# rapport 2012:5

# Interlaboratory Comparison on POPs in Food 2012



# Thirteenth Round of an International Study

Nanna Bruun Bremnes Line Småstuen Haug Sharon Lynn Broadwell Georg Becher





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Interlaboratory Comparison on POPs in Food 2012 Thirteenth Round of an International Study

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# Summary

In 2012, the thirteenth round of the Interlaboratory Comparison on POPs in Food was conducted on the determination of the 2,3,7,8-chlorinated dibenzo-p-dioxins (PCDDs) and dibenzofurans (PCDFs) as well as dioxin-like non-ortho and mono-ortho chlorinated biphenyls (PCBs) in three different food items. In addition, laboratories could voluntarily determine and report six PCBs, polybrominated diphenyl ethers (PBDEs) and hexabromocyclododecanes (HBCDs).

The objectives of this interlaboratory comparison study were

- a) To offer a tool for quality assurance for the participating laboratories
- b) To assess the between laboratory reproducibility
- c) To assess the readiness of expert laboratories world-wide to determine levels of chlorinated and brominated persistent organic pollutants in regular foodstuffs

The 2012 study was performed on sample homogenates of reindeer meat, halibut filet and cod liver oil. In addition, six standard solutions were provided containing known concentrations of PCDDs/ PCDFs, non-ortho PCBs, mono-ortho PCBs, PBDEs, indicator PCBs and  $\alpha$ -HBCD.

The test materials were sent to 94 laboratories in 36 different countries in January 2012, and results were returned from 90 of these laboratories by the deadline in April. Most laboratories analyzed all the three food items. A draft report was made available on our webpage www.fhi.no/ILC in July and was presented for the participants and other interested parties at the DIOXIN 2012 Symposium in Cairns, Australia.

This report presents the reported results for all seventeen 2,3,7,8-substituted PCDDs/PCDFs, the non-ortho substituted PCBs #77, 81, 126 and 169 and the eight mono-ortho substituted PCBs #105, 114, 118, 123, 156, 157, 167, 189 in three food items on a fresh weight and lipid weight basis.

In addition, the results for eight PBDEs #28, 47, 99, 100, 153, 154, 183 and 209, six indicator PCBs #28, 52, 101, 138, 153 and 180, and total HBCDs as well as the  $\alpha$ -,  $\beta$ - and  $\gamma$ -isomers were reported from those laboratories that voluntarily determined their concentrations.

Non-detected congeners were assigned a concentration corresponding to the reported detection limit except for PBDEs, indicator PCBs and HBCDs where non-detects were removed from the data set.

The consensus concentration (assigned value) for each analyte in the three food samples was determined as follows: The median of all reported concentrations for each analyte was calculated. All values above two times the median were removed from the calculation. The consensus median and consensus mean as well as standard deviation (SD) were calculated from the remaining data.

Toxic equivalents (TEQs) were calculated from the consensus values of individual congeners using the toxic equivalency factors derived by WHO in 1998 and 2005.

Z-scores for the PCDD/PCDF TEQs were calculated for each laboratory using  $\pm 20$  % of the consensus TEQs (from 2012 on WHO<sub>2005</sub> TEFs were used and not WHO<sub>1998</sub> TEFs as in the previous reports) as a value for target standard deviation ( $\sigma$ ). Further, Z-scores were calculated for the non-ortho PCB TEQ, the mono-ortho PCB TEQ, the total TEQ, the sum of six indicator PCBs, the sum of eight PBDEs, total HBCD, and the three isomers of HBCD and for each single congener in all three matrices.

The consensus values of the standard solutions were calculated as mentioned above with the exception of the removal of all values exceeding  $\pm 50$  % of the median prior to the final calculation of the consensus median and mean.

The consensus values for the lipid content were calculated by first excluding results deviating more than two SD from the mean of all values, and then re-calculating the median, mean and SD.

For the determination of total TEQs in the three food samples, Z-scores within  $\pm 1$  were obtained by 79-80 % of the laboratories. The majority of the laboratories (89-95 %) reported results for total TEQ with a trueness of  $\pm 40$  % for all food samples (Z-score  $\pm 2$ ). The relative standard deviation (RSD) calculated for the total TEQ after removal of outliers was 12-16 %. It is therefore concluded that the performance of laboratories worldwide in determining dioxin-like compounds is generally good for the food samples included in this study.

For the different food samples, between 57-62 laboratories reported results for all the six indicator PCBs, 30-36 laboratories reported concentrations for all seven of the tetra- to hepta-BDEs and 22-23 laboratories reported concentrations for BDE-209. The concentrations of the sum of seven PBDEs on fresh weight basis were 18 (14 %), 800 (12 %) and 6442 (14 %) pg/g in reindeer meat, halibut filet and cod liver oil, respectively, with average RSD given in parentheses.

The consensus concentrations for BDE-209 were 16 (n=22), 21 (n=24) and 35 (n=23) pg/g fresh weight

in reindeer meat, halibut filet and cod liver oil, respectively. The corresponding RSD on fresh weight basis were 48, 41 and 75 %. The sums of concentrations on fresh weight basis for six indicator PCBs were 873 pg/g (31 %) in reindeer meat, 8262 pg/g (32 %) in halibut filet and 67005 pg/g (26 %) in cod liver oil. Average RSDs are given in parentheses.

The consensus concentrations calculated for HBCDs are just indicative values as only few laboratories reported results (n=8 to 12).

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## Introduction

In order to ensure consumer protection and reduce human exposure to dioxins and dioxin-like PCBs through food consumption, many countries request frequent monitoring of the presence of these toxic pollutants in food and feed. Thus, there is a large demand for chemical laboratories that are able to determine these contaminants at low levels. It is usually required by the authorities that laboratories performing such measurements are accredited according to ISO standards and prove their competence by successful participation in interlaboratory studies.

This study is the thirteenth round of a world-wide interlaboratory comparison study on dioxin-like compounds in food organized by the Department of Exposure and Risk Assessment, Division of Environmental Medicine, Norwegian Institute of Public Health (NIPH), Oslo, Norway.

The exercise took place from January 2012, when the samples were shipped to the laboratories for analysis, to the reporting deadline in April 2012, when the last reports on the results were received. A draft report was made available to the participants on our webpage (http://www.fhi.no/ILC) in July and was presented during the DIOXIN 2012 Symposium in Cairns, Australia.

The main objective of this exercise was to assess the between laboratory reproducibility of dioxin-like compounds analyses in frequently consumed foods and provide a QA/QC instrument for each participating laboratory to contribute to its proficiency. Participants were also asked to voluntarily determine the concentrations of eight PBDEs, six indicator PCBs and HBCD in the food samples in order to assess the readiness of laboratories to analyze these persistent organic pollutants.

All of the participants from previous rounds of this series of "Interlaboratory Comparisons on POPs in Food" were invited to participate. In addition, several other laboratories announced their participation. There was no limit to the total number of participating laboratories. The 90 laboratories that submitted results, and thereby contributed to the study results, are presented in Table 1.

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Agenzia Regionale Protezione Ambiente Del Piemonte, Polo Microinquinanti Grugliasco (Torino), Italy	CCL Nutricontrol  Veghel, The Netherlands
<b>ALS Czech Republic, s.r.o</b> . Pardubice, Czech Republic	<b>Cenpro Technology Co</b> Kao Hsiung City, Taiwan
<b>ALS Environmental (Burlington)</b> Burlington, Ontario, Canada	Central Lab of Residue Analysis of Pesticides and Heavy Metals in Foods Giza, Egypt
ALS Laboratory Group (Center of Excellence) Edmonton, Alberta, Canada	CHELAB SRL, Unità Locale di Lusciano Lusciano (CE), Italy
<b>Analytical Perspectives</b> Wilmington, NC, USA	Chemical and Veterinary Analytical Institute Münsterland-Emscher-Lippe (CVUA-MEL) Muenster, Germany
ASAE (Food Safety and Economic Authority) Lisboa, Portugal	Chemisches und mikrobiologisches Institut UEG GmbH Wetzlar, Germany
<b>AsureQuality Limited - Wellington Laboratory</b> Wellington, New Zealand	Chemisches und Veterinäruntersuchungsamt (CVUA Freiburg, Germany
<b>Bálint Analitika LTD.</b> Budapest, Hungary	China National Center of Food Safety Risk Assessment (CFSA) Beijing, China
<b>Bayerisches Landesamt für Umwelt</b> Augsburg, Germany	<b>Danish Veterinary and Food Administration</b> Ringsted, Denmark
<b>Bioassay and Safety Assessment Laboratory</b> Shanghai, China	Dioxin laboratory of Comprehensive test center of Chinese Academy of Inspection and Quarantine Beijing, China
<b>BioDetection Systems</b> Amsterdam, The Netherlands	<b>Environmental Laboratory - IQS</b> Barcelona, Spain
BLS-Analytik GmbH & Co.KG Bad Kissingen, Germany	Eurofins GfA Lab Service GmbH Hamburg, Germany
CALTAX Des Moines, IOWA, United States	FDA, Arkansas Regional Lab, Dioxin Group Jefferson, Arkansas, USA
Canadian Food Inspection Agency (CFIA) Calgary, Alberta, Canada	Food GmbH Jena Analytik & Consulting Jena, Germany
CARSO-LSEHL Lyon Cedex 07, France	Government Laboratory  Hong Kong SAR, China

Health Canada, Food Research Division, Health Products and Food Branch Ottawa, Canada	<b>LUFA Rostock der LMS</b> Rostock, Germany
Hubei Dioxin Lab Wuhan, Hubei Province, China	Marchwood Scientific Services Southampton, UK
Institute of Aquaculture Stirling, Scotland, UK	Marino SRL Santa Maria A Vico, Italia
Institute of Environmental Assessment and Water Research (IDAEA-CSIC) Barcelona, Spain	mas   münster analytical solutions gmbh Münster , Germany
Instituto "G. CAPORALE"  Teramo, Italy	MicroPolluants Technologie Saint Julien lès Metz, France
Istituto Zooprofilattico Sperimentale delle Regioni Lazio e Toscana Roma, Italy	Ministry of Food, Agriculture and Livestock, National Food Reference Laboratory Ankara, Turkey
Istituto zooprofilattico sperimentale Lombardia Emilia Romagna Bologna, Italy	<b>National Cheng Kung University</b> Tainan, Taiwan
Japan Food Research Laboratories Tokyo, Japan	National Institute for Health and Welfare Kuopio, Finland
<b>La Drome Laboratoire</b> Valence, France	National Institute of Nutrition and Food Safety Beijing, China
LABERCA Nantes, France	National Institute of Nutrition and Seafood Research- NIFES Bergen, Norway
<b>Laboratory of Vendee (LEAV)</b> la Roche sur Yon, France	National Measurement Institute, Dioxin AnalysisUnit - Pymble Sydney, Australia
<b>Landesamt für Umweltschutz Sachsen-Anhalt</b> Halle, Germany	National Tsing Hua University/ GMLab, Department of Chemistry Hsinchu, Taiwan
Landesbetrieb Hessisches Landeslabor Standort Wiesbaden Wiesbaden, Germany	NCSR "Demokritos" Athens, Greece
Landesuntersuchungsamt, Institut für Lebensmittelchemie Speyer, Germany	NEOTRON SPA Modena, Italy
Landwirtschaftliche Untersuchungs- und Forschungsanstalt Speyer, Germany	Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit Braunschweig, Germany
<b>LUFA Nord-West, Institute for Feed Analysis</b> Oldenburg, Germany	Nofalab BV Schiedam, The Netherlands

NOFER Institute Of Occupational Medicine Lodz, Poland	Super Micro Mass Research & Technology Center Niaosong Township, Kaohsiung County, Taiwan
Norwegian Institute for Air Research (NILU) Kjeller, Norway	The Food and Environment Research Agency (FERA) York, UK
<b>Oekometric</b> Bayreuth, Germany	<b>TLR International laboratories</b> Rotterdam, The Netherlands
Pacific Rim Laboratories Inc. Surrey, British Columbia, Canada	U. S. EPA/Environmental Chemistry Laboratory Stennis Space Center, Mississippi, USA
R&C LAB SRL Altavilla Vicentina , Italy	<b>Umeå University</b> Umeå, Sweden
Research and Productivity Council Fredericton, New Brunswick, Canada	Umweltbundesamt GmbH Vienna, Austria
SGS Belgium NV, division IAC Antwerpen, Belgium	University of Liège, CART Liège, Belgium
SGS Institut Fresenius GmbH Bayreuth, Germany	Wellington Laboratories Inc. Guelph, Ontario, Canada
SGS North America Inc. Wilmington, NC, USA	Wessling Laboratorien GmbH Altenberge, Germany
Shanghai Municipal Center for Disease Control and Prevention Shanghai, China	<b>Western Region Laboratory</b> Burnaby, British Columbia, Canada
Shenzhen Center for Disease Control & Prevention Shenzhen, China	Worthies Engineering Consultants Corp. Environmental Analysis Lab Taichung, Taiwan
<b>Shimadzu Techno-Research, INC.</b> Kyoto, Japan	Zavod za zdravstveno varstvo Maribor Institut za varstvo okolja Maribor, Slovenia
<b>State Laboratory</b> County Kildare, Ireland	Zhejiang Provincial Center for Disease Control and Prevention (ZJCDC) HangZhou, China
<b>Sun Dream Environmental Technology Corporation</b> Taichung City, Taiwan	Örebro University, MTM Research Centre Dioxin Laboratory Örebro, Sweden

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# Design and practical implementation

#### Study design and reporting of results

As in the previous rounds of this interlaboratory comparison studies, the test material chosen represented naturally contaminated food samples. The analytes to be determined were all seventeen 2,3,7,8-substituted PCDDs/PCDFs, the four non-ortho substituted PCBs #77, 81, 126 and 169 and the eight mono-ortho substituted PCBs #105, 114, 118, 123, 156, 157, 167 and 189. In addition, laboratories were asked to determine on a voluntary basis eight PBDEs #28, 47, 99, 100, 153, 154, 183 and 209, six indicator PCBs #28, 52, 101, 138, 153 and 180, total HBCDs and it's three isomers ( $\alpha$ -,  $\beta$ -,  $\gamma$ -HBCD). The six PCB congeners belong together with the mono-ortho PCB #118 to the selection of PCBs commonly referred to as ICES-7 (ICES-7: Report of the ICES Advisory Committee, 2010; Book 7).

The analysis should be performed using the laboratories' own methods for sample preparation and instrumental analysis, their own standards and quantification procedures and their own method for lipid determination.

It was recommended that laboratories determine as many as possible of the 2,3,7,8-substituted PCDDs/ PCDFs, dioxin-like PCBs, PBDEs, indicator PCBs and HBCDs. The report was to include the determined lipid percent for the reindeer meat and halibut filet. In addition, the actual sample and lipid amount (g) for each determination should be reported. For each sample, laboratories were to report the found concentration on fresh weight basis for each congener which was detected (e.g.  $S/N \ge 3$ ) as well as the level of determination (LOD, e.g., S/N = 3). Non-detected congeners (e.g. S/N < 3) were to be marked "ND" in the comments column of the Report forms.

In addition, six standard solutions containing known concentrations were to be analyzed using the laboratory's own quantification standards and methods. The standard solutions consisted of the following components:

- 1) seventeen 2,3,7,8-substituted PCDDs/PCDFs
- 2) four non-ortho PCBs
- 3) eight mono-ortho PCBs

- 4) eight PBDEs
- 5) six indicator PCBs
- 6) a-HBCD

The results were reported in separate forms.

The test materials consisted of reindeer meat,
halibut filet and cod liver oil. The laboratories could
choose to analyze one, two or all three food samples.

Each participating laboratory was given a specific code by the co-coordinators. In the present report, the participants are presented in the tables and figures by their unique laboratory codes. The participants have access to their own code only and laboratory codes were not revealed to third parties.

When received by the co-coordinators, the raw data from the laboratories were entered into a database. A draft report was generated and made available to all participants on the Internet in July 2012. The draft of the final report was discussed during the DIOXIN 2012 Symposium in August in Cairns, Australia.

# Collection, preparation, and distribution of samples

Samples shipped to the participants comprised one to three of the following:

- Reindeer meat (~100 g)
- Halibut filet (~100 g)
- Cod liver oil (~15 g)

The test materials consisted of natural products and were not fortified with standards.

The reindeer meat was first chopped into manageable pieces. The homogenization was then performed by repeatedly grinding the meat in a grinder. A similar procedure was adopted for the halibut filet. The homogeneity of these materials was tested using an approach developed at NIPH. The rationale for and description of the test method is given in Appendix E. The homogeneity of the cod liver oil was ensured by stirring the material with a magnetic stirrer for 30 minutes at 38°C.

Sub-samples of at least 100 g of reindeer meat (R), 100 g of halibut filet (H) were placed into carefully cleaned screw-cap polystyrene bottles while 15 g of cod liver oil was placed into amber glass ampoules. All samples were stored at –20°C until shipment. The frozen samples were shipped to the participating laboratories marked as test material R, H and C.

#### Statistical analysis

Based on experiences from previous rounds, we have chosen the following approach for the calculation of the consensus concentrations for each of the congeners:

For PCDDs/PCDFs and dioxin-like PCBs congenerby-congener medians were calculated from the food sample data of all reporting laboratories using the detection limit as concentration for non-detected congeners (upperbound concentration).

For PBDEs, indicator PCBs and HBCD, non-detected congeners were removed from the data set prior to consensus calculation. Outliers were defined as those values exceeding twice the median of all values and were removed from the data set.

The consensus values were defined as the median of the remaining data for each congener. In addition, the consensus mean and SD were calculated from this data set for each congener. Those congener data which had been removed prior to consensus calculation are marked in the tables presenting the individual results.

For the standard solutions, outliers were defined as those values outside  $\pm 50$  % of the median of all reported values. Consensus median, mean and SD were calculated from the remaining data. The consensus of the lipid content was calculated as the mean after removal of values outside  $\pm 2$ SD.

TEQs were calculated from the consensus values for PCDDs/PCDFs, non-ortho PCBs, and mono-ortho PCBs, using the toxic equivalency factors derived by WHO in 1998 and 2005. As the detection limit was used for the concentration of non-detects, these TEQs represent upper bound concentrations.

Z-scores for PCDD/PCDF TEQ as well as for the non-ortho PCB TEQ, the mono-ortho PCB TEQ, the total TEQ (WHO<sub>2005</sub>TEFs) the sum of six indicator PCBs, the sum of eight PBDEs, total HBCDs and for each congener were calculated for each laboratory according to the following equation:

$$z = (x - X)/\sigma$$

Where x = reported value; X = consensus value (assigned value);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20 % of the consensus was used, i.e.

Z-scores between +1 and -1 reflect a deviation of  $\pm 20$  % from the consensus value.

#### The final report and certificate

The draft of the final report was prepared by the co-coordinators and published on the web in july 2012. The draft was presented at the DIOXIN2012 Symposium in August in Cairns, Australia.

A certificate, stating the participant's code, will be sent to each participant contributing to the results at the end of 2012. The final report will be made available to the participants in pdf format at http://www.fhi.no/ILC.

#### Co-ordination

The study was initiated and carried out by the Department of Exposure and Risk Assessment, Division of Environmental Medicine, Norwegian Institute of Public Health, Oslo, Norway. Members of the co-ordination committee were:

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# Results

90 laboratories in 36 different countries submitted their results within the dead line and the results will be presented in the following chapters. Any participating laboratory will be able to compare its performance congener by congener with the other laboratories. Since variations in performances are based on several factors, it is recommended that each laboratory carefully evaluates the factors that, favorably or unfavorably, have contributed to its performance. A general reader of the report can without access to the laboratory codes get a general picture of the analytical performance of laboratories world-wide for determining dioxins, dioxin-like PCBs, indicator PCBs, PBDEs and HBCD in regular foods.

In Appendix C the consensus statistics are given on fresh and lipid weight basis for concentrations and TEQ values of individual congeners, a summary of TEQ values for each food item, and the Z-score plots based on a target deviation of  $\pm 20$  %.

Further, the results of the lipid determinations are presented.

Finally, individual results reported by the laboratories for each congener are given for reindeer meat, halibut filet and cod liver oil in Appendix 2, 3 and 4.

#### Summarising comments on results

#### PCDDs/PCDFs

#### Analyte solution

Concentrations for PCDDs/PCDFs were reported by 80 laboratories. The average RSD for the 17 congeners was 9.5 % ranging from 8.3 % for 1,2,3,4,6,7,8,9-OCDD to 13 % for 1,2,3,4,6,7,8,9-OCDF. The calculation of Z-scores for the TEQs (target 13.6 pg TEQ/ $\mu$ L) of the PCDD/PCDF standard solution showed that 96 % of the laboratories were within the range of  $\pm$ 20 % of the consensus value. This demonstrates the high quality of the calibration solutions used by the laboratories.

#### Reindeer meat

For the reindeer meat sample, PCDD/PCDF results from 71 laboratories were received. The consensus TEQ (total TEQ based on WHO  $_{2005}$  TEFs) was 1.0 pg TE/g fresh

weight and 7.9 pg TE/g lipid. The average RSD was 33 % ranging from 21-62 % for 2,3,4,7,8-PeCDF and 1,2,3,4,6,7,8,9-OCDF respectively. Z-scores within  $\pm 1$  were obtained by 77 % of the laboratories and 92 % of the laboratories had Z-scores within  $\pm 2$ .

#### Halibut filet

PCDD/PCDF concentrations in the halibut filet sample were reported by 78 laboratories. The consensus TEQ was 0.43 pg TEQ/g fresh weight and 2.7 pg TEQ/g lipid. The average RSD was 36 % ranging from 18-64 % (2,3,4,7,8-PeCDF and 1,2,3,4,6,7,8,9-OCDF respectively). Z-scores were within  $\pm 1$  for 85 % of the laboratories and within  $\pm 2$  for 92 % of the laboratories.

#### Cod liver oil

For the sample of cod liver oil 77 laboratories determined PCDD/PCDF concentrations. The consensus TEQ was 9.6 pg/g. The average RSD was 40 % ranging from 18-67 % (2,3,7,8-TCDF and 1,2,3,4,6,7,8,9-OCDF respectively). Z-scores for PCDD/PCDF TEQ within  $\pm 1$  were obtained by 80 % of the laboratories and 95 % had Z-scores within  $\pm 2$ .

#### Dioxin-like PCBs

#### Analyte solution

The 12 dioxin-like PCBs in the analyte solution were analyzed and reported by 78-79 laboratories. The RSDs for the different congeners were 8.1-10 % with an average of 9.2 %.

#### Reindeer meat

Dioxin-like PCB concentrations in reindeer meat were reported from 71 laboratories. The concentrations of the 12 congeners varied between 0.61 pg/g fresh weight (CB-81) and 320 pg/g fresh weight (CB-118). The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 24 % ranging from 18 % for CB-105 to 35 % for CB-123.

The dioxin-like PCBs contribute 68% to the total TEQ in the sample with CB-126 as the main contributor (64%).

#### Halibut filet

The number of laboratories that measured and reported dioxin-like PCB concentrations in halibut filet were 78. The concentrations ranged from 0.78 pg/g fresh weight for CB-81 to 1532 pg/g fresh weight for CB-118. The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 22 % ranging from 16 % for CB-105 to 41 % for CB-123.

The dioxin-like PCBs contribute to about 69 % of the total TEQ in the sample with CB-126 as the main contributor (58 %).

#### Cod liver oil

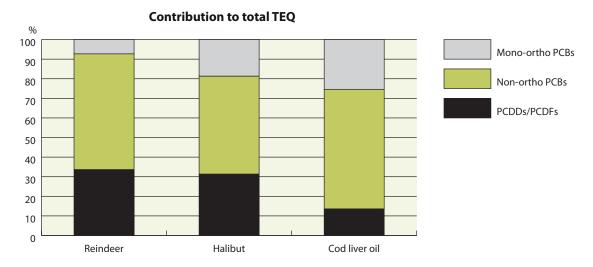
Dioxin-like PCBs in cod liver oil were reported by 79 laboratories. Levels were ranging from 4.2 pg/g fresh weigh for CB-81 to 13600 pg/g fresh weight for CB-118. The average RSD for concentrations of individual dioxin-like PCB congeners on fresh weight basis was 22 % ranging from 15 % for CB-105 to 38 % for CB-81. The contribution of the dioxin-like PCBs to the total TEQ was about 85 % with CB-126 as the main contributor (73 %).

#### Total TEQ

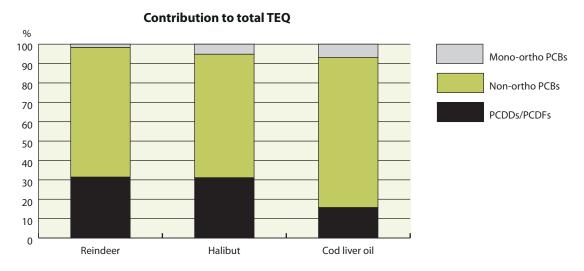
The total TEQ for reindeer meat was 1.0 pg TEQ/g fresh weight and 7.9 pg TEQ/g lipid weight (WHO TEF<sub>2005</sub>). For halibut filet the total TEQ was 1.4 pg TEQ/g fresh weight and 8.7 pg TEQ/g lipid weight, and for cod liver oil 9.6 g TEQ/g.

The RSDs for total TEQs on fresh weight basis calculated from the RSD of individual congeners were 15 % for reindeer meat, 10 % for halibut filet and 10 % for cod liver oil.

In Figure 1 and 2 the contribution of the three groups of dioxin-like compounds is depicted based on WHO TEF $_{1998}$  and WHO TEF $_{2005}$ , respectively. For all three food-items included in this study the dioxin-like PCBs contributed to 68 % or more of the total TEQs (using WHO TEF $_{2005}$ ), demonstrating the importance of PCBs for the determination of the total TEQ related toxic potency of food samples.



**Figure 1.** The contribution of PCDDs/PCDFs, non-ortho PCBs and mono-ortho PCBs to the total TEQ calculated using the WHO<sub>1008</sub> TEFs, in the three food samples.



**Figure 2.** The contribution of PCDDs/PCDFs, non-ortho PCBs and mono-ortho PCBs to the total TEQ calculated using the WHO $_{2005}$  TEFs, in the three food samples.

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#### Indicator PCBs

#### Analyte solution

65 laboratories reported indicator PCBs in the analyte solution. The average RSD was 12 % ranging form 11 to 13 %.

#### Reindeer meat

For the reindeer meat sample indicator PCB results were received from 58 laboratories. The concentrations were varying between 14 pg/g fresh weight (CB-52) and 445 pg/g fresh weight (CB-153). The RSDs were ranging from 23 to 42 % for CB-180 and CB-52 respectively, with an average of 31 % for all indicator PCBs. The consensus median for the sum of indicator PCBs was 873 pg/g fresh weight.

#### Halibut filet

Within the deadline, 61 laboratories reported results of indicator PCBs in the halibut filet sample. The concentrations ranged from 368 pg/g fresh weight (CB-28) to 2621 pg/g fresh weight (CB-153) with a consensus median for the sum of indicator PCBs of 8262 pg/g fresh weight. The average RSD was 31 %, ranging from 29 to 39 %.

#### Cod liver oil

Results were obtained from 63 laboratories. The concentrations of indicator PCBs in the cod liver oil sample were ranging from 2109 pg/g fresh weight (CB-28) to 24000 pg/g (CB-153) and the consensus median for the sum was 67005 pg/g fresh weight. The average RSD was 26 %, ranging from 20 to 36 %.

#### **PBDEs**

#### Analyte solution

The tri- to hepta-PBDE standard solution was analyzed by 39 laboratories and 26 laboratories reported values for BDE-209. The RSDs were between 9.4-13 % for all congeners

#### Reindeer meat

The PBDE concentrations in reindeer meat were reported by 31 laboratories, except for BDE-209 for which 22 results were received. The consensus concentrations were in the range from 0.51 pg/g fresh weight for BDE-28 to 7.7 pg/g fresh weight for BDE-153. The consensus concentration for BDE-209 was 16 pg/g fresh weight. The sum of tri- to hepta-BDEs was 18 pg/g fresh weight. The range of RSDs on fresh weight basis was 19-48 %, with an average of 37 % including BDE-209.

#### Halibut filet

Within the deadline, 37 laboratories had reported results for tri- to hepta-PBDEs in halibut filet and 24 laboratories had reported results for BDE-209. The consensus concentrations varied between 0.55 pg/g fresh weight (BDE-183) and 544 pg/g fresh weight (BDE-47). The concentration for BDE-209 was 21 pg/g fresh weight. The sum of tri- to heptaBDEs was 800 pg/g fresh weight. The RSD calculated from the concentrations on fresh weight ranged from 15-49 %, with an average of 25 % for PBDEs including BDE-209

#### Cod liver oil

37 laboratories reported results for tri- to hepta-PBDEs in cod liver oil, and 23 reported results for BDE-209. The concentrations varied between 5.5 pg/g fresh weight (BDE-183) and 4560 pg/g (BDE-47). The concentration for BDE-209 was 35 pg/g. The sum of tri- to hepta-BDEs was 6442 pg/g fresh weight. The RSDs for the individual congeners were ranging from 17 to 43 % with an average of 32 % including BDE-209.

#### **HBCDs**

Also in this round of the study, total HBCDs and the isomers  $\alpha$ -,  $\beta$ - and  $\gamma$ -HBCD could be determined and reported. A total of 14 laboratories reported  $\alpha$ -HBCD in the standard solution and 13 laboratories reported one or more of the three isomers in the food samples. The consensus concentrations for the sum of individual HBCD isomers were 7.2 pg/g fresh weight for reindeer meat, and 370 and 5922 pg/g fresh weight for halibut filet and cod liver oil, respectively. Since only few laboratories reported HBCDs, these results must be regarded as indicative values.

#### Lipid content

The mean and RSDs (in parentheses) for the lipid contents of the food samples were calculated to be 13 % (15 %) for reindeer meat and 16 % (12 %) for halibut filet. Cod liver oil was assumed to consist of 100 % lipids.

# Acknowledgements

The laboratories are acknowledged for their participation in this interlaboratory comparison and their interest in its overall objectives, thereby making it clear that they value good analytical performance. All the individual analysts are acknowledged for their contributions to the results.

We are grateful to Cambridge Isotope Laboratories, Inc. for providing the standard solutions for this interlaboratory study. We thank Aage Pedersen AS, Tana, for providing the reindeer meat and The National Institute of Nutrition and Seafood Research (NIFES), Bergen, for providing the halibut filet. The cod liver oils were a kind gift from Axellus AS, Oslo.

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# Appendix A:

Participant's affiliations and addresses

#### **Appendix A: Affiliations and addresses of participants**

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# Appendix B:

Study announcement and instructions for participants

# **Announcement for Interlaboratory Comparison on POPs in Food 2012**

#### Introduction

We herby announce the 13<sup>th</sup> round of the Interlaboratory Comparison on the Determination of POPs in Food. The study is open for academic, regulatory as well as commercial laboratories world-wide. The organizer of this study is the Department of Exposure and Risk Assessment, Division of Environmental Medicine, Norwegian Institute of Public Health (NIPH), Oslo, Norway.

The study is scheduled to take place from January to April 2012. A draft report will be available prior to the evaluation meeting which will take place at the Dioxin 2012 Symposium in August, Cairns, Australia. The final report will be available to the participants by December 2012 together with a certificate for participation.

#### **Objectives**

The objectives of this exercise are to assess the interlaboratory consistency in results from analyses of dioxins, PCBs, PBDEs and HBCD in regular foods known to contribute to the intake in the general population and to assess the world-wide readiness and capacity in analysing these halogenated persistent organic pollutants in food. The study also serves as a quality assurance instrument for the participating laboratories.

#### **Participants**

We encourage all laboratories world-wide working in this field to participate and assess their analytical performance. Participants are requested to completely fill out the Registration Form and mark the desired sample types and what analytes they intend to determine.

#### **Analytical requirements**

In this interlaboratory comparison, all the seventeen 2, 3, 7, 8-substituted PCDDs and PCDFs, the four non-ortho PCBs, CB-77, 81, 126 and 169 as well as the eight mono-ortho PCBs, CB-105, 114, 118, 123, 156, 157, 167, and 189 will be assessed. In addition, you are invited to determine six marker PCBs, eight PBDEs and HBCD. The concentration of the following congeners can be reported: CB-28, 52, 101, 138, 153 and 180 and BDE-28, 47, 99, 100, 153, 154, 183 and 209. The concentration of  $\alpha$ -HBCD,  $\beta$ -HBCD and  $\gamma$ -HBCD as well as the total of these isomers will also be assessed. The test materials consist of three fresh food homogenates. You can choose to analyse one, two or all three of the food items. We encourage you to determine as many analytes as possible. You are further requested to determine and report the lipid content of the foods.

We also include standard solutions of all analytes that should be analysed as solutions of known concentration, which may be used to check your own calibration solutions.

#### **Test material**

The test materials consist of three unfortified natural food product homogenates, Reindeer meat (labelled R)  $\sim$ 100 g, Halibut filet (labelled H)  $\sim$ 100 g and Cod liver oil (labelled C)  $\sim$ 15 g, and will be distributed by an international courier service to the participating laboratories.

#### **Please note:**

In order to avoid delay at customs, please inform us if there are import restrictions for any of these samples in your country.

#### **Instructions for analysis and reporting**

Further detailed instructions and reporting forms will be sent by e-mail simultaneously with the dispatch of the samples in January.

In short, laboratories should:

- use their own standard operation procedures for extraction clean-up and instrumental determination
- use their own reference standards for identification and quantification
- report a single concentration for each analyte in each food matrix determined on fresh weight basis
- report limits of detection for all measured analytes in each food item
- report the lipid content

#### Time schedule

Announcement	December 2011	
Return of registration form	<b>December 16, 2011</b>	
Shipment of test material	January 16, 2012	
Confirmation of receipt of test material by participant	Within 7 days	
Reporting of test results a)	April 20, 2012	
Publication of draft report on web-site	August 2012	
Evaluation meeting at Dioxin 2012 in Cairns, Australia	August 2012	
Final report available to all participants	November 2012	

a) Please be sure that your results are reported on time as there will be **no extension of the deadline.** 

#### **Participation fee**

To all laboratories that have received the test materials, a corresponding invoice in Norwegian kroner (NOK) will be sent. The participation fee for any combination of the analytes in one food item is 9 000 NOK, for two food items 11 200 NOK, and for the complete set of all three food items the fee is 13 400 NOK.

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### **Interlaboratory Comparison on Dioxins in Food 2012**

#### **Instructions for participants**

#### January 2012

#### 1. Introduction

This is the 13<sup>th</sup> Round of the Interlaboratory Comparison Study on the Determination of POPs in Food organised by the Department of Exposure and Risk Assessment, Norwegian Institute of Public Health, Oslo, Norway. The objective of this exercise is to assess the interlaboratory comparability of the results from analyses of all dioxins and dioxin-like PCBs included in the WHO-TEF schemes in regular foods. Participants may also determine and report concentrations of six marker PCBs, eight polybrominated diphenylethers (PBDEs) and hexabromocyclododecane (HBCD). The exercise serves as a quality assurance instrument for the participating laboratories. A further objective is to assess the world-wide readiness and capacity for the determination of dioxin-like compounds, marker PCBs, PBDEs and HBCD in food. Instructions for the analysis and submission of results are given below.

#### Please read these instructions carefully before starting the experimental work.

The participating laboratories will collaboratively assess the interlaboratory comparability in the analytical performance for determination of:

• dioxins and furans: all seventeen 2,3,7,8-substituted PCDDs and PCDFs

• non-ortho PCBs: CB-77, 81, 126 and 169

• mono-ortho PCBs: CB-105, 114, 118, 123, 156, 157, 167 and 189.

• marker PCBs: CB-28, 52, 101, 138, 153 and 180

in samples of Reindeer meat (R), Halibut filet (H) and Cod liver oil (C). The mentioned analytes should also be determined in the respective six standard solutions. For HBCD, concentrations of  $\alpha$ -HBCD,  $\beta$ -HBCD and  $\gamma$ -HBCD as well as the total of these isomers will be assessed. Both results from GC-MS and LC-MS or LC-MS/MS are welcome.

#### 2. Participants

A list of participants is attached. Ninety-one laboratories have announced their participation in the study.

#### 3. Design of the study

#### 3.1 Test materials

#### Samples

One standard solution of each:

- EDF-5008-50 with PCDDs/PCDFs at concentrations 2:5:10 pg/µl for tetra:penta-hexa-hepta:octa chlorinated dibenzo-p-dioxins/-dibenzo furans respectively
- EC-4986/1000 with non-ortho PCBs at concentration 10 pg/μl
- EC-4987/100 with mono-ortho PCBs at concentration 100 pg/μl
- EC-5179/50 with marker PCBs at concentration 100 pg/μl
- EO-5103/100 with PBDEs at concentration 25 pg/μl, except BDE-209 at 100 pg/μl
- ULM-4834-S/100 with α-HBCD at a concentration 500 pg/µl

#### One sample of each

- ca. 100 g reindeer meat
- ca. 100 g halibut filet
- ca. 15 g cod liver oil, lipid content 100%

#### **Fortification**

The samples are prepared from regular market foods. There is no fortification or spiking of the PCDD, PCDF, PCB, PBDE or HBCD analytes in the food samples.

#### **Shipment**

The samples are fresh frozen food homogenates. They are distributed by DHL and should reach the receiving laboratory in good condition within a few days. The airwaybill numbers will be made available for the participants to trace the shipment at <a href="http://www.dhl.com">http://www.dhl.com</a>.

#### 3.2 Coding

#### Coding of laboratories

Upon arrival of the samples in the participant's laboratory, the Microsoft excel file named "Participant confirmation", shall be filled in and **immediately** returned to the co-ordinators by e-mail or telefax. The code of the laboratory will then be given by the co-ordinators. The laboratory codes will not be revealed to the other participants or to third parties.

#### Coding of samples

Reindeer meat R
Halibut filet H
Cod liver oil C

The above sample coding is marked on the sample bottles.

#### 3.3 Analytical procedure

#### Methods to be used

Laboratories shall use

- their own methods for sample preparation and instrumental analysis
- their own internal- and quantification standards
- their own lipid determination procedure

#### Standard solutions

The standard solutions should be analysed using the laboratory's own quantification standards and methods and the results shall be reported.

