE-max		0.985	1.07	0.982	0.990	1.88	1.88
% Lipid		0.15	0.11	0.12	0.082	0.34	0.17

(a)-Concentrations should be considered a maximum. The GC column used is not specific for this isomer.
U-Undetected at low standard based detection limits.
EMPC-A peak was detected that did not meet the method identification criteria. The peak areas were used to calculate an Estimated Maximum Possible Concentration for the detection limit.

Table 8. Lobster Meat Native Results Summary (pg/g lipid weight)

Isomer	Field ID Extract ID MS Filename Sample Weight(g)	Method Blank 39783 F17V11.RPT 50.9	L-Jewel 1 39762 F17V14.RPT 51.77	L-Jewel 2 39763 F17V15.RPT 51.06	L-Jewel 3 39764 F17V16.RPT 50.63	L-Jewel 4 39765 F17V17.RPT 50.8	LNM 1 39766 F17V18.RPT 50.76
2,3,7,8-TCDF(a)		U(65.5)	115	U(83.1 EMPC)	U(120)	54.4	U(66 EMPC)
2,3,7,8-TCDD		U(65.5)	U(178 EMPC)	U(83.1)	U(120)	U(28.8)	U(56.5)
1,2,3,7,8-PeCDF		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
2,3,4,7,8-PeCDF		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
1,2,3,7,8-PeCDD		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
1,2,3,4,7,8-HxCDF		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
1,2,3,6,7,8-HxCDF		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
2,3,4,6,7,8-HxCDF		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
1,2,3,7,8,9-HxCDF		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
1,2,3,4,7,8-HxCDD		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
1,2,3,6,7,8-HxCDD		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
1,2,3,7,8,9-HxCDD		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
1,2,3,4,6,7,8-HpCDF		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
1,2,3,4,7,8,9-HpCDF		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
1,2,3,4,6,7,8-HpCDD		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
OCDF		U(655)	U(885)	U(831)	U(1200)	U(288)	U(565)
OCDD		1160.0	1630.0	U(831)	U(1200)	U(387 EMPC)	U(565)
Total TCDF		U(65.5)	115	U(83.1)	U(120)	54.4	U(56.5)
Total TCDD		U(65.5)	190	U(83.1)	U(120)	U(28.8)	U(56.5)
Total PeCDF		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
Total PeCDD		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
Total HxCDF		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
Total HxCDD		U(328)	U(443)	U(415)	U(599)	306	U(283)
Total HpCDF		U(328)	U(443)	U(415)	U(599)	U(144)	U(283)
Total HpCDD		U(328)	U(443)	U(415)	U(599)	201	U(283)
ITE-min		1.16	13.1	0	0	5.44	0
ITE-max		658	981	832	1093	291	568
% Lipid		0.15	0.11	0.12	0.082	0.34	0.17

(a)-Concentrations should be considered a maximum. The GC column used is not specific for this isomer.

U-Undetected at low standard based detection limits.

EMPC-A peak was detected that did not meet the method identification criteria. The peak areas were used to calculate an Estimated Maximum Possible Concentration for the detection limit.

Table 8. (Continued)

Isomer	Field ID Extract ID MS Filename Sample Weight(g)	LNM 2 39767 F17V19.RPT 50.03	LNM 3 39768 F22V11.RPT 50.8	LNM 4 39769 F22V12.RPT 51.33	L-Jewel 1 39778 (MS) F18VQ48.RPT 25.54	L-Jewel 1 39779 (MSD) F18VQ49.RPT 25.18
2,3,7,8-TCDF(a)		U(106 EMPC)	U(60.6 EMPC)	U(175 EMPC)	5320	7760
2,3,7,8-TCDD		U(89.2)	U(61.8)	U(139)	4930	7690
1,2,3,7,8-PeCDF		U(446)	U(257)	U(691)	24900	34500
2,3,4,7,8-PeCDF		U(446)	U(257)	U(691)	23500	31800
1,2,3,7,8-PeCDD		U(446)	U(257)	U(691)	31700	47400
1,2,3,4,7,8-HxCDF		U(446)	U(257)	U(691)	24000	31900
1,2,3,6,7,8-HxCDF		U(446)	U(257)	U(691)	22700	31900
2,3,4,6,7,8-HxCDF		U(446)	U(257)	U(691)	20200	27500
1,2,3,7,8,9-HxCDF		U(446)	U(257)	U(691)	20100	27700
1,2,3,4,7,8-HxCDD		U(446)	U(257)	U(691)	28500	40800
1,2,3,6,7,8-HxCDD		U(446)	U(257)	U(691)	24800	35900
1,2,3,7,8,9-HxCDD		U(446)	U(257)	U(691)	27100	39500
1,2,3,4,6,7,8-HpCDF		U(446)	U(257)	U(691)	26300	35500
1,2,3,4,7,8,9-HpCDF		U(446)	U(257)	U(691)	21800	29800
1,2,3,4,6,7,8-HpCDD		U(446)	U(257)	U(691)	20700	29200
OCDF		U(892)	U(515)	U(1380)	46100	66400
OCDD		U(892)	544.0	3100.0	56300	81800
Total TCDF		U(89.2)	U(51.5)	U(138)	5320	8190.0
Total TCDD		U(89.2)	U(61.8)	U(139)	4930	7690
Total PeCDF		U(446)	U(257)	U(691)	50600	68800
Total PeCDD		U(446)	U(257)	U(691)	31700	47400
Total HxCDF		U(446)	U(257)	U(691)	87100	119000
Total HxCDD		U(446)	U(257)	U(691)	78900	115000
Total HpCDF		U(446)	U(257)	U(691)	48600	65800
Total HpCDD		U(446)	U(257)	U(691)	20700	29200
ITE-min		0	0.544	3.1	51837	74404
ITE-max		895	526	1391	51837	74404
% Lipid		0.11	0.19	0.071	0.17	0.12

Table 9. Lobster Tomalley Native Results Summary (pg/g whole weight)