#### General

Beware of the high risk of background contamination and positive blank values when analysing food samples with levels of dioxins, PCBs, PBDEs and HBCD in the low ppt range.

Use sample size according to expected levels of dioxins for the determinations in order to achieve a detection level that leaves as few as possible analytes as non-detected. The sample amount dispatched is not meant for replicate analyses.

The samples might become inhomogeneous during freezing and transport. Re-homogenise all received material of each food item before any portion is taken out for analysis.

#### 4. Reporting

#### 4.1 Results to be reported

Laboratories are recommended to report as many as possible of the congeners mentioned in chapter 1.

The reports <u>must</u> include the determined lipid percent for reindeer meat and halibut filet. Also, the actual sample amount (g) for each determination must be reported.

The analytical report must include concentrations for all the congeners in all the samples on fresh weight basis, see Report forms B, C, D for PCDD/PCDF and dioxin-like PCBs and Report form 2, 3, 4 for marker PCBs, PBDEs and HBCD.

Laboratories must report one concentration on fresh weight basis for each congener which is detected  $(S/N \ge 3)$ , as well as the limit of determination (LOD, S/N = 3) for each sample. Non-detected congeners (S/N < 3) must be marked ND in the Comments column of the Report form. Please note that the LOD will be used as concentration of non-detected congeners.

#### 4.2 Checklist

Please use the attached checklist before returning the Report forms with your results.

#### 4.3 Submitting results

Three Microsoft Excel files are provided to each participant comprising:

#### **Participants confirmation**

• confirmation of receiving test materials

#### Report form dioxins and dioxinlike PCBs

• analytical data, Report forms A, B, C and D

#### Report form marker PCBs, PBDEs and HBCD

• analytical data, Report forms 1, 2, 3 and 4

Participants are requested to submit their reports electronically to avoid possible transcription errors.

#### Please, do not alter rows or columns in the original Report forms!

The electronic report shall be sent to <u>dioxin@fhi.no</u> within the deadline.

If necessary, a hard copy of the Report forms can be provided. Please contact one of the coordinators. If a hard copy report is used, it shall either be faxed to: + 47 21 07 66 86 or mailed to:

Norwegian Institute of Public Health att. Georg Becher P.O. Box 4403 Nydalen N-0403 Oslo, Norway

#### Deadline

The reports must be in our hands no later than April 20, 2012 to enable us to prepare the draft report for the Dioxin 2012 Symposium in Cairns, Australia. There will be no extension of this deadline. A confirmation for the receipt of your results will be sent to you by e-mail within a week.

#### 5. Statistical evaluations

Prior to the final report, a draft version will be prepared based on the data reported by April 20th. The co-ordinators will calculate mean, median and between-laboratory standard deviations for each congener. Outliers will be removed, and consensus values will be calculated. In case of extreme deviation from normal distribution, appropriate procedures will be used to get a best available estimate of the true value. For the dioxin-like compounds, TEQ values will be calculated for each laboratory and a consensus TEQ value based on the consensus of the congeners. Z-scores will be calculated for laboratories' results for PCDD/PCDF TEQs and PCB TEQs.

Statistical results based on the reported data as well as other important information from the evaluation of the data, will be discussed during a consultation meeting in August at the Dioxin 2012 Symposium in Cairns, Australia.

#### 6. Final report

The final report will be prepared by the co-ordinators. All participants will be presented by their laboratory code. A draft will be published on the Internet in the beginning of August. The results will be discussed during the Dioxin 2012 Symposium in Cairns, Australia. The final report will be available by November 2012. The report will be available in an electronic version on <a href="http://www.fhi.no">http://www.fhi.no</a>. Certificates of participation in the study will be given to all laboratories submitting results.

#### **7. Fee**

To all laboratories that have received the materials, an invoice will be sent. The participation fee for any combination of the 29 dioxin-like congeners, six marker PCBs, 8 PBDEs and HBCD is

- NOK 9000 for one food item
- NOK 11200 for two food items
- NOK 13400 for the complete set of all three food items.

Up to six standard solutions will be distributed free of charge to all participants, dependent on which analytes the participating laboratories intend to determine.

Invoices will be sent out after we have received the Participant confirmation from the participants.

#### 8. Time schedule

Announcement	December 2011
Return of registration form	<b>December 16, 2011</b>
Shipment of test material	January 23, 2012
Confirmation of receipt of test material by participant	Within 7 days
Reporting of test results a)	April 20, 2012
Publication of draft report on web-site	August 2012
Evaluation meeting at Dioxin 2012 Cairns, Australia	August 2012
Final report available to all participants	November 2012

# a) Please be sure that your results are reported in time as there will be **no extension of the deadline.**

#### 9. Co-ordinators of the study

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## **Interlaboratory Comparison on Dioxins in Food 2012**

### Checklist

In order to avoid possible misunderstandings and errors when reporting your results, we here give a list of possible pitfalls. Please, check this list and your Report forms before reporting your results.

Are the results for each congener filled out in the correct order? Be especially aware of 2,3,4,6,7,8- and 1,2,3,7,8,9-HxCDF, and PCB 81.
Are all congener results reported in $pg/\mu l$ for standards and $pg/g$ for samples?
Are both concentration and LOD reported for each congener?
Are sample amount and measured lipid content filled in?
Are not detected congeners marked with ND in the Comments column?

# Appendix C:

## Summary results

Consensus of congener concentrations Consensus of TEQ values Consensus statistics Laboratories´ reported TEQs Lipid determination Laboratories´ Z-scores Z-score plots

### Consensus of congener concentrations

	Reinde	er meat	Halib	ut filet	Cod li	ver oil
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
2,3,7,8-TCDD	0.039	0.31	0.048	0.30	0.31	0.31
1,2,3,7,8-PeCDD	0.13	0.98	0.066	0.42	0.11	0.11
1,2,3,4,7,8-HxCDD	0.12	0.94	0.0076	0.048	0.036	0.036
1,2,3,6,7,8-HxCDD	0.14	1.1	0.068	0.43	0.33	0.33
1,2,3,7,8,9-HxCDD	0.016	0.13	0.0088	0.055	0.075	0.075
1,2,3,4,6,7,8-HpCDD	0.14	1.1	0.050	0.31	0.17	0.17
1,2,3,4,6,7,8,9-OCDD	0.48	3.7	0.15	0.97	0.24	0.24
2,3,7,8-TCDF	0.091	0.71	1.63	10	6.5	6.5
1,2,3,7,8-PeCDF	0.022	0.17	0.14	0.90	1.1	1.1
2,3,4,7,8-PeCDF	0.29	2.2	0.42	2.7	0.70	0.70
1,2,3,4,7,8-HxCDF	0.14	1.1	0.035	0.22	0.20	0.20
1,2,3,6,7,8-HxCDF	0.10	0.79	0.041	0.26	0.38	0.38
2,3,4,6,7,8-HxCDF	0.060	0.46	0.042	0.26	0.35	0.35
1,2,3,7,8,9-HxCDF	0.0060	0.046	0.0057	0.036	0.034	0.034
1,2,3,4,6,7,8-HpCDF	0.060	0.46	0.021	0.13	0.15	0.15
1,2,3,4,7,8,9-HpCDF	0.010	0.077	0.0080	0.050	0.050	0.050
1,2,3,4,6,7,8,9-OCDF	0.030	0.23	0.020	0.13	0.10	0.10
PCB 77	0.75	5.8	16	102	90	90
PCB 126	6.6	51	8.1	51	70	70
PCB 169	0.96	7.4	2.4	15	14	14
PCB 81	0.61	4.7	0.78	4.9	4.2	4.2
PCB 105	139	1080	517	3248	4748	4748
PCB 114	9.8	76	33	209	304	304
PCB 118	320	2478	1532	9637	13600	13600
PCB 123	2.7	21	20	127	198	198
PCB 156	50	384	136	854	1467	1467
PCB 157	13	102	39	247	434	434
PCB 167	17	134	80	503	839	839
PCB 189	3.9	30	10	64	117	117

fw. - fresh weight lw. - lipid weight

### Consensus of congener concentrations

	Reinde	er meat	Halib	ut filet	Cod li	ver oil
	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.	pg/g fw.	pg/g lw.
CB 28	48	369	368	2314	2109	2109
CB 52	12	92	999	6280	5680	5680
CB 101	27	208	1596	10041	9108	9108
CB 138	182	1407	2020	12704	19484	19484
CB 153	445	3446	2621	16485	24000	24000
CB 180	160	1239	658	4138	6624	6624
BDE 28	0.51	3.9	35	219	243	243
BDE 47	3.6	28	544	3423	4560	4560
BDE 99	3.3	25	26	164	80	80
BDE 100	0.88	6.8	92	577	889	889
BDE 153	7.7	60	17	107	21	21
BDE 154	0.91	7.0	86	540	643	643
BDE 183	1.3	10	0.55	3.4	5.5	5.5
BDE 209	16	125	21	130	35	35
α-HBCD	3.0	23	388	2443	5390	5390
β-HBCD	0.56	4.3	6.0	38	321	321
γ-HBCD	3.9	31	13	82	370	370
Tot HBCD	7.2	56	370	2327	5922	5922
Sum PCB	873	6763	8262	51963	67005	67005
Sum BDE without 209	18	141	800	5034	6442	6442
Sum BDE	34	266	821	5164	6477	6477

fw. - fresh weight lw. - lipid weight

#### Consensus of TEQs

TEF<sub>2006</sub>

2006	Reinde	er meat	Halibi	ut filet	Cod li	ver oil
	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.
2,3,7,8-TCDD	0.039	0.31	0.048	0.30	0.31	0.31
1,2,3,7,8-PeCDD	0.13	0.98	0.066	0.42	0.11	0.11
1,2,3,4,7,8-HxCDD	0.012	0.094	0.00076	0.0048	0.0036	0.0036
1,2,3,6,7,8-HxCDD	0.014	0.11	0.0068	0.043	0.033	0.033
1,2,3,7,8,9-HxCDD	0.0016	0.013	0.00088	0.0055	0.0075	0.0075
1,2,3,4,6,7,8-HpCDD	0.0014	0.011	0.00050	0.0031	0.0017	0.0017
1,2,3,4,6,7,8,9-OCDD	0.00014	0.0011	0.000046	0.00029	0.000071	0.000071
2,3,7,8-TCDF	0.0091	0.071	0.16	1.0	0.65	0.65
1,2,3,7,8-PeCDF	0.00067	0.0052	0.0043	0.027	0.032	0.032
2,3,4,7,8-PeCDF	0.087	0.67	0.13	0.80	0.21	0.21
1,2,3,4,7,8-HxCDF	0.014	0.11	0.0035	0.022	0.020	0.020
1,2,3,6,7,8-HxCDF	0.010	0.079	0.0041	0.026	0.038	0.038
2,3,4,6,7,8-HxCDF	0.0060	0.046	0.0042	0.026	0.035	0.035
1,2,3,7,8,9-HxCDF	0.00060	0.0046	0.00057	0.0036	0.0034	0.0034
1,2,3,4,6,7,8-HpCDF	0.00060	0.0046	0.00021	0.0013	0.0015	0.0015
1,2,3,4,7,8,9-HpCDF	0.00010	0.00077	0.000080	0.00050	0.00050	0.00050
1,2,3,4,6,7,8,9-OCDF	0.0000090	0.000070	0.0000060	0.000038	0.000030	0.000030
PCB 77	0.000075	0.00058	0.0016	0.010	0.0090	0.0090
PCB 126	0.66	5.1	0.81	5.1	7.0	7.0
PCB 169	0.029	0.22	0.072	0.45	0.42	0.42
PCB 81	0.00018	0.0014	0.00023	0.0015	0.0013	0.0013
PCB 105	0.0042	0.032	0.015	0.097	0.14	0.14
PCB 114	0.00029	0.0023	0.0010	0.0063	0.0091	0.0091
PCB 118	0.010	0.074	0.046	0.29	0.41	0.41
PCB 123	0.000082	0.00064	0.00060	0.0038	0.0059	0.0059
PCB 156	0.0015	0.012	0.0041	0.026	0.044	0.044
PCB 157	0.00040	0.0031	0.0012	0.0074	0.013	0.013
PCB 167	0.00052	0.0040	0.0024	0.015	0.025	0.025
PCB 189	0.00012	0.00091	0.00030	0.0019	0.0035	0.0035
PCDDs/PCDFs	0.32	2.5	0.43	2.7	1.5	1.5
Non-ortho PCBs	0.68	5.3	0.88	5.5	7.4	7.4
Mono-ortho PCBs	0.017	0.13	0.071	0.45	0.65	0.65
Total TEQ	1.0	7.9	1.4	8.7	9.6	9.6

fw. - fresh weight lw- - lipid weight

#### Consensus of TEQs

TEF1998

1EF1998	Reinde	er meat	Halib	ut filet	Cod li	ver oil
	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.	pg TE/g fw.	pg TE/g lw.
2,3,7,8-TCDD	0.039	0.31	0.048	0.30	0.31	0.31
1,2,3,7,8-PeCDD	0.13	0.98	0.066	0.42	0.11	0.11
1,2,3,4,7,8-HxCDD	0.012	0.094	0.00076	0.0048	0.0036	0.0036
1,2,3,6,7,8-HxCDD	0.014	0.11	0.0068	0.043	0.033	0.033
1,2,3,7,8,9-HxCDD	0.0016	0.013	0.00088	0.0055	0.0075	0.0075
1,2,3,4,6,7,8-HpCDD	0.0014	0.011	0.00050	0.0031	0.0017	0.0017
1,2,3,4,6,7,8,9-OCDD	0.000048	0.00037	0.000015	0.00010	0.000024	0.000024
2,3,7,8-TCDF	0.0091	0.071	0.16	1.02	0.65	0.65
1,2,3,7,8-PeCDF	0.0011	0.0087	0.0072	0.045	0.054	0.054
2,3,4,7,8-PeCDF	0.15	1.1	0.21	1.3	0.35	0.35
1,2,3,4,7,8-HxCDF	0.014	0.11	0.0035	0.022	0.020	0.020
1,2,3,6,7,8-HxCDF	0.010	0.079	0.0041	0.026	0.038	0.038
2,3,4,6,7,8-HxCDF	0.0060	0.046	0.0042	0.026	0.035	0.035
1,2,3,7,8,9-HxCDF	0.00060	0.0046	0.00057	0.0036	0.0034	0.0034
1,2,3,4,6,7,8-HpCDF	0.00060	0.0046	0.00021	0.0013	0.0015	0.0015
1,2,3,4,7,8,9-HpCDF	0.00010	0.00077	0.000080	0.00050	0.00050	0.00050
1,2,3,4,6,7,8,9-OCDF	0.0000030	0.000023	0.0000020	0.000013	0.000010	0.000010
PCB 77	0.000075	0.00058	0.0016	0.010	0.0090	0.0090
PCB 126	0.66	5.1	0.81	5.1	7.0	7.0
PCB 169	0.010	0.074	0.024	0.15	0.14	0.14
PCB 81	0.000061	0.00047	0.000078	0.00049	0.00042	0.00042
PCB 105	0.014	0.11	0.052	0.32	0.47	0.47
PCB 114	0.0049	0.038	0.017	0.10	0.15	0.15
PCB 118	0.032	0.25	0.15	0.96	1.4	1.4
PCB 123	0.00027	0.0021	0.0020	0.013	0.020	0.020
PCB 156	0.025	0.19	0.068	0.43	0.73	0.73
PCB 157	0.0066	0.051	0.020	0.12	0.22	0.22
PCB 167	0.00017	0.0013	0.00080	0.0050	0.0084	0.0084
PCB 189	0.00039	0.0030	0.0010	0.0064	0.012	0.012
PCDDs/PCDFs	0.38	3.0	0.52	3.3	1.6	1.6
Non-ortho PCBs	0.67	5.2	0.83	5.2	7.2	7.2
Mono-ortho PCBs	0.083	0.64	0.31	2.0	3.0	3.0
Total TEQ	1.1	8.8	1.7	10	12	12

fw. - fresh weight

lw- - lipid weight

## **Analyte solution**

	Target value	Consensus	Median all values	Consensus	Standard	Relative standard	No. of values	No. of values
	pg/μl	median, pg/μl	pg/μl	mean, pg/μl	deviation, pg/μl	deviation, %	reported	removed
2,3,7,8-TCDD	2.0	2.0	2.0	2.0	0.17	8.4	80	1
1,2,3,7,8-PeCDD	5.0	4.8	4.8	4.8	0.41	8.5	80	2
1,2,3,4,7,8-HxCDD	5.0	4.8	4.8	4.8	0.43	9.0	80	1
1,2,3,6,7,8-HxCDD	5.0	4.8	4.8	4.8	0.44	9.1	80	1
1,2,3,7,8,9-HxCDD	5.0	5.1	5.1	5.1	0.58	11	80	0
1,2,3,4,6,7,8-HpCDD	5.0	4.9	4.9	4.9	0.43	8.7	80	0
1,2,3,4,6,7,8,9-OCDD	10.0	9.8	9.8	9.8	0.81	8.3	80	1
2,3,7,8-TCDF	2.0	1.9	1.9	1.9	0.22	12	80	0
1,2,3,7,8-PeCDF	5.0	5.0	5.0	4.9	0.50	10	80	1
2,3,4,7,8-PeCDF	5.0	4.8	4.8	4.7	0.44	9.3	80	1
1,2,3,4,7,8-HxCDF	5.0	4.9	4.9	4.9	0.42	8.6	80	0
1,2,3,6,7,8-HxCDF	5.0	5.0	5.0	4.9	0.42	8.6	80	0
2,3,4,6,7,8-HxCDF	5.0	5.0	5.0	4.9	0.43	8.7	80	0
1,2,3,7,8,9-HxCDF	5.0	4.9	4.9	4.9	0.48	10	80	0
1,2,3,4,6,7,8-HpCDF	5.0	4.9	4.9	4.8	0.43	9.0	80	0
1,2,3,4,7,8,9-HpCDF	5.0	5.0	5.0	5.0	0.50	10	80	0
1,2,3,4,6,7,8,9-OCDF	10	9.7	9.7	9.7	1.23	13	80	0
PCB 77	10	10	10	10	0.91	9.1	79	2
PCB 126	10	10	10	10	0.88	8.4	79	2
PCB 169	10	10	10	10	0.96	9.3	79	2
PCB 81	10	10	10	10	1.0	10	78	2
PCB 105	100	104	104	102	8.3	8.1	79	1
PCB 114	100	102	102	102	9.2	9.1	79	1
PCB 118	100	101	100	100	9.6	10	79	1
PCB 123	100	103	102	102	9.0	8.9	79	1
PCB 156	100	104	104	105	9.8	9.4	79	1
PCB 157	100	103	103	104	11	10.2	79	1
PCB 167	100	103	103	103	8.7	8.5	79	1
PCB 189	100	103	103	104	10	9.8	79	1

### Reindeer meat, fresh weight

	Consensus	Median all values	Consensus	Standard	Relative standard	No. of values	No. of values	No. of reported
	median, pg/g	pg/g	mean, pg/g	deviation, pg/g	deviation, %	reported	removed	non-detects
2,3,7,8-TCDD	0.039	0.040	0.038	0.012	31	71	2	10
1,2,3,7,8-PeCDD	0.13	0.13	0.12	0.034	28	71	1	2
1,2,3,4,7,8-HxCDD	0.12	0.12	0.12	0.026	22	71	1	2
1,2,3,6,7,8-HxCDD	0.14	0.14	0.14	0.034	24	71	1	3
1,2,3,7,8,9-HxCDD	0.016	0.018	0.017	0.0054	33	71	14	17
1,2,3,4,6,7,8-HpCDD	0.14	0.14	0.14	0.036	25	71	6	3
1,2,3,4,6,7,8,9-OCDD	0.48	0.50	0.49	0.16	32	71	9	4
2,3,7,8-TCDF	0.091	0.093	0.096	0.027	28	71	1	1
1,2,3,7,8-PeCDF	0.022	0.024	0.024	0.0084	36	71	11	12
2,3,4,7,8-PeCDF	0.29	0.29	0.28	0.060	21	71	0	0
1,2,3,4,7,8-HxCDF	0.14	0.14	0.14	0.031	22	71	2	3
1,2,3,6,7,8-HxCDF	0.10	0.10	0.10	0.026	26	71	1	4
2,3,4,6,7,8-HxCDF	0.060	0.062	0.064	0.020	31	71	4	7
1,2,3,7,8,9-HxCDF	0.0060	0.0081	0.0067	0.0036	54	71	19	46
1,2,3,4,6,7,8-HpCDF	0.060	0.062	0.063	0.022	34	71	10	9
1,2,3,4,7,8,9-HpCDF	0.010	0.012	0.010	0.0057	55	71	19	35
1,2,3,4,6,7,8,9-OCDF	0.030	0.044	0.035	0.022	62	71	21	25
PCB 77	0.75	0.80	0.78	0.27	34	71	12	6
PCB 126	6.6	6.6	6.3	1.6	26	71	0	1
PCB 169	0.96	0.98	0.94	0.21	23	70	6	5
PCB 81	0.61	0.62	0.59	0.17	29	71	5	6
PCB 105	139	139	137	24	18	71	1	0
PCB 114	9.8	9.8	9.5	2.1	22	71	2	4
PCB 118	320	320	309	67	22	71	1	0
PCB 123	2.7	2.8	2.7	0.95	35	71	5	9
PCB 156	50	50	48	11	22	71	1	0
PCB 157	13	13	13	2.7	21	71	2	2
PCB 167	17	17	17	3.8	22	71	0	2
PCB 189	3.9	3.9	3.9	0.77	20	71	5	5

### Halibut filet, fresh weight

	Consensus	Median all values	Consensus	Standard	Relative standard	No. of values	No. of values	No. of reported
	median, pg/g	pg/g	mean, pg/g	deviation, pg/g		reported	removed	non-detects
2,3,7,8-TCDD	0.048	0.049	0.049	0.013	26	78	3	4
1,2,3,7,8-PeCDD	0.066	0.066	0.065	0.016	25	78	3	4
1,2,3,4,7,8-HxCDD	0.0076	0.010	0.0081	0.0034	42	78	20	29
1,2,3,6,7,8-HxCDD	0.068	0.069	0.067	0.016	23	78	2	6
1,2,3,7,8,9-HxCDD	0.0088	0.010	0.0093	0.0043	46	78	18	33
1,2,3,4,6,7,8-HpCDD	0.050	0.054	0.051	0.015	29	78	12	11
1,2,3,4,6,7,8,9-OCDD	0.15	0.17	0.16	0.057	35	78	15	11
2,3,7,8-TCDF	1.6	1.6	1.6	0.30	18	78	1	1
1,2,3,7,8-PeCDF	0.14	0.14	0.14	0.028	20	78	1	0
2,3,4,7,8-PeCDF	0.42	0.42	0.43	0.091	21	78	0	0
1,2,3,4,7,8-HxCDF	0.035	0.037	0.037	0.013	36	78	8	11
1,2,3,6,7,8-HxCDF	0.041	0.041	0.042	0.011	26	78	5	8
2,3,4,6,7,8-HxCDF	0.042	0.043	0.043	0.012	27	78	6	9
1,2,3,7,8,9-HxCDF	0.0057	0.010	0.0069	0.0044	64	78	18	56
1,2,3,4,6,7,8-HpCDF	0.021	0.030	0.026	0.012	47	78	22	17
1,2,3,4,7,8,9-HpCDF	0.0080	0.010	0.0085	0.0051	60	78	21	51
1,2,3,4,6,7,8,9-OCDF	0.020	0.031	0.023	0.013	58	78	27	34
PCB 77	16	16	16	3.6	22	78	0	1
PCB 126	8.1	8.1	7.8	1.6	20	78	3	1
PCB 169	2.4	2.4	2.3	0.56	24	78	2	3
PCB 81	0.78	0.82	0.75	0.25	33	76	12	8
PCB 105	517	517	509	79	16	78	0	0
PCB 114	33	33	33	6.3	19	78	0	0
PCB 118	1532	1532	1499	249	17	78	0	0
PCB 123	20	21	19	8.0	41	78	8	5
PCB 156	136	136	134	22	16	78	0	0
PCB 157	39	39	39	7.3	18	78	1	0
PCB 167	80	81	78	13	16	78	4	0
PCB 189	10	10	10	2.4	24	78	0	4

## Cod liver oil, fresh weight

	Consensus	Median all values	Consensus	Standard	Relative standard	No. of values	No. of values	No. of reported
	median, pg/g	pg/g	mean, pg/g	deviation, pg/g	deviation, %	reported	removed	non-detects
2,3,7,8-TCDD	0.31	0.32	0.31	0.088	28	77	1	5
1,2,3,7,8-PeCDD	0.11	0.11	0.11	0.044	38	77	10	13
1,2,3,4,7,8-HxCDD	0.036	0.050	0.043	0.026	61	77	15	54
1,2,3,6,7,8-HxCDD	0.33	0.34	0.34	0.087	26	77	1	4
1,2,3,7,8,9-HxCDD	0.075	0.083	0.080	0.029	36	77	12	20
1,2,3,4,6,7,8-HpCDD	0.17	0.19	0.18	0.064	36	77	11	15
1,2,3,4,6,7,8,9-OCDD	0.24	0.33	0.26	0.15	56	77	23	20
2,3,7,8-TCDF	6.5	6.5	6.3	1.1	18	77	0	1
1,2,3,7,8-PeCDF	1.1	1.1	1.1	0.28	26	77	1	1
2,3,4,7,8-PeCDF	0.70	0.71	0.71	0.18	26	77	4	2
1,2,3,4,7,8-HxCDF	0.20	0.21	0.21	0.066	31	77	10	8
1,2,3,6,7,8-HxCDF	0.38	0.38	0.39	0.10	26	77	1	3
2,3,4,6,7,8-HxCDF	0.35	0.35	0.36	0.10	28	77	2	5
1,2,3,7,8,9-HxCDF	0.034	0.050	0.043	0.029	66	77	15	52
1,2,3,4,6,7,8-HpCDF	0.15	0.17	0.16	0.074	45	77	17	14
1,2,3,4,7,8,9-HpCDF	0.050	0.060	0.056	0.032	58	77	12	48
1,2,3,4,6,7,8,9-OCDF	0.10	0.16	0.12	0.082	67	77	23	39
PCB 77	90	90	88	18	20	79	2	1
PCB 126	70	70	67	15	23	79	1	1
PCB 169	14	14	14	2.9	21	79	2	2
PCB 81	4.2	4.6	4.1	1.6	38	79	13	10
PCB 105	4748	4764	4688	714	15	79	1	0
PCB 114	304	305	304	61	20	79	1	0
PCB 118	13600	13600	13148	2324	18	79	0	0
PCB 123	198	207	190	62	33	79	10	3
PCB 156	1467	1467	1481	245	17	79	0	0
PCB 157	434	434	436	76	17	79	1	0
PCB 167	839	841	819	150	18	79	4	1
PCB 189	117	117	117	26	22	79	0	1

### **Analyte solution**

	Target value	Median, pg/μl all values	Median, pg/μl outliers removed	Mean, pg/μl all values	Mean, pg/μl outliers removed
	pg/μl				
CB 28	100	96	96	98	96
CB 52	100	96	96	111	97
CB 101	100	97	97	129	97
CB 138	100	97	97	141	98
CB 153	100	98	98	122	96
CB 180	100	98	98	102	98
BDE 28	25	25	25	25	25
<b>BDE 47</b>	25	24	24	24	24
BDE 99	25	25	25	24	24
BDE 100	25	24	24	24	24
BDE 153	25	25	25	25	25
BDE 154	25	24	24	24	24
BDE 183	25	24	24	24	24
BDE 209	100	94	95	88	92
α-HBCD *	500	485	485	477	477

	Relative standard deviation, %	Relative standard deviation, %	Number of reported	Number of reported
	all values	outliers removed	values	outliers
CB 28	42	13	65	4
CB 52	123	13	65	3
CB 101	218	11	65	3
CB 138	257	13	65	2
CB 153	176	12	65	2
CB 180	43	13	64	2
BDE 28	11	11	39	0
<b>BDE 47</b>	10	10	39	0
BDE 99	9.4	9.4	39	0
BDE 100	11	11	39	0
BDE 153	10	10	39	0
BDE 154	10	10	39	0
BDE 183	11	11	38	0
BDE 209	24	13	26	1
α-HBCD *	7.6	7.6	14	0

<sup>\* :</sup> Indicative value due to few reported values

Reindeer meat, fresh weight

	Median, pg/g	Median, pg/g	Median, pg/g	Mean, pg/g	Mean, pg/g	Mean, pg/g
	all values	outliers removed	outliers and NDs removed	all values	outliers removed	outliers and NDs removed
CB 28	49	49	48	96	46	47
CB 52	14	12	12	75	13	13
CB 101	29	27	27	96	28	27
CB 138	185	182	182	267	190	190
CB 153	448	445	445	558	426	426
CB 180	165	160	160	238	155	155
BDE 28	0.6	0.5	0.5	1.2	0.5	0.5
BDE 47	4.5	3.7	3.6	34	4.0	4.0
BDE 99	3.4	3.3	3.3	44	3.5	3.4
BDE 100	1.0	0.9	0.9	9	1.0	0.9
BDE 153	7.8	7.7	7.7	13	7.7	7.8
BDE 154	1.0	0.9	0.9	5.1	0.9	1.0
BDE 183	1.4	1.3	1.3	3.8	1.3	1.4
BDE 209	20	15	16	45	13	14
α-HBCD *	20	17	3.0	17	14	3.0
β-HBCD *	10	10	0.6	11	7.9	0.6
γ-HBCD *	20	10	3.9	39	11	3.9
Tot HBCD *	65	40	7.2	66	50	7.2

	Relative standard deviation, %	Relative standard deviation, %	Relative standard deviation, %	Number of reported	Number of outliers	Number of reported NDs
	all values	outliers removed	outliers and NDs removed	values		
CB 28	206	34	32	58	7	6
CB 52	286	47	42	58	17	8
CB 101	291	33	29	58	10	4
CB 138	150	31	31	58	5	1
CB 153	156	26	26	58	3	1
CB 180	178	23	23	57	4	1
BDE 28	140	50	47	31	8	6
<b>BDE 47</b>	373	34	35	31	9	1
BDE 99	482	32	32	31	7	2
<b>BDE 100</b>	455	44	38	31	9	5
BDE 153	179	20	19	31	2	1
BDE 154	363	35	34	31	6	3
BDE 183	284	46	46	30	5	7
BDE 209	138	60	48	22	8	3
α-HBCD *	75	53	55	11	1	9
β-HBCD *	116	70	**	12	1	11
γ-HBCD *	129	64	115	11	4	8
Tot HBCD *	88	79	91	8	1	5

<sup>\*:</sup> Indicative value due to few reported values

<sup>\*\* :</sup> Not relevant

Halibut filet, fresh weight

	Median, pg/g	Median, pg/g	Median, pg/g	Mean, pg/g	Mean, pg/g	Mean, pg/g
	all values	outliers removed	outliers and NDs removed	all values	outliers removed	outliers and NDs removed
CB 28	396	368	368	472	394	394
CB 52	1000	999	999	1020	956	955
CB 101	1593	1593	1596	1538	1538	1547
CB 138	2020	2010	2020	1977	1937	1952
CB 153	2622	2621	2621	2556	2494	2494
CB 180	661	660	658	660	646	639
BDE 28	36	35	35	45	35	36
<b>BDE 47</b>	544	544	544	534	534	534
BDE 99	26	26	26	29	28	28
BDE 100	92	92	92	92	92	94
BDE 153	17	17	17	17	16	16
BDE 154	86	86	86	87	87	87
BDE 183	1.0	0.60	0.5	2.9	0.67	0.62
BDE 209	28	21	21	45	24	24
α-HBCD *	393	388	388	452	405	405
β-HBCD *	18	13	6.0	50	17	9.3
γ-HBCD *	14	12	13	50	15	13
Tot HBCD *	370	370	370	389	389	389

	Relative standard deviation, %	Relative standard deviation, %	Relative standard deviation, %	Number of reported	Number of outliers	Number of reported NDs
	all values	outliers removed	outliers and NDs removed	values		
CB 28	56	39	39	61	8	1
CB 52	45	30	31	61	2	1
CB 101	30	30	30	61	0	1
CB 138	38	36	35	61	1	1
CB 153	34	30	30	61	1	0
CB 180	33	29	29	60	1	1
<b>BDE 28</b>	61	22	15	37	5	1
<b>BDE 47</b>	18	18	18	37	0	0
<b>BDE 99</b>	36	24	24	36	1	0
<b>BDE 100</b>	21	21	13	36	0	1
<b>BDE 153</b>	37	19	19	37	1	0
<b>BDE 154</b>	21	21	21	37	0	0
<b>BDE 183</b>	197	46	49	36	13	10
<b>BDE 209</b>	106	51	41	24	5	2
α-HBCD *	40	17	17	12	1	0
β-HBCD *	211	80	81	13	3	10
γ-HBCD *	224	40	11	12	2	9
Tot HBCD *	9.0	9.0	9.0	9	0	0

<sup>\*:</sup> Indicative value due to few reported values

Cod liver oil, fresh weight

	Median, pg/g	Median, pg/g	Median, pg/g	Mean, pg/g	Mean, pg/g	Mean, pg/g
	all values	outliers removed	outliers and NDs removed	all values	outliers removed	outliers and NDs removed
CB 28	2154	2124	2109	2264	2171	2157
CB 52	5680	5680	5680	0 5448	5448	5448
CB 101	9116	9108	9108	9362	9057	9057
CB 138	19484	19484	19484	20341	20341	20341
CB 153	24000	24000	24000	23611	23611	23611
CB 180	6624	6624	6624	6680	6680	6680
BDE 28	254	243	243	340	243	243
<b>BDE 47</b>	4560	4560	4560	4360	4360	4360
BDE 99	83	80	80	112	79	81
BDE 100	889	889	889	889	889	889
BDE 153	22	21	21	41	21	21
BDE 154	650	647	643	684	659	660
BDE 183	6.0	5.6	5.5	48	5.8	5.6
BDE 209	80	35	35	209	51	53
α-HBCD *	5410	5390	5390	6240	5637	5637
β-HBCD *	371	371	321	361	361	356
γ-HBCD *	399	370	370	515	317	346
Tot HBCD *	5922	5922	5922	6243	6243	6243

	Relative standard deviation, %	Relative standard deviation, %	Relative standard deviation, %	Number of reported	Number of outliers	Number of reported NDs
	all values	outliers removed	outliers and NDs removed	values		
CB 28	41	35	36	63	2	1
CB 52	23	23	23	63	0	0
CB 101	32	20	20	63	1	0
CB 138	31	31	31	63	0	0
CB 153	25	25	25	63	0	0
CB 180	23	23	23	62	0	0
BDE 28	59	17	17	37	8	1
<b>BDE 47</b>	20	20	20	37	0	0
BDE 99	104	31	26	37	4	3
<b>BDE 100</b>	25	25	25	37	0	0
BDE 153	254	31	26	37	4	4
BDE 154	29	19	20	37	1	1
BDE 183	453	41	43	36	5	9
BDE 209	155	82	75	23	7	8
α-HBCD *	35	15	15	11	1	0
β-HBCD *	22	22	25	11	0	2
γ-HBCD *	93	42	24	12	2	2
Tot HBCD *	13	13	13	8	0	0

<sup>\*:</sup> Indicative value due to few reported values

### Laboratories' reported TEQs, sum indicator PCB and sum BDE without BDE 209

TEF <sub>2006</sub>	Median	Mean	SD	RSD	Min	Max	Reporting
	pg/g	pg/g	pg/g	%	pg/g	pg/g	laboratories
Reindeer meat, fresh weight							
PCDD/PCDF TEQ	0.33	1.5	9.6	629	0.040	81	71
Non-ortho PCB TEQ	0.69	0.67	0.16	24	0.043	1.4	71
Mono-ortho PCB TEQ	0.017	0.017	0.0068	40	0.0024	0.067	71
Total TEQ	1.0	2.1	9.4	450	0.086	82	74
Sum indicator PCB	897	1326	2128	160	1.0	15780	58
Sum BDE without BDE 209	21	110	425	384	15	2391	31
Halibut filet, fresh weight							
PCDD/PCDF TEQ	0.44	0.55	0.15	28	0.14	1.6	78
Non-ortho PCB TEQ	0.89	0.92	0.36	39	0.36	3.2	78
Mono-ortho PCB TEQ	0.071	0.070	0.011	16	0.015	0.089	78
Total TEQ	1.4	1.4	0.42	29	0.48	3.7	81
Sum indicator PCB	8435	8212	2369	29	8.5	15770	61
Sum BDE without BDE 209	810	804	140	17	255	1076	37
Cod liver oil, fresh weight							
PCDD/PCDF TEQ	1.5	1.8	0.53	30	0.81	5.4	77
Non-ortho PCB TEQ	7.5	7.5	3.4	46	0.70	34	79
Mono-ortho PCB TEQ	0.66	0.66	0.18	27	0.34	2.0	79
Total TEQ	9.7	9.7	3.4	35	2.1	36	81
Sum indicator PCB	67190	67601	13766	20	80	108263	63
Sum BDE without BDE 209	6483	6471	1121	17	3693	10160	37

### Laboratories' reported TEQs, sum indicator PCB and sum BDE without BDE 209

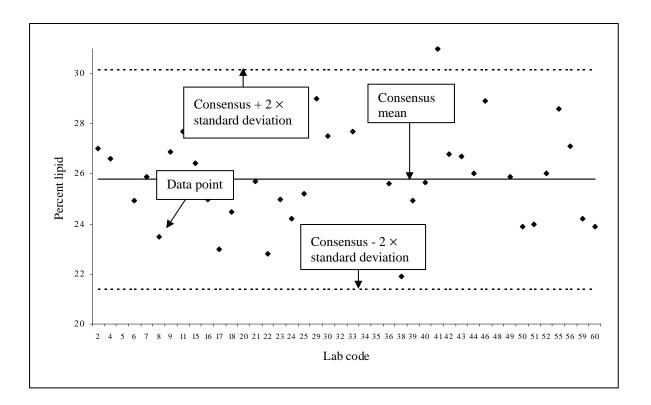
TEF <sub>1998</sub>	Median	Mean	SD	RSD	Min	Max	Reporting
	pg/g	pg/g	pg/g	%	pg/g	pg/g	laboratories
Reindeer meat, fresh weight							
PCDD/PCDF TEQ	0.39	1.5	9.6	629	0.050	81	71
Non-ortho PCB TEQ	0.67	0.64	0.16	25	0.037	1.3	71
Mono-ortho PCB TEQ	0.083	0.084	0.033	39	0.019	0.32	71
Total TEQ	1.1	2.2	9.5	428	0.11	82	72
Sum indicator PCB	897	1326	2128	160	1.0	15780	58
Sum BDE without BDE 209	21	110	425	384	15	2391	31
Halibut filet, fresh weight							
PCDD/PCDF TEQ	0.53	0.55	0.16	29	0.21	1.7	78
Non-ortho PCB TEQ	0.84	0.87	0.36	41	0.19	3.1	78
Mono-ortho PCB TEQ	0.31	0.31	0.048	16	0.07	0.43	78
Total TEQ	1.7	1.7	0.45	26	0.56	4.0	79
Sum indicator PCB	8435	8212	2369	29	8.5	15770	61
Sum BDE without BDE 209	810	804	140	17	255	1076	37
Cod liver oil, fresh weight							
PCDD/PCDF TEQ	1.7	1.8	0.58	33	0.87	5.8	77
Non-ortho PCB TEQ	7.2	7.2	3.4	48	0.57	34	79
Mono-ortho PCB TEQ	3.0	3.0	0.67	22	1.6	7.3	79
Total TEQ	12	12	3.5	29	4.1	38	79
Sum indicator PCB	67190	67601	13766	20	80	108263	63
Sum BDE without BDE 209	6483	6471	1121	17	3693	10160	37

### Presentation of results for lipid determination

Removal of outliers and calculation of consensus were done by the following procedure:

- 1. The mean was calculated from all the reported data.
- 2. Values outside a range of  $\pm$  2 × the standard deviation of this mean were defined as outliers and removed from the data set.
- 3. Mean, standard deviation and median were re-calculated from the remaining data. This mean was called consensus.