Isomer	Field ID Extract ID MS Filename Sample Weight (g)	Method Blank 39760 F17V11.RPT 9.95	TNM 1 39770 F22V13.RPT 11.2	TNM 2 39771 F22V14.RPT 10.1	TNM 3 39772 F18VQ42.RPT 7.11	TNM 4 39773 F18VQ43.RPT 10.4	T-Jewel 1 39774 F18VQ44.RPT 10.18
2,3,7,8-TCDF(a)		U(.503)	19.7	18.9	16.2	19.5	23.6
2,3,7,8-TCDD		U(.503)	1.98	2.2	U(.703 EMPC)	U(2.19 EMPC)	2.37
1,2,3,7,8-PeCDF		U(2.51)	2.68	U(2.69 EMPC)	U(3.52)	U(2.4)	U(3.37 EMPC)
2,3,4,7,8-PeCDF		U(2.51)	7.84	8.23	5.95	U(5.52 EMPC)	9.23
1,2,3,7,8-PeCDD		U(2.51)	4.49	U(5.17 EMPC)	U(4.78 EMPC)	4.31	6.91
1,2,3,4,7,8-HxCDF		U(2.51)	U(2.23)	U(2.48)	U(3.52)	U(2.4)	2.67
1,2,3,6,7,8-HxCDF		U(2.51)	U(2.23)	U(2.48)	U(3.52)	U(2.4)	U(2.46)
2,3,4,6,7,8-HxCDF		U(2.51)	U(2.23)	U(2.48)	U(3.52)	U(2.4)	5.17
1,2,3,7,8,9-HxCDF		U(2.51)	U(2.23)	U(2.48)	U(3.52)	U(2.4)	U(2.46)
1,2,3,4,7,8-HxCDD		U(2.51)	U(2.23)	U(2.48)	U(3.52)	U(2.4)	U(3.5 EMPC)
1,2,3,6,7,8-HxCDD		U(2.51)	5.64	5.84	6.23	6.22	9.89
1,2,3,7,8,9-HxCDD		U(2.51)	U(2.23)	U(2.48)	U(3.52)	U(2.4)	3.81
1,2,3,4,6,7,8-HpCDF		U(2.51)	U(2.23)	U(2.48)	U(3.52)	U(2.4)	U(2.46)
1,2,3,4,7,8,9-HpCDF		U(2.51)	U(2.23)	U(2.48)	U(3.52)	U(2.4)	U(2.46)
1,2,3,4,6,7,8-HpCDD		U(2.51)	13.90	12.9	16.60	13.9	19.8
OCDF		U(5.03)	U(4.46)	U(4.95)	U(7.03)	U(4.81)	U(4.91)
OCDD		8.9	24.9	23.2	38.7	46.9	32.5
Total TCDF		U(.503)	62.8	50.9	56.3	60.8	54
Total TCDD		U(.503)	13.4	3.74	12.7	8.51	10.6
Total PeCDF		U(2.51)	32.6	20.7	31.6	21.7	42.2
Total PeCDD		U(2.51)	23.7	22.3	19.3	20.6	24.9
Total HxCDF		U(2.51)	11.5	11.4	11.3	11.3	24.7
Total HxCDD		U(2.51)	42.7	43.6	43.5	43.2	60.4
Total HpCDF		U(2.51)	U(2.23)	U(2.48)	U(3.52)	U(2.4)	U(2.46)
Total HpCDD		U(2.51)	35.1	31.4	38	31.6	44.5
ITE-min		0.00888	11.0	8.94	5.42	4.91	15.2
ITE-max		5.04	12.4	13.2	10.9	11.5	16.2
% Lipid		16.81	15.85	11.69	18.28	14.95	21.42

(a)-Concentrations should be considered a maximum. The GC column used is not specific for this isomer.

U-Undetected at low standard based detection limits.

EMPC-A peak was detected that did not meet the method identification criteria. The peak areas were used to calculate an Estimated Maximum Possible Concentration for the detection limit.

Table 9 (Continued)

Isomer	T-Jewel 2 39775 F18VQ45.RPT 10.16	T-Jewel 3 39776 F18VQ46.RPT 10.27	T-Jewel 4 39777 F18VQ47.RPT 10.17	TNM 3 39780(MS) F18VQ410.RPT 7.07	TNM 3 39781(MSD) F18VQ411.RPT 7.01
2,3,7,8-TCDF(a)	29	20.6	20.2	54.4	50.9
2,3,7,8-TCDD	U(3.27 EMPC)	1.93	U(1.86 EMPC)	31.1	32
1,2,3,7,8-PeCDF	U(3.55 EMPC)	2.65	2.86	149	156
2,3,4,7,8-PeCDF	10.8	7.06	7.08	146	146
1,2,3,7,8-PeCDD	7.37	U(6.2 EMPC)	4.03	198	205
1,2,3,4,7,8-HxCDF	U(2.46)	U(2.43)	U(2.46)	147	147
1,2,3,6,7,8-HxCDF	U(2.46)	U(2.43)	U(2.46)	146	143
2,3,4,6,7,8-HxCDF	2.46	U(2.43)	U(2.46)	130	125
1,2,3,7,8,9-HxCDF	U(2.46)	U(2.43)	U(2.46)	123	116
1,2,3,4,7,8-HxCDD	3.54	U(2.43)	U(2.46)	169	170
1,2,3,6,7,8-HxCDD	11.4	7.99	7	153	155
1,2,3,7,8,9-HxCDD	U(3.64 EMPC)	U(2.72 EMPC)	2.62	171	162
1,2,3,4,6,7,8-HpCDF	U(2.46)	U(2.43)	U(2.46)	163	163
1,2,3,4,7,8,9-HpCDF	U(2.46)	U(2.43)	U(2.46)	131	136
1,2,3,4,6,7,8-HpCDD	14.2	14.2	15.7	144.0	138.0
OCDF	U(4.92)	U(4.87)	U(4.92)	276.0	275.0
OCDD	25.6	25.4	26.8	369.0	349.0
Total TCDF	55.7	43.9	47.8	100	84.5
Total TCDD	6.19	7.6	6.83	38.1	37
Total PeCDF	37.1	31.6	27.2	302	327
Total PeCDD	18.2	18.1	25.2	207	216
Total HxCDF	13.7	9.03	10.4	562	546
Total HxCDD	54.4	42.9	43.5	527	515
Total HpCDF	U(2.46)	U(2.43)	U(2.46)	297	302
Total HpCDD	32.6	32.1	35.9	167	161
ITE-min	13.9	8.62	8.86	325	327
ITE-max	18.5	13.3	12.0	325	327
% Lipid	14.51	18.26	19.5	20.69	21.61

Table 10. Lobster Tomalley Native Results Summary (pg/g lipid weight)