The diagram shows the reported data with consensus and consensus  $\pm$  the new standard deviation  $\times$  2.



#### **Z-Scores of lipid content**

Z-scores of lipid content were calculated for each laboratory according to the following equation:

$$z = (x - X)/\sigma$$

where x = reported value; X = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm$  20% from the consensus value.

## Lipid determination for Reindeer meat

Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
2	12.7		63	2.20	outlier			
3	13.6		64	12.5				
4	11.6		67	12.9				
5	13.4		68	12.0				
6	13.1		69	11.9				
8	14.1		70	12.8				
9	14.1		71	13.3				
10	13.5		72	11.6				
11	13.1		74	12.0				
12	11.5		76	14.2				
13	13.1		79	13.2				
15	6.03		80	13.1				
16	12.1		81	13.8				
17	13.9		84	10.7				•
18	6.50		85	14.9				
19	10.8		88	15.5				
20	13.5		89	13.3				
23	14.2		90	13.0				•
26	12.3		91	13.1				•
27	12.8		92	15.5				
28	13.1		93	12.1				r
29	9.10		95	12.7				•
32	11.0		96	12.4				
34	14.0		97	12.5				
35	14.6		100	11.6				•
36	12.5		102	12.5				r
38	12.9		107	17.6				
39	13.0		110	13.0				
40	14.7							
42	9.14							
44	13.6							
45	13.6					<u> </u>		
46	12.7							•
47	10.3							
48	13.2							
50	8.40							
52	13.0							
53	12.4							•
55 56	16.3					<u> </u>		•
56	10.7 13.7					<u> </u>		•
57 58								
58	11.8					<u> </u>		•
60	12.9 13.0					<u> </u>		•
61	12.9							
		ontlia.						
62	39.1	outlier						

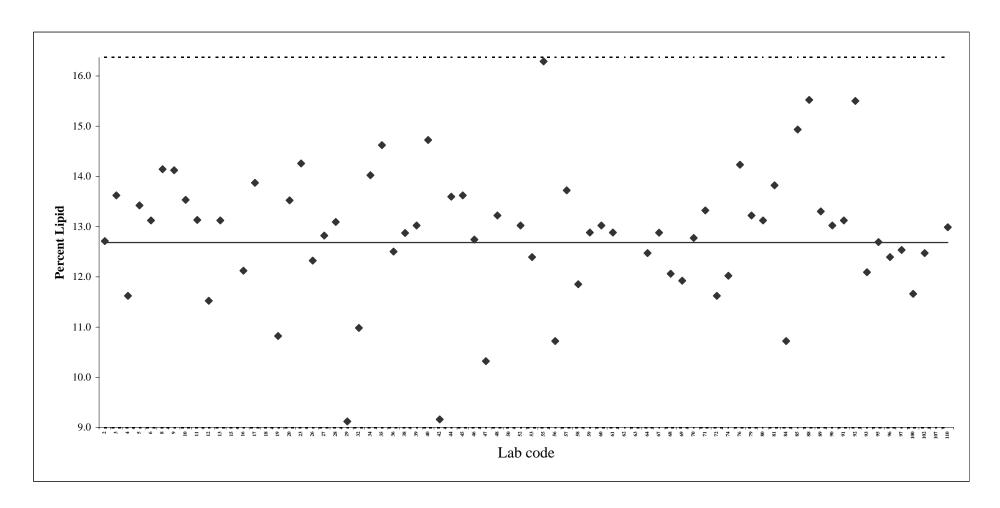
Mean	Standard deviation	Relative standard deviation	Median
12.7	1.84	14.6	12.9

## Lipid determination for Halibut filet

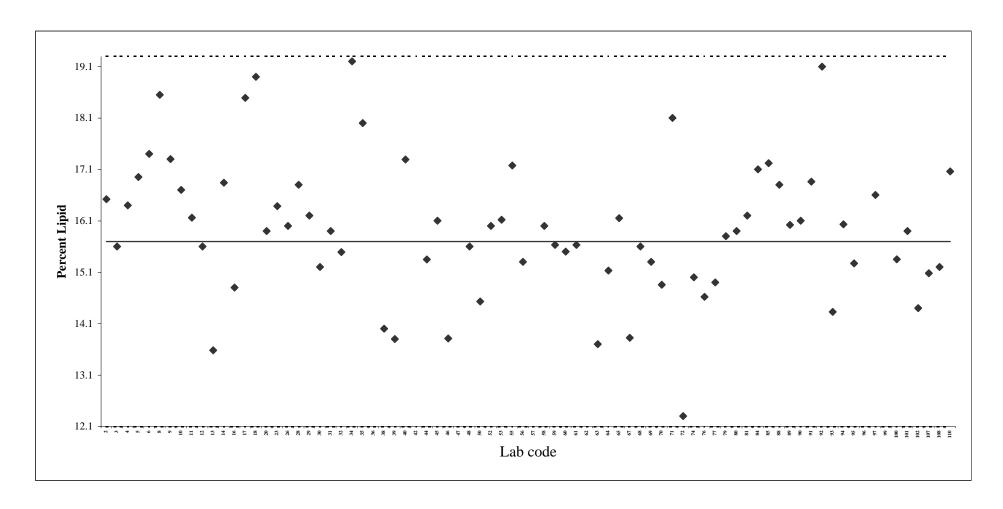
Lab code	% lipid	Notes	Lab code	% lipid	Notes	Lab code	% lipid	Notes
2	16.5		63	13.7				
3	15.6		64	15.1				
4	16.4		65	16.2				
5	17.0		67	13.8				
6	17.4		68	15.6				
8	18.6		69	15.3				
9	17.3		70	14.9				
10	16.7		71	18.1				
11	16.2		72	12.3				
12	15.6		74	15.0				
13	13.6		76	14.6				
14	16.8		77	14.9				
16	14.8		79	15.8				
17	18.5		80	15.9				
18	18.9		81	16.2				
20	15.9		84	17.1				
23	16.4		85	17.2				
26	16.0		88	16.8				
28	16.8		89	16.0				
29	16.2		90	16.1				
30	15.2		91	16.9				
31	15.9		92	19.1				
32	15.5		93	14.3				
34	19.2		94	16.0				
35	18.0		95	15.3				
36	19.6		96	10.1				
38	14.0		97	16.6				
39	13.8		99	12.0				•
40	17.3		100	15.4				
42	11.6		101	15.9				
44	15.3		102	14.4				
45	16.1		107	15.1				
46	13.8		108	15.2				,
47	11.7		110	17.1				•
48	15.6							•
50	14.5							•
52	16.0							•
53	16.1							
55	17.2							
56	15.3							
57	10.6							
58	16.0							•
59	15.6							
60	15.5							
61	15.6							
62	51.5	outlier						

Mean	Standard deviation	Relative standard deviation	Median
15.7	1.80	11.5	15.9

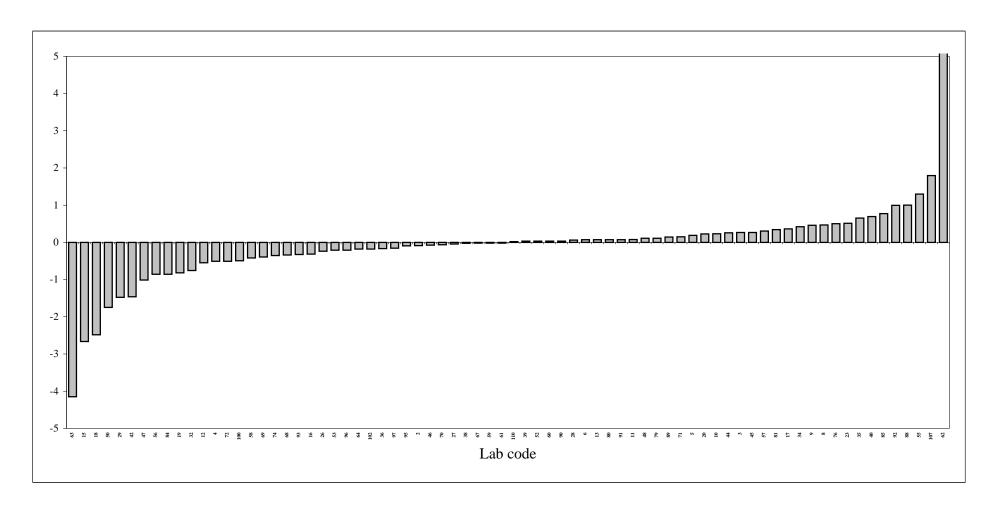
## Lipid determination; Reindeer meat



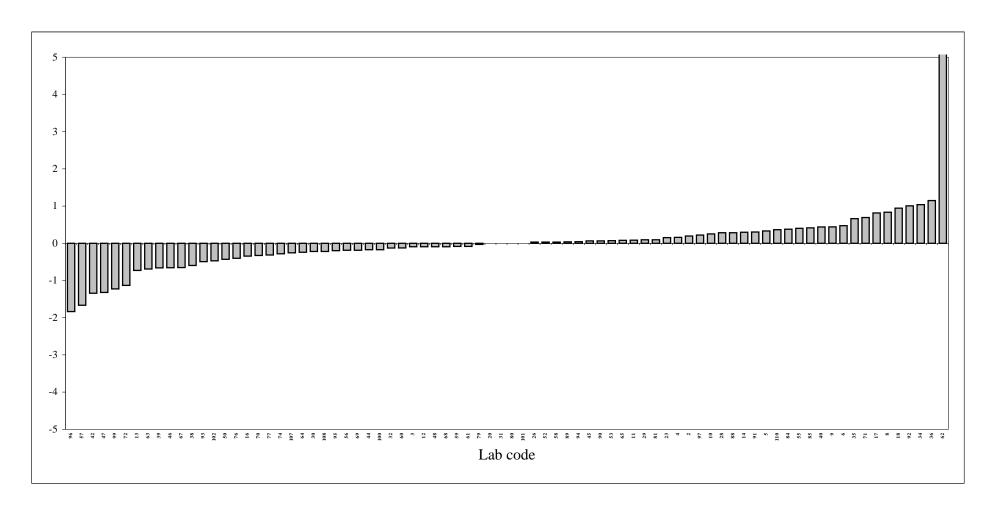
## Lipid determination; Halibut filet



## **Z-score lipid determination; Reindeer meat**



## **Z-score lipid determination; Halibut filet**



#### **Laboratories Z-scores: Analyte Solution**

LABCODE:	Sum TE totalt	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum u/209
1	0.15	0.11	0.60	0.043		
2	0.11	0.090	0.39	0.081	-0.038	0.10
3	-0.78	-0.38				
4	-0.17	-0.22	0.37	0.10	0.026	
5	-0.0078	0.018	-0.39	0.36	0.33	-0.061
6	-0.29	-0.32	0.0086	0.14	0.0034	
7	0.023	0.034	-0.11	0.012		
8	-0.66	-0.74	0.22	0.19	-0.24	0.38
9	0.30	0.28	0.49	0.25	0.53	0.077
10	-0.42	0.014 -0.050	-0.21	0.025	-0.14	
11 12	-0.062 -0.19	-0.030	0.95	0.66	-0.14	0.81
13	-0.19	-0.38	-0.35	0.63	-0.17	0.56
14	0.092	0.053	0.49	0.55	-0.17	0.50
15	0.44	0.38	1.2	0.48	1.4	
16	-0.085	-0.12	0.39	0.030	0.082	0.071
17	-0.48	-0.09	-4.5	-4.5	0.34	0.0.2
18	-0.42	-0.46	0.0090	0.077	-0.47	
19						
20	-0.30	-0.37	0.44	0.24	-0.13	0.17
0				-		
0						
23	0.16	0.18	-0.079	0.061		
0						
0						
26	0.020	-0.0028	0.29	0.051	0.73	
27 28	-0.44	-0.47 -0.033	-0.21	-0.19	0.065	
20 29	-0.056	-0.033	-0.28	-0.33		
30	0.0089	-0.040	0.53	0.46	-0.54	-0.15
31	3.4	-0.12	47	0.16	-0.54	-0.13
32	0.065	0.045	0.36	-0.28	-0.19	
0	0.002	0.0 15	0.50	0.20	0.17	
34	-0.21	-0.26	0.47	-0.38	-0.41	-0.92
35	0.042	-0.026	0.77	0.74	0.082	
36	0.45	0.43	0.68	0.36		
37					0.28	0.22
38	0.023	-0.0092	0.40	0.13	0.20	-0.0046
39	0.0016	-0.033	0.36	0.42	0.24	
40	-0.24	-0.31	0.45	0.19	-0.15	
41	-1.1	-1.1	-0.071	-0.54	0.69	
42	-0.23	-0.27	0.21	0.54	-4.7	
0 44	0.19	0.17	0.38	0.24		0.0078
44 45	-0.091	-0.15	0.61	0.24		0.0078
46	0.32	0.26	1.1	0.62	0.58	0.056
47	-0.92	-0.97	-0.46	-0.27	0.50	0.050
48	0.29	0.32	0.052	-0.30	-0.066	
49	-0.50	-0.50	-0.42	-0.61	-0.81	
50						
51	-0.25	-0.27	-0.11	0.37	-0.25	-0.017
52						
53	0.071	0.049	0.33	0.17	0.72	
0	0.000	0.11	0.0020	0.00	0.12	
55 56	-0.088	-0.11	0.0028	0.80	0.12	
56 57	0.30	0.32	0.049	0.40	-1.9	-0.50
58	-0.21	-0.21	-0.31	0.40	0.31	0.17
59	-0.37	-0.41	-0.033	0.71	-0.0094	0.34
60	-0.0043	-0.0063	-0.0088	0.17	0.32	-0.27
61	-0.37	-0.40	-0.22	0.66	-0.090	0.45
62	-0.15	-0.15	-0.18	-0.068		
0						
64	-0.20	-0.20	-0.14	-0.35	-0.43	-0.13
65	-0.050	-0.082	0.34	0.0065		-0.36
0	2.25					
67	-0.22	-0.26	0.25	-0.050	0.27	
68 60	0.0086	-0.0029	0.11	0.25	0.37	
69 70	-4.6 -0.23	-0.23	-0.24 -0.39	0.27 0.30	74 0.25	-0.23
70 71	0.55	0.57	0.18	0.30	0.25	0.013
72	-0.69	-0.82	0.74	0.72	-0.65	0.013
73	-0.12	-0.10	-0.33	-0.043	0.00	55
. •						

### Laboratories Z-scores: Analyte Solution (continued)

LABCODE:	Sum TE totalt	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum u/209
74	-0.49	-0.49	-0.50	-0.15	-0.68	
0						
76	0.014	-0.010	0.35	-0.26	0.17	0.83
77	-0.11	-0.11	-0.13	0.14	0.087	-0.45
0						
79	0.48	0.38	1.7	0.89	0.86	
80	-0.16	-0.15	-0.35	0.16	0.046	
81	-0.021	-0.045	0.20	0.41	0.17	-0.10
0						
0						
84	-0.096	-0.12	0.12	0.51	0.18	0.54
85	0.13	0.14	0.089	-0.25		0.18
0						
0						
88	-0.26	-0.35	0.77	0.33	0.093	
89	-0.034	-0.083	0.41	0.88	1.1	
90	-2.4	-2.5	-0.58	-1.72	-2.2	-0.91
91	-0.17	-0.20	0.097	0.060	-0.013	
92	-0.30	-0.36	0.28	0.67		
93	-0.084	-0.10	0.093	0.036	0.015	
94	0.10	0.11	0.034	0.22	-0.11	-0.50
95	-0.015	-0.044	0.43	-0.57	-0.26	-0.38
96	-0.14	-0.22	0.78	0.70	0.54	0.10
97	-0.49	-0.56	0.41	-0.64	-1.4	
0		0.044	0.40		0.40	0.10
99	0.072	0.061	0.29	-0.37	-0.40	-0.68
100	-0.13	-0.16	0.15	0.82	-2.1	-0.60
101	-1.5	-1.7	-0.092	-0.073	0.022	
0						
0						
0						
0						
0	0.14	0.17	0.20	0.26	1.1	0.20
107	0.14	0.17	-0.30	0.36	-1.1	-0.29
108 0					0.074	0.14
110	0.00	-0.058	0.66	0.47	0.60	-0.0064
110	0.00	-0.038	0.00	0.47	0.00	-0.0004

#### **Laboratories Z-scores: Reindeer Meat**

LABCODE:	Sum TE totalt	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum u/209
1 2	0.48	0.26	0.60	0.13	0.039	
3	-3.0	1.5	0.00	0.13	0.039	
4	-0.22	-1.2	0.26	-0.73	-0.41	
5	-0.35	0.11	-0.58	0.56	0.61	1.0
6	0.042	0.039	0.042	0.080	0.49	
7						
8	-0.034	0.56	-0.24	-3.2	-0.064	5.6
9	0.27	0.23	0.30	-0.081	0.59	1.3
10	0.52	0.35	0.60	0.59	0.24	
11 12	0.24 0.14	0.90 -0.14	-0.068 0.26	-0.14 0.22	-0.24 2.5	47
13	-0.074	0.36	-0.31	1.1	0.70	0.71
14	-0.074	0.50	-0.51	1.1	0.70	0.71
15	-4.6	-4.4	-4.7	-4.3	-1.3	
16	-0.04	-0.22	0.061	-0.47	-0.57	-0.78
17	-0.18	-0.10	-0.23	0.53	2.9	
18	-0.12	-0.24	-0.059	-0.11	0.058	
19	-0.89	-0.17	-1.2	-1.3	-1.3	
20	0.13	-0.20	0.29	-0.20	-0.49	-0.16
21						
22	1.0	1.7	0.07	0.20		
23 24	-1.2	-1.7	-0.97	0.28		
24 25						
26	0.013	-0.28	0.16	-0.38	-5.0	
27	394	1249	-0.87	0.26	1.7	
28	-2.4	-2.0	-2.5	-2.7		
29	-1.5	-1.7	-1.4	-1.2		
30						
31						
32	-0.50	0.015	-0.74	-0.68	0.22	
33	0.12	0.004	0.16	0.15	0.025	2.0
34	0.13	0.084	0.16	0.15	0.036	2.0
35 36	-0.40 0.89	5.3 1.6	-3.1 0.57	0.23 0.076	0.37	
37	0.89	1.0	0.57	0.070		
38	-0.30	-0.028	-0.42	-0.74	-0.087	3.1
39	-0.94	-0.58	-1.1	-1.9	-1.35	5.1
40	0.29	0.16	0.35	0.14	-0.32	
41						
42	-1.9	-1.5	-2.10	-0.30	29	
43		0.070		0.40		0.4.4
44	0.37	0.058	0.52	0.60		0.16
45 46	0.89 -0.14	0.73 0.057	0.96 -0.23	0.70 -0.51	0.22	-0.20
47	-0.14	0.34	-0.23	-0.47	-0.23	-0.20
48	1.0	-0.17	1.6	0.90	0.97	
49	-10	****	-14	****	***	
50	0.12	-0.23	0.30	-0.24	0.77	
51						
52	-0.10	0.41	-0.36	0.42	1.2	
53	0.10	-0.18	0.24	-0.33	1.6	
54 55	0.45	-0.46	0.88	0.50	5.4	
55 56	0.45 0.49	-0.46 2.3	-0.39	0.50 1.3	0.20	-0.074
50 57	0.49	0.40	0.050	-0.15	-1.2	1.5
58	-0.41	-0.47	-0.39	-0.15	0.045	1.3
59	0.65	0.58	0.67	1.4	0.67	0.063
60	-1.5	-1.1	-1.7	-1.4	-0.62	9.1
61	0.47	0.35	0.51	1.2	0.76	-0.094
62	0.35	0.88	0.11	0.048		
63	-3.0	0.22	0.15	0 :-	0.01	0.42
64	-0.24	0.23	-0.46	-0.47	-0.84	0.13
65 66						
67	-0.23	-0.63	-0.045	-0.15		
68	0.62	0.52	0.67	0.56	0.61	
69	-2.0	0.52	-0.65	-0.16	-0.89	
70	-0.59	0.057	-0.90	-0.17	0.79	0.36
71	0.37	0.68	0.23	0.15	0.17	-0.37
72	0.11	0.062	0.14	-0.013	0.039	-0.26
73						

### Laboratories Z-scores: Reindeer Meat (continued)

LABCODE:	Sum TE totalt	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	<b>Sum Indicator PCB</b>	Sum u/209
74	-0.29	-0.24	-0.32	-0.33	-0.27	
75						
76	-1.7	-1.5	-1.8	-0.024	-0.53	653
77						
78						
79	1.2	2.0	0.85	0.49	0.090	
80	-0.54	-0.70	-0.47	0.068	-0.15	
81	0.32	0.12	0.41	0.47	0.66	0.47
82						
83						
84	-0.63	-0.97	-0.47	-0.67	-0.83	-0.47
85	0.12	-0.040	0.20	0.10		-0.50
86						
87						
88	0.42	0.018	0.62	0.29	0.56	
89	0.35	0.013	0.51	0.35	0.60	
90	-0.62	-0.85	-0.50	-1.1	0.12	5.6
91	0.56	0.00	0.84	0.25		
92	3.1	6.9	1.4	0.18		
93	0.55	0.93	0.38	0.086	85	
94						
95	-0.73	-2.1	-0.091	-0.10	0.0058	2.9
96	0.25	0.37	0.19	0.44	0.15	-0.49
97	0.83	0.79	0.86	0.60	0.18	
98						
99						
100	-0.23	0.23	-0.44	-0.18	-0.60	1.9
101						
102	0.66					
0						
0						
0						
0						
107	3.8	0.59	5.1	15	25	12
108						
0						
110	0.18	0.18	0.17	0.71	2.5	30

#### **Laboratories Z-scores: Halibut Filet**

LABCODE:	Sum TE totalt	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	Sum Indicator PCB	Sum u/209
1	0.16	0.20	0.11	0.0050	0.10	0.0027
2 3	0.16 -3.3	0.29 0.62	0.11	0.0059	-0.19	-0.0027
4	-0.044	-0.28	0.12	-0.62	-0.24	
5	-0.23	0.17	-0.55	1.3	1.1	0.042
6	0.72	0.88	0.67	0.33	0.54	****
7						
8	-0.97	-0.43	-1.3	-0.16	-1.5	-3.4
9	-0.043	0.059	-0.079	-0.22	0.11	-0.44
10	0.20	0.32	0.11	0.49		
11	0.16	0.31	0.12	-0.18	-0.067	
12	0.13	-0.28	0.34	0.024	0.14	0.82
13	-0.60	-0.89	-0.49	-0.20	-0.034	0.44
14	0.36	0.11	0.50	0.066		
15 16	-0.24	-0.32	-0.18	-0.54	-0.62	-0.38
17	0.27	1.2	-0.18	0.72	0.48	-0.36
18	0.60	0.21	0.78	0.61	1.7	
19	-0.54	-0.0078	-0.78	-0.77	1.7	
20	-0.072	-0.13	-0.013	-0.45	-0.55	-0.19
21						
22						
23	0.79	3.5	-0.49	0.19		
24						
25						
26	0.060	0.057	0.088	-0.26	-5.0	
27						
28	-2.2	-2.0	-2.3	-2.4		
29	0.23	0.64	0.061	-0.077	0.07	0.50
30	0.50	0.50	0.46	1.1	0.37	0.52
31 32	-0.012 -0.47	-0.050 0.20	-0.019 -0.79	0.31 -0.65	0.48	
33	-0.47	0.20	-0.79	-0.03	0.46	
34	0.78	1.0	0.75	-0.11	0.035	0.14
35	-2.0	-0.53	-3.0	0.18	-0.25	0.14
36	-0.65	-0.33	-0.76	-1.2	0.20	
37						
38	-0.55	-0.32	-0.61	-1.2	-0.77	-0.98
39	0.36	0.25	0.46	-0.13	1.8	
40	0.74	-0.033	1.2	0.25	1.1	
41	0.00	0.40	0.70		4.0	
42	-0.39	-0.13	-0.60	0.66	-1.0	
43	0.42	0.26	0.79	0.65		0.60
44 45	0.42 0.41	-0.36 0.36	0.78 0.48	0.65 -0.24		-0.60
46	1.7	0.59	2.2	0.77	0.85	0.62
47	-1.7	-1.9	-1.7	-1.4	0.03	0.02
48	-0.020	-0.22	0.075	0.0091	-0.73	
49						
50	0.20	0.47	0.047	0.40	0.80	
51						
52	-0.34	0.0011	-0.57	0.37	0.034	
53	0.17	0.042	0.26	-0.17	1.6	
54 55	5.4	1.9	7.5	0.48	4.5	
55 56	0.028	2.8	7.5 -1.4	0.48 0.95	4.5 -0.16	0.13
50 57	3.8	-0.72	-1.4 6.4	-0.42	-0.16 -1.5	0.13
58	-0.25	-0.72	-0.25	-0.42	0.10	0.37
59	-0.022	0.16	-0.17	0.65	0.86	1.7
60	-0.86	-0.39	-1.1	-0.53	-0.19	-1.2
61	-0.060	0.43	-0.37	0.81	0.91	0.52
62	0.35	-0.011	0.51	0.48		
63	-1.0					
64	-0.28	-0.44	-0.18	-0.49	-0.97	-0.42
65	0.31	0.47	0.25	0.021		1.2
66	0.15	0.07	0.10	0.15		
67 68	-0.15 0.71	-0.87	0.18	0.17	1.0	
68 69	0.71 -1.9	1.1	0.53 -0.49	0.66 0.14	1.2 0.56	
70	0.59	0.11	0.87	-0.069	-0.060	0.058
70	0.39	1.1	-0.37	-0.16	0.41	0.038
72	-0.60	-0.86	-0.45	-0.91	-0.59	-1.1
73						
	-	=	-	•	-	•

### Laboratories Z-scores: Halibut Filet (continued)

LABCODE:	Sum TE totalt	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	<b>Sum Indicator PCB</b>	Sum u/209
74	-0.0053	0.32	-0.17	0.056	0.13	
75						
76	-1.6	-0.24	-2.4	-0.73	-1.1	-0.036
77	-0.14	0.64	-0.52	-0.059	0.60	0.095
78						
79	0.41	0.61	0.32	0.22	0.029	
80	-0.83	-0.97	-0.86	0.33	-0.23	
81	0.043	-0.13	0.10	0.40	0.75	0.089
82						
83						
84	-0.19	-0.62	0.027	-0.28	0.11	-0.096
85	-0.22	-0.58	-0.040	-0.29		-0.82
86						
87						
88	0.51	0.34	0.60	0.36	0.51	
89	0.07	-0.14	0.15	0.42	0.48	
90	-1.5	-3.4	-0.63	-0.93	-0.41	-0.22
91	1.0	0.14	1.5	1.1		
92	-0.63	-0.67	-0.60	-0.66		
93	0.39	0.40	0.46	-0.53	-0.86	
94	-0.75	0.65	-1.4	-0.85	0.39	-0.48
95	-0.14	-0.081	-0.16	-0.20	-0.12	0.0042
96	0.43	0.69	0.27	0.87	1.1	1.0
97	1.0	1.3	0.92	0.72	0.55	
98						
99	0.32	0.60	0.14	0.88	1.0	-0.22
100	3.7	13	-0.54	-0.51	-0.50	0.46
101	8.4	0.20	13	0.59	-5.0	
102	0.32					
0						
0						
0						
0 107	-1.1	0.45	-1.6	-4.0	-4.5	0.55
107	2.2	3.7	-1.6 1.6	0.35	-4.5 -0.64	0.55
0	2.2	3.7	1.0	0.55	-U.0 <del>4</del>	
110	0.37	0.17	0.48	0.11	0.45	0.98
110	0.57	0.17	0.40	0.11	0.75	0.70

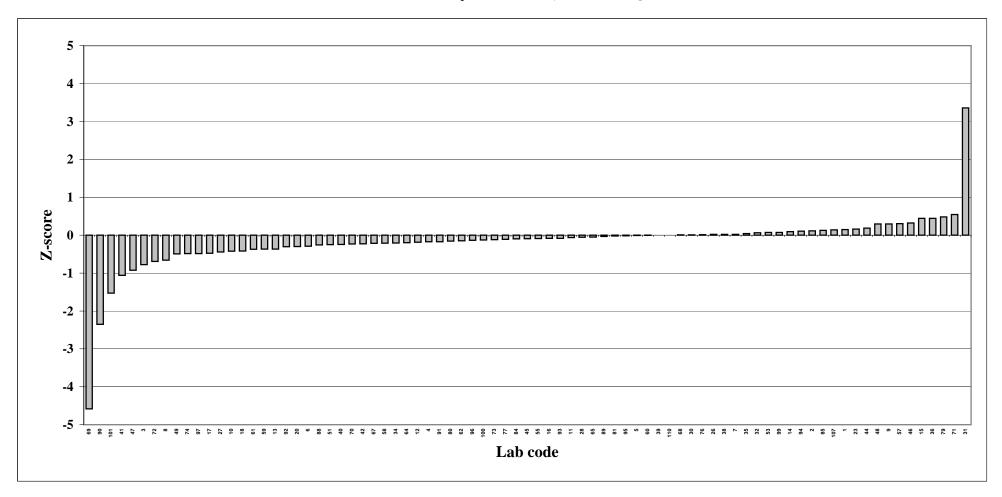
#### Laboratories Z-scores: Cod Liver Oil

LABCODE:				Sum TE mono-orto PCB	Sum Indicator PCB	Sum u/209
1	0.035	1.8	-0.34	0.51		
2	0.22	0.23	0.44	-2.3	-0.21	-0.15
3						
4	-0.31	-0.54	-0.20	-1.1	-0.81	
5	-0.63	-0.12	-0.85	0.77	0.86	-0.36
6	0.10	0.79	-0.024	0.037	0.43	
7	-0.14	-1.4	0.17	-0.81		
8	-3.9	-2.2	-4.5	-0.13	-0.025	0.59
9	-0.0086	-0.037	0.0037	-0.086	-0.15	-0.69
10	0.62	0.19	0.67	0.97		
11	0.083	0.85	-0.048	-0.15	0.26	
12	0.11	-0.25	0.19	0.061	0.15	1.1
13	-0.051	0.23	-0.17	0.66	-0.41	1.4
14	0.12	-0.082	0.23	-0.71	-0.41	1.4
	0.12	-0.062	0.23	-0.71		
15	0.12	0.10	0.071	0.40	0.20	0.10
16	-0.12	-0.19	-0.071	-0.48	-0.28	0.12
17	-0.44	-0.071	-0.55	0.045	-0.29	
18	0.30	0.026	0.36	0.23	0.55	
19						
20	0.52	0.83	0.52	-0.25	-0.22	-0.0012
21						
22						
23	-0.74	0.64	-1.0	-0.32		
24						
25						
26	-0.29	-0.18	-0.29	-0.47	-5.0	
27	-0.36	1.4	-0.27	0.68	0.87	
28	-1.4	-0.90	-1.5	-1.61	0.07	
29	0.35	1.9	0.069	0.17		
30	0.33	-0.21	0.069	0.17	-0.24	0.032
31	-0.083	-0.19	-0.054	-0.17	-0.24	0.032
					0.56	
32	-1.3	0.066	-1.7	-0.55	0.56	
33	0.54	0.20	0.54	0.22	0.021	0.005
34	0.54	0.38	0.64	-0.22	-0.021	0.095
35	-1.7	-0.25	-3.1	10	0.12	
36	0.039	1.1	-0.12	-0.54		
37	-1.9	-0.11	-2.4	-0.008	-0.95	-2.1
38	0.27	1.0	0.18	-0.42	0.22	-0.069
39	0.15	0.23	0.20	-0.61	-0.43	
40	1.2	0.24	1.5	0.069	-0.23	
41	0.19	-0.046	0.27	-0.16	2.0	
42	0.41	-0.18	0.27	3.4	2.4	
43						
44	0.43	-0.80	0.68	0.30		0.19
45	0.34	0.63	0.37	-0.66		
46	0.17	0.61	0.044	0.58	0.46	-0.81
47	-1.8	-2.0	-1.8	-1.5	****	
48	0.49	-1.40	0.86	0.45	-0.52	
49	-0.90	-0.41	-0.98	-1.0	-1.1	
50	0.030	0.11	-0.0026	0.21	0.50	
51	-0.53	0.40	-0.79	0.24	-0.22	0.97
52	-0.33	-0.90	-0.19	-0.35	-0.22	0.77
53	-0.31	-0.11	-0.19	-0.53 -0.53	1.1	
	-0.30	-0.11	-0.32	-0.55	1.1	
54 55	1.2	2.0	1.1	0.42	2.1	
55	1.3	2.6	1.1	0.42	3.1	0.1-
56 	0.74	13	-1.8	1.1	0.014	0.45
57	14	-1.5	18	-0.41	-1.2	-0.54
58	-0.57	-0.29	-0.60	-0.80	-0.21	-0.16
59	-0.20	0.19	-0.34	0.50	0.58	0.80
60	-0.17	0.48	-0.36	0.53	0.65	-0.79
61						
62						
63	3.4					
64	0.12	-0.11	0.2	-0.59	-0.64	-0.53
65	-2.2	-2.1	-2.24	-2.381		-2.13
66				· <del></del>		
67	0.77	-0.023	0.94	0.709		
68	-0.19	0.94	-0.45	0.27	0.60	
69	-0.19	0.74	-0.43	0.47	1.25	
70		0.83	0.44	0.49		0.21
70	0.50	0.83	0.44	0.49	0.396	0.31
	0.60	0.66	0.7	0.19	0.10	0.12
72	0.68	0.66	0.7		-0.10	-0.12
73	0.012	2.1	-0.36	-0.33		

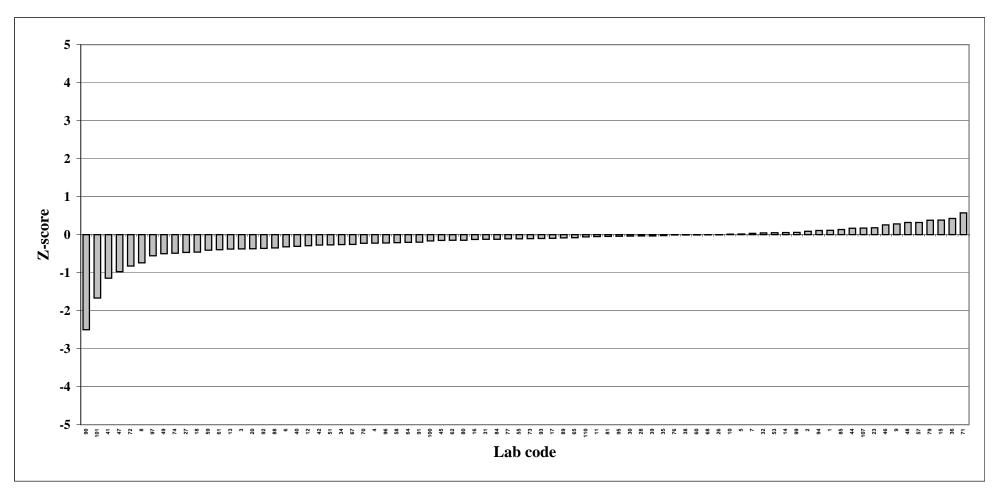
### Laboratories Z-scores: Cod Liver Oil (continued)

LABCODE:	Sum TE totalt	Sum TE PCDD/PCDF	Sum TE non-ortho PCB	Sum TE mono-orto PCB	<b>Sum Indicator PCB</b>	Sum u/209
74						
75						
76	-1.52	0.47	-2.0	0.00	0.97	0.033
77	0.073	0.94	-0.10	0.12	1.0	-0.24
78						
79	0.73	2.7	0.39	0.16	-0.060	
80	-0.67	-1.1	-0.70	0.52	-0.076	
81	0.087	0.61	-0.018	0.12	0.49	-0.28
82						
83						
84	0.072	-0.42	0.17	0.026	0.094	0.10
85	0.42	0.10	0.51	0.071		-0.32
86						
87						
88	0.64	0.69	0.67	0.22	0.25	
89	0.38	1.7	0.13	0.40	0.48	
90	-1.1	-1.4	-1.0	-1.2	-0.58	-0.029
91	0.16	-0.32	0.25	0.15	-0.56	
92	0.77	0.98	0.74	0.59		
93	0.32	0.27	0.36	-0.069	-0.72	
94	-1.2	1.3	-1.7	-0.15	0.35	-0.82
95	0.044	0.10	0.043	-0.067	0.20	0.11
96	0.16	0.56	0.075	0.29	-1.3	0.64
97	0.69	1.2	0.63	0.31	0.26	
98						
99						
100	-0.65		0.22	-0.99	-0.35	0.38
101						
102	0.19					
0						
0						
0						
0						
107	1.2	0.018	1.5	-0.20	0.83	0.51
108	0.42	3.7	-0.19	0.10	-0.58	
0					-1.3	2.9
110	0.36	0.26	0.42	-0.21	0.14	0.18