Isomer	Field ID Extract ID MS Filename Sample Weight (g)	Method Blank 39760 F17V11.RPT 9.95	TNM 1 39770 F22V13.RPT 11.2	TNM 2 39771 F22V14.RPT 10.1	TNM 3 39772 F18VQ42.RPT 7.11	TNM 4 39773 F18VQ43.RPT 10.4
2,3,7,8-TCDF(a)		U(2.99)	124	162	88.6	130
2,3,7,8-TCDD		U(2.99)	12.5	18.8	8.26	U(14.6 EMPC)
1,2,3,7,8-PeCDF		U(14.9)	16.9	U(23 EMPC)	U(19.2)	U(16.1)
2,3,4,7,8-PeCDF		U(14.9)	49.5	70.4	32.6	U(36.9 EMPC)
1,2,3,7,8-PeCDD		U(14.9)	28.3	U(44.2 EMPC)	U(26.1 EMPC)	28.8
1,2,3,4,7,8-HxCDF		U(14.9)	U(14.1)	U(21.2)	U(19.2)	U(16.1)
1,2,3,6,7,8-HxCDF		U(14.9)	U(14.1)	U(21.2)	U(19.2)	U(16.1)
2,3,4,6,7,8-HxCDF		U(14.9)	U(14.1)	U(21.2)	U(19.2)	U(16.1)
1,2,3,7,8,9-HxCDF		U(14.9)	U(14.1)	U(21.2)	U(19.2)	U(16.1)
1,2,3,4,7,8-HxCDD		U(14.9)	U(14.1)	U(21.2)	U(19.2)	U(16.1)
1,2,3,6,7,8-HxCDD		U(14.9)	35.6	50	34.1	41.6
1,2,3,7,8,9-HxCDD		U(14.9)	U(14.1)	U(21.2)	U(19.2)	U(16.1)
1,2,3,4,6,7,8-HpCDF		U(14.9)	U(14.1)	U(21.2)	U(19.2)	U(16.1)
1,2,3,4,7,8,9-HpCDF		U(14.9)	U(14.1)	U(21.2)	U(19.2)	U(16.1)
1,2,3,4,6,7,8-HpCDD		U(14.9)	87.9	110	91.0	93
OCDF		U(29.9)	U(28.2)	U(42.3)	U(38.5)	U(32.2)
OCDD		52.8	157	198	212.0	313.0
Total TCDF		U(2.99)	396	435	308	407
Total TCDD		U(2.99)	84.6	32	69.5	56.9
Total PeCDF		U(14.9)	206	177	173	145
Total PeCDD		U(14.9)	149	191	106	138
Total HxCDF		U(14.9)	72.3	97.2	62	75.6
Total HxCDD		U(14.9)	270	373	238	289
Total HpCDF		U(14.9)	U(14.1)	U(21.2)	U(19.2)	U(16.1)
Total HpCDD		U(14.9)	221	269	208	212
ITE-min		0.0528	69.2	76.5	38.0	32.8
ITE-max		29.9	78.0	113	63.9	76.7
% Lipid		16.81	15.85	11.69	18.28	14.95

(a)-Concentrations should be considered a maximum. The GC column used is not specific for this isomer.

U-Undetected at low standard based detection limits.

EMPC-A peak was detected that did not meet the method identification criteria. The peak areas were used to calculate an Estimated Maximum Possible Concentration for the detection limit.

Table 10 (Continued)

Isomer	T-Jewel 1 39774 F18VQ44.RPT 10.18	T-Jewel 2 39775 F18VQ45.RPT 10.16	T-Jewel 3 39776 F18VQ46.RPT 10.27	T-Jewel 4 39777 F18VQ47.RPT 10.17	TNM 3 39780(MS) F18VQ410.RPT 7.07	TNM 3 39781(MSD) F18VQ411.RPT 7.01
2,3,7,8-TCDF(a)	110	200	113	104	263	235
2,3,7,8-TCDD	11.1	U(22.5 EMPC)	10.6	U(9.54 EMPC)	151	148
1,2,3,7,8-PeCDF	U(15.7 EMPC)	U(24.5 EMPC)	14.5	14.7	719	722
2,3,4,7,8-PeCDF	43.1	74.7	38.7	36.3	704	675
1,2,3,7,8-PeCDD	32.3	50.8	U(33.9 EMPC)	20.7	958	949
1,2,3,4,7,8-HxCDF	12.5	U(17)	U(13.3)	U(12.6)	710	678
1,2,3,6,7,8-HxCDF	U(11.5)	U(17)	U(13.3)	U(12.6)	706	661
2,3,4,6,7,8-HxCDF	24.1	17	U(13.3)	U(12.6)	630	578
1,2,3,7,8,9-HxCDF	U(11.5)	U(17)	U(13.3)	U(12.6)	594	536
1,2,3,4,7,8-HxCDD	U(16.3 EMPC)	24.4	U(13.3)	U(12.6)	816	788
1,2,3,6,7,8-HxCDD	46.2	78.6	43.7	35.9	741	719
1,2,3,7,8,9-HxCDD	17.8	U(25.1 EMPC)	U(14.9 EMPC)	13.4	826	749
1,2,3,4,6,7,8-HpCDF	U(11.5)	U(17)	U(13.3)	U(12.6)	787	754
1,2,3,4,7,8,9-HpCDF	U(11.5)	U(17)	U(13.3)	U(12.6)	633	631
1,2,3,4,6,7,8-HpCDD	92.6	97.6	78	81	698.0	640
OCDF	U(22.9)	U(33.9)	U(26.7)	U(25.2)	1340.0	1270
OCDD	152.0	176.0	139.0	137.0	1790.0	1620.0
Total TCDF	252	384	240	245	484	391
Total TCDD	49.3	42.7	41.6	35	184	171
Total PeCDF	197	256	173	139	1460	1510
Total PeCDD	116	126	99.1	129	1000	1000
Total HxCDF	115	94.7	49.5	53.4	2720	2520
Total HxCDD	282	375	235	223	2550	2380
Total HpCDF	U(11.5)	U(17)	U(13.3)	U(12.6)	1440	1400
Total HpCDD	208	225	176	184	808	744
ITE-min	70.9	95.9	47.3	45.5	1571	1514
ITE-max	75.9	128	72.6	61.6	1571	1514
% Lipid	21.42	14.51	18.26	19.5	20.69	21.61

Table 11. Lobster Meat Native Results Summary (pg/g whole weight)