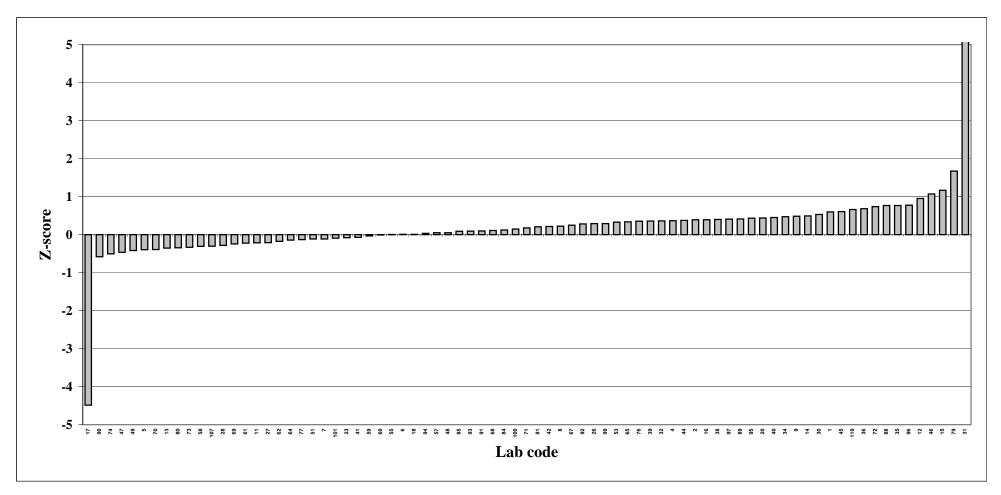
## **Z-score analyte solution; total TEQ**



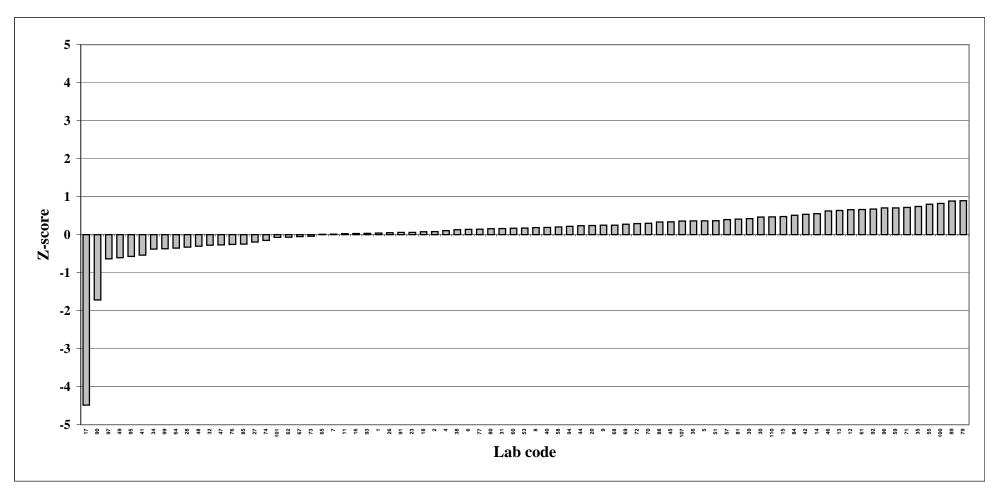
### **Z-score analyte solution; PCDD/PCDF TEQ**



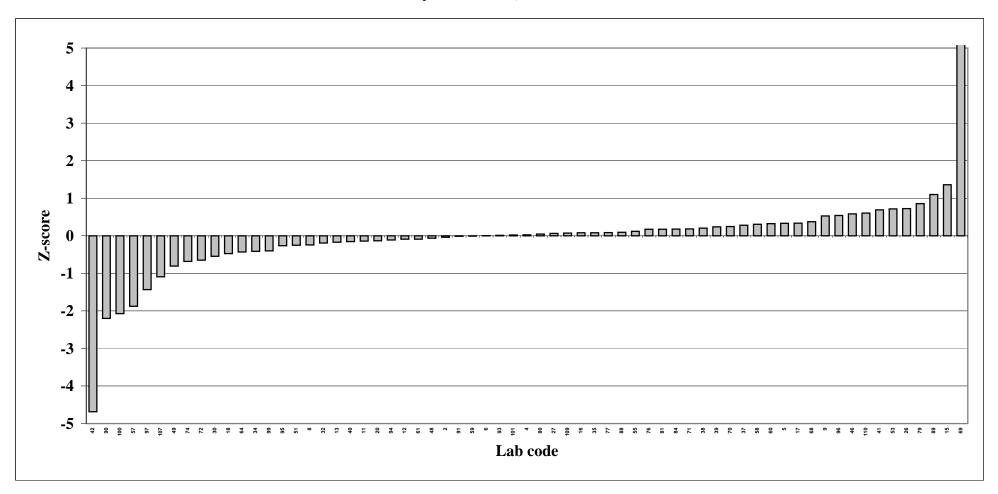
#### **Z-score analyte solution; non-ortho PCB TEQ**



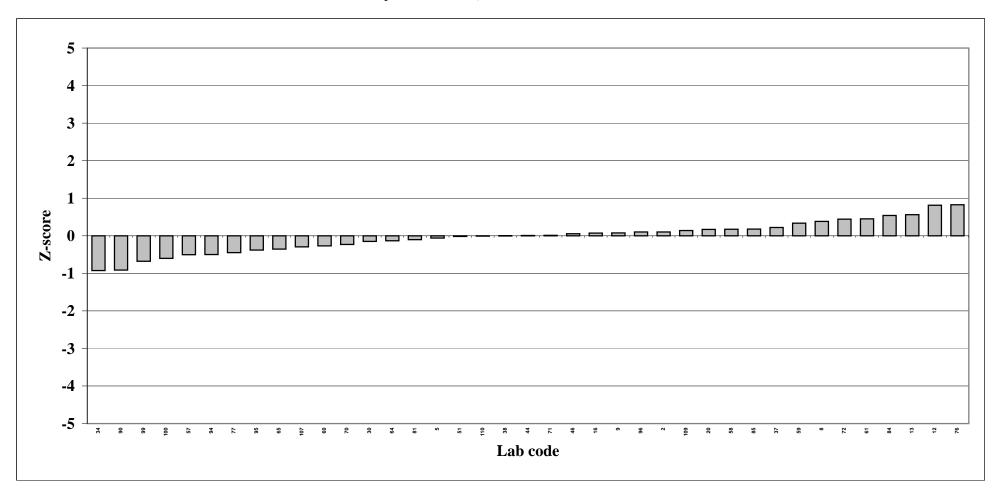
#### **Z-score analyte solution; mono-ortho PCB TEQ**



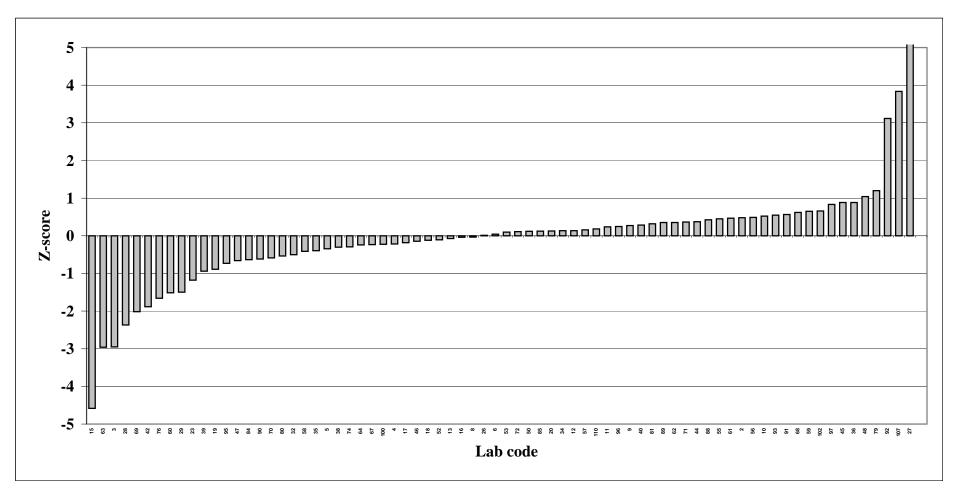
## **Z**-score analyte solution; sum indicator PCB



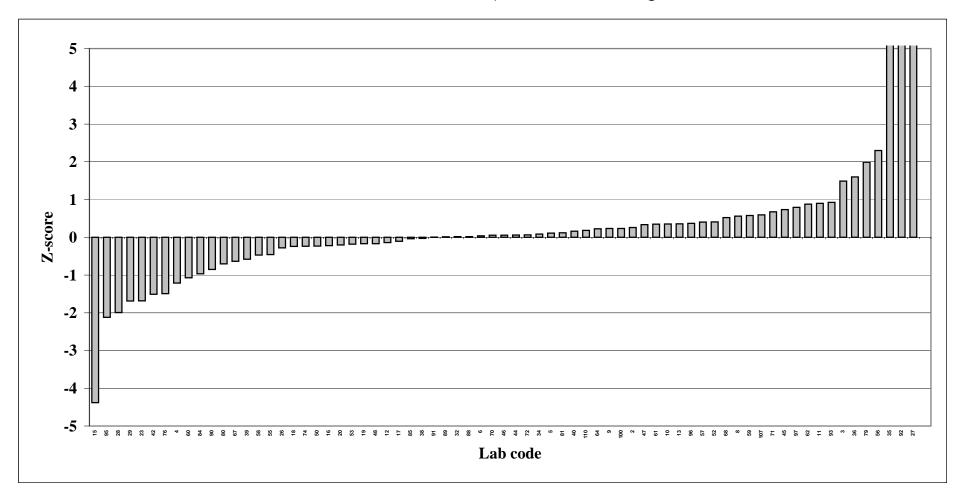
### **Z-score analyte solution; sum PBDE without BDE-209**



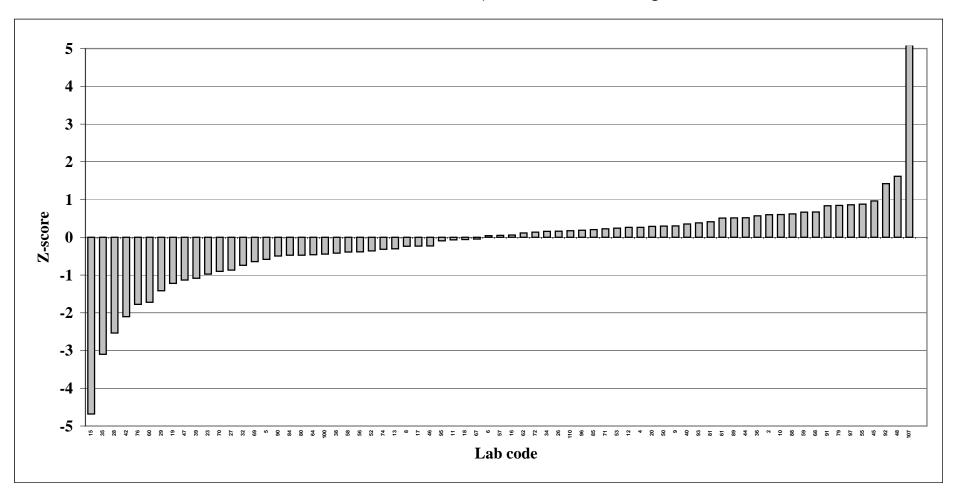
#### **Z-score Reindeer meat; total TEQ**



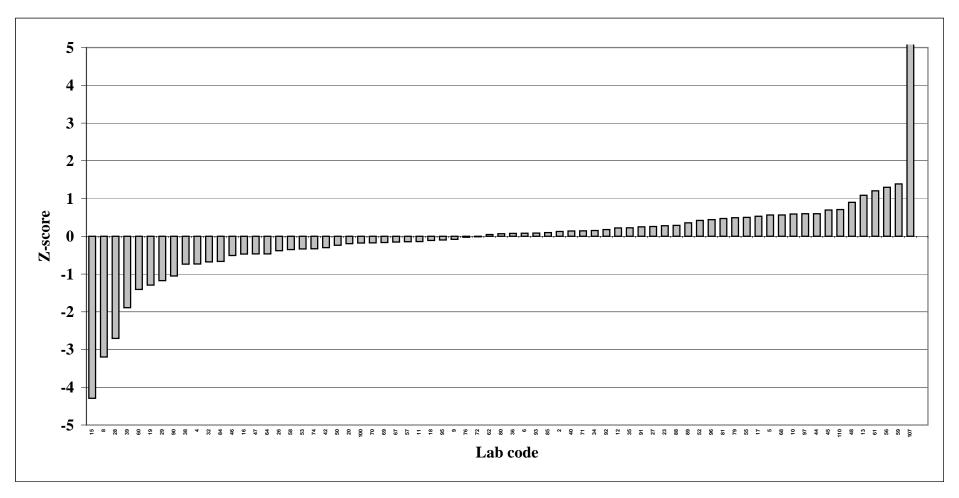
### **Z-score Reindeer meat; PCDD/PCDF TEQ**



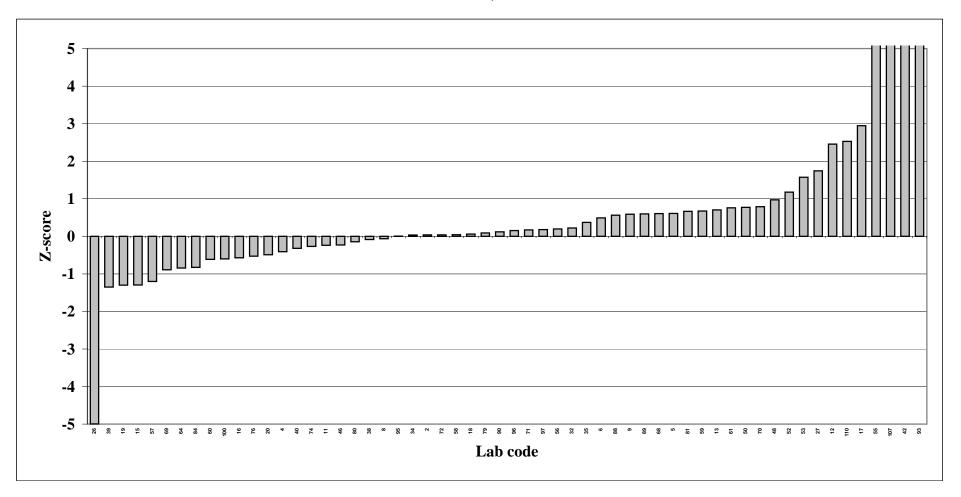
### **Z-score Reindeer meat; non-ortho PCB TEQ**



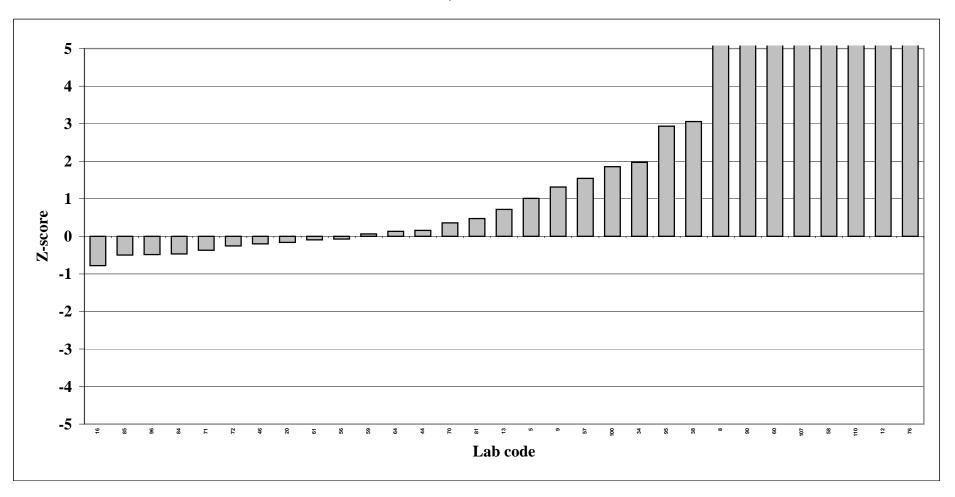
#### **Z-score Reindeer meat; mono-ortho PCB TEQ**



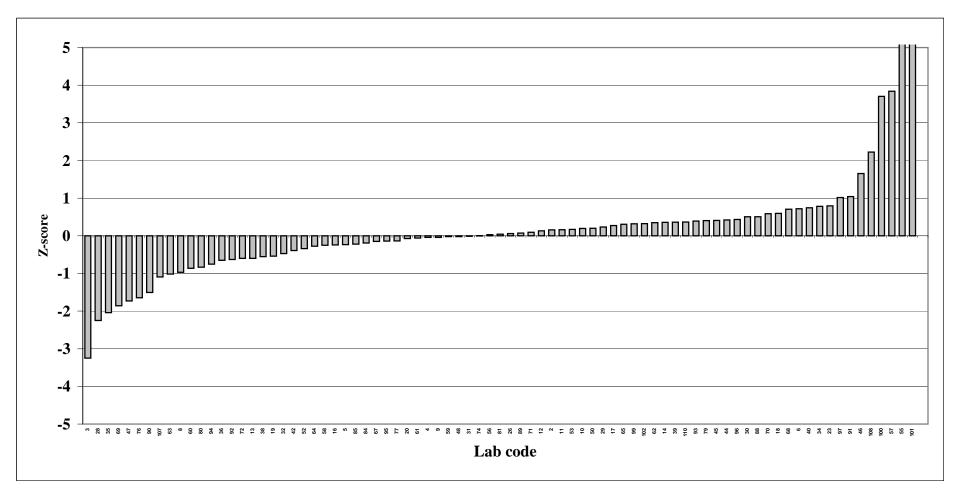
#### **Z-score Reindeer meat; sum indicator PCB**



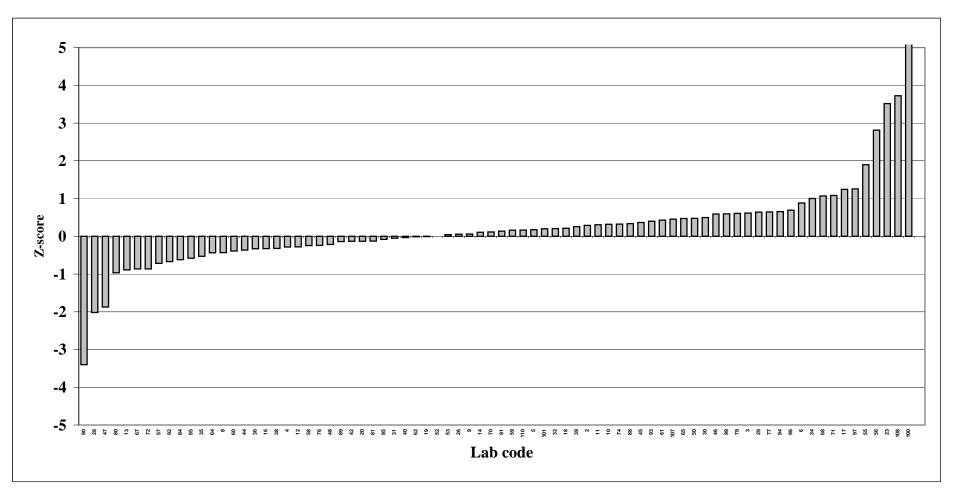
### **Z-score Reindeer meat; sum PBDE without BDE-209**



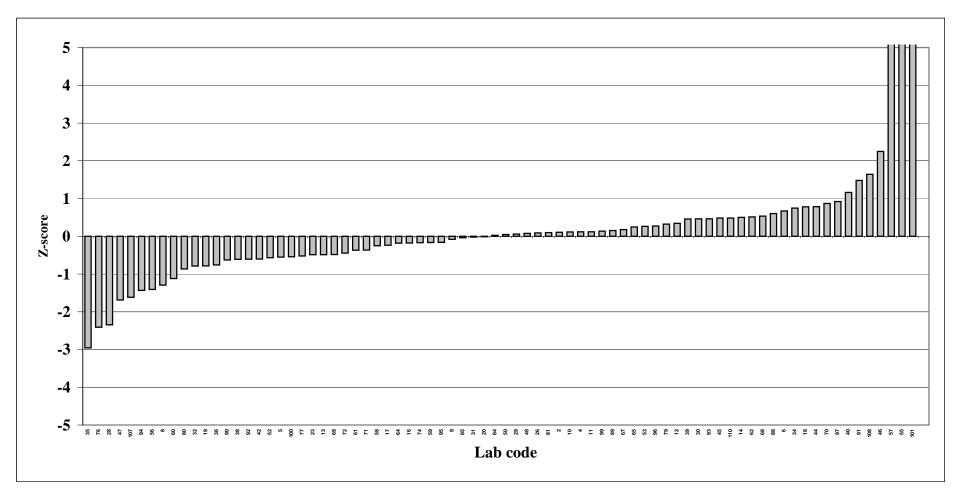
### **Z-score Halibut filet; total TEQ**



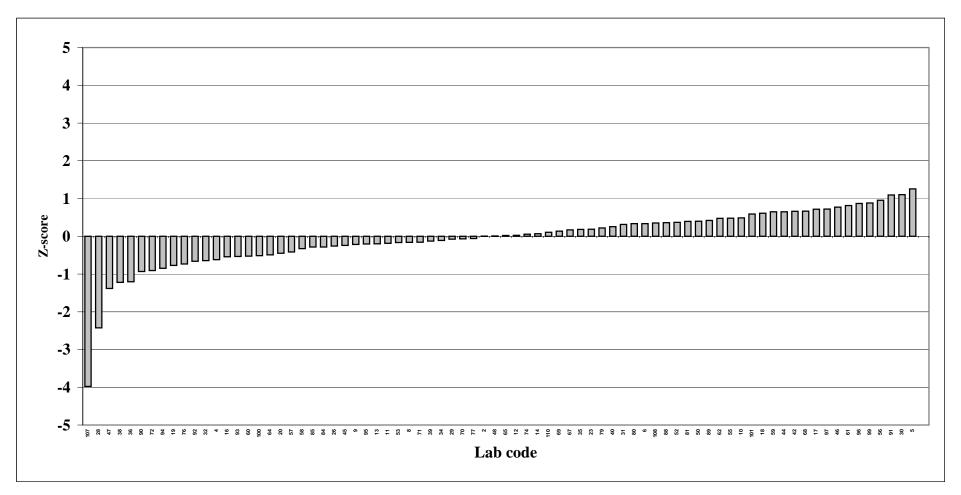
### **Z-score Halibut filet; PCDD/PCDF TEQ**



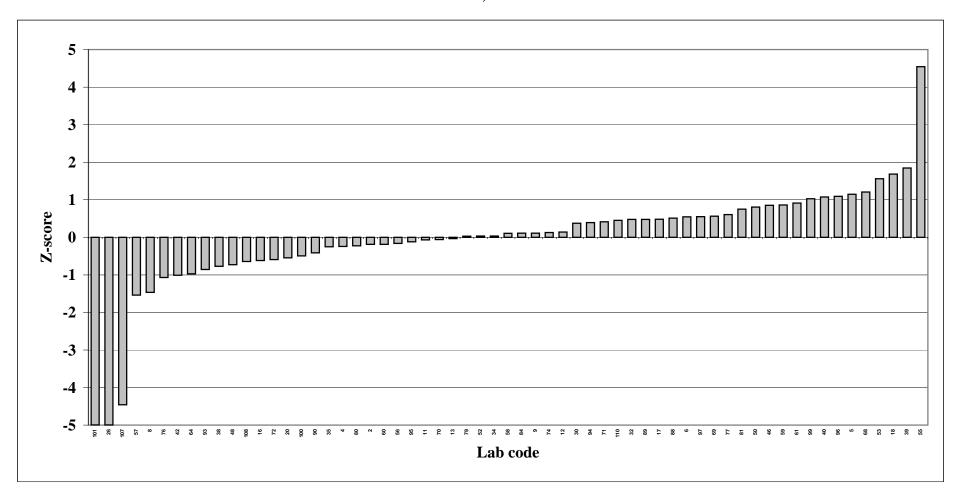
### **Z-score Halibut filet; non-ortho PCB TEQ**



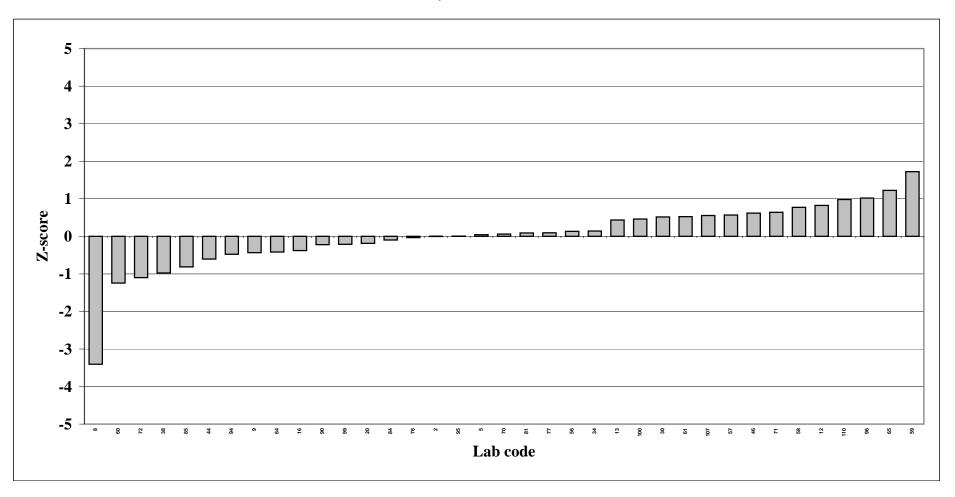
#### **Z-score Halibut filet; mono-ortho PCB TEQ**



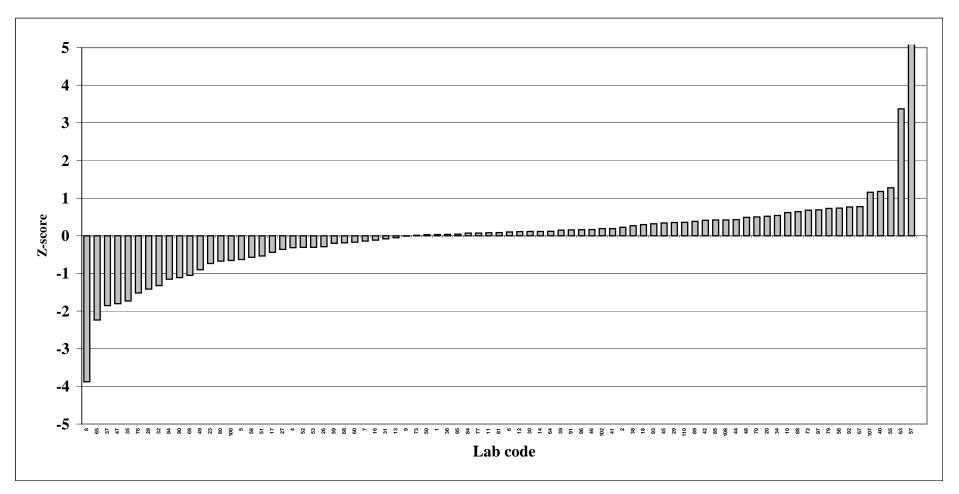
#### **Z-score** Halibut filet; sum indicator PCB



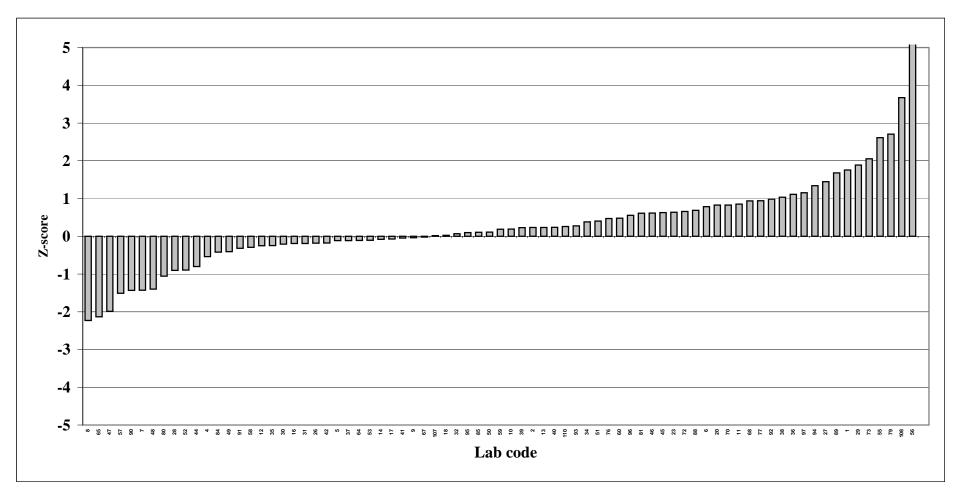
### **Z-score Halibut filet; sum PBDE without BDE-209**



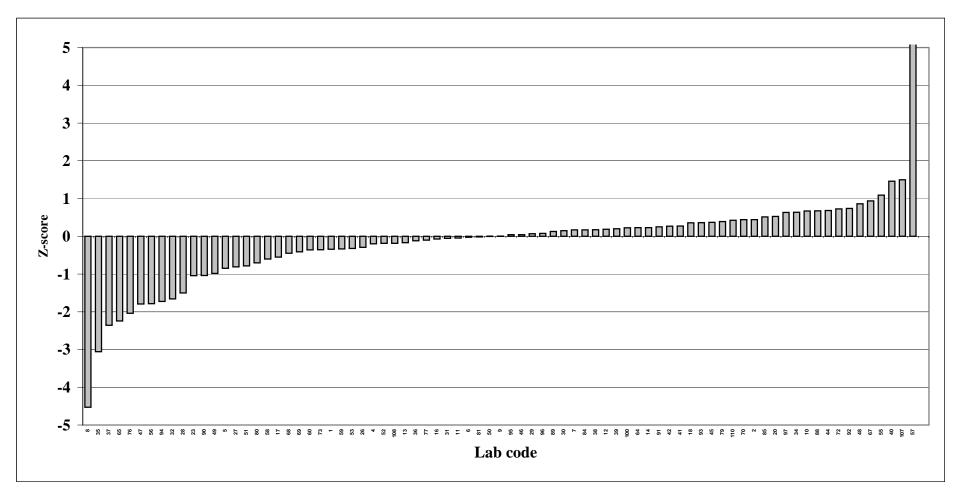
### **Z-score Cod liver oil; total TEQ**



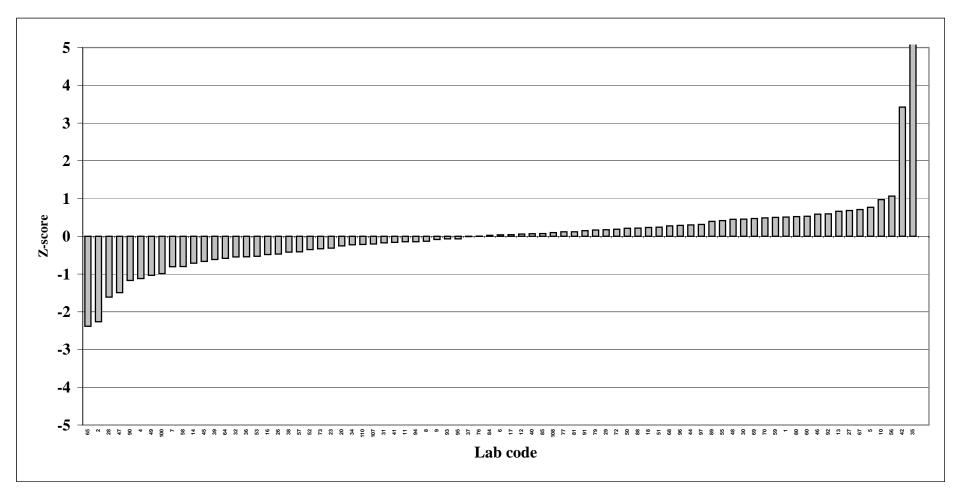
### **Z-score Cod liver oil; PCDD/PCDF TEQ**



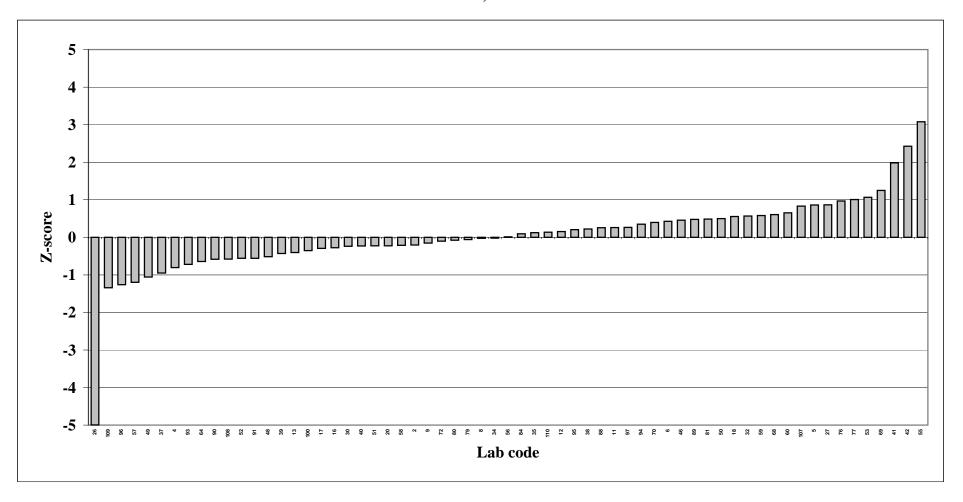
### **Z-score Cod liver oil; non-ortho PCB TEQ**



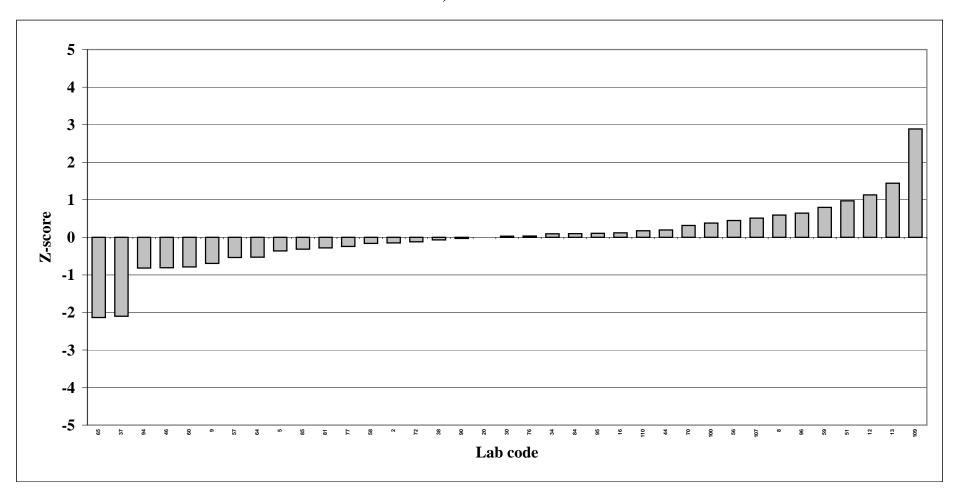
### **Z-score Cod liver oil; mono-ortho PCB TEQ**



### **Z-score Cod liver oil; sum indicator PCB**



### **Z-score Cod liver oil; sum PBDE without BDE-209**



## Appendix D:

WHO TEFs for human risk assessment

WHO TEFs for human risk assessment based on the conclusions of the World Health
Organisation Meeting in Stockholm, Sweden, 15-18 June 1997 and International Programme on Chemical Safety expert meeting in Geneva, June 2005
(M. van den Berg et al., Environ Health Perspect 1998;106:775-792; M. van den Berg et al., Toxicological sciences 93(2), 223-241 (2006))

Congener	TEF values	TEF values	Congener	TEF values	TEF values
	(1998)	(2006)		(1998)	(2006)
"Dioxins"			"Dioxin-like" PCBs		
Polychlorinated dibenzo-p-dioxins (PCDDs)			Non-ortho PCBs		
2,3,7,8-TCDD	1	1	PCB 77	0.0001	0.0001
1,2,3,7,8-PeCDD	1	1	PCB 81	0.0001	0.0003
1,2,3,4,7,8-HxCDD	0.1	0.1	PCB 126	0.1	0.1
1,2,3,6,7,8-HxCDD	0.1	0.1	PCB 169	0.01	0.03
1,2,3,7,8,9-HxCDD	0.1	0.1			
1,2,3,4,6,7,8-HpCDD	0.01	0.01			
OCDD	0.0001	0.0003			
Polychlorinated dibenzofurans (PCDFs)			Mono-ortho PCBs		
2,3,7,8-TCDF	0.1	0.1	PCB 105	0.0001	0.00003
1,2,3,7,8-PeCDF	0.05	0.03	PCB 114	0.0005	0.00003
2,3,4,7,8-PeCDF	0.5	0.3	PCB 118	0.0001	0.00003
1,2,3,4,7,8-HxCDF	0.1	0.1	PCB 123	0.0001	0.00003
1,2,3,6,7,8-HxCDF	0.1	0.1	PCB 156	0.0005	0.00003
1,2,3,7,8,9-HxCDF	0.1	0.1	PCB 157	0.0005	0.00003
2,3,4,6,7,8-HxCDF	0.1	0.1	PCB 167	0.00001	0.00003
1,2,3,4,6,7,8-HpCDF	0.01	0.01	PCB 189	0.0001	0.00003
1,2,3,4,7,8,9-HpCDF	0.01	0.01			
OCDF	0.0001	0.0003			

Abbreviations used: "T" = tetra; "Pe" = penta; "Hx" = hexa; "Hp" = hepta; "O" = octa; "CDD" = chlorodibenzo-p-dioxin; "CDF" = chlorodibenzofuran; "CB" = chlorobiphenyl.