Isomer	Field ID Extract ID MS Filename Sample Weight(g)	Method Blank 39760 E18VQ63.RPT 50.9	L-Jewel 1 39739 E18VQ66.RPT 51.77	L-Jewel 2 39740 E18VQ67.RPT 51.06	L-Jewel 3 39741 E18VQ68.RPT 50.63	L-Jewel 4 39742 E18VQ69.RPT 50.8	LNM 1 39743 E18VQ610.RPT 50.76
77-TCB		U(.878 EMPC)	2.28	1.75	1.87	3.66	2.45
123-PeCB		U(.299 EMPC)	U(.46 EMPC)	0.266	U(.199)	U(.195)	U(.257)
118-PeCB		7.95	80.7	57.1	75.3	205	61.3
114-PeCB		U(.374 EMPC)	1.3	U(.831 EMPC)	1.23	U(2.67 EMPC)	U(1.07 EMPC)
105-PeCB		3.19	23.4	16.2	23	54.4	18.4
126-PeCB		U(.565 EMPC)	U(.332)	U(.279)	U(.314 EMPC)	U(.485 EMPC)	U(.31)
167-HxCB		0.712	4.78	U(2.16 EMPC)	U(4.87 EMPC)	6.14	U(3.42 EMPC)
156-HxCB		0.794	6.36	3.76	5.98	13.8	3.81
157-HxCB		U(.351 EMPC)	U(.981)	1.05	1.62	U(3.40EMPC)	U(.918)
169-HxCB		0.536	U(.844)	U(.68)	U(.573)	U(1.0)	U(.85)
180-HpCB		11.6	312	32.2	42.6	139	31.7
170-HpCB		3.47	76.5	13	20.3	43.7	14.6
189-HpCB		U(.37 EMPC)	1.71	1.11	1.24	U(1.0)	U(1.01 EMPC)
ITE-min		0.00734	0.0264	0.0124	0.0178	0.00873	0.0129
ITE-max		0.0647	0.0685	0.0475	0.0550	0.0703	0.0535
% Lipid		0.15	0.11	0.12	0.082	0.34	0.17

U-Undetected at low standard based detection limits.
EMPC-A peak was detected that did not meet the method identification criteria.
The peak areas were used to calculate an Estimated Maximum Possible Concentration for the detection limit.
J-Corresponding labeled analog is outside of the MRI criteria of 25-150%.

Table 11. (Continued)

Isomer	Field ID Extract ID MS Filename Sample Weight(g)	LNM 2 39744 E18VQ611.RPT 50.03	LNM 3 39745 E18VQ612.RPT 50.8	LNM 4 39746 E19V11.RPT 51.33	L-Jewel 1 39755 (MS) E19V112.RPT 25.54	L-Jewel 1 39756 (MSD) E19V113.RPT 25.18
77-TCB		2.44	1.64	2.2	143	146
123-PeCB		U(.273)	U(.125)	U(.0519)	158	156
118-PeCB		82.8	53.5	63.6	252	249
114-PeCB		1.06	0.811	1.11	210	226
105-PeCB		24.5	15.9	20.5	189	189
126-PeCB		U(.338)	U(.283 EMPC)	0.174	166	163
167-HxCB		U(4.63 EMPC)	2.87	3.26	215	217
156-HxCB		5.29	3.35	4.11	162	157
157-HxCB		1.59	U(.428)	U(1.07 EMPC)	151	151
169-HxCB		U(.887)	U(.147)	U(.406)	150	155
180-HpCB		35.5	22.5	35.3	468	454
170-HpCB		17.2	10.9	14.8	273	279
189-HpCB		1.01	U(.686 EMPC)	0.504	190	283
ITE-min		0.0181	0.0112	0.0314	18.5	18.3
ITE-max		0.0608	0.0412	0.0360	18.5	18.3
% Lipid		0.11	0.19	0.071	0.17	0.12

Table 12. Lobster Meat Native Results Summary (pg/g lipid weight)

Isomer	Field ID Extract ID MS Filename Sample Weight(g)	Method Blank 39760 E18VQ63.RPT 50.9	L-Jewel 1 39739 E18VQ66.RPT 51.77	L-Jewel 2 39740 E18VQ67.RPT 51.06	L-Jewel 3 39741 E18VQ68.RPT 50.63	L-Jewel 4 39742 E18VQ69.RPT 50.8	LNM 1 39743 E18VQ610.RPT 50.76
77-TCB		U(586 EMPC)	2090	1490	2270	1070	1410
123-PeCB		U(200 EMPC)	U(421 EMPC)	226	U(241)	U(57.2)	U(147)
118-PeCB		5300	74000	48400	91400	60000	35200
114-PeCB		U(249 EMPC)	1190	U(705 EMPC)	1500	U(783 EMPC)	U(615 EMPC)
105-PeCB		2130	21400	13800	27900	16000	10500
126-PeCB		U(377 EMPC)	U(305)	U(236)	U(381 EMPC)	U(142)	U(178)
167-HxCB		475	4380	U(1840 EMPC)	U(5910 EMPC)	1800	U(1960 EMPC)
156-HxCB		530	5830	3190	7260	4040	2190
157-HxCB		U(234 EMPC)	U(899)	890	1970	U(996EMPC)	U(526)
169-HxCB		358	U(774) J	U(576)	U(695)	U(1000) J	U(488)
180-HpCB		7740	286000	27300	51700	40700	18200
170-HpCB		2320	70100	11100	24600	12800	8350
189-HpCB		U(247 EMPC)	1570	938	1500	U(1000) J	U(578 EMPC)
ITE-min		4.90	24.2	10.5	21.6	2.56	7.39
ITE-max		43.2	62.9	40.2	66.7	27.6	30.7
% Lipid		0.15	0.11	0.12	0.082	0.34	0.17

U-Undetected at low standard based detection limits.
EMPC-A peak was detected that did not meet the method identification criteria.
The peak areas were used to calculate an Estimated Maximum Possible Concentration for the detection limit.
J-Corresponding labeled analog is outside of the MRI criteria of 25-150%.

Table 12 (Continued)

Isomer	Field ID Extract ID MS Filename Sample Weight(g)	LNM 2 39744 E18VQ611.RPT 50.03	LNM 3 39745 E18VQ612.RPT 50.8	LNM 4 39746 E19V11.RPT 51.33	L-Jewel 1 39755 (MS) E19V112.RPT 25.54	L-Jewel 1 39756 (MSD) E19V113.RPT 25.18
77-TCB		1910	856	3130	83700	121000
123-PeCB		U(244)	U(65.5)	U(73.6)	92500	130000
118-PeCB		73900	28000	90200	147000	207000
114-PeCB		943	424	1580	123000	188000
105-PeCB		21900	8290	29100	111000	157000
126-PeCB		U(302)	U(148 EMPC)	247	96900	135000
167-HxCB		U(4130 EMPC)	1500	4620	125000	181000
156-HxCB		4710	1750	5830	94400	131000
157-HxCB		1420	U(224)	U(1510 EMPC)	88200	126000
169-HxCB		U(791)	U(76.8)	U(576)	87900	129000
180-HpCB		31600	11700	50100	274000	377000
170-HpCB		15300	5720	21000	159000	232000
189-HpCB		902	U(359 EMPC)	715	111000	236000
ITE-min		16.0	5.85	44.6	10830	15175
ITE-max		54.2	21.6	51.1	10830	15175
% Lipid		0.11	0.19	0.071	0.17	0.12

Table 13. Lobster Tomalley Native Results Summary (pg/g whole weight)

Isomer	Field ID Extract ID MS Filename Sample Weight (g)	Method Blank 39760 E18VQ63.RPT 9.95	TNM 1 39747 E19V12.RPT 11.2	TNM 2 39748 E19V13.RPT 10.1	TNM 3 39749 E19V14.RPT 7.11	TNM 4 39750 E19V15.RPT 10.4	T-Jewel 1 39751 E19V16.RPT 10.18
77-TCB		U(4.49 EMPC)	786	697	471	457	579
123-PeCB		U(1.53 EMPC)	U(.0519)	401	229	243	385
118-PeCB		40.7	U(25500 EMPC) D	U(22000 EMPC) D	23100	U(19900 EMPC) D	U(21000 EMPC) D
114-PeCB		U(1.91 EMPC)	622	568	369	383	557
105-PeCB		16.3	12000	11100	7800	7730	10800
126-PeCB		U(2.89 EMPC)	U(144 EMPC)	152	U(97.7 EMPC)	116	162
167-HxCB		3.64	2840	2550	1890	1920	2880
156-HxCB		4.06	2790	2590	1840	1820	3220
157-HxCB		U(1.79 EMPC)	821	767	550	538	862
169-HxCB		2.74	28.7	U(25.3 EMPC)	U(18.8 EMPC)	18.2	35.8
180-HpCB		59.4	19200	19700	12700	13400	42300
170-HpCB		17.8	7040	7200	5310	5110	29200
189-HpCB		U(1.89 EMPC)	U(.864)	127	167	112	278
ITE-min		0.0375	4.92	19.6	5.42	14.9	23.7
ITE-max		0.331	21.9	22.1	15.4	16.8	25.8
% Lipid		16.8	15.9	11.7	18.3	15.0	21.4

U-Undetected at low standard based detection limits.
EMPC-A peak was detected that did not meet the method identification criteria.
The peak areas were used to calculate an Estimated Maximum Possible Concentration for the detection limit.
Shaded values exceeds the upper limit of calibration but the signal is not saturated. The concentration given should be considered an estimate.
D-Represents a saturated peak signal. The concentration given should be considered an estimated value.

Table 13. (Continued)

Isomer	Field ID Extract ID MS Filename Sample Weight (g)	T-Jewel 2 39752 E19V17.RPT 10.16	T-Jewel 3 39753 E19V18.RPT 10.27	T-Jewel 4 39754 E19V19.RPT 10.17	TNM 3 39757 (MS) E19V114.RPT 7.07	TNM 3 39758 (MSD) E19V115.RPT 7.01
77-TCB		437	529	486	530	974
123-PeCB		294	533	208	295	870
118-PeCB		U(19900 EMPC) D	U(20900 EMPC) D	U(18800 EMPC) D	U(23200 EMPC) D	22700
114-PeCB		399	660	480	422	1130
105-PeCB		8300	11700	8850	8770	8080
126-PeCB		120	175	128	134	713
167-HxCB		2170	3500	2230	2190	2680
156-HxCB		2150	3730	2440	2060	2350
157-HxCB		641	1060	670	619	1090
169-HxCB		23.3	28.4	24.7	U(27.2 EMPC)	564
180-HpCB		21200	28000	26800	15000	13200
170-HpCB		7350	10900	9560	6010	6140
189-HpCB		147	183	144	177	774
ITE-min		15.9	23.4	17.3	16.9	83.7
ITE-max		17.9	25.5	19.1	19.5	83.7
% Lipid		14.5	18.3	19.5	20.7	21.6

Table 14. Lobster Tomalley Native Results Summary (pg/g lipid weight)

Isomer	Field ID Extract ID MS Filename Sample Weight (g)	Method Blank 39760 E18VQ63.RPT 9.95	TNM 1 39747 E19V12.RPT 11.2	TNM 2 39748 E19V13.RPT 10.1	TNM 3 39749 E19V14.RPT 7.11	TNM 4 39750 E19V15.RPT 10.4	T-Jewel 1 39751 E19V16.RPT 10.18
77-TCB		U(26.7 EMPC)	4960	5960	2580	3060	2700
123-PeCB		U(9.11 EMPC)	U(.328)	3430	1250	1630	1800
118-PeCB		242	U(161000 EMPC) D	U(188000 EMPC) D	126000	U(133000 EMPC) D	U(98100 EMPC) D
114-PeCB		U(11.4 EMPC)	3930	4860	2020	2560	2600
105-PeCB		97.1	76000	94900	42700	51700	50300
126-PeCB		U(17.2 EMPC)	U(906 EMPC)	1300	U(535 EMPC)	776	754
167-HxCB		21.7	17900	21800	10400	12800	13400
156-HxCB		24.2	17600	22200	10100	12200	15000
157-HxCB		U(10.7 EMPC)	5180	6560	3010	3600	4020
169-HxCB		16.3	181	U(216 EMPC)	U(103 EMPC)	122	167
180-HpCB		353	121000	168000	69300	89400	198000
170-HpCB		106	44400	61600	29100	34100	136000
189-HpCB		U(11.2 EMPC)	U(5.45)	1090	914	749	1300
ITE-min		0.223	31.1	168	29.6	99.4	110
ITE-max		1.97	138	189	84.2	113	120
% Lipid		16.8	15.9	11.7	18.3	15.0	21.4

U-Undetected at low standard based detection limits.
EMPC-A peak was detected that did not meet the method identification criteria.
The peak areas were used to calculate an Estimated Maximum Possible Concentration for the detection limit.
Shaded values exceeds the upper limit of calibration but the signal is not saturated.
The concentration given should be considered an estimate.
D-Represents a saturated peak signal. The concentration given should be considered an estimated value.