# Appendix E:

Homogeneity testing

## Homogeneity testing of test materials for "Interlaboratory Comparison on Dioxins in Food" organised by the Norwegian Institute of Public Health

#### Introduction

The International Harmonized Protocol for the Proficiency Testing of Analytical Chemistry Laboratories (Pure Appl Chem 2006;78:145-96) states that "The bulk material prepared for the proficiency test must be sufficient homogeneous and stable, in respect of each analyte, to ensure that all laboratories receive distribution units that do not differ to any consequential degree in mean analyte concentration. The scheme provider must clearly state the procedure used to establish the homogeneity of the test material".

The protocol requires that the variation in composition among the distributed units is negligible in relation to variation introduced by the measurements conducted by the participants of the proficiency test (PT). The estimated variation between the samples ( $s_{sam}$ ) should be less than 30% of the target standard deviation ( $\sigma_p$ ), i.e.,  $s_{sam} < 0.3 \sigma_p$ .

Further the protocol states that homogeneity testing is required to reassure the participants in proficiency testing schemes that the distributed units of the test material are sufficiently similar. The test specified calls for the selection of ten or more units at random after the putative homogenized material has been split and packaged into discrete samples for distribution. The material from each sample is then analyzed in duplicate, under randomized repeatability conditions (that is, all in one run) using a method with sufficient analytical precision. The value of  $\sigma_{sam}$  is then estimated from the mean squares after one-way analysis of variance (ANOVA).

Much depends on the quality of the analytical results of the homogeneity testing. If the analytical precision  $(\sigma_{an})$  of the homogeneity test is not small, important sampling variation may be obscured by analytical variation. We may get a non-significant result when testing for heterogeneity, not because it is not present, but the test has no power to detect it. It is recommended that the analytical (repeatability) precision of the method used in the homogeneity test should satisfy  $\sigma_{an} < 0.5 \ \sigma_p$ 

#### Consequences for the Interlaboratory Comparison on Dioxins in Food

Below follows the consequences for the Interlaboratory Comparison on Dioxin in Food;

1.

The protocol recommends duplicate analysis of at least 10 distribution units. Due to limited amount of test material in each distribution unit and the requirement for sufficiently low analytical standard deviation, the test analysis has to be restricted to PCB, e.g., 6 indicator PCB or CB-153. It is, however, questionable whether analysis of indicator PCB also reflects the distribution of dioxins and other contaminants in the sample, as the test material is often prepared by mixing specifically contaminated material with background contaminated material in order to achieve a sufficient contamination level. Therefore, the distribution of PCBs in the sample might not be relevant for the distribution of dioxins in the sample. The analytical precision of the method used in the homogeneity test should be less than half of the target standard deviation, i.e.,  $\sigma_{an} < 0.5 \sigma_{p}$ . For determination of dioxins, the target standard deviation may be approximated by the requirement for trueness (Commission Regulation (EC) No 1883/2006) of  $\pm$  20% for total TEQ, i.e., the analytical precision should be less than 10%. This is unrealistic to achieve for the determination of dioxins.

#### 2.

The homogeneity testing using, e.g., the determination of indicator PCBs, requires the analysis of at least 60 samples prior to shipment of the distribution units to the participants. This causes problems for the time schedule of the sample preparation and involves high costs.

#### **3.**

The laboratory conducting the homogeneity test on PT analytes would have access to the test material and knowledge of contamination levels prior to the start of the PT and would therefore not be qualified for participation in the PT.

#### **Conclusion**

A valid testing of homogeneity of the test materials of the Interlaboratory Comparison (ILC) on Dioxins in Food with respect to the distribution of dioxins and dioxin-like PCBs is not guaranteed using indicator PCBs. It is doubtful that the analytical precision is small enough to detect a lack in sufficient homogeneity. Given the need for annually testing three different matrices for homogeneity, alternative, rapid and low cost homogeneity tests using surrogate should be applied.

#### Present approach for homogeneity testing for the ILC on Dioxins in Food

The Harmonized Protocol states under Chapter Testing for sufficient homogeneity: "Tests for sufficient homogeneity are in practice never wholly satisfactory... However, given that sufficient homogeneity is a reasonable prior assumption (because proficiency testing scheme providers do their best to ensure it), and that the cost [and time-consumption] of testing for it is often high, it is sensible to make the main emphasis the avoidance of "Type 1 errors" (that is, false rejection of a satisfactory material).

Having this in mind and the facts that it is impossible to determine all analytes for homogeneity testing of food test material and that a single indicator analyte not necessarily reflects the distribution of the other analytes, we have developed an approach that ensures that the test material is thoroughly blended and evenly distributed among the individual test bottles. The homogeneity testing of solid samples is based on the principle of measuring electrolytic conductivity after addition of sodium chloride to a small portion of the coarsely blended test material. A demonstration of homogeneous distribution of the added salt in the sub samples would indicate our ability to evenly blend the food matrix, i.e., with this approach we ensure the efficiency of our blending procedure. This is especially of importance when blending highly contaminated food matrices with background contaminated food matrices.

When testing homogeneity of the food samples, sodium chloride was added to about 10% of the test material in such an amount that the conductivity was about doubled compared to the natural conductivity. This sub-sample was added to the total sample. For example, to 1 kg of homogenised chicken meat, 150 g NaCl were added resulting in an addition of 1% NaCl to the final test material of 15 kg. Conductivity measurements are performed as follows: boiling water is added to 10.0g of the test material, and the resulting dispersion is ultrasonicated. After centrifugation, the extract is filtered through folded paper filters and allowed to cool to room temperature. The electrolytic conductivity of the water extract is measured using a conductivity meter.

Homogeneity of the test material was demonstrated by comparing the conductivity in water extracts of 10 samples from the same bottle (variation within bottles), and in extracts from 10 different bottles (variation between bottles).

#### **Example**

As an example, the relative standard deviation (RSD) of 10 conductivity measurements within a sample bottle containing chicken meat homogenate was 2%. The RSD for the measurement of samples from 10 different, randomly selected bottles was 3%. The contribution of the inhomogeneity to the total variation, calculated from  ${\rm RSD}^2_{\rm inhomogeneity} = {\rm RSD}^2_{\rm between} - {\rm RSD}^2_{\rm within}^1$  was 2.2% and hence small and acceptable. The total uncertainty for the determination of PCDD/Fs is usually considerably larger, so the measured contribution of inhomogeneity to the total uncertainty can be neglected

<sup>&</sup>lt;sup>1</sup>G. Becher, L.S. Haug, C. Thomsen, World-wide comparison on the quality of analytical determinations of PCDDs/PCDFs and dioxin-like PCBs in food, Talanta 63 (2004) 1115-1122.

### Appendix 1:

Presentation of results for analyte solution

#### **Appendix 1: Presentation of results: Analyte solution**

Statistic calculations for PCDDs, PCDFs, dioxin-like PCBs, indicator PCBs, PBDEs and α-HBCD

The analyte solution contained

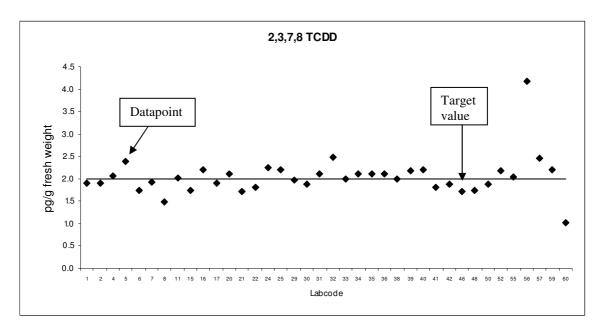
- PCDDs/PCDFs at concentrations of 2:5:10 pg/µl for tetra:penta-hexa-hepta:octa chlorinated dibenzodioxins/furans respectively.
- Non-ortho PCBs at concentration of 10 pg/μl.
- Mono-ortho PCBs and indicator PCBs at concentration of 100 pg/μl.
- PBDE at a concentration of 25 pg/µl, except BDE-209 at 100 pg/µl.
- α-HBCD at a concentration of 500 pg/μl.

These concentrations are called the congeners' target value.

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

- 1. The median was calculated from all the reported data.
- 2. Values outside a range of 50 % to 150 % of this median, were defined as outliers and removed from the data set.
- 3. Median, mean and standard deviation were re-calculated from the remaining data. This median and mean were called consensus median and mean.

The diagram shows the target value and the reported data. Values outside a range of 50 % to 150 % of "median of all values", were defined as outliers and are not shown in the plot.



#### **Z-Scores of individual congeners**

Z-scores of each congener were calculated for each laboratory according to the following equation:

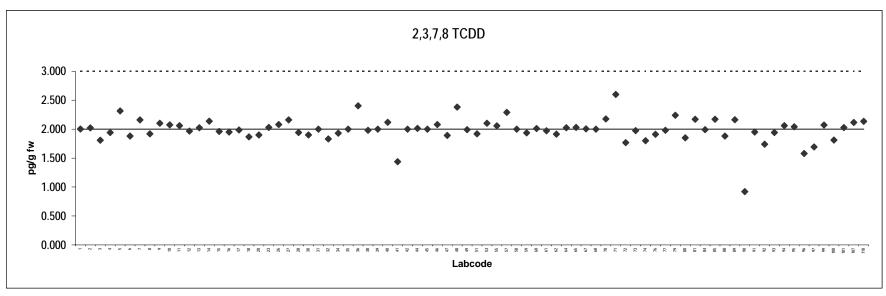
$$z = (x - X)/\sigma$$

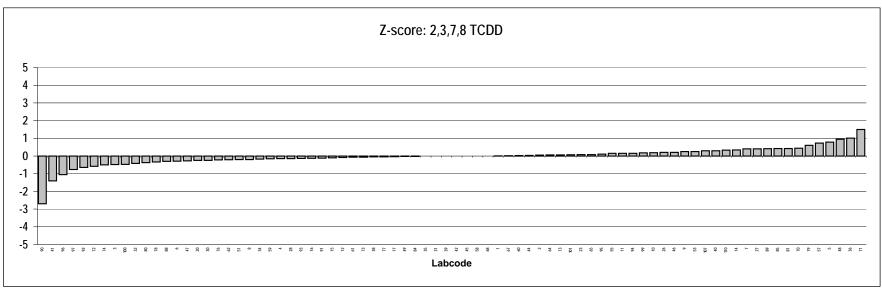
Where x = reported value; X = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm$  20% from the consensus value.

### Analyte solution Congener: 2,3,7,8 TCDD

Tabaada	Como mala for	NI <sub>0</sub> 4 <sub>00</sub>	Tab aada	Cama mala for	Notes
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.0		59	1.9	
2 3	2.0		60	2.0	
3	1.8		61	2.0	
4	1.9		62	1.9	
5	2.3		64	2.0	
6	1.9		65	2.0	
7	2.2		67	2.0	
8	1.9		68	2.0	
9	2.1		70	2.2	
10	2.1		71	2.6	
11	2.1		72	1.8	
12	2.0		73	2.0	
13	2.0		74	1.8	
14	2.1		76	1.9	
15	2.0		77	2.0	
16	1.9		79	2.2	
17	2.0		80	1.9	
18	1.9		81	2.2	
20	1.9		84	2.0	
23	2.0		85	2.2	
26	2.1		88	1.9	
27	2.2		89	2.2	
28	1.9		90	0.92	Outlier
30	1.9		91	2.0	
31	2.0		92	1.7	
32	1.8		93	1.9	
34	1.9		94	2.1	
35	2.0		95	2.0	
36	2.4		96	1.6	
38	2.0		97	1.7	
39	2.0		99	2.1	
40	2.1		100	1.8	
41	1.4		101	2.0	
42	2.0		107	2.1	
44	2.0		110	2.1	
45	2.0				
46	2.1				
47	1.9				
48	2.4				
49	2.0				
51	1.9				
53	2.1				
55	2.1				
57	2.3				
58	2.0				

Consensus median, pg/g	2.0
Median all values pg/g	2.0
Consensus mean, pg/g	2.0
Standard deviation, pg/g	0.17
Relative standard deviation, %	8.4
No. of values reported	80
No. of values removed	1
No. of reported non-detects	0

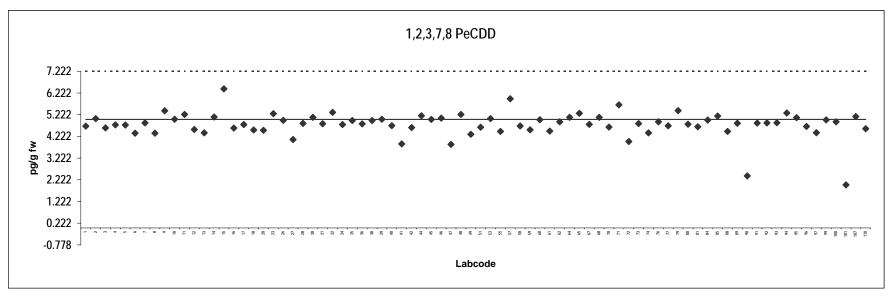


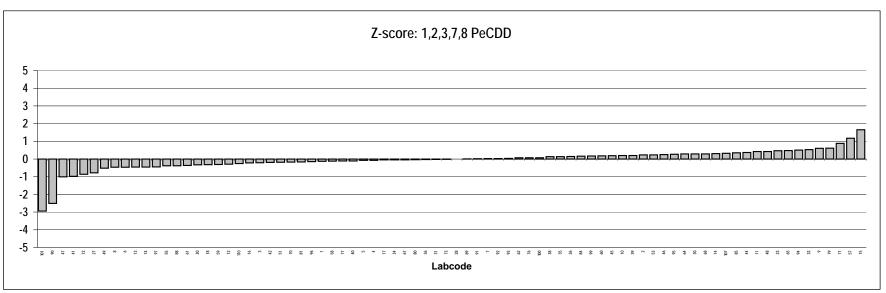


# Analyte solution Congener: 1,2,3,7,8 PeCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4.7		59	4.5	
2	5.0		60	5.0	
3	4.6		61	4.5	
4	4.8		62	4.9	
5	4.7		64	5.1	
6	4.4		65	5.3	
7	4.8		67	4.8	
8	4.4		68	5.1	
9	5.4		70	4.6	
10	5.0		71	5.7	
11	5.2		72	4.0	
12	4.5		73	4.8	
13	4.4		74	4.4	
14	5.1		76	4.9	
15	6.4		77	4.7	
16	4.6		79	5.4	
17	4.8		80	4.8	
18	4.5		81	4.7	
20	4.5		84	5.0	
23	5.3		85	5.2	
26	5.0		88	4.5	
27	4.1		89	4.8	
28	4.8		90	2.4	Outlier
30	5.1		91	4.8	
31	4.8		92	4.8	
32	5.3		93	4.8	
34	4.8		94	5.3	
35	5.0		95	5.1	
36	4.8		96	4.7	
38	5.0		97	4.4	
39	5.0		99	5.0	
40	4.7		100	4.9	
41	3.9		101	2.0	Outlier
42	4.6		107	5.1	
44	5.2		110	4.6	
45	5.0				
46	5.1				
47	3.9				
48	5.2				
49	4.3				
51	4.6				
53	5.0				
55	4.4				
57	6.0				
58	4.7				

4.8
4.8
4.8
0.41
8.5
80
2
0

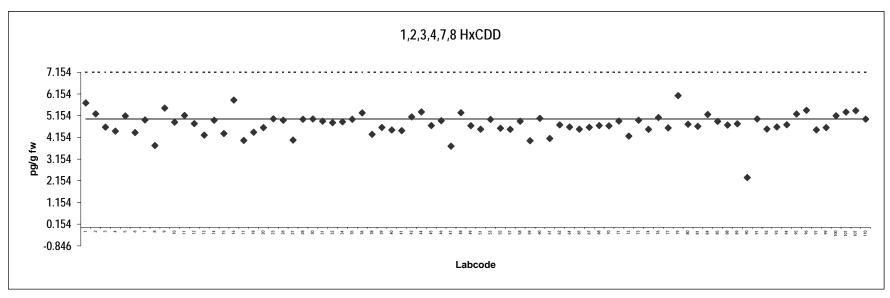


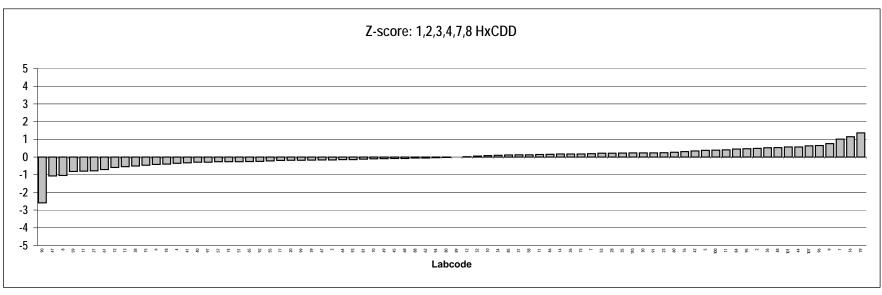


### **Analyte solution** Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.7	110165	59	4.0	110163
2	5.2		60	5.0	
2 3	4.6		61	4.1	
4	4.4		62	4.7	
5	5.1		64	4.6	
6	4.4		65	4.5	
7	5.0		67	4.6	
8	3.8		68	4.7	
9	5.5		70	4.7	
10	4.9		71	4.9	
11	5.2		72	4.2	
12	4.8		73	4.9	
13	4.3		74	4.5	
14	4.9		76	5.1	
15	4.3		77	4.6	
16	5.9		79	6.1	
17	4.0		80	4.8	
18	4.4		81	4.7	
20	4.6		84	5.2	
23	5.0		85	4.9	
26	4.9		88	4.7	
27	4.0		89	4.8	
28	5.0		90	2.3	Outlier
30	5.0		91	5.0	
31	4.9		92	4.5	
32	4.8		93	4.6	
34	4.9		94	4.7	
35	5.0		95	5.2	
36	5.3		96	5.4	
38	4.3		97	4.5	
39	4.6		99	4.6	
40	4.5		100	5.2	
41	4.5		101	5.3	
42	5.1		107	5.4	
44	5.3		110	5.0	
45	4.7				
46	4.9				
47	3.8				
48	5.3				
49	4.7				
51	4.5				
53	5.0				
55	4.6				
57	4.5				
58	4.9				

Consensus median, pg/g	4.8
Median all values pg/g	4.8
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.43
Relative standard deviation, %	9.0
No. of values reported	80
No. of values removed	1
No. of reported non-detects	0

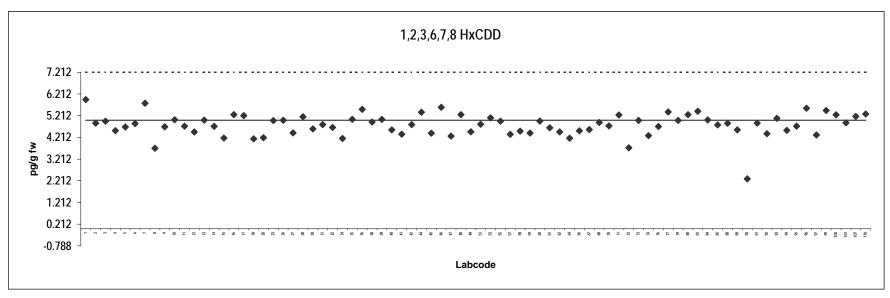


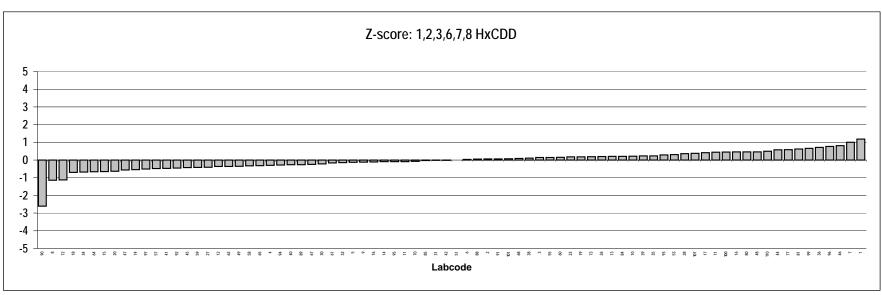


### **Analyte solution** Congener: 1,2,3,6,7,8 HxCDD

					ongener:
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	6.0		59	4.4	
2	4.9		60	5.0	
3	5.0		61	4.7	
4	4.5		62	4.5	
5	4.7		64	4.2	
6	4.8		65	4.5	
7	5.8		67	4.6	
8	3.7		68	4.9	
9	4.7		70	4.7	
10	5.0		71	5.2	
11	4.7		72	3.7	
12	4.5		73	5.0	
13	5.0		74	4.3	
14	4.7		76	4.7	
15	4.2		77	5.4	
16	5.3		79	5.0	
17	5.2		80	5.3	
18	4.1		81	5.4	
20	4.2		84	5.0	
23	5.0		85	4.8	
26	5.0		88	4.9	
27	4.4		89	4.6	
28	5.2		90	2.3	Outlier
30	4.6		91	4.9	
31	4.8		92	4.4	
32	4.7		93	5.1	
34	4.2		94	4.5	
35	5.0		95	4.7	
36	5.5		96	5.6	
38	4.9		97	4.3	
39	5.0		99	5.5	
40	4.6		100	5.3	
41	4.4		101	4.9	
42	4.8		107	5.2	
44	5.4		110	5.3	
45	4.4				
46	5.6				
47	4.3				
48	5.3				
49	4.5				
51	4.8				
53	5.1				
55	5.0				
57	4.4				
58	4.5				

Consensus median, pg/g	4.8
Median all values pg/g	4.8
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.44
Relative standard deviation, %	9.1
No. of values reported	80
No. of values removed	1
No. of reported non-detects	0

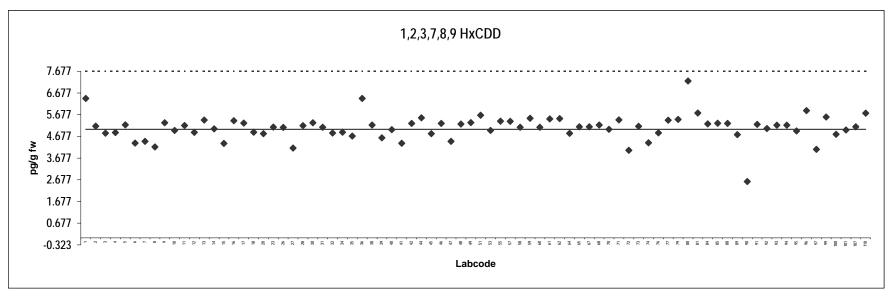


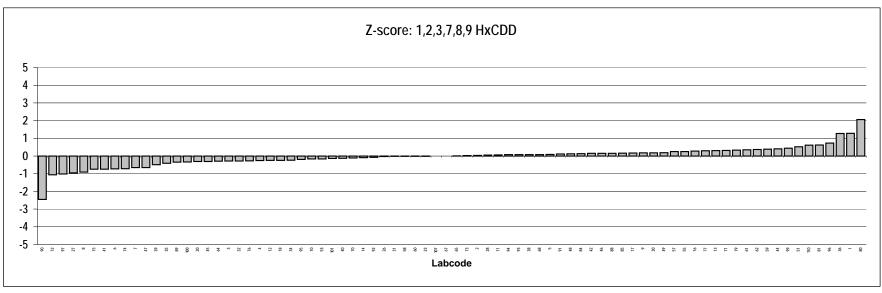


### **Analyte solution** Congener: 1,2,3,7,8,9 HxCDD

				•	ongener:
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	6.4		59	5.5	
2 3	5.2		60	5.1	
3	4.8		61	5.5	
4	4.9		62	5.5	
5 6	5.2		64	4.8	
6	4.4		65	5.1	
7	4.5		67	5.1	
8	4.2		68	5.2	
9	5.3		70	5.0	
10	4.9		71	5.4	
11	5.2		72	4.0	
12	4.9		73	5.1	
13	5.4		74	4.4	
14	5.0		76	4.8	
15	4.4		77	5.4	
16	5.4		79	5.5	
17	5.3		80	7.2	
18	4.9		81	5.8	
20	4.8		84	5.3	
23	5.1		85	5.3	
26	5.1		88	5.3	
27	4.1		89	4.8	
28	5.2		90	2.6	
30	5.3		91	5.2	
31	5.1		92	5.0	
32	4.8		93	5.2	
34	4.9		94	5.2	
35	4.7		95	4.9	
36	6.4		96	5.9	
38	5.2		97	4.1	
39	4.6		99	5.6	
40	5.0		100	4.8	
41	4.4		101	5.0	
42	5.3		107	5.1	
44	5.5		110	5.7	
45	4.8				
46	5.3				
47	4.5				
48	5.2				
49	5.3				
51	5.7				
53	5.0				
55	5.4				
57	5.4				
58	5.1				

Consensus median, pg/g	5.1
Median all values pg/g	5.1
Consensus mean, pg/g	5.1
Standard deviation, pg/g	0.58
Relative standard deviation, %	11
No. of values reported	80
No. of values removed	0
No. of reported non-detects	0



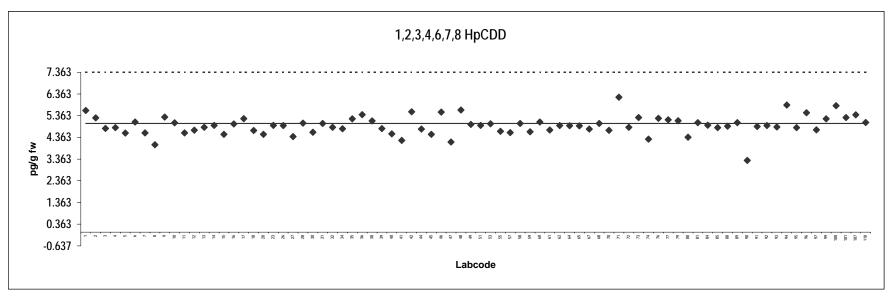


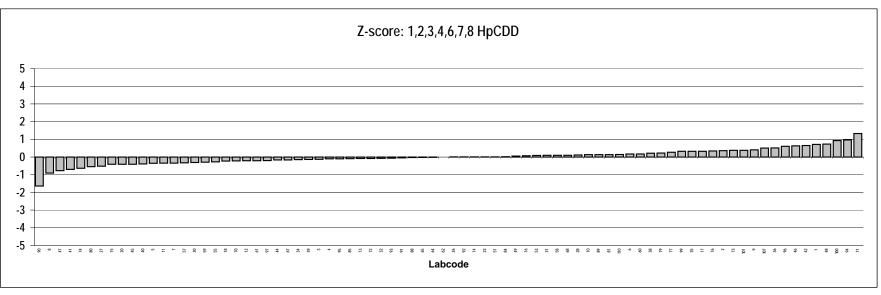
Analyte solution Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
		Notes			Notes
1	5.6		59	4.6	
2 3	5.3		60	5.1	
3	4.8		61	4.7	
4	4.8		62	4.9	
5	4.6		64	4.9	
6	5.1		65	4.9	
7	4.6		67	4.7	
8	4.0		68	5.0	
9	5.3		70	4.7	
10	5.0		71	6.2	
11	4.6		72	4.8	
12	4.7		73	5.3	
13	4.8		74	4.3	
14	4.9		76	5.2	
15	4.5		77	5.2	
16	5.0		79	5.1	
17	5.2		80	4.4	
18	4.7		81	5.0	
20	4.5		84	4.9	
23	4.9		85	4.8	
26	4.9		88	4.9	
27	4.4		89	5.0	
28	5.0		90	3.3	
30	4.6		91	4.9	
31	5.0		92	4.9	
32	4.8		93	4.8	
34	4.8		94	5.9	
35	5.2		95	4.8	
36	5.4		96	5.5	
38	5.1		97	4.7	
39	4.8		99	5.2	
40	4.5		100	5.8	
41	4.2		101	5.3	
42	5.5		107	5.4	
44	4.7		110	5.0	
45	4.5				
46	5.5				
47	4.2				
48	5.6				
49	5.0				
51	4.9				
53	5.0				
55	4.6				
57	4.6				
58	5.0				

#### Consensus median, pg/g Median all values pg/g Consensus mean, pg/g 4.9 4.9 4.9

Standard deviation, pg/g	0.43
Relative standard deviation, %	8.7
No. of values reported	80
No. of values removed	0
No. of reported non-detects	0



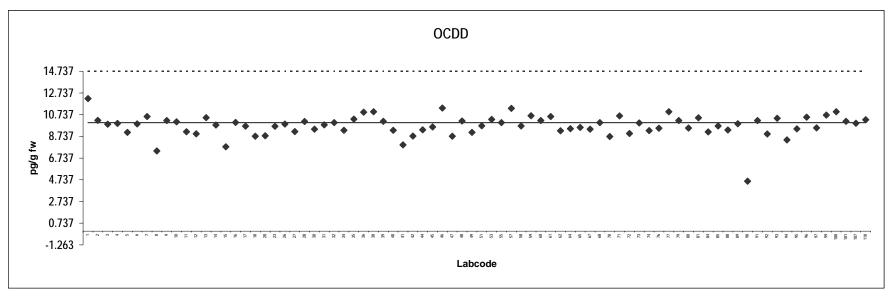


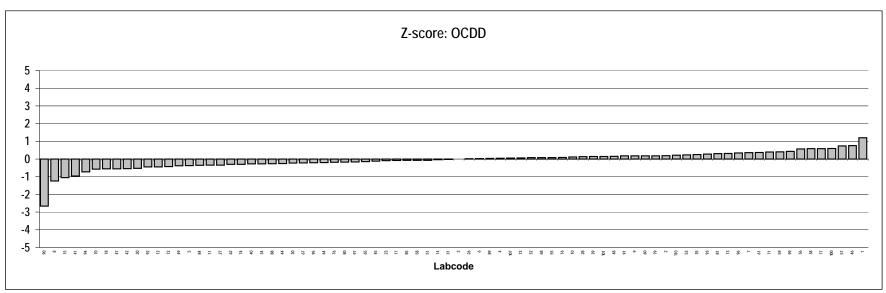
# Analyte solution Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	12		59	11	
2	10		60	10	
3	9.8		61	11	
4	9.9		62	9.2	
5	9.1		64	9.4	
6	9.9		65	9.6	
7	11		67	9.4	
8	7.4		68	10	
9	10		70	8.7	
10	10		71	11	
11	9.2		72	9.0	
12	9.0		73	10.0	
13	10		74	9.3	
14	9.8		76	9.5	
15	7.8		77	11	
16	10		79	10	
17	9.7		80	9.5	
18	8.8		81	10	
20	8.8		84	9.1	
23	9.7		85	9.7	
26	9.9		88	9.3	
27	9.2		89	9.9	
28	10		90	4.6	Outlier
30	9.4		91	10	
31	9.8		92	9.0	
32	10		93	10	
34	9.3		94	8.4	
35	10		95	9.4	
36	11		96	11	
38	11		97	9.5	
39	10		99	11	
40	9.3		100	11	
41	8.0		101	10	
42	8.8		107	10.0	
44	9.3		110	10	
45	9.6				
46	11				
47	8.8				
48	10				
49	9.1				
51	9.7				
53	10				
55	10				
57	11				
58	9.7				

Consenus	statistics	

9.8 9.8
9.8
7.0
9.8
0.81
8.3
80
1
0

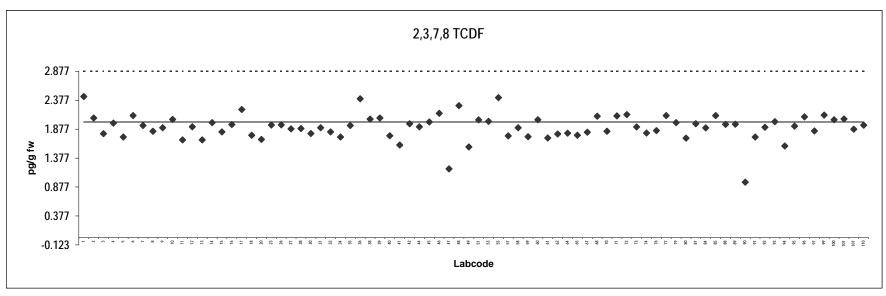


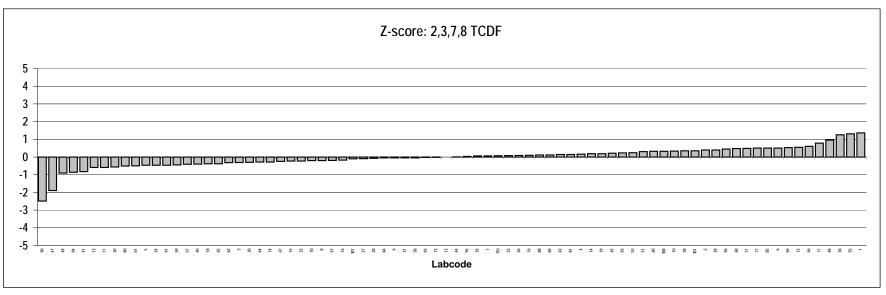


### **Analyte solution** Congener: 2,3,7,8 TCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	2.4		59	1.7	
2 3	2.1		60	2.0	
3	1.8		61	1.7	
4	2.0		62	1.8	
5	1.7		64	1.8	
6	2.1		65	1.8	
7	1.9		67	1.8	
8	1.8		68	2.1	
9	1.9		70	1.8	
10	2.0		71	2.1	
11	1.7		72	2.1	
12	1.9		73	1.9	
13	1.7		74	1.8	
14	2.0		76	1.9	
15	1.8		77	2.1	
16	2.0		79	2.0	
17	2.2		80	1.7	
18	1.8		81	2.0	
20	1.7		84	1.9	
23	1.9		85	2.1	
26	2.0		88	2.0	
27	1.9		89	2.0	
28	1.9		90	0.96	
30	1.8		91	1.7	
31	1.9		92	1.9	
32	1.8		93	2.0	
34	1.7		94	1.6	
35	1.9		95	1.9	
36	2.4		96	2.1	
38	2.1		97	1.8	
39	2.1		99	2.1	
40	1.8		100	2.0	
41	1.6		101	2.1	
42	2.0		107	1.9	
44	1.9		110	1.9	
45	2.0				
46	2.2				
47	1.2				
48	2.3				
49	1.6				
51	2.0				
53	2.0				
55	2.4				
57	1.8				
58	1.9				

Consensus median, pg/g	1.9
Median all values pg/g	1.9
Consensus mean, pg/g	1.9
Standard deviation, pg/g	0.22
Relative standard deviation, %	12
No. of values reported	80
No. of values removed	0
No. of reported non-detects	0

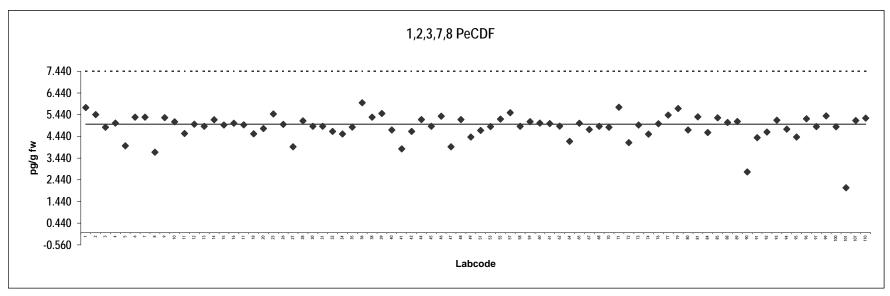


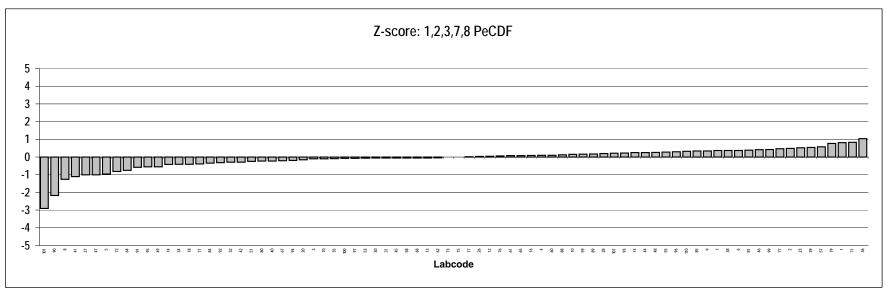


# Analyte solution Congener: 1,2,3,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.8		59	5.1	
2	5.4		60	5.1	
3	4.9		61	5.0	
4	5.1		62	4.9	
5	4.0		64	4.2	
6	5.3		65	5.0	
7	5.3		67	4.8	
8	3.7		68	4.9	
9	5.3		70	4.9	
10	5.1		71	5.8	
11	4.6		72	4.1	
12	5.0		73	5.0	
13	4.9		74	4.5	
14	5.2		76	5.0	
15	5.0		77	5.4	
16	5.0		79	5.7	
17	5.0		80	4.7	
18	4.6		81	5.3	
20	4.8		84	4.6	
23	5.5		85	5.3	
26	5.0		88	5.1	
27	4.0		89	5.1	
28	5.2		90	2.8	
30	4.9		91	4.4	
31	4.9		92	4.6	
32	4.7		93	5.2	
34	4.6		94	4.8	
35	4.9		95	4.4	
36	6.0		96	5.3	
38	5.3		97	4.9	
39	5.5		99	5.4	
40	4.7		100	4.9	
41	3.9		101	2.1	Outlier
42	4.7		107	5.2	Outilei
44	5.2		110	5.3	
45	4.9		110	3.3	
46	5.4				
47	4.0				
48	5.2				
49	4.4				
51	4.4				
53	4.7				
55	5.2				
55 57	5.2 5.5				
	3.5 4.9				
58	4.9				