Table 14 (Continued)

Isomer	Field ID Extract ID MS Filename Sample Weight (g)	T-Jewel 2 39752 E19V17.RPT 10.16	T-Jewel 3 39753 E19V18.RPT 10.27	T-Jewel 4 39754 E19V19.RPT 10.17	TNM 3 39757 (MS) E19V114.RPT 7.07	TNM 3 39758 (MSD) E19V115.RPT 7.01
77-TCB		3010	2900	2490	2560	4510
123-PeCB		2030	2920	1070	1430	4030
118-PeCB		U(137000 EMPC) D	U(114000 EMPC) D	U(96200 EMPC) D	U(112000 EMPC) D	105000
114-PeCB		2750	3620	2460	2040	5240
105-PeCB		57200	64200	45400	42400	37400
126-PeCB		824	959	657	646	3300
167-HxCB		15000	19200	11400	10600	12400
156-HxCB		14800	20400	12500	9950	10900
157-HxCB		4420	5830	3430	2990	5030
169-HxCB		161	156	127	U(132 EMPC)	2610
180-HpCB		146000	153000	137000	72300	61100
170-HpCB		50700	59700	49100	29100	28400
189-HpCB		1010	1000	741	855	3580
ITE-min		109	128	88.5	81.6	388
ITE-max		123	140	98.1	94.1	388
% Lipid		14.5	18.3	19.5	20.7	21.6

Table 15. Lobster Meat Labeled Analog Recoveries (%)

Labeled Analog	Field ID Extract ID MS Filename Sample Weight (g)	Method Blank 39783 F17V11.RPT 50.9	L-Jewel 1 39762 F17V14.RPT 51.8	L-Jewel 2 39763 F17V15.RPT 51.1	L-Jewel 3 39764 F17V16.RPT 50.6	L-Jewel 4 39765 F17V17.RPT 50.8	LNM 1 39766 F17V18.RPT 50.8
13C-2,3,7,8-TCDF		54.4	51.6	64.5	74.9	76.9	58.5
13C-2,3,7,8-TCDD		52.6	40.9	48.8	59.3	59.0	44.2
13C-1,2,3,7,8-PeCDF		69	38.2	68.3	64.7	63.5	67
13C-1,2,3,7,8-PeCDD		59.9	35.1	54.3	69.6	67.1	60.3
13C-1,2,3,6,7,8-HxCDF		70	78.5	74.5	77.9	75.1	62.3
13C-1,2,3,6,7,8-HxCDD		76	72	64	65.7	62.9	54.9
13C-1,2,3,4,6,7,8-HpCDF		87.9	62.1	61	67.3	61.4	55
13C-1,2,3,4,6,7,8-HpCDD		82.1	66.4	69.8	73.9	69.7	60.5
13C-OCDD		84.1	49.3	65.8	68.3	67.6	61.6

Labeled Analog	Field ID Extract ID MS Filename Sample Weight (g)	LNM 2 39767 F17V19.RPT 50.0	LNM 3 39768 F22V11.RPT 50.8	LNM 4 39769 F22V12.RPT 51.3	L-Jewel 1 39778 (MS) F18VQ48.RPT 25.5	L-Jewel 1 39779 (MSD) F18VQ49.RPT 25.2	LCS 39782 F17V12.RPT 10
13C-2,3,7,8-TCDF		65.5	33	51.4	65.2	38.7	64.8
13C-2,3,7,8-TCDD		47.3	33.2	51.7	60.7	35.3	53.4
13C-1,2,3,7,8-PeCDF		74.9	34.8	48.8	71.8	41.7	63.6
13C-1,2,3,7,8-PeCDD		58.9	26.8	39.9	63.6	33.4	52.1
13C-1,2,3,6,7,8-HxCDF		73.2	44.8	69.8	76	49.2	75.5
13C-1,2,3,6,7,8-HxCDD		62.5	42.2	64.9	69	41.3	70.7
13C-1,2,3,4,6,7,8-HpCDF		60.3	33.3	53	64	36.8	77.1
13C-1,2,3,4,6,7,8-HpCDD		72.6	43.4	65	74.8	44.4	82.6
13C-OCDD		71.3	44.5	65	73.1	40.3	80.8

Table 15. (Continued)

Labeled Analog	Field ID Extract ID MS Filename Sample Weight (g)	Average	Standard Deviation
13C-2,3,7,8-TCDF		58.0	14.4
13C-2,3,7,8-TCDD		48.0	9.83
13C-1,2,3,7,8-PeCDF		57.4	15.0
13C-1,2,3,7,8-PeCDD		50.9	15.6
13C-1,2,3,6,7,8-HxCDF		68.1	12.1
13C-1,2,3,6,7,8-HxCDD		59.9	10.6
13C-1,2,3,4,6,7,8-HpCDF		55.5	11.5
13C-1,2,3,4,6,7,8-HpCDD		64.1	11.5
13C-OCDD		60.7	11.7

Table 16. Lobster Tomalley Labeled Analog Recoveries (%)

Labeled Analog	Field ID Extract ID MS Filename Sample Weight	Method Blank 39760 F17V11.RPT 9.95	TNM 1 39770 F22V13.RPT 11.2	TNM 2 39771 F22V14.RPT 10.1	TNM 3 39772 F18VQ42.RP 7.11	TNM 4 39773 F18VQ43.RP 10.4	T-Jewel 1 39774 F18VQ44.RP 10.18	T-Jewel 2 39775 F18VQ45.RP 10.16
13C-2,3,7,8-TCDF		54.4	67.6	67.8	72.4	65.1	69.6	71.4
13C-2,3,7,8-TCDD		52.6	69.8	70.3	64.7	58.6	65	65.2
13C-1,2,3,7,8-PeCDF		69	64.8	63.0	71.3	69.5	69.6	81.9
13C-1,2,3,7,8-PeCDD		59.9	52.4	48.7	58.1	57	59.9	76.2
13C-1,2,3,6,7,8-HxCDF		70	81.9	85.9	72.5	73.4	81	81.5
13C-1,2,3,6,7,8-HxCDD		76	76	80.7	64.1	69.3	75.1	79.7
13C-1,2,3,4,6,7,8-HpCDF		87.9	65.6	67	53.9	65.3	69	76.2
13C-1,2,3,4,6,7,8-HpCDD		82.1	72.6	77	66.9	79.7	79.1	84.9
13C-OCDD		84.1	80.2	74.2	56.4	79.5	76.6	83.1

Labeled Analog	Field ID Extract ID MS Filename Sample Weight	T-Jewel 3 39776 18VQ46.RP 10.27	T-Jewel 4 39777 18VQ47.RP 10.17	TNM 3 39780(MS) 18VQ410.RP 7.07	TNM 3 39781(MSD) 18VQ411.RP 7.01	LCS 39782 F17V12.RPT 10	Average	Standard Deviation
13C-2,3,7,8-TCDF		66.6	68.4	65	64.4	64.8	67.8	2.71
13C-2,3,7,8-TCDD		62.7	65	62.4	59.7	53.4	64.4	3.78
13C-1,2,3,7,8-PeCDF		69.8	68.4	77.2	67.3	63.6	70.3	5.58
13C-1,2,3,7,8-PeCDD		58.0	59.7	66.5	57.0	52.1	59.4	7.54
13C-1,2,3,6,7,8-HxCDF		77.5	79.3	70.7	72.1	75.5	77.6	5.17
13C-1,2,3,6,7,8-HxCDD		70.6	74.2	68	68.7	70.7	72.6	5.37
13C-1,2,3,4,6,7,8-HpCDF		68.3	67.5	62	60	77.1	65.5	5.92
13C-1,2,3,4,6,7,8-HpCDD		77	76.5	77.7	69.2	82.6	76.1	5.25
13C-OCDD		79.7	73.3	76.9	70.1	80.8	75.0	7.56

Table 17. Lobster Meat Labeled Analog Recoveries (%)

Labeled Analog	Field ID Extract ID MS Filename Sample Weight	Method Blank 39760 E18VQ63.RPT 50.9	L-Jewel 1 39739 E18VQ66.RP 51.8	L-Jewel 2 39740 E18VQ67.RP 51.1	L-Jewel 3 39741 E18VQ68.RP 50.6	L-Jewel 4 39742 E18VQ69.RP 50.8	LNM 1 39743 18VQ610.RP 50.8	LNM 2 39744 18VQ611.RP 50.0
13C-77-TCB		105	91.3	93.7	90.6	84	69.2	90.8
13C-118-PeCB		106	92.9	89.2	84.4	83.3	71.3	90.5
13C-105-PeCB		103	92.5	86.3	85.2	82.4	73.1	87.3
13C-126-PeCB		97.6	82.9	83.7	77.7	78.2	67.8	84.1
13C-156-HxCB		107	102	97.2	89.6	110	77.5	92.8
13C-169-HxCB		113	166 J	130	126	213 J	117	129
13C-180-HpCB		107	118	106	100	164 J	87.5	106

J-The labeled analog recovery is outside of the MRI criteria of 25-150%.

Labeled Analog	Field ID Extract ID MS Filename Sample Weight	LNM 3 39745 18VQ612.RP 50.8	LNM 4 39746 E19V11.RPT 51.3	L-Jewel 1 39755 E19V112.RPT 25.5	L-Jewel 1 39756 E19V113.RPT 25.2	LCS 39759 E18VQ64.RPT 10	Average	Standard Deviation
13C-77-TCB		81.6	95.7	103	64.0	97.8	86.4	12.0
13C-118-PeCB		78.2	94.0	98.4	62.9	94.7	84.5	11.0
13C-105-PeCB		76.8	87.4	94.9	57.6	91.9	82.4	10.9
13C-126-PeCB		72.8	68.8	93.2	58.0	91.2	76.7	10.1
13C-156-HxCB		88.8	85.4	109	65.0	95.1	91.7	13.9
13C-169-HxCB		131	128	150	83.4	99.8	137	34.0
13C-180-HpCB		101	85.2	107	60.3	94.0	104	26.6

Table 18. Lobster Tomalley Labeled Analog Recoveries (%)

Labeled Analog	Field ID Extract ID MS Filename Sample Weight	Method Blank 39760 E18VQ63.RPT 9.95	TNM 1 39747 E19V12.RPT 11.2	TNM 2 39748 E19V13.RPT 10.1	TNM 3 39749 E19V14.RPT 7.11	TNM 4 39750 E19V15.RPT 10.4	T-Jewel 1 39751 E19V16.RPT 10.18	T-Jewel 2 39752 E19V17.RPT 10.16
13C-77-TCB		105	77.6	92.7	88.1	80.5	93.5	85.4
13C-118-PeCB		106	85.2	99.0	92.8	87.8	103	89.1
13C-105-PeCB		103	83.8	98.4	93.7	87.2	101	90.4
13C-126-PeCB		97.6	86.6	98.4	91.0	85.2	101	95.4
13C-156-HxCB		107	105	118	108	101	122	116
13C-169-HxCB		113	115	128	127	118	128	123
13C-180-HpCB		107	88.5	97.9	90.1	84.3	108	93.8

Labeled Analog	Field ID Extract ID MS Filename Sample Weight	T-Jewel 3 39753 E19V18.RPT 10.27	T-Jewel 4 39754 E19V19.RPT 10.17	TNM 3 39757 E19V114.RPT 7.07	TNM 3 39758 E19V115.RPT 7.01	LCS 39759 E18VQ64.RPT 10	Average	Standard Deviation
13C-77-TCB		95.6	98.7	103	64.0	97.8	87.9	11.5
13C-118-PeCB		98.8	101	98.4	62.9	94.7	91.8	11.8
13C-105-PeCB		98.3	101	94.9	57.6	91.9	90.6	13.0
13C-126-PeCB		98.3	102	93.2	58.0	91.2	90.9	12.9
13C-156-HxCB		113	121	109	65.0	95.1	108	16.5
13C-169-HxCB		111	120	150	83.4	99.8	120	16.8
13C-180-HpCB		86.9	95.2	107	60.3	94.0	91.2	13.5

Table 19. MS/MSD Recoveries (%) for Lobster Meat

Isomer	Spike Level Total pg	Field ID Extract ID MS File	TNM 3 39772 F18VQ42.RPT	TNM 3 39780(MS) F18VQ410.RPT	TNM 3 39781(MSD) F18VQ411.RPT	%RPD(a)	TNM 3 (MS) % Recovery	TNM 3 (MSD) % Recovery	Average Recovery
2378TCDF(a)	200		16.2	54.4	50.9	6.6	135	122	129
2378TCDD	200		U(.703 EMPC)	31.1	32.0	2.9	110	112	111
12378PeCDF	1000		U(3.52)	149	156	4.6	105	109	107
23478PeCDF	1000		5.95	146	146	0.0	99.0	98.0	98.5
12378PeCDD	1000		U(4.78 EMPC)	198	205	3.5	140	144	142
123478HxCDF	1000		U(3.52)	147	147	0.0	104	103	104
123678HxCDF	1000		U(3.52)	146	143	2.1	103	100	102
234678HxCDF	1000		U(3.52)	130	125	3.9	92.0	88.0	90.0
123789HxCDF	1000		U(3.52)	123	116	5.9	87.0	81.0	84.0
123478HxCDD	1000		U(3.52)	169	170	0.6	119	119	119
123678HxCDD	1000		6.23	153	155	1.3	104	104	104
123789HxCDD	1000		U(3.52)	171	162	5.4	121	114	118
1234678HpCDF	1000		U(3.52)	163	163	0.0	115	114	115
1234789HpCDF	1000		U(3.52)	131	136	3.7	93.0	95.0	94.0
1234678HpCDD	1000		16.6	144	138	4.3	90.0	85.0	87.5
12346789OCDF	2000		U(7.03)	276	275	0.4	98.0	96.0	97.0
12346789OCDD	2000		38.7	369	349	5.6	117	109	113