Consensus median, pg/g 5.0	Consenus statistics	
Consensus mean, pg/g  4.9	Median all values pg/g	5.0
Standard deviation, pg/g  Relative standard deviation, %  10	Standard deviation, pg/g	0.50
No. of values reported 80 No. of values removed 1 No. of reported non-detects 0	No. of values removed	80 1 0



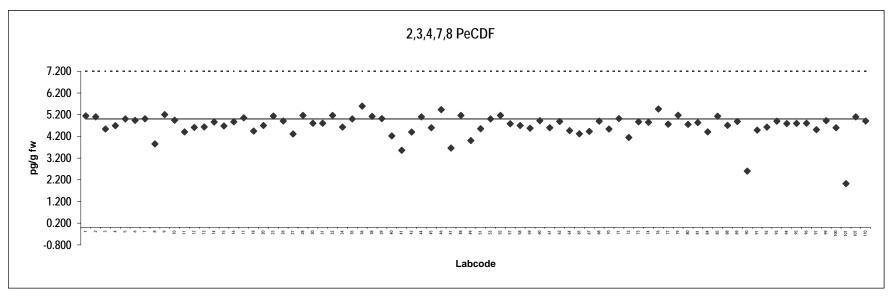


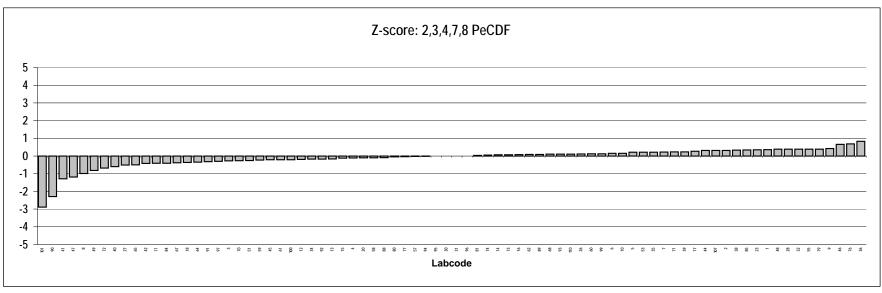
### **Analyte solution** Congener: 2,3,4,7,8 PeCDF

					Congener
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.1		59	4.6	
2 3	5.1		60	4.9	
3	4.5		61	4.6	
4	4.7		62	4.9	
5	5.0		64	4.5	
6	4.9		65	4.3	
7	5.0		67	4.4	
8	3.9		68	4.9	
9	5.2		70	4.5	
10	4.9		71	5.0	
11	4.4		72	4.1	
12	4.6		73	4.9	
13	4.6		74	4.9	
14	4.9		76	5.5	
15	4.7		77	4.8	
16	4.9		79	5.2	
17	5.1		80	4.8	
18	4.4		81	4.8	
20	4.7		84	4.4	
23	5.1		85	5.1	
26	4.9		88	4.7	
27	4.3		89	4.9	
28	5.2		90	2.6	
30	4.8		91	4.5	
31	4.8		92	4.6	
32	5.2		93	4.9	
34	4.6		94	4.8	
35	5.0		95	4.8	
36	5.6		96	4.8	
38	5.1		97	4.5	
39	5.0		99	4.9	
40	4.2		100	4.6	
41	3.6		101	2.0	Outlier
42	4.4		107	5.1	
44	5.1		110	4.9	
45	4.6				
46	5.4				
47	3.7				
48	5.2				
49	4.0				
51	4.6				
53	5.0				
55	5.2				
57	4.8				
58	4.7				
58	4./				

#### Consenus statistics Consensus median, pg/g 4.8

Median all values pg/g	4.8
Consensus mean, pg/g	4.7
Standard deviation, pg/g	0.44
Relative standard deviation, %	9.3
No. of values reported	80
No. of values removed	1
No. of reported non-detects	0

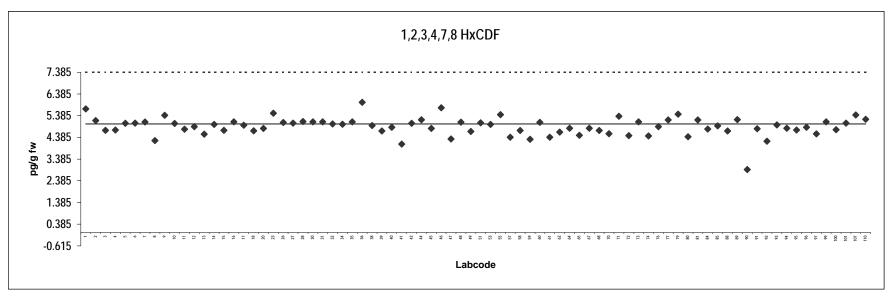


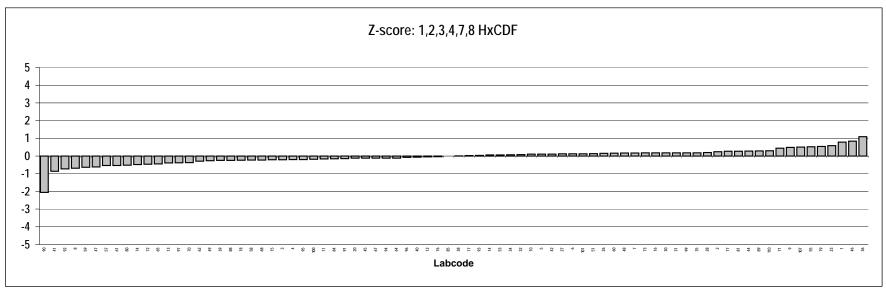


# Analyte solution Congener: 1,2,3,4,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.7	110165	59	4.3	Hotes
2	5.2		60	5.1	
2 3	4.7		61	4.4	
4	4.7		62	4.6	
5	5.0		64	4.8	
6	5.0		65	4.6	
7	5.1		67	4.8	
8	4.2		68	4.8	
9	5.4		70	4.7	
10	5.0		70	5.4	
11	4.8		72	4.5	
12	4.8		73	5.1	
13	4.5		74	4.5	
14	5.0		74 76	4.9	
15	4.7		70 77	5.2	
16	5.1		79	5.5	
17	4.9		80	3.3 4.4	
18	4.9		81	5.2	
20	4.7		84	4.8	
23	5.5		85	4.8 4.9	
26	5.1		88	4.7	
27	5.0		89	5.2	
28	5.1		90	2.9	
30	5.1		91	4.8	
31	5.1		92	4.2	
32	5.0		93	5.0	
34	5.0		94	4.8	
35	5.1		95	4.7	
36	6.0		95 96	4.7	
38	4.9		90 97	4.5	
39	4.7		99	5.1	
40	4.9		100	4.7	
41	4.1		101	5.0	
42	5.0		107	5.4	
44	5.2		110	5.2	
45	4.8		110	3.2	
46	5.8				
47	4.3				
48	5.1				
49	4.7				
51	5.1				
53	5.0				
55	5.4				
57	4.4				
58	4.7				
50	4./				

Consenus statistics						
Consensus median, pg/g	4.9					
Median all values pg/g	4.9					
Consensus mean, pg/g	4.9					
Standard deviation, pg/g	0.42					
Relative standard deviation, %	8.6					
No. of values reported	80					
No. of values removed	0					
No. of reported non-detects	0					

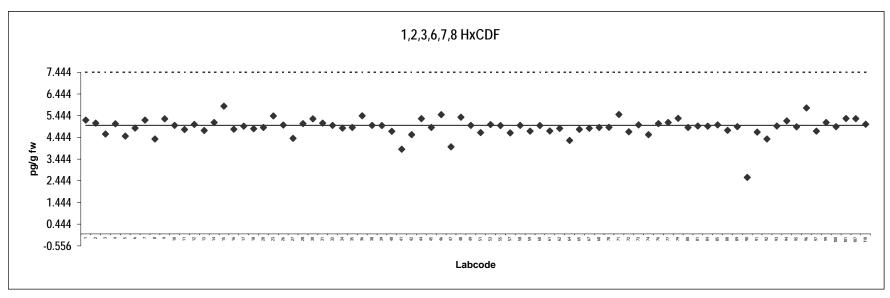


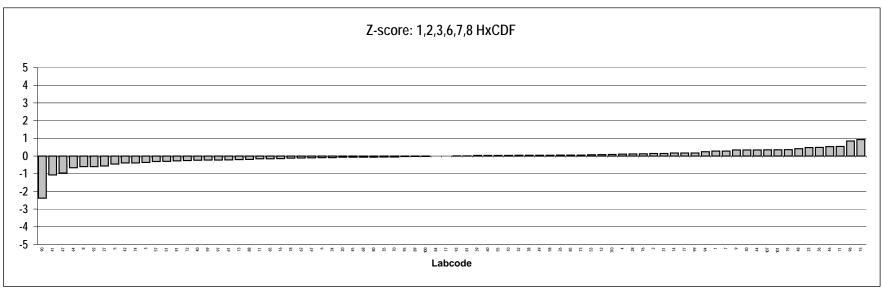


### **Analyte solution** Congener: 1,2,3,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.2	110165	59	4.7	110163
	5.1		60	5.0	
2 3	4.6		61	4.7	
1	5.1		62	4.9	
4 5	4.5		64	4.3	
6	4.9		65	4.8	
7	5.2		67	4.9	
8	4.4		68	4.9	
9	5.3		70	4.9	
10	5.0		71	5.5	
11	4.8		72	4.7	
12	5.0		73	5.0	
13	4.8		74	4.6	
13	5.1		74 76	5.1	
	5.9		70 77	5.1	
15					
16	4.8		79 80	5.3	
17	5.0			4.9	
18	4.8		81	5.0	
20	4.9		84	5.0	
23	5.4		85	5.0	
26	5.0		88	4.8	
27	4.4		89	4.9	
28	5.1		90	2.6	
30	5.3		91	4.7	
31	5.1		92	4.4	
32	5.0		93	5.0	
34	4.9		94	5.2	
35	4.9		95	4.9	
36	5.4		96	5.8	
38	5.0		97	4.7	
39	5.0		99	5.1	
40	4.7		100	4.9	
41	3.9		101	5.3	
42	4.6		107	5.3	
44	5.3		110	5.0	
45	4.9				
46	5.5				
47	4.0				
48	5.4				
49	5.0				
51	4.7				
53	5.0				
55	5.0				
57	4.7				
58	5.0				

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	4.9
Standard deviation, pg/g	0.42
Relative standard deviation, %	8.6
No. of values reported	80
No. of values removed	0
No. of reported non-detects	0

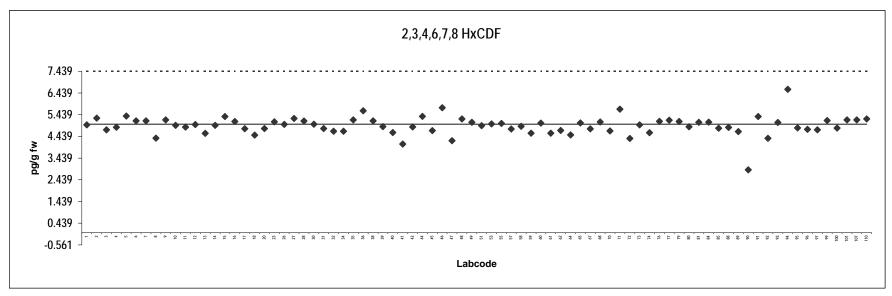


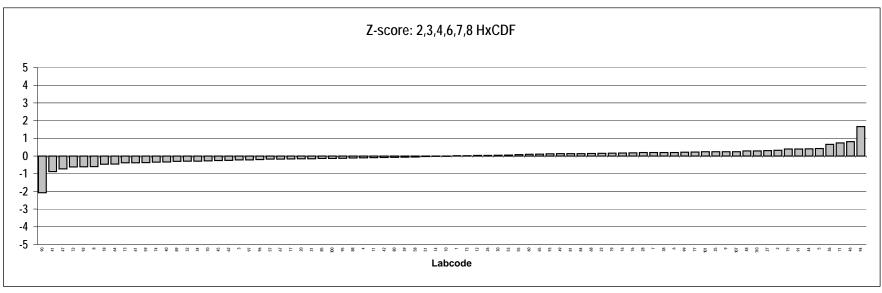


# Analyte solution Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.0		59	4.6	
2	5.3		60	5.1	
3	4.7		61	4.6	
4	4.9		62	4.7	
5	5.4		64	4.5	
6	5.2		65	5.1	
7	5.2		67	4.8	
8	4.4		68	5.1	
9	5.2		70	4.7	
10	4.9		71	5.7	
11	4.9		72	4.3	
12	5.0		73	5.0	
13	4.6		74	4.6	
14	4.9		76	5.1	
15	5.4		77	5.2	
16	5.1		79	5.1	
17	4.8		80	4.9	
18	4.5		81	5.1	
20	4.8		84	5.1	
23	5.1		85	4.8	
26	5.0		88	4.9	
27	5.3		89	4.7	
28	5.1		90	2.9	
30	5.0		91	5.4	
31	4.8		92	4.4	
32	4.7		93	5.1	
34	4.7		94	6.6	
35	5.2		95	4.8	
36	5.6		96	4.8	
38	5.2		97	4.7	
39	4.9		99	5.2	
40	4.6		100	4.8	
41	4.1		101	5.2	
42	4.9		107	5.2	
44	5.4		110	5.2	
45	4.7				
46	5.8				
47	4.2				
48	5.2				
49	5.1				
51	4.9				
53	5.0				
55	5.0				
57	4.8				
58	4.9				

Consenus statistics					
Consensus median, pg/g	5.0				
Median all values pg/g	5.0				
Consensus mean, pg/g	4.9				
Standard deviation, pg/g	0.43				
Relative standard deviation, %	8.7				
No. of values reported	80				
No. of values removed	0				
No. of reported non-detects	0				

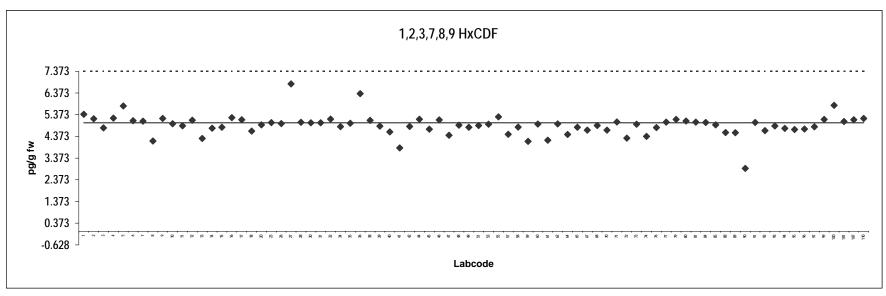


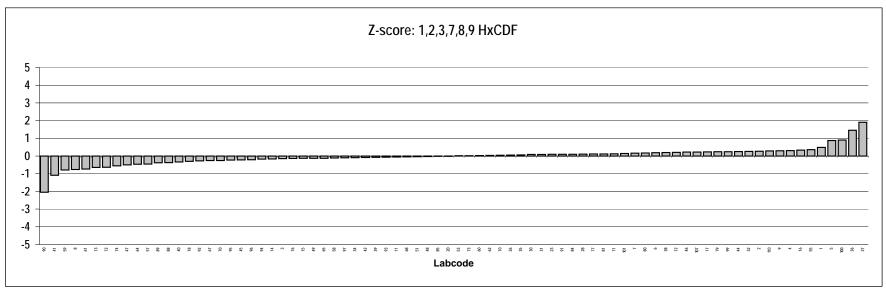


# Analyte solution Congener: 1,2,3,7,8,9 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.4		59	4.1	
2	5.2		60	4.9	
3	4.8		61	4.2	
4	5.2		62	4.9	
5	5.8		64	4.5	
6	5.1		65	4.8	
7	5.1		67	4.7	
8	4.2		68	4.9	
9	5.2		70	4.7	
10	5.0		71	5.0	
11	4.9		72	4.3	
12	5.1		73	4.9	
13	4.3		74	4.4	
14	4.7		76	4.8	
15	4.8		77	5.0	
16	5.2		79	5.2	
17	5.1		80	5.1	
18	4.6		81	5.0	
20	4.9		84	5.0	
23	5.0		85	4.9	
26	5.0		88	4.6	
27	6.8		89	4.5	
28	5.0		90	2.9	
30	5.0		91	5.0	
31	5.0		92	4.6	
32	5.2		93	4.9	
34	4.8		94	4.7	
35	5.0		95	4.7	
36	6.3		96	4.7	
38	5.1		97	4.8	
39	4.8		99	5.2	
40	4.6		100	5.8	
41	3.8		101	5.1	
42	4.8		107	5.1	
44	5.2		110	5.2	
45	4.7				
46	5.1				
47	4.4				
48	4.9				
49	4.8				
51	4.9				
53	4.9				
55 57	5.3				
57	4.5				
58	4.8				

Consenus statistics						
G 1: /	4.0					
Consensus median, pg/g	4.9					
Median all values pg/g	4.9					
Consensus mean, pg/g	4.9					
Standard deviation, pg/g	0.48					
Relative standard deviation, %	10					
No. of values reported	80					
No. of values removed	0					
No. of reported non-detects	0					

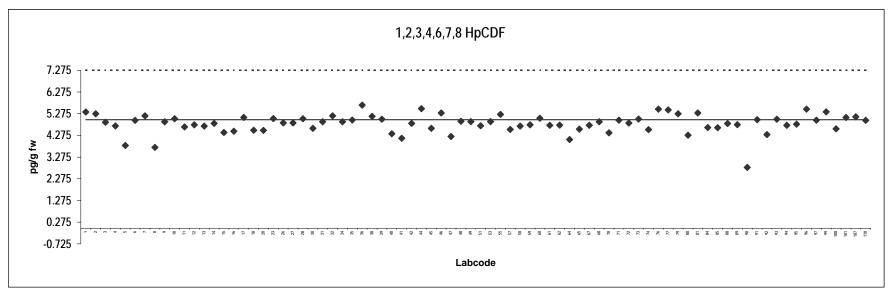


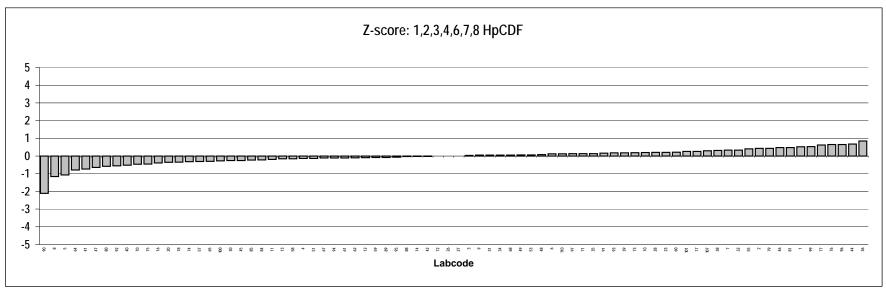


Analyte solution Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Cono nala fre	Notes	Lab code		Notes
	Conc. pg/g fw.	Notes		Conc. pg/g fw.	Notes
1	5.4		59	4.8	
2 3	5.3		60	5.1	
3	4.9		61	4.7	
4	4.7		62	4.7	
5	3.8		64	4.1	
6	5.0		65	4.6	
7	5.2		67	4.7	
8	3.7		68	4.9	
9	4.9		70	4.4	
10	5.0		71	5.0	
11	4.7		72	4.8	
12	4.8		73	5.0	
13	4.7		74	4.5	
14	4.8		76	5.5	
15	4.4		77	5.5	
16	4.5		79	5.3	
17	5.1		80	4.3	
18	4.5		81	5.3	
20	4.5		84	4.6	
23	5.0		85	4.6	
26	4.9		88	4.8	
27	4.9		89	4.8	
28	5.0		90	2.8	
30	4.6		91	5.0	
31	4.9		92	4.3	
32	5.2		93	5.0	
34	4.9		94	4.7	
35	5.0		95	4.8	
36	5.7		96	5.5	
38	5.2		97	5.0	
39	5.0		99	5.4	
40	4.3		100	4.6	
41	4.1		101	5.1	
42	4.8		107	5.1	
44	5.5		110	5.0	
45	4.6				
46	5.3				
47	4.2				
48	4.9				
49	4.9				
51	4.7				
53	4.9				
55	5.2				
57	4.6				
58	4.7				

Consensus median, pg/g	4.9
Median all values pg/g	4.9
Consensus mean, pg/g	4.8
Standard deviation, pg/g	0.43
Relative standard deviation, %	9.0
No. of values reported	80
No. of values removed	0
No. of reported non-detects	0

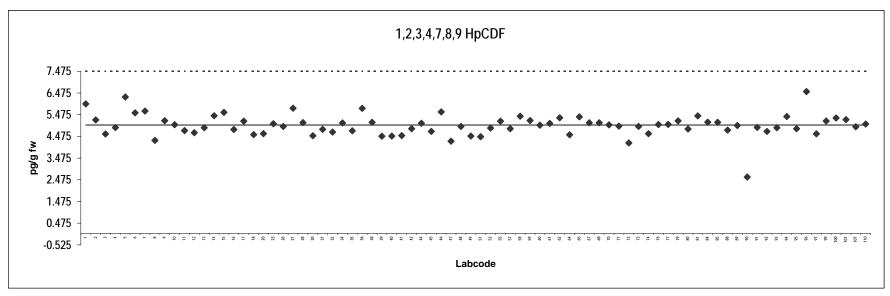


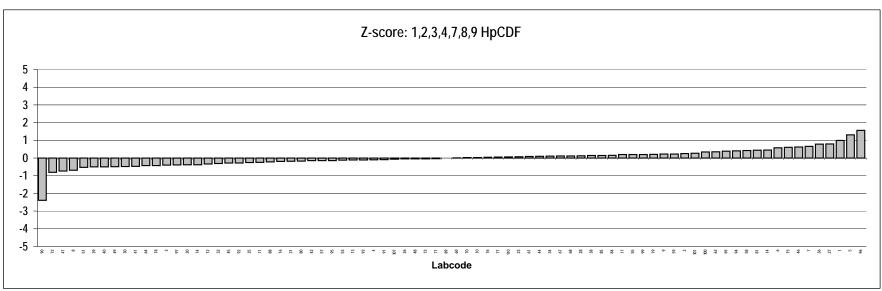


# Analyte solution Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	6.0		59	5.2	
2	5.2		60	5.0	
3	4.6		61	5.1	
4	4.9		62	5.3	
5	6.3		64	4.6	
6	5.6		65	5.4	
7	5.6		67	5.1	
8	4.3		68	5.1	
9	5.2		70	5.0	
10	5.0		71	4.9	
11	4.7		72	4.2	
12	4.6		73	4.9	
13	4.9		74	4.6	
14	5.4		76	5.0	
15	5.6		77	5.0	
16	4.8		79	5.2	
17	5.2		80	4.8	
18	4.6		81	5.4	
20	4.6		84	5.1	
23	5.1		85	5.1	
26	4.9		88	4.8	
27	5.8		89	5.0	
28	5.1		90	2.6	
30	4.5		91	4.9	
31	4.8		92	4.7	
32	4.7		93	4.9	
34	5.1		94	5.4	
35	4.7		95	4.8	
36	5.8		96	6.5	
38	5.1		97	4.6	
39	4.5		99	5.2	
40	4.5		100	5.3	
41	4.5		101	5.2	
42	4.8		107	4.9	
44	5.1		110	5.0	
45	4.7				
46	5.6				
47	4.3				
48	4.9				
49	4.5				
51	4.5				
53	4.9				
55 57	5.2				
57	4.8				
58	5.4				

Consensus median, pg/g	5.0
Median all values pg/g	5.0
Consensus mean, pg/g	5.0
Standard deviation, pg/g	0.50
Relative standard deviation, %	10
No. of values reported	80
No. of values removed	0
No. of reported non-detects	0

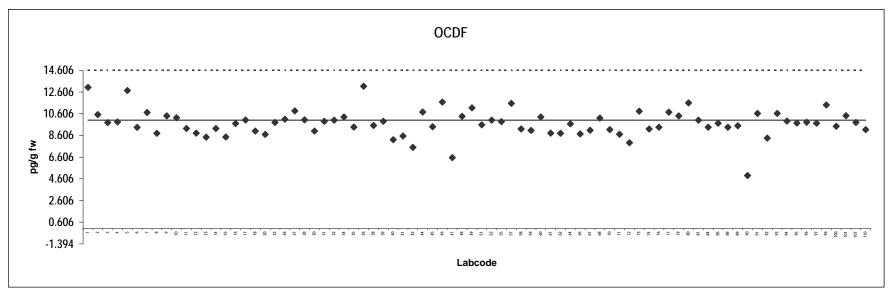


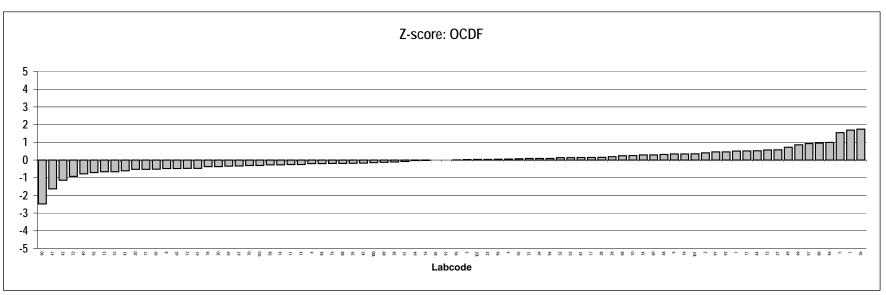


### **Analyte solution**Congener: OCDF

					Cons
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	13		59	9.1	
2 3	11		60	10	
	9.8		61	8.8	
4	9.8		62	8.8	
5	13		64	9.7	
6	9.3		65	8.7	
7	11		67	9.1	
8	8.8		68	10	
9	10		70	9.1	
10	10		71	8.7	
11	9.2		72	7.9	
12	8.8		73	11	
13	8.4		74	9.2	
14	9.2		76	9.4	
15	8.5		77	11	
16	9.7		79	10	
17	10		80	12	
18	9.0		81	10	
	8.7				
20 23			84	9.3 9.7	
	9.8		85		
26	10		88	9.4	
27	11		89	9.5	
28	10		90	4.9	
30	9.0		91	11	
31	9.9		92	8.4	
32	10		93	11	
34	10		94	9.9	
35	9.4		95	9.7	
36	13		96	9.8	
38	9.5		97	9.7	
39	9.9		99	11	
40	8.2		100	9.5	
41	8.5		101	10	
42	7.5		107	9.8	
44	11		110	9.1	
45	9.4				
46	12				
47	6.6				
48	10				
49	11				
51	9.6				
53	10				
55	9.9				
57	12				
58	9.2				

Consensus median, pg/g	9.7
Median all values pg/g	9.7
Consensus mean, pg/g	9.7
Standard deviation, pg/g	1.2
Relative standard deviation, %	13
No. of values reported	80
No. of values removed	0
No. of reported non-detects	0



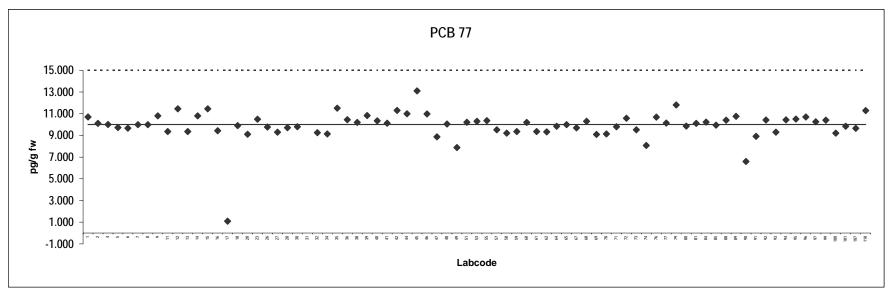


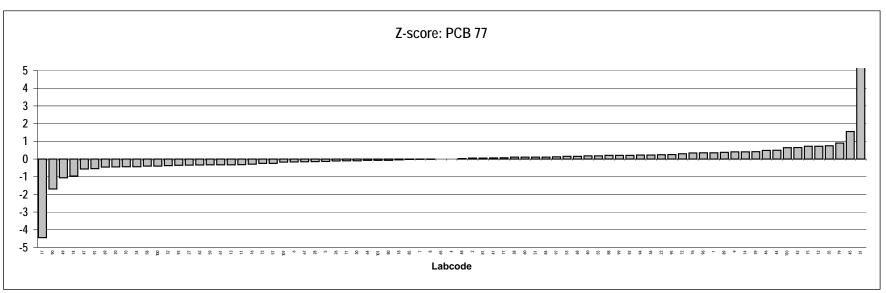
### Analyte solution Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11		61	9.3	
2	10		62	9.3	
4	10		64	9.8	
5	9.7		65	10.0	
6	9.7		67	9.7	
7	10.0		68	10	
8	10.0		69	9.1	
9	11		70	9.1	
11	9.4		71	9.8	
12	11		72	11	
13	9.3		73	9.5	
14	11		74	8.1	
15	11		76	11	
16	9.4		77	10	
17	1.1	Outlier	79	12	
18	9.9		80	9.9	
20	9.1		81	10	
23	10		84	10	
26	9.8		85	9.9	
27	9.3		88	10	
28	9.7		89	11	
30	9.8		90	6.6	
31	103	Outlier	91	8.9	
32	9.3		92	10	
34	9.1		93	9.3	
35	12		94	10	
36	10		95	11	
38	10		96	11	
39	11		97	10	
40	10		99	10	
41	10		100	9.2	
42	11		101	9.8	
44	11		107	9.6	
45	13		110	11	
46	11				
47	8.9				
48	10				
49	7.9				
51	10				
53	10				
55	10				
57	9.5				
58	9.2				
59	9.3				
60	10				

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.91
D 1 .: . 1 11 1 .: .: 0/	0.1

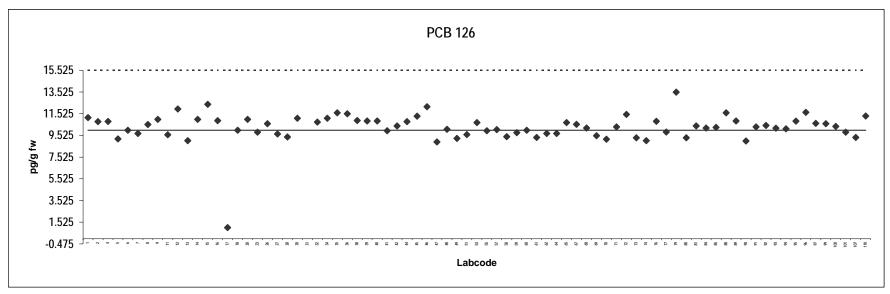
Standard deviation, pg/g	0.91
Relative standard deviation, %	9.1
No. of values reported	79
No. of values removed	2
No. of reported non-detects	0

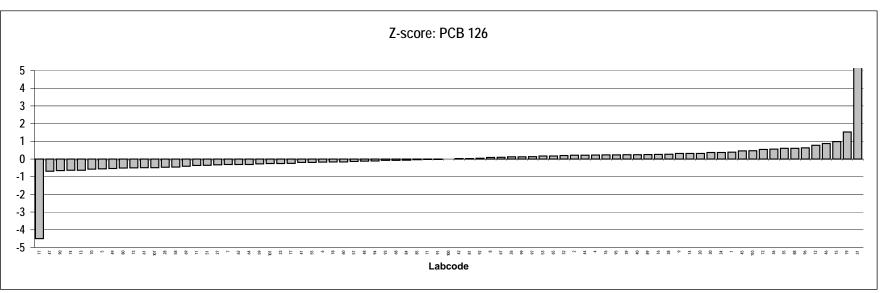




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11		61	9.3	
2	11		62	9.7	
4	11 9.2		64	9.7	
5	9.2		65	11	
6	10.0		67	11	
7	9.7		68	10	
8	11		69	9.5	
9	11		70	9.2	
11	9.6		71	10	
12	12		72	11	
13	9.0		73	9.3	
14	11		74	9.0	
15	12		76	11	
16	11		77	9.8	
17	1.0	Outlier	79	14	
18	10		80	9.3	
20	11		81	10	
23	9.8		84	10	
26	11		85	10	
27	9.7		88	12	
28	9.4		89	11	
30	11		90	9.0	
31	104	Outlier	91	10	
32	11		92	10	
34	11		93	10	
35	12		94	10	
36	12		95	11	
38	11		96	12	
39	11		97	11	
40	11		99	11	
41	10.0		100	10	
42	10		101	9.8	
44	11		107	9.3	
45	11		110	11	
46	12				
47	8.9				
48	10				
49	9.2				
51	9.6				
53	11				
55	10.0				
57	10				
58	9.4				
59	9.8				
60	10				

Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.88
Relative standard deviation, %	8.4
No. of values reported	79
No. of values removed	2
No. of reported non-detects	0

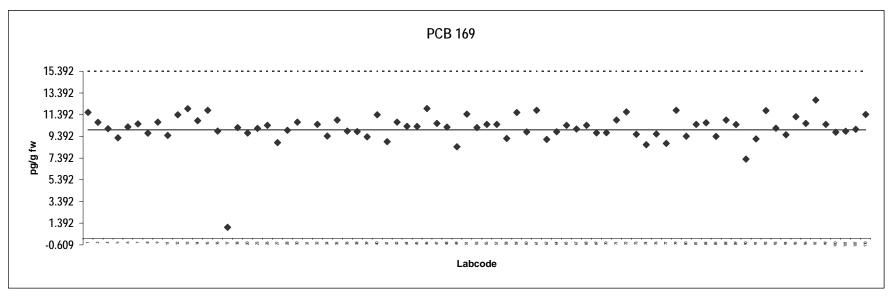


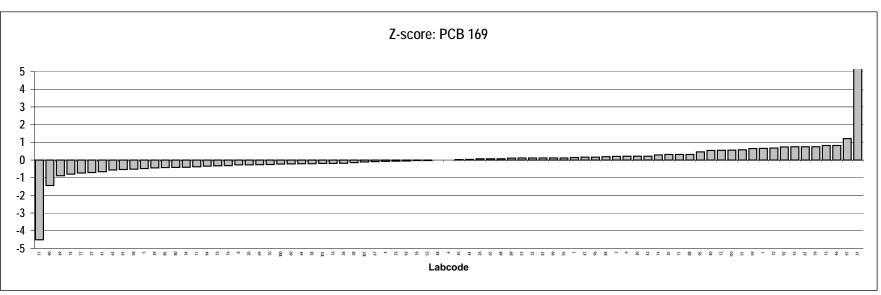


Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	12		61	12	
2	11		62	9.1	
4	10		64	9.8	
5	9.3		65	10	
6	10		67	10	
7	11		68	10	
8	9.7		69	9.7	
9	11		70	9.7	
11	9.5		71	11	
12	11		72	12	
13	12		73	9.6	
14	11		74	8.6	
15	12		76	9.6	
16	9.9		77	8.7	
17	1.0	Outlier	79	12	
18	10		80	9.4	
20	9.7		81	11	
23	10		84	11	
26	10		85	9.4	
27	8.8		88	11	
28	10.0		89	10	
30	11		90	7.3	
31	101	Outlier	91	9.2	
32	11		92	12	
34	9.4		93	10	
35	11		94	9.5	
36	9.9		95	11	
38	9.8		96	11	
39	9.3		97	13	
40	11		99	11	
41	8.9		100	9.8	
42	11		101	9.9	
44	10		107	10	
45	10		110	11	
46	12				
47 48	11				
	10 8.4				
49 51	8.4 11				
53	10				
55	10				
55 57	10				
58	9.2				
58 59	12				
60	9.8				
OU	9.0				

Consenus	statistics

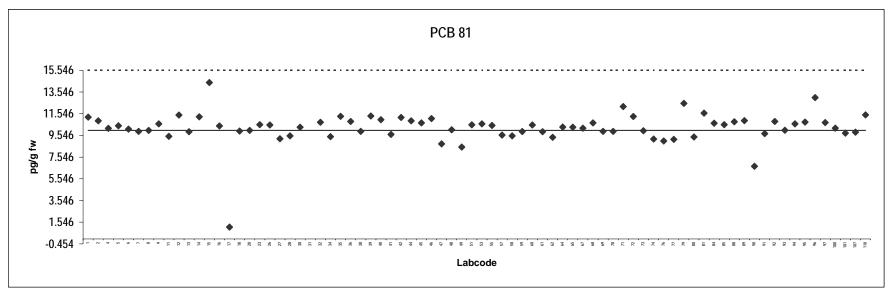
Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	0.96
Relative standard deviation, %	9.3
No. of values reported	79
No. of values removed	2
No. of reported non-detects	0

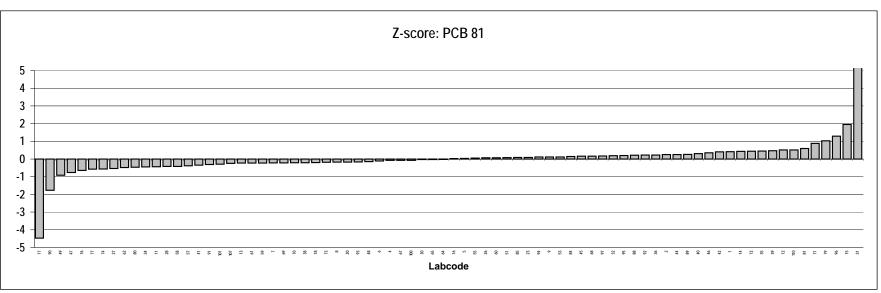




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	11		61	9.9	
2	11		62	9.4	
4	10		64	10	
5	10		65	10	
6	10		67	10	
7	9.9		68	11	
8	10		69	9.9	
9	11		70	9.9	
11	9.4		71	12	
12	11		72	11	
13	9.9		73	10.0	
14	11		74	9.2	
15	14		76	9.0	
16	10		77	9.2	
17	1.1	Outlier	79	13	
18	10.0		80	9.4	
20	10		81	12	
23	11		84	11	
26	11		85	11	
27	9.2		88	11	
28	9.5		89	11	
30	10		90	6.7	
31	103	Outlier	91	9.7	
32	11		92	11	
34	9.4		93	10	
35	11		94	11	
36	11		95	11	
38	9.9		96	13	
39	11		97	11	
40	11		100	10	
41	9.6		101	9.8	
42	11		107	9.8	
44	11		110	11	
45	11				
46	11				
47	8.8				
48	10				
49	8.5				
51	11				
53	11				
55	10				
57	9.6				
58	9.5				
59	9.9				
60	11				