(a)-Percent Relative Difference=(high-low)/average X 100

Isomer	Spike Level Total pg	Field ID Extract ID MS File	TNM 3 39749 E19V14.RPT	TNM 3 (MS) 39757 E19V114.RPT	TNM 3 (MSD) 39758 E19V115.RPT	%RPD(a)	TNM 3 (MS) % Recovery	TNM 3 (MSD) % Recovery	Average Recovery
77-TCB	4000		471	530	974	59.0 (b)	8.0	71.0	40
123-PeCB	4000		229	295	870	98.7 (b)	9.0	90	50
118-PeCB	4000		23100	U(23200 EMPC)	22700	NC	NC	-56.0	NC
114-PeCB	4000		369	422	1130	91.2 (b)	7.00	107	57
105-PeCB	4000		7800	8770	8080	8.19	137	39.0	88
126-PeCB	4000		U(97.7 EMPC)	134	713	NC	19.0	100	NC
167-HxCB	4000		1890	2190	2680	20.1	42.0	111	77
156-HxCB	4000		1840	2060	2350	13.2	31.0	72.0	52
157-HxCB	4000		550	619	1090	55.1 (b)	10.0	76.0	43
169-HxCB	4000		U(18.8 EMPC)	U(27.2 EMPC)	564	NC	NC	79.0	NC
180-HpCB	4000		12700	15000	13200	12.8	325	70.0	198
170-HpCB	4000		5310	6010	6140	2.14	99	116	108
189-HpCB	4000		167	177	774	126 (b)	1.00	85	43

(a)-Percent Relative Difference=(high-low)/average X 100
(b)-Value grater than 20% RPD

Table 20. MS/MSD Recoveries (%) for Lobster Tomalley

Isomer	Spike Level Total pg	Field ID Extract ID MS File	L-Jewel 1 39762 F17V14.RPT	L-Jewel 1 (MS) 39778 (MS) F18VQ48.RPT	L-Jewel 1 (MSD) 39779 (MSD) F18VQ49.RPT	%RPD(a)	L-Jewel 1 (MS) % Recovery	L-Jewel 1 (MSD) % Recovery	Average Recovery
2378TCDF(a)	200		0.125	9.1	9.33	2.5	115	116	116
2378TCDD	200		U(.194 EMPC)	8.44	9.26	9.3	108	117	113
12378PeCDF	1000		U(.483)	42.7	41.5	2.9	109	104	107
23478PeCDF	1000		U(.483)	40.2	38.3	4.8	103	96.0	100
12378PeCDD	1000		U(.483)	54.3	57	4.9	139	144	142
123478HxCDF	1000		U(.483)	41	38.4	6.5	105	97.0	101
123678HxCDF	1000		U(.483)	38.9	38.3	1.6	99.0	96.0	97.5
234678HxCDF	1000		U(.483)	34.5	33	4.4	88.0	83.0	85.5
123789HxCDF	1000		U(.483)	34.3	33.3	3.0	88.0	84.0	86.0
123478HxCDD	1000		U(.483)	48.7	49.1	0.8	124	124	124
123678HxCDD	1000		U(.483)	42.4	43.2	1.9	108	109	109
123789HxCDD	1000		U(.483)	46.4	47.6	2.6	119	120	120
1234678HpCDF	1000		U(.483)	45	42.7	5.2	115	108	112
1234789HpCDF	1000		U(.483)	37.4	35.8	4.4	96.0	90.0	93.0
1234678HpCDD	1000		U(.483)	35.5	35.2	0.8	91.0	89.0	90.0
12346789OCDF	2000		U(.966)	78.9	79.8	1.1	101	100	101
12346789OCDD	2000		1.78	96.3	98.4	2.2	121	122	122

(a)-Percent Relative Difference=(high-low)/average X 100

Isomer	Spike Level Total pg	Field ID Extract ID MS File	L-Jewel 1 39739 E18VQ66.RPT	L-Jewel 1 (MS) 39755 E19V112.RPT	L-Jewel 1 (MSD) 39756 E19V113.RPT	%RPD(a)	L-Jewel 1 (MS) % Recovery	L-Jewel 1 (MSD) % Recovery	Average Recovery
77-TCB	5000		2.28	143	146	2.1	72.0	72.0	72.0
123-PeCB	5000		U(.46 EMPC)	158	156	1.3	81.0	79.0	80.0
118-PeCB	5000		80.7	252	249	1.2	88.0	85.0	86.5
114-PeCB	5000		1.30	210	226	7.3	107	113	110
105-PeCB	5000		23.4	189	189	0.0	85.0	83.0	84.0
126-PeCB	5000		U(.332)	166	163	1.8	85.0	82.0	83.5
167-HxCB	5000		4.78	215	217	0.9	107	107	107
156-HxCB	5000		6.36	162	157	3.1	80.0	76.0	78.0
157-HxCB	5000		U(.981)	151	151	0.0	77.0	76.0	76.5
169-HxCB	5000		U(.844)	150	155	3.3	77.0	78.0	77.5
180-HpCB	5000		312	468	454	3.0	80.0	72.0	76.0
170-HpCB	5000		76.5	273	279	2.2	100	102	101
189-HpCB	5000		1.71	190	283	39.3 (b)	96.00	142	119

(a)-Percent Relative Difference=(high-low)/average X 100
(b)-Value grater than 20% RPD

Table 21. Lab Control Spike Results

Isomer	Spike Level pg/g	Field ID Extract ID	LCS 39782	% Recovery
2378TCDF	20		17	87.0
2378TCDD	20		24.6	123
12378PeCDF	100		106	106
23478PeCDF	100		97	97.0
12378PeCDD	100		124	124
123478HxCDF	100		116	116
123678HxCDF	100		117	117
234678HxCDF	100		96.4	96.4
123789HxCDF	100		87.5	87.5
123478HxCDD	100		116	116
123678HxCDD	100		105	105
123789HxCDD	100		117	117
1234678HpCDF	100		116	116
1234789HpCDF	100		91.3	91.3
1234678HpCDD	100		85.1	85.1
12346789OCDF	200		187	93.5
12346789OCDD	200		226	113

Isomer	Spike Level pg/g	Field ID Extract ID	LCS 39759	% Recovery
77-TCB	500		357	71.4 **J**
123-PeCB	500		368	73.6 **J**
118-PeCB	500		415	83.0
114-PeCB	500		525	105
105-PeCB	500		413	82.6
126-PeCB	500		406	81.2
167-HxCB	500		628	126 **J**
156-HxCB	500		404	80.8
157-HxCB	500		389	77.8
169-HxCB	500		396	79.2
180-HpCB	500		414	82.8
170-HpCB	500		430	86.0
189-HpCB	500		428	85.6

J- Recovery outside of the MRI adopted criteria of 75-125%.