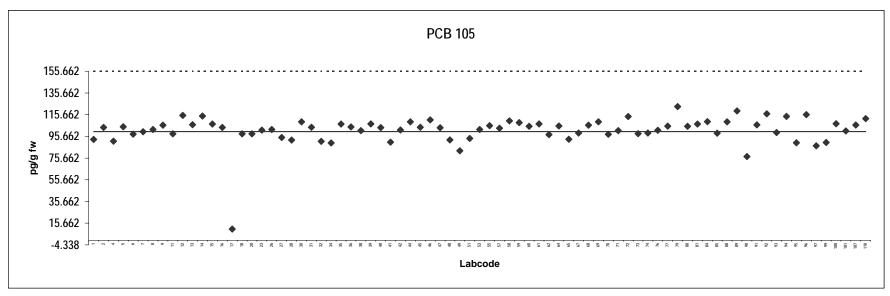
Consensus median, pg/g	10
Median all values pg/g	10
Consensus mean, pg/g	10
Standard deviation, pg/g	1.0
Relative standard deviation, %	10
No. of values reported	78
No. of values removed	2
No. of reported non-detects	0
No. of reported non-detects	0

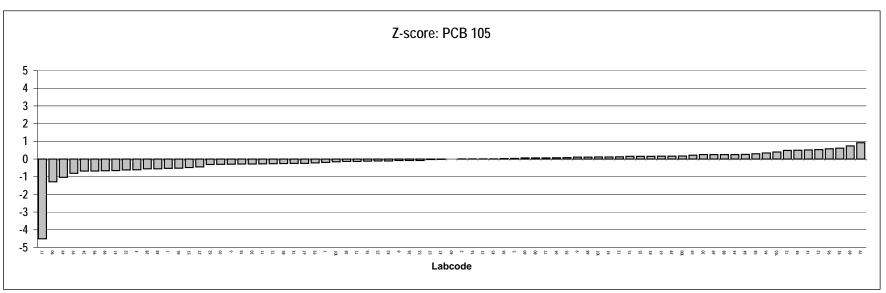




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	93		61	107	
2	104		62	97	
4	91		64	105	
5	105		65	93	
6	98		67	99	
7	100		68	106	
8	102		69	109	
9	106		70	97	
11	98		71	101	
12	115		72	114	
13	106		73	98	
14	114		74	99	
15	107		76	101	
16	104		77	105	
17	10	Outlier	79	123	
18	98		80	105	
20	98		81	107	
23	101		84	109	
26	102		85	99	
27	95		88	109	
28	92		89	119	
30	109		90	77	
31	104		91	106	
32	91		92	117	
34 35	90 107		93 94	99 114	
36	107		94 95	90	
38	104		95 96	116	
39	107		97	87	
40	104		99	90	
41	90		100	107	
42	102		101	101	
44	109		107	106	
45	104		110	112	
46	111		110	112	
47	104				
48	92				
49	82				
51	94				
53	102				
55	105				
57	103				
58	110				
59	108				
60	105				

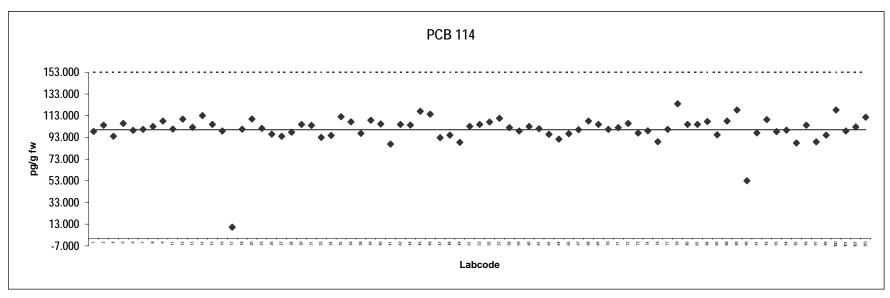
Consensus median, pg/g	104
Median all values pg/g	104
Consensus mean, pg/g	102
Standard deviation, pg/g	8.3
Relative standard deviation, %	8.1
No. of values reported	79
No. of values removed	1
No. of reported non-detects	0

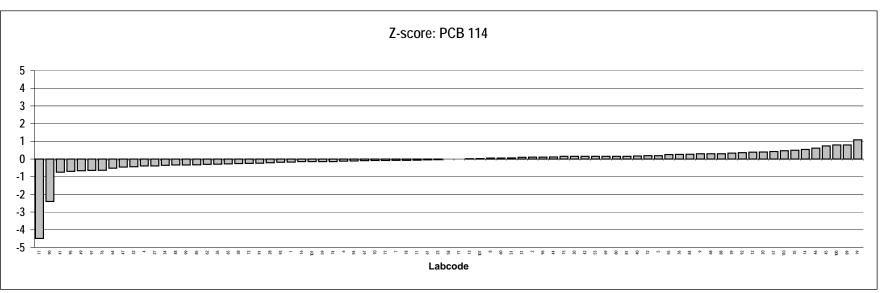




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	98		61	101	
2	104		62	96	
4	94		64	91	
5	106		65	96	
6	99		67	100	
7	100		68	108	
8	103		69	105	
9	108		70	100	
11	101		71	102	
12	110		72	106	
13	102		73	97	
14	113		74	99	
15	105		76	89	
16	99		77	100	
17	10	Outlier	79	124	
18	101		80	105	
20	110		81	105	
23	101		84	108	
26	96		85	95	
27	94		88	108	
28	98		89	118	
30	105		90	53	
31	104		91	97	
32	93		92	109	
34	95		93	98	
35	112		94	100	
36	107		95	88	
38	97		96	104	
39	109		97	89	
40	105		99	95	
41	87		100	118	
42	105		101	99	
44	104		107	103	
45	117		110	112	
46	114				
47	93				
48	95				
49	88				
51	103				
53	105				
55	107				
57	111				
58	102				
59	99				
60	103				

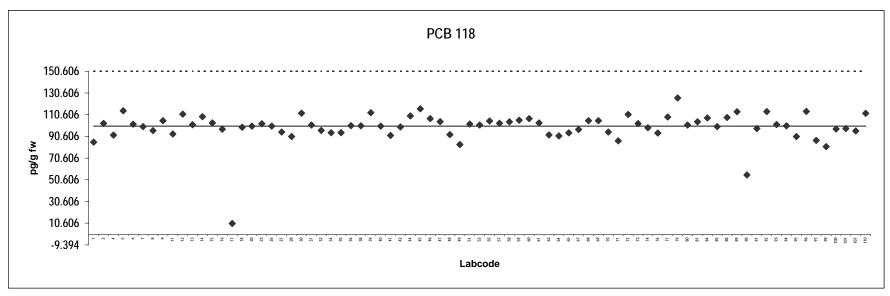
Consensus median, pg/g	102
Median all values pg/g	102
Consensus mean, pg/g	102
Standard deviation, pg/g	9.2
Relative standard deviation, %	9.1
No. of values reported	79
No. of values removed	1
No. of reported non-detects	0

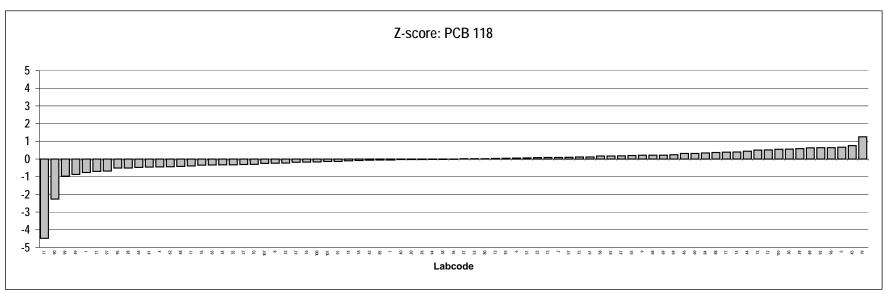




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	85		61	103	
2	102		62	92	
4	92		64	91	
5	114		65	94	
6	102		67	97	
7	100		68	105	
8	96		69	105	
9	105		70	95	
11	93		71	87	
12	111		72	111	
13	101		73	102	
14	109		74	99	
15	103		76	94	
16	97		77	108	
17	10	Outlier	79	126	
18	99		80	101	
20	100		81	104	
23	102		84	108	
26	100		85	100	
27	95		88	108	
28	90		89	113	
30	112		90	55	
31	101		91	98	
32	96		92	114	
34	94		93	101	
35	94		94	100	
36	100		95	90	
38	100		96	114	
39	112		97	87	
40	100		99	81	
41	91		100	97	
42	99		101	98	
44	109		107	96	
45	116		110	112	
46	107				
47	104				
48	92				
49	83				
51	102				
53	101				
55	105				
57	103				
58	104				
59	106				
60	107				

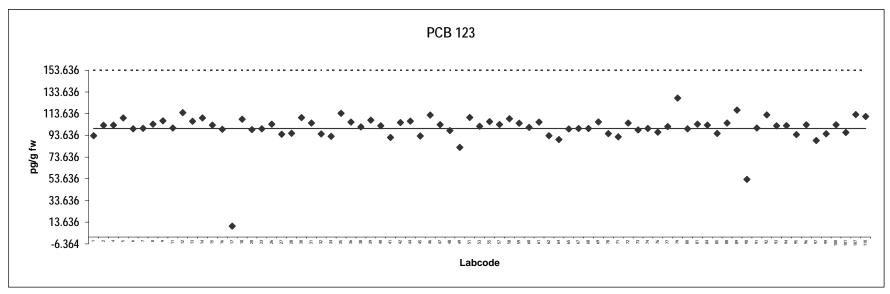
Consensus median, pg/g	101
Median all values pg/g	100
Consensus mean, pg/g	100
Standard deviation, pg/g	9.6
Relative standard deviation, %	10
No. of values reported	79
No. of values removed	1
No. of reported non-detects	0

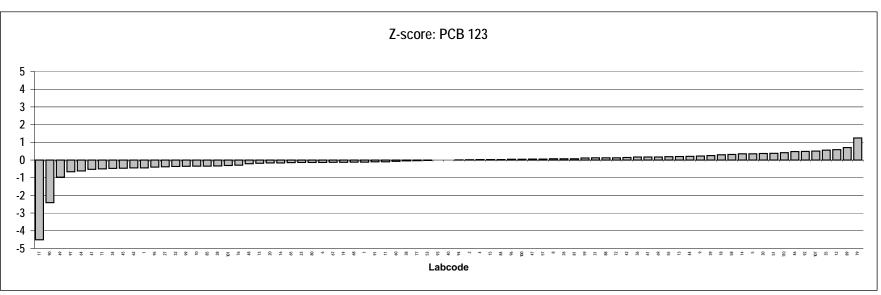




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	93		61	106	
2	103		62	93	
4	103		64	90	
5	110		65	100	
6	100		67	100	
7	100		68	100	
8	104		69	106	
9	107		70	95	
11	100		71	92	
12	115		72	105	
13	107		73	99	
14	110		74	100	
15	103		76	97	
16	99		77	102	
17	10.0	Outlier	79	128	
18	109		80	100	
20	99		81	104	
23	100		84	103	
26	104		85	95	
27	95		88	105	
28	95		89	117	
30	110		90	53	
31	105		91	100	
32	95		92	113	
34	93		93	102	
35	114		94	103	
36	106		95	94	
38	102		96	103	
39	108		97	89	
40	102		99	95	
41	92		100	103	
42	105 107		101 107	96 113	
44					
45	93		110	111	
46 47	112 103				
48	98				
48	98 83				
51	83 110				
53	102				
55	102				
57	104				
58	109				
59	105				
60	101				

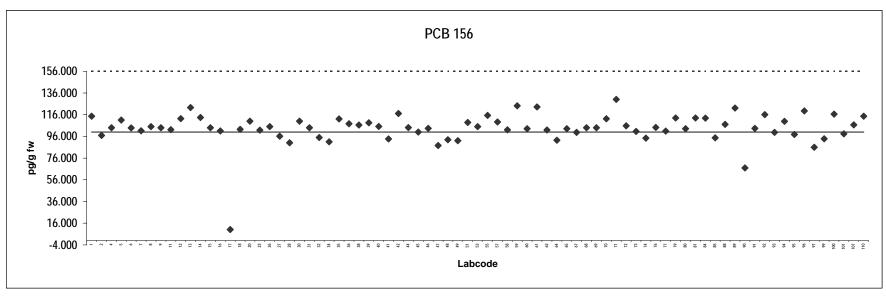
103
102
102
9.0
9
79
1
0

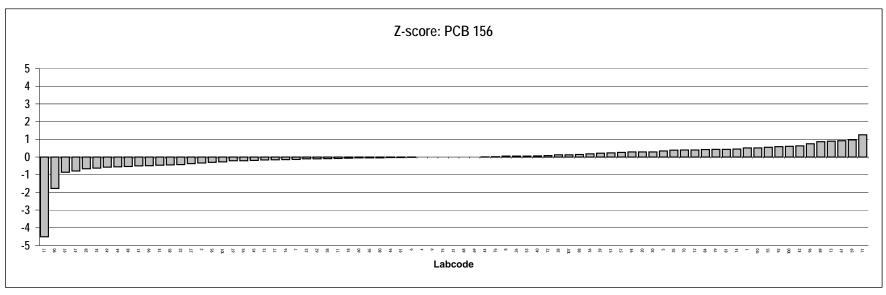




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	115		61	123	
2	97		62	102	
4	104		64	92	
5	111		65	103	
6	104		67	100	
7	101		68	104	
8	105		69	104	
9	104		70	112	
11	102		71	130	
12	112		72	106	
13	123		73	100	
14	113		74	94	
15	104		76	104	
16	101		77	101	
17	10	Outlier	79	113	
18	103		80	103	
20	110		81	113	
23	102		84	113	
26	105		85	95	
27	96		88	107	
28	90		89	122	
30	110		90	67	
31	104		91	103	
32	95		92	116	
34	91		93	100	
35	112		94	110	
36	108		95	98	
38	107		96	119	
39	108		97	86	
40	105		99	94	
41	94		100	117	
42	117 104		101 107	98 107	
44					
45	100		110	115	
46 47	103 88				
47	93				
48	93 92				
51	109				
53	105				
55	115				
57	109				
58	102				
59	124				
60	103				

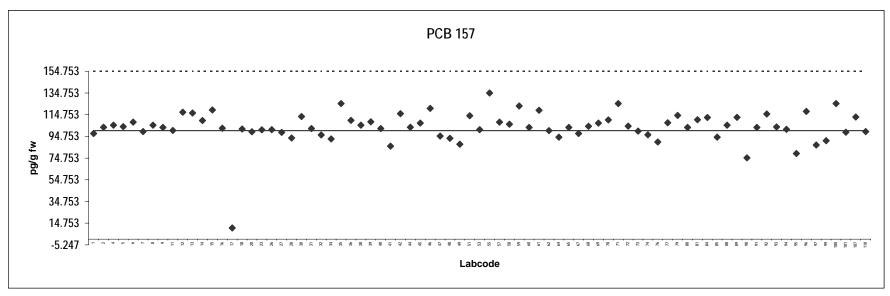
Consensus median, pg/g	104
Median all values pg/g	104
Consensus mean, pg/g	105
Standard deviation, pg/g	9.8
Relative standard deviation, %	9.4
No. of values reported	79
No. of values removed	1
No. of reported non-detects	0

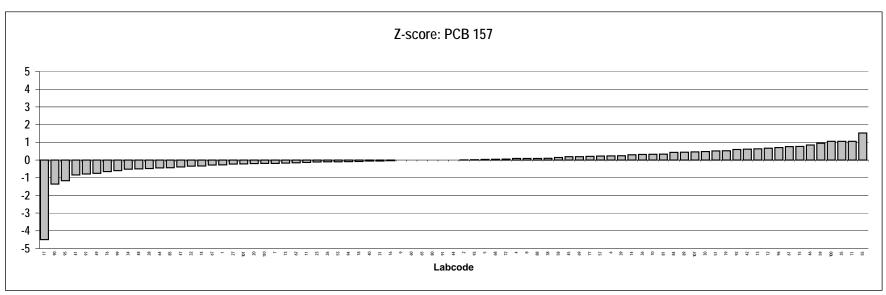




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	97		61	119	
2	103		62	100	
4	105		64	94	
5 6	104		65	103	
6	108		67	97	
7	99		68	104	
8	105		69	107	
9	103		70	110	
11	100		71	125	
12	117		72	104	
13	116		73	100	
14	109		74	96	
15	119		76	90	
16	102		77	107	
17	10	Outlier	79	114	
18	102		80	103	
20	99		81	110	
23	101		84	112	
26	101		85	94	
27	98		88	105	
28	93		89	112	
30	113		90	75	
31	102		91	103	
32	96		92	115	
34	92		93 94	103	
35 36	125 110		94 95	101 79	
38	105		95 96	118	
39	103		90 97	87	
40	108		99	91	
41	86		100	125	
42	116		101	99	
44	103		107	113	
45	107		110	99	
46	121		110	**	
47	95				
48	93				
49	87				
51	114				
53	101				
55	135				
57	108				
58	106				
59	123				
60	103				

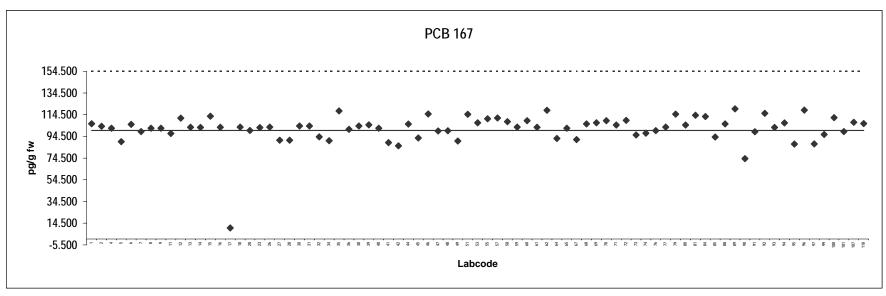
Consensus median, pg/g	103
Median all values pg/g	103
Consensus mean, pg/g	104
Standard deviation, pg/g	11
Relative standard deviation, %	10
No. of values reported	79
No. of values removed	1
No. of reported non-detects	0

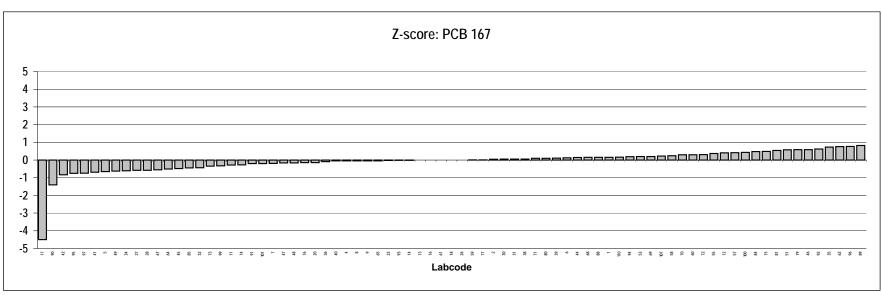




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	106		61	103	
2	104		62	118	
4	102		64	93	
5 6	90		65	102	
6	106		67	92	
7	99		68	106	
8	102		69	107	
9	102		70	109	
11	97		71	105	
12	111		72	109	
13	103		73	96	
14	103		74	97	
15	113		76	100	
16	103		77	103	
17	10	Outlier	79	115	
18	103		80	105	
20	100		81	114	
23	103		84	113	
26	103		85	94	
27	91		88	106	
28	91		89	120	
30	104		90	74	
31	104		91	99	
32	94		92	116	
34	91		93	103	
35 36	118 101		94 95	107 87	
38	101		95 96	119	
39	104		90 97	88	
40	103		99	96	
41	89		100	112	
42	86		101	99	
44	106		107	107	
45	93		110	106	
46	115		110	100	
47	100				
48	100				
49	90				
51	115				
53	107				
55	111				
57	112				
58	108				
59	103				
60	109				

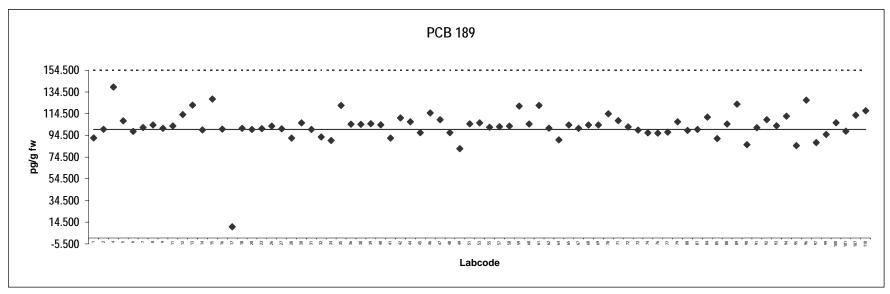
103
103
103
8.7
8.5
79
1
0

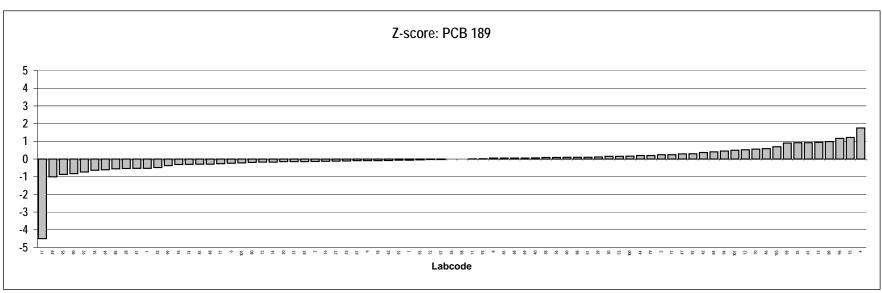




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	92		61	122	
2	100		62	101	
4	139		64	90	
5 6	108		65	104	
6	98		67	101	
7	102		68	104	
8	104		69	104	
9	101		70	114	
11	103		71	108	
12	114		72	102	
13	122		73	99	
14	99		74	97	
15	128		76	97	
16	100		77	98	
17	10	Outlier	79	107	
18	101		80	99	
20	100		81	100	
23	101		84	111	
26	103		85	92	
27	101		88	105	
28	92		89	123	
30	106		90	86	
31	100		91	102	
32	93		92	109	
34	90		93	103	
35	122		94 95	112	
36 38	105 105		95 96	85 127	
38	105		96 97	127	
40	103		97	88 95	
40	92		100	106	
41	92 111		100	98	
44	107		107	113	
45	97		110	117	
46	115		110	117	
47	109				
48	97				
49	82				
51	105				
53	106				
55	102				
57	102				
58	103				
59	122				
60	105				

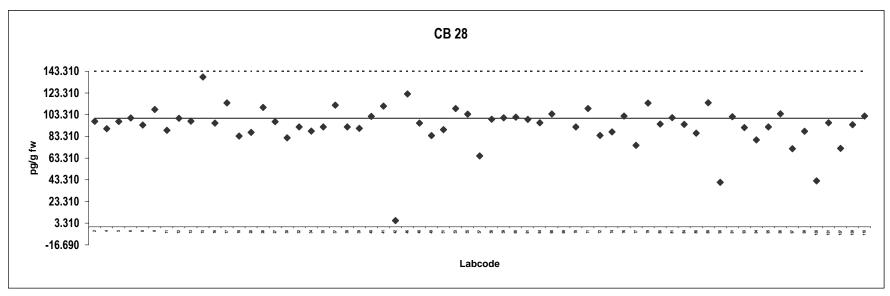
Consensus median, pg/g	103
Median all values pg/g	103
Consensus mean, pg/g	104
Standard deviation, pg/g	10
Relative standard deviation, %	10
No. of values reported	79
No. of values removed	1
No. of reported non-detects	0

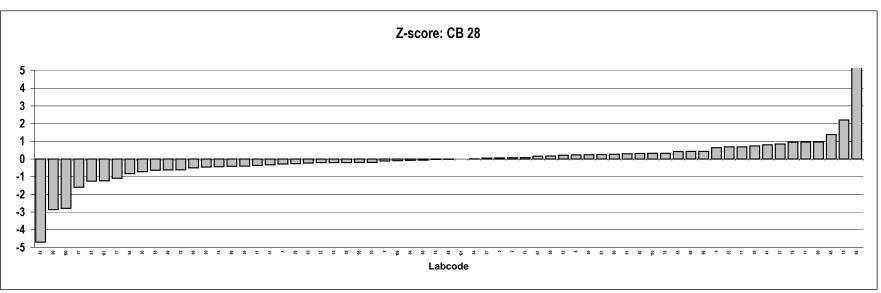




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	97		77	75	
4	90		79	114	
5	97		80	95	
6	100		81	101	
8	94		84	94	
9	108		88	86	
11	89		89	114	
12	100		90	41	Outlier
13	97		91	101	
15	138		93	91	
16	95		94	80	
17	114		95	92	
18	84		96	104	
20	87		97	72	
26	110		99	88	
27	97		100	42	Outlier
30	82		101	96	
32	92		107	72	
34	88		109	94	
35	92		110	102	
37	112				
38	92				
39	91				
40	102				
41	111				
42	5.8	Outlier			
46	122				
48	96				
49	84				
51	89				
53	109				
55	104				
57	65				
58	99				
59	100				
60	101				
61	99				
64	96				
68	104				
69	387	Outlier			
70	92				
71	109				
72	84				
74	87				
76	102				

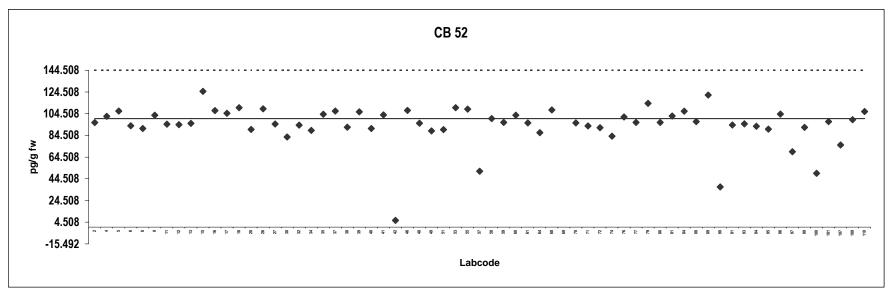
Constitus statistics	
Consensus median ma/s	96
Consensus median, pg/g	, ,
Median all values pg/g	96
Consensus mean, pg/g	96
Standard deviation, pg/g	12
Relative standard deviation, %	13
No. of values reported	65
No. of values removed	4
No. of reported non-detects	0

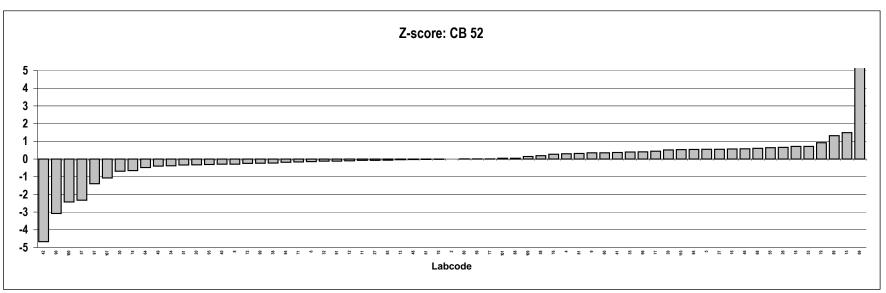




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	96		77	97	
4	102		79	114	
5	107		80	96	
6	93		81	102	
8	91		84	107	
9	103		88	97	
11	95		89	122	
12	94		90	37	Outlier
13	96		91	94	
15	125		93	95	
16	107		94	93	
17	105		95	90	
18	110		96	104	
20	90		97	69	
26	109		99	92	
27	95		100	49	
30	83		101	97	
32	94		107	76	
34	89		109	99	
35	104		110	106	
37	107				
38	92				
39	106				
40	91				
41	103	0.41			
42	6.2 107	Outlier			
46					
48 49	96 89				
51	90				
53	110				
55	109				
57	52				
58	100				
59	96				
60	103				
61	96				
64	87				
68	108				
69	1190	Outlier			
70	96	Outilei			
70	93				
72	92				
74	84				
76	102				

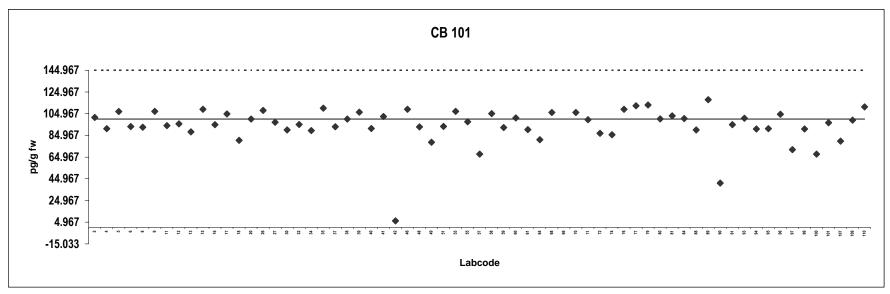
Consensus median, pg/g	96
Median all values pg/g	96
Consensus mean, pg/g	97
Standard deviation, pg/g	13
Relative standard deviation, %	13
No. of values reported	65
No. of values removed	3
No. of reported non-detects	0

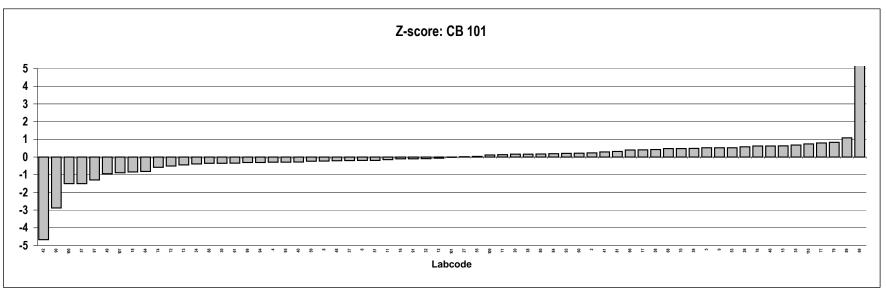




Lab code	Cono nala fre	Notes	Lab code	Cono nala fre	Notes
		Notes		Conc. pg/g fw.	Notes
2 4	101		77 79	112	
5	91 107		80	113 100	
5	107				
6	93		81	103	
8 9	92		84	100	
	107		88	90	
11	94		89	118	0 11
12	96		90	41	Outlier
13	88		91	95	
15	109		93	101	
16	95		94	91	
17	105		95	91	
18	80		96	104	
20	100		97	72	
26	108		99	91	
27	97		100	68	
30	90		101	97	
32	95		107	80	
34	89		109	99	
35	110		110	111	
37	93				
38	100				
39	106				
40	91				
41	102				
42	6.3	Outlier			
46	109				
48	93				
49	79				
51	93				
53	107				
55	98				
57	68				
58	105				
59	92				
60	101				
61	90				
64	81				
68	106				
	2360	Outlier			
69	2360 106	Outner			
70	106 99				
71					
72	87				
74	86				
76	109				

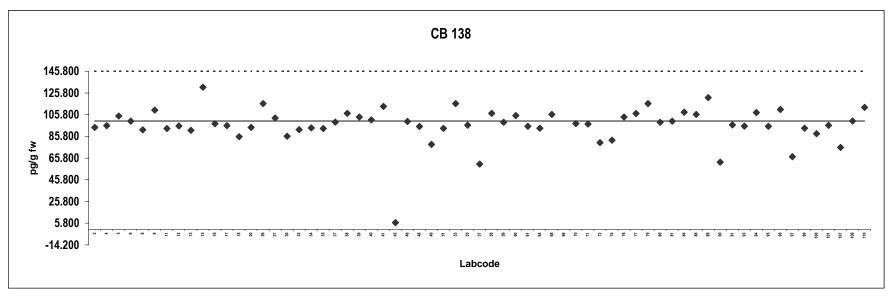
	0.7
Consensus median, pg/g	97
Median all values pg/g	97
Consensus mean, pg/g	97
Standard deviation, pg/g	11
Relative standard deviation, %	11
No. of values reported	65
No. of values removed	3
No. of reported non-detects	0

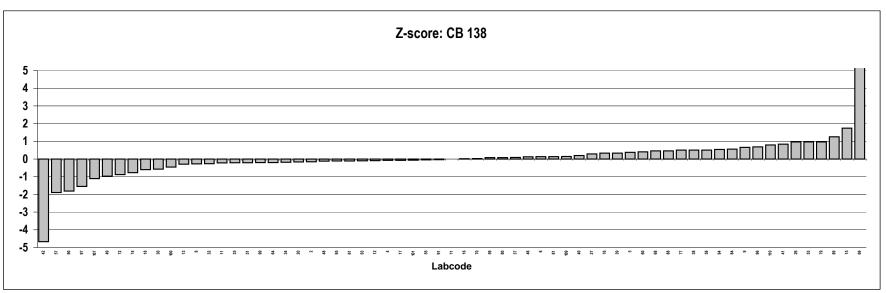




г		C / C	<b>T</b> . (		C / C	Cong
L	Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
	2	94		77	107	
	4	96		79	116	
	5	105		80	99	
	6	100		81	100	
	8	92		84	108	
	9	110		88	106	
	11	93		89	122	
	12	95		90	62	
	13	91		91	96	
	15	131		93	95	
	16	97		94	108	
	17	96		95	95	
	18	86		96	111	
	20	94		97	67	
	26	116		99	93	
	27	103		100	88	
	30	86		101	96	
	32	92		107	76	
	34	94		109	100	
	35	93		110	113	
	37	99				
	38	107				
	39	104				
	40	101				
	41	113				
	42	6.4	Outlier			
	46	100				
	48	95				
	49	78				
	51	93				
	53	116				
	55	96				
	57	60				
	58	107				
	59	99				
	60	105				
	61	95				
	64	93				
	68	106				
	69	3010	Outlier			
	70	98				
	71	97				
	72	80				
1	74	82				
	76	104				
L	70	104				

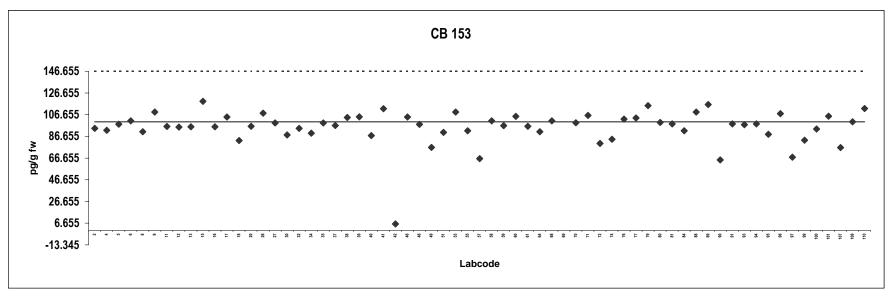
Consensus median, pg/g	97
Median all values pg/g	97
Consensus mean, pg/g	98
Standard deviation, pg/g	13
Relative standard deviation, %	13
No. of values reported	65
No. of values removed	2
No. of reported non-detects	0

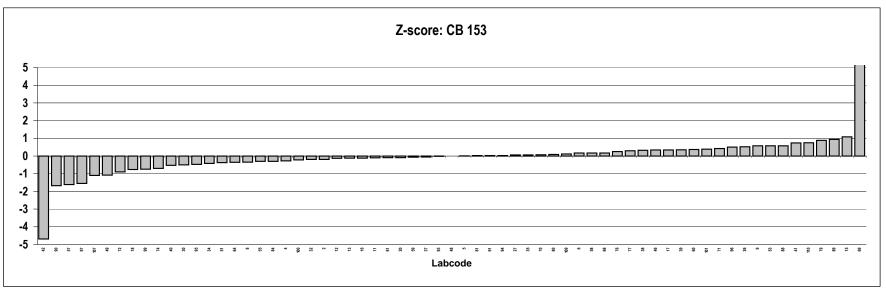




					Cong
Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
2	94		77	104	
4	92		79	115	
5	98		80	100	
6	101		81	98	
8	91 109		84	92	
9	109		88	109	
11	96		89	116	
12	95		90	65	
13	95		91	98	
15	119		93	97	
16	95		94	98	
17	104		95	89	
18	83		96	108	
20	96		97	67	
26	108		99	83	
27	99		100	93	
30	88		101	105	
32	94		107	76	
34	90		109	100	
35	99		110	112	
37	97				
38	104				
39	105				
40	87				
41	112	0.41			
42	6.0	Outlier			
46	104				
48	98				
49	77				
51	90				
53	109				
55	92				
57 58	66 101				
58 59	96				
60	96 105				
61	96				
64	96 91				
68	101				
69	1820	Outlier			
70	99	Outilei			
70	106				
72	80				
74	84				
76	103				

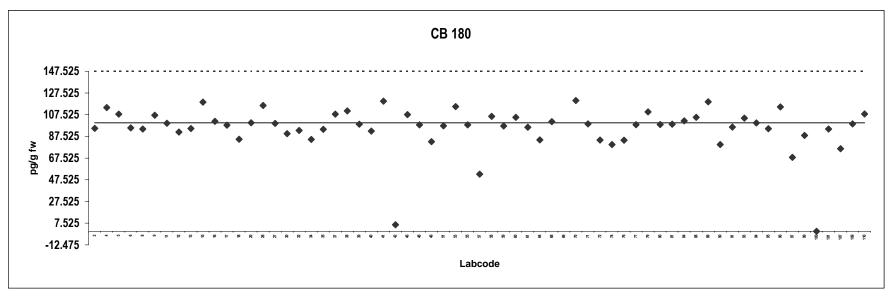
Consensus median, pg/g	98
Median all values pg/g	98
Consensus mean, pg/g	96
Standard deviation, pg/g	11
Relative standard deviation, %	12
No. of values reported	65
No. of values removed	2
No. of reported non-detects	0

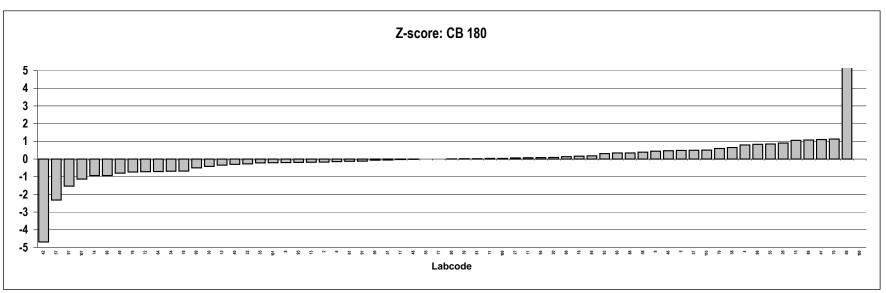




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	95		77	98	
4	114		79	110	
5	108		80	98	
6	95		81	99	
8	94		84	102	
9	107		88	105	
11	100		89	119	
12	91		90	80	
13	95		91	96	
15	119		93	104	
16	101		94	100	
17	98		95	95	
18	85		96	115	
20	100		97	68	
26	116		99	88	
27	100		100	not reported	Outlier,ND
30	90		101	94	
32	93		107	76	
34	85		109	99	
35	94		110	108	
37	108				
38	111				
39	99				
40	92				
41	120				
42	6.1	Outlier			
46	108				
48	98				
49	83				
51	97				
53	115				
55	98				
57	53				
58	106				
59	97				
60	105				
61	96				
64	84				
68	101				
69	422	Outlier			
70	121				
71	99				
72	84				
74	80				
76	84				

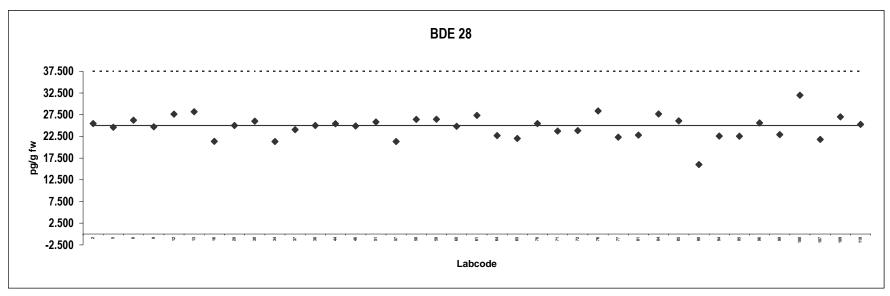
·	
Consensus median, pg/g	98
Median all values pg/g	98
Consensus mean, pg/g	98
Standard deviation, pg/g	13
Relative standard deviation, %	13
No. of values reported	64
No. of values removed	2
No. of reported non-detects	1

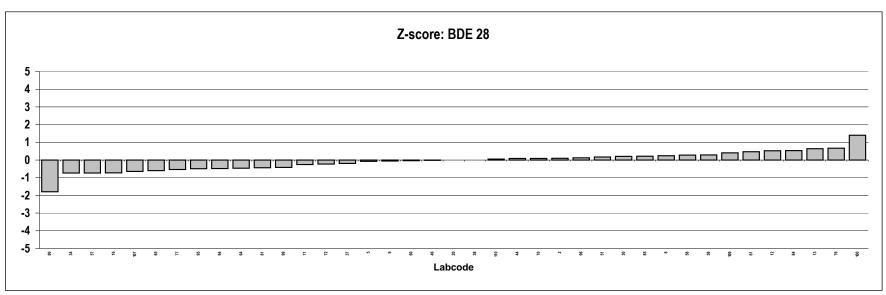




Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
2 5 8	25				
5	25				
8	26				
9 12	25 28				
12	28				
13	28				
16	21				
20	25				
30	26				
34	21				
37	24				
38	25 25				
44	25 25				
46	25				
51	26				
57 58	21 26				
58 59	26 26				
60	26 25				
61	25 27				
64	23				
65	23				
70	22 25				
71	24				
72	24				
76	28				
77	22				
81	23				
84	28				
85	26				
90	16				
94	23				
95	23				
96	26				
99	23				
100	32				
107	22				
109	27				
110	25				

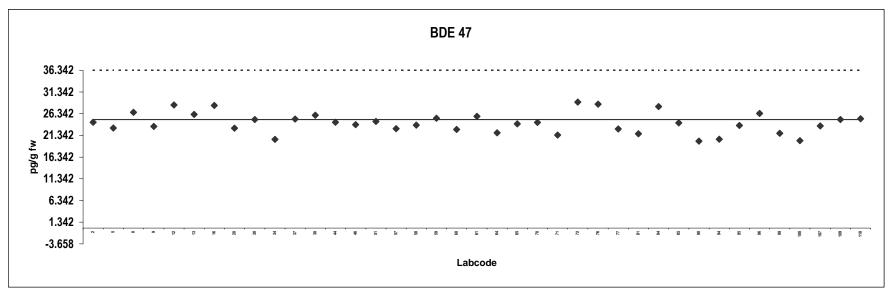
Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	2.7
Relative standard deviation, %	11
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0

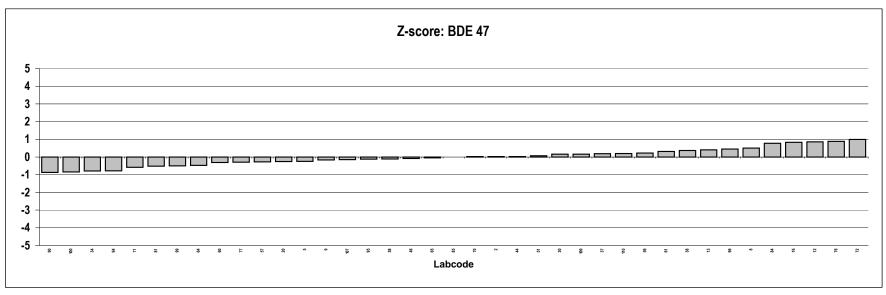




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
	24			100	
2 5 8	23 27				
8	27				
9 12	23				
12	28				
13	26				
16	28				
20	23				
30	25				
34	20				
37	25				
38	26				
44	24				
46	24				
51	25				
57	23				
58	24				
59	25				
60	23				
61	26				
64	22				
65	24				
70 71	24 21				
71 72	29				
76	29 29				
77	23				
81	23				
84	28				
85	26 24				
90	20				
94	20				
95	24				
96	26				
99	22				
100	20				
107	24				
109	25				
110	25				
	<del></del>				

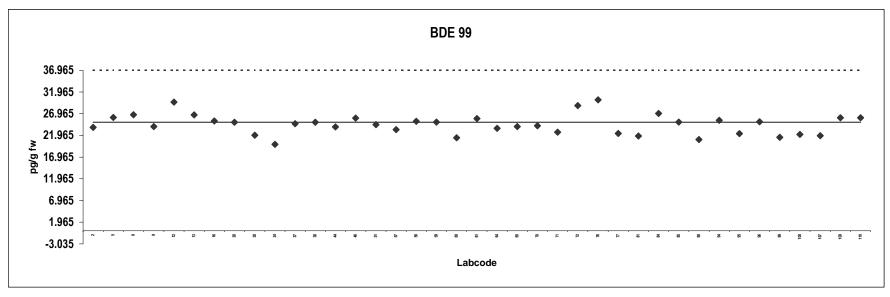
Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2.4
Relative standard deviation, %	10
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0

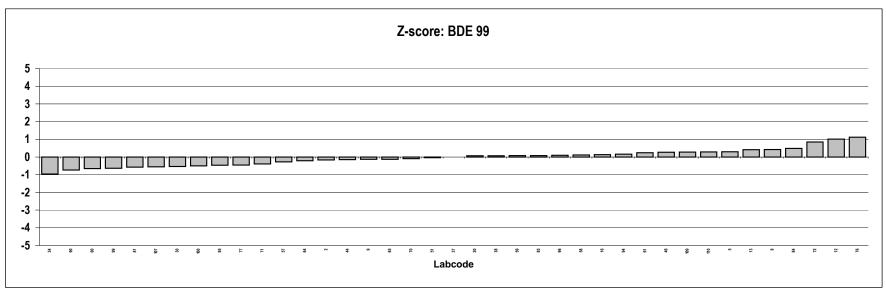




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
	24			100	
2 5 8	26				
8	27				
9 12	24				
12	30				
13	27				
16	25				
20	25				
30	22				
34	20				
37	25				
38	25				
44	24				
46	26				
51	24				
57 <b>5</b> 0	23				
58	25				
59	25				
60	21				
61	26 24				
64	24				
65 70	24 24				
70	23				
72	23 29				
76	30				
77	22				
81	22				
84	27				
85	25				
90	21				
94	25				
95	22				
96	25				
99	22				
100	22				
107	22				
109	26				
110	26				

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	24
Standard deviation, pg/g	2.3
Relative standard deviation, %	9.4
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0

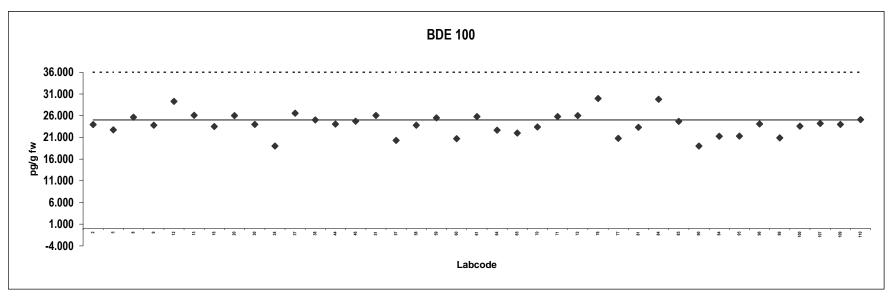


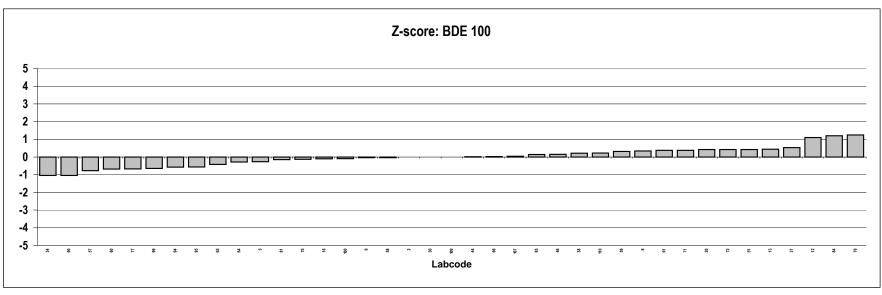


Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
2 5 8	24				
5	23				
8	26				
9 12	24				
12	29				
13	26				
16	24				
20	26				
30	24				
34	19				
37	27				
38	25				
44	24				
46	25				
51	26				
57	20				
58 59	24 25				
59	25				
60 61	21 26				
64	23				
65	23 22				
70	23				
70	25 26				
72	26				
76	30				
77	21				
81	23				
84	30				
85	25				
90	19				
94	21				
95	21				
96	24				
99	21				
100	24				
107	24				
109	24				
110	25				

### Consensus median, pg/g 24

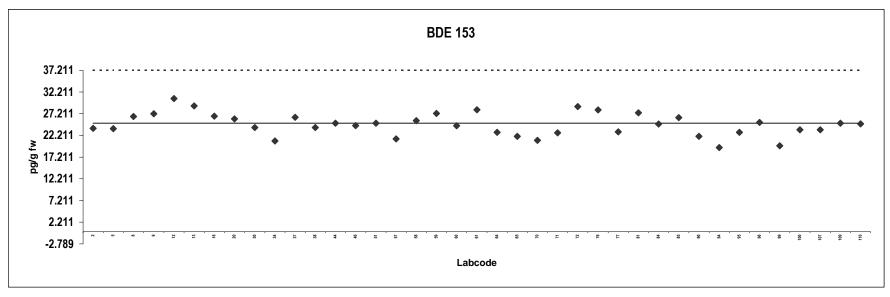
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2.6
Relative standard deviation, %	11
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0

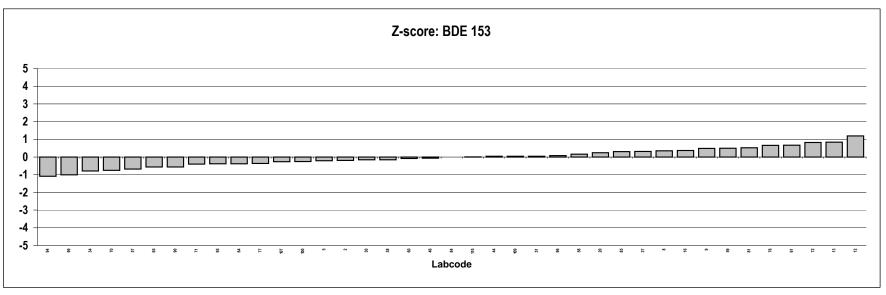




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
	24				
2 5 8	24				
8	27				
9 12	27				
12	31				
13	29				
16	27				
20	26				
30	24				
34	21				
37	26				
38	24				
44	25				
46	24				
51	25				
57 58	21 26				
58 59	26 27				
60	24				
61	28				
64	23				
65	22				
70	21				
71	23				
72	29				
76	28				
77	23				
81	27				
84	25				
85	26				
90	22				
94	19				
95	23				
96	25				
99	20				
100	24				
107	23				
109	25				
110	25				

Consensus median, pg/g	25
Median all values pg/g	25
Consensus mean, pg/g	25
Standard deviation, pg/g	2.6
Relative standard deviation, %	10
No. of values reported	39
No. of values removed	0
No. of reported non-detects	0



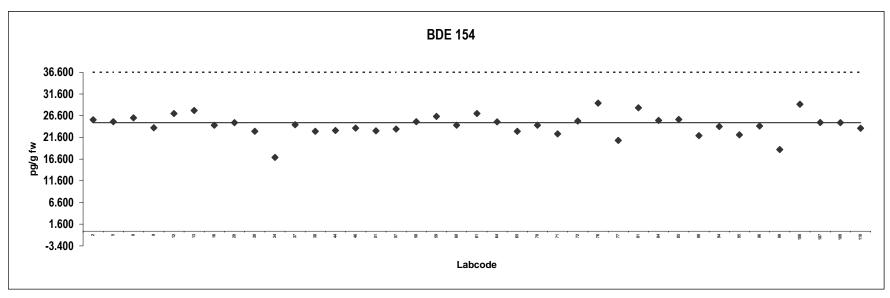


Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
2 5 8	26				
5	25				
8	26				
9 12	24 27				
12	27				
13	28				
16	24				
20	25				
30	23				
34	17				
37	25				
38	23				
44	23				
46	24				
51	23				
57	24				
58	25				
59	26				
60	24				
61	27				
64	25				
65	23				
70	24				
71	22				
72	25				
76	30				
77	21				
81	28				
84	25				
85	26				
90	22				
94	24				
95	22				
96	24				
99	19				
100	29				
107	25				
107	25 25				
110	23 24				
110	24				
1					
L					

#### Consenus statistics Consensus median, pg/g Median all values pg/g 24 24 Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % 24 2.5 10 No. of values reported 39 No. of values removed 0

0

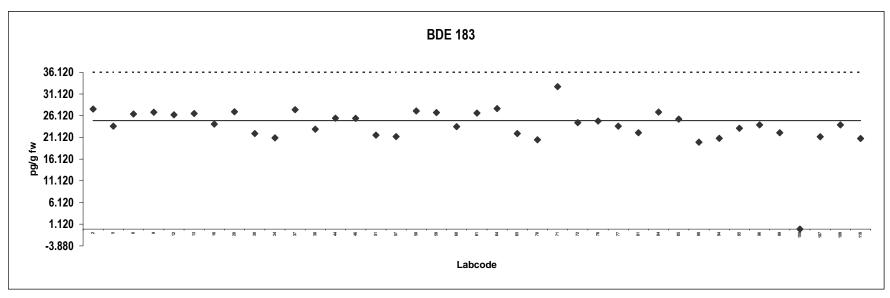
No. of reported non-detects

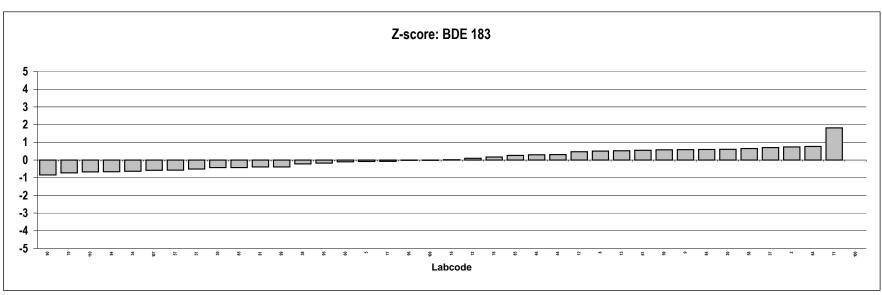




2 5 8	-		Notes	Lab code	Conc. pg/g fw.	Notes
		Conc. pg/g fw.			100	
5		24				
8		26				
9		27				
12		26				
13		27				
16		24				
20		27				
30		22				
34		21				
37		27				
38		23				
44		26				
46		25				
51		22				
57		21				
58		27				
59		27				
60		24				
61		27				
64		28				
65		22				
70		21				
71		33				
72		25				
76		25				
77		24				
81		22				
84		27				
85		25				
90		20				
94		21 23				
95 96		23 24				
96		24 22				
100		not reported	Outlier,ND			
100		not reported 21	Junet, ND			
107		24				
110		21				
110		∠1				

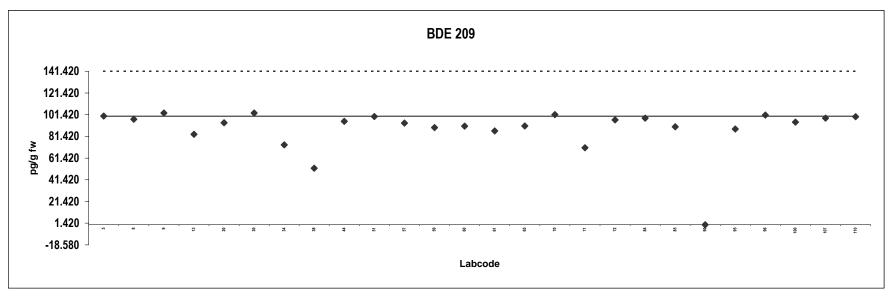
	24
Consensus median, pg/g	24
Median all values pg/g	24
Consensus mean, pg/g	24
Standard deviation, pg/g	2.8
Relative standard deviation, %	11
No. of values reported	38
No. of values removed	0
No. of reported non-detects	1

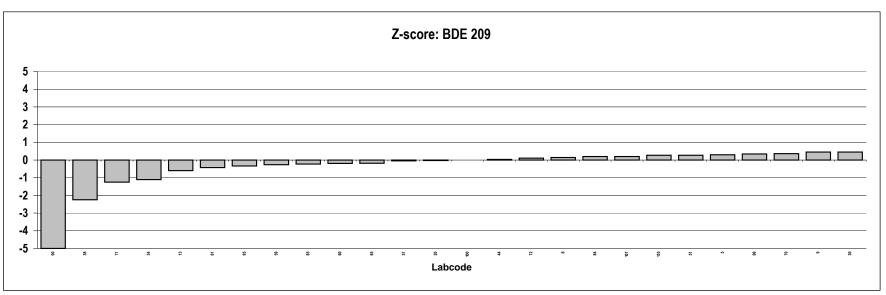




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
5 8 9	100			F8-8	- 12 122
8	97 103				
9	103				
13	83				
20	94				
30	103				
34	74				
38	52				
44	95				
51	100				
57	94				
59	90				
60	91				
61	86				
61 65	91				
70	101				
71	71				
72	97				
84	98				
85	90	0 41 170			
90	0.0	Outlier,ND			
95	88				
96	101				
100	95				
107	98				
110	100				

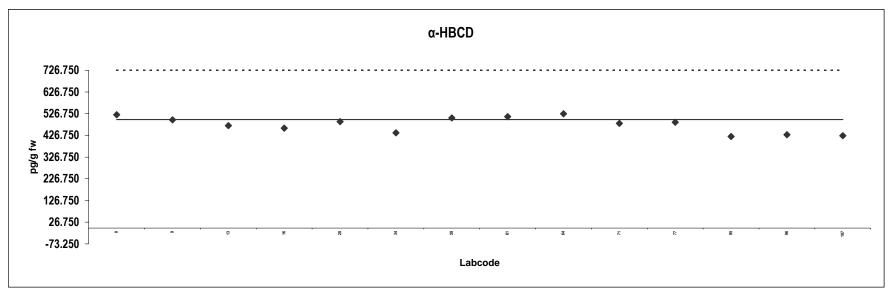
Consensus median, pg/g	95
Median all values pg/g	94
Consensus mean, pg/g	92
Standard deviation, pg/g	12
Relative standard deviation, %	13
No. of values reported	26
No. of values removed	1
No. of reported non-detects	1

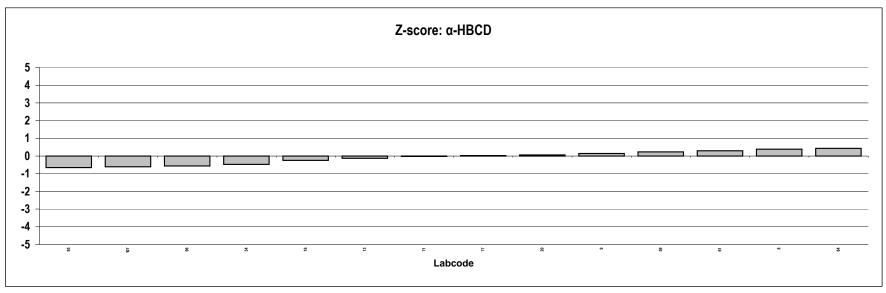




Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
8 9 13	522			100	
9	498 472				
16	460				
16 20	490				
34 59	439 507				
61	507 513				
64	513 526				
71 77	482 487				
95	421				
96	430				
107	425				

Consensus median, pg/g	485
Median all values pg/g	485
Consensus mean, pg/g	477
Standard deviation, pg/g	36
Relative standard deviation, %	7.6
No. of values reported	14
No. of values removed	0
No. of reported non-detects	0





## Appendix 2:

Presentation of results for reindeer meat

### **Appendix 2: Presentation of results: Reindeer meat**

#### Statistic calculations for PCDDs, PCDFs and dioxin-like PCBs

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

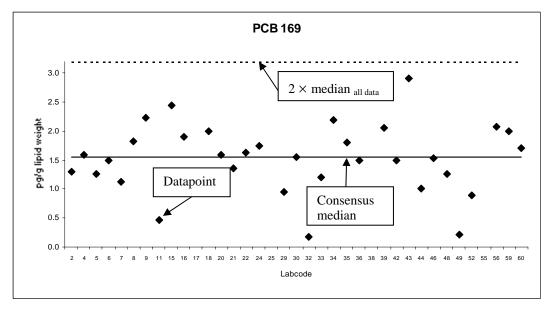
- 1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
- 2. Values exceeding  $2 \times$  this median, were defined as outliers and removed from the data set.
- 3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.

#### Statistic calculations for indicator PCBs, PBDEs and HBCD

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

- 1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners (NDs).
- 2. Values exceeding  $2 \times$  this median, were defined as outliers and removed from the data set. The NDs were also removed.
- 3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.
- 4. For comparison, median, mean and standard deviation were also calculated without removing NDs.

The diagram shows the reported data up to approximately the limit for outliers ( $2 \times$  the first median).



#### **Z-Scores of individual congeners**

Z-scores of each congener were calculated for each laboratory according to the following equation:

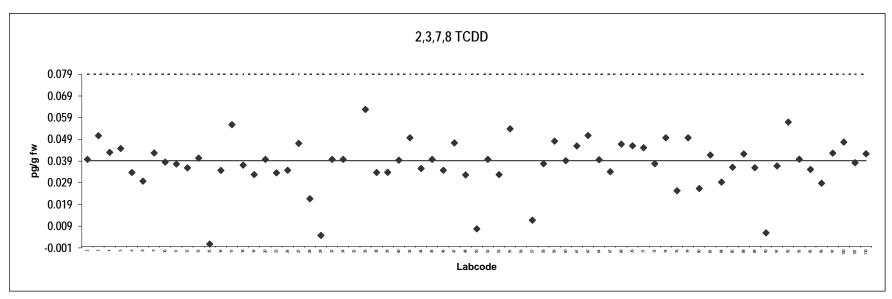
$$z = (x - X)/\sigma$$

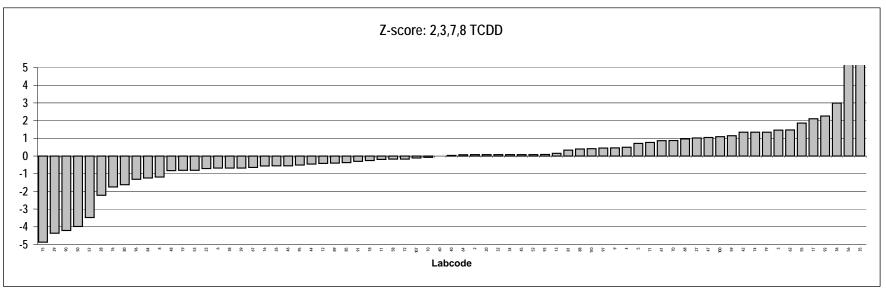
where x = reported value; X = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm$  20% from the consensus value.

Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.040		62	0.051	
3	0.051		64	0.040	
4	0.043		67	0.034	
5	0.045		68	0.047	
6	0.034		70	0.046	
8	0.030	ND	71	0.045	
9	0.043		72	0.038	
10	0.039		74	0.050	ND
11	0.038		76	0.026	
12	0.036		79	0.050	
13	0.041		80	0.027	
15	0.0010	ND	81	0.042	
16	0.035		84	0.030	
17	0.056	ND	85	0.036	
18	0.037		88	0.043	
19	0.033		89	0.036	
20	0.040		90	0.0062	ND
23	0.034		91	0.037	
26	0.035		92	0.057	
27	0.047		93	0.040	
28	0.022		95	0.035	
29	0.0050	ND	96	0.029	
32	0.040		97	0.043	
34	0.040		100	0.048	
35	0.38	Outlier	107	0.039	
36	0.063		110	0.043	
38	0.034				
39	0.034				
40	0.040				
42	0.050	ND			
44	0.036				
45	0.040				
46	0.035				
47	0.048				
48	0.033				
50	0.0080	ND			
52	0.040				
53	0.033				
55	0.054				
56	0.095	Outlier,ND			
57	0.012	ND			
58	0.038				
59	0.048				
60	0.039				
61	0.046				

Consensus median, pg/g	0.039
Median all values pg/g	0.040
Consensus mean, pg/g	0.038
Standard deviation, pg/g	0.012
Relative standard deviation, %	31
No. of values reported	71
No. of values removed	2
No. of reported non-detects	10

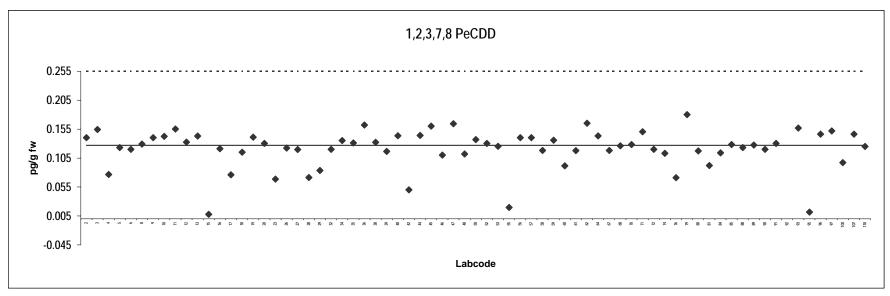


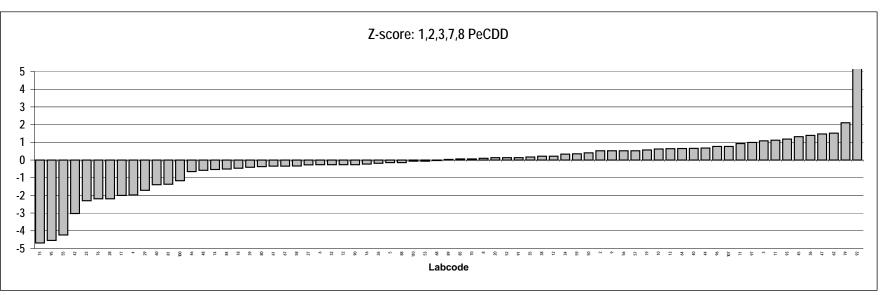


**Congener: 1,2,3,7,8 PeCDD** 

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
		Notes			Notes
2 3	0.14		62 64	0.17	
4	0.15			0.14	
5	0.077 0.12		67 68	0.12 0.13	
5			70		
6 8	0.12		70	0.13	
8	0.13		71	0.15	
9	0.14		72	0.12	
10	0.14		74	0.11	
11	0.15		76	0.071	
12	0.13		79	0.18	
13	0.14		80	0.12	
15	0.0077		81	0.092	
16	0.12		84	0.11	
17	0.076		85	0.13	
18	0.12		88	0.12	
19	0.14		89	0.13	
20	0.13		90	0.12	
23	0.068		91	0.13	
26	0.12		92	0.33	Outlier
27	0.12		93	0.16	
28	0.071		95	0.011	
29	0.083		96	0.15	
32	0.12		97	0.15	
34	0.14		100	0.097	
35	0.13		107	0.15	
36	0.16		110	0.12	
38	0.13				
39	0.12				
40	0.14				
42	0.050				
44	0.14				
45	0.16				
46	0.11				
47	0.16				
48	0.11				
50	0.14				
52	0.13				
53	0.13				
55	0.019	ND			
56	0.14	ND			
57	0.14				
58	0.12				
59	0.14				
60	0.091				
61	0.12				

Consensus median, pg/g	0.13 0.13
Median all values pg/g	0.13
Consensus mean, pg/g	0.12
Standard deviation, pg/g	0.034
Relative standard deviation, % No. of values reported	28 71
No. of values removed	1
No. of reported non-detects	2



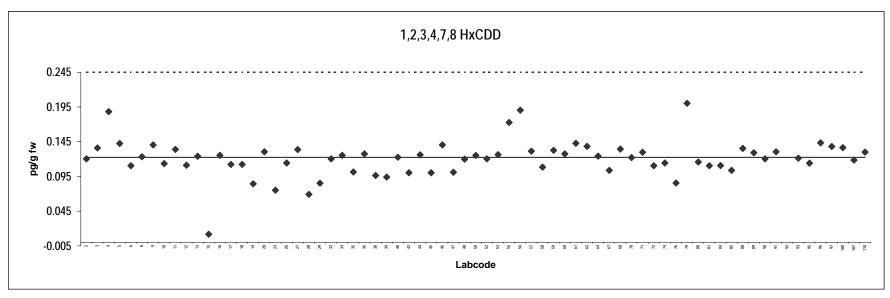


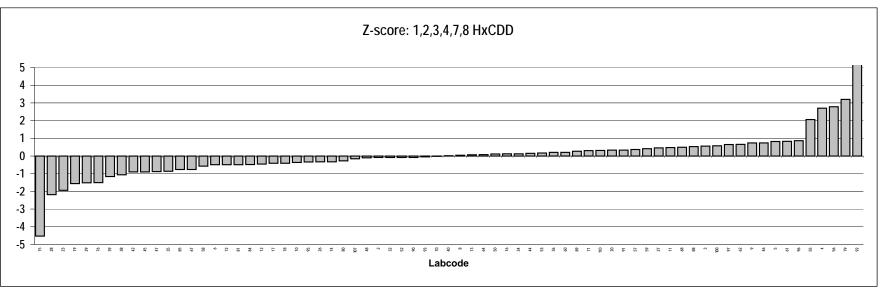
**Congener: 1,2,3,4,7,8 HxCDD** 

					ongener:
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2 3	0.12		62	0.14	
3	0.14		64	0.12	
4	0.19		67	0.10	
5	0.14		68	0.13	
6	0.11		70	0.12	
8	0.12		71	0.13	
9	0.14		72	0.11	
10	0.11		74	0.11	
11	0.13		76	0.085	
12	0.11		79	0.20	
13	0.12		80	0.12	
15	0.011		81	0.11	
16	0.12		84	0.11	
17	0.11		85	0.10	
18	0.11		88 89	0.14	
19 20	0.084 0.13		89 90	0.13 0.12	
23	0.13		90	0.12	
26	0.073		92	0.13	Outlier
27	0.11		93	0.34	Outlief
28	0.069		95 95	0.12	
29	0.085		96	0.14	
32	0.12		97	0.14	
34	0.13		100	0.14	
35	0.10		107	0.12	
36	0.13		110	0.13	
38	0.096			*****	
39	0.094				
40	0.12				
42	0.10	ND			
44	0.13				
45	0.10				
46	0.14				
47	0.10				
48	0.12				
50	0.12				
52	0.12				
53	0.13				
55	0.17				
56	0.19	ND			
57	0.13				
58	0.11				
59	0.13				
60	0.13				
61	0.14				

Consenus statistics		
Consensus median, pg/g Median all values pg/g Consensus mean, pg/g	0.12 0.12 0.12	
Standard deviation, pg/g	0.026	
Relative standard deviation, %	22	
No. of values reported	71	
No. of values removed	I 1	

No. of reported non-detects

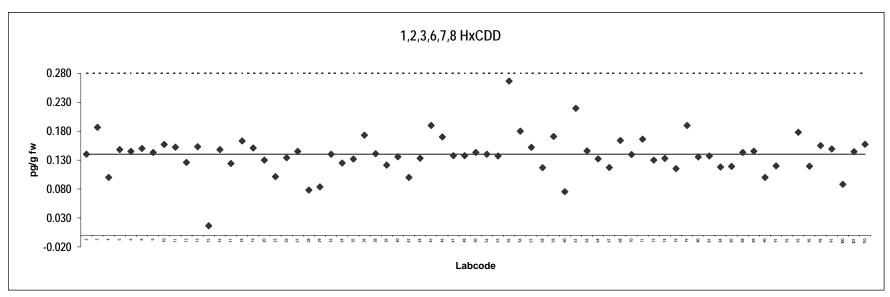


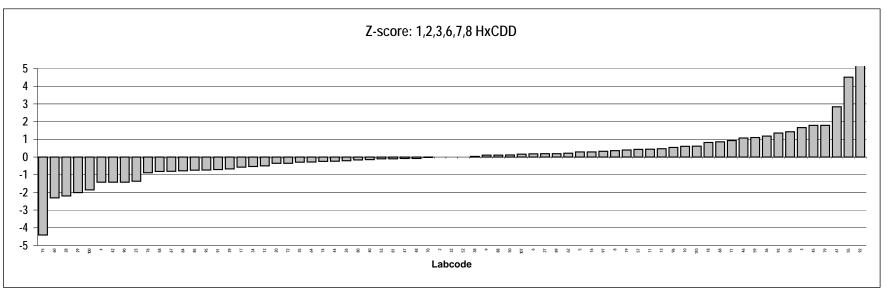


Congener: 1,2,3,6,7,8 HxCDD

Notes
Outlier
ND
ND
1

Consensus median, pg/g	0.14
Median all values pg/g	0.14
Consensus mean, pg/g	0.14
Standard deviation, pg/g	0.034
Relative standard deviation, %	24
No. of values reported	71
No. of values removed	1
No. of reported non-detects	3

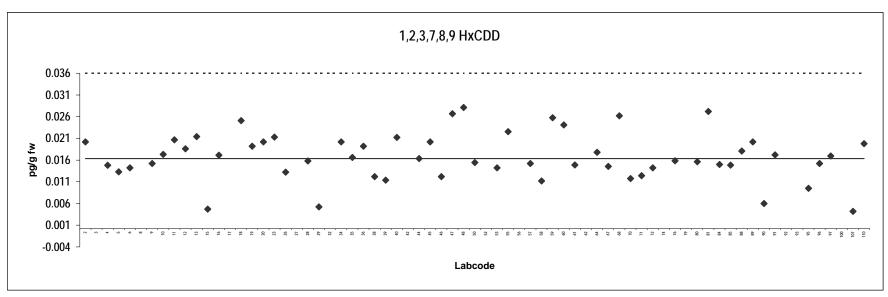


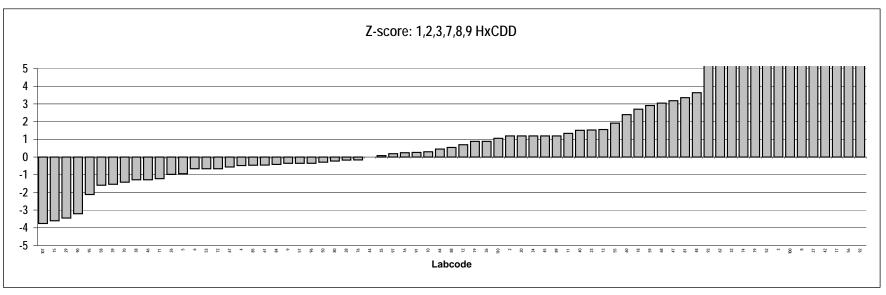


Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.020		62	0.039	Outlier,ND
3	0.089	Outlier	64	0.018	
4	0.015	ND	67	0.014	
5	0.013		68	0.026	
6	0.014		70	0.012	
8	0.10	Outlier	71	0.012	
9	0.015		72	0.014	
10	0.017		74	0.050	Outlier,ND
11	0.020		76	0.016	
12	0.018		79	0.056	Outlier
13	0.021		80	0.015	
15	0.0045		81	0.027	
16	0.017		84	0.015	
17	0.13	Outlier,ND	85	0.015	
18	0.025		88	0.018	
19	0.019		89	0.020	
20	0.020		90	0.0058	ND
23	0.021		91	0.017	
26	0.013		92	0.26	Outlier
27	0.10	Outlier,ND	93	0.039	Outlier
28	0.016		95	0.0093	
29	0.0050	ND	96	0.015	
32	0.050	Outlier,ND	97	0.017	
34	0.020		100	0.090	Outlier,ND
35	0.016		107	0.0040	ND
36	0.019		110	0.020	
38	0.012				
39	0.011				
40	0.021				
42	0.10	Outlier,ND			
44	0.016				
45	0.020				
46	0.012				
47	0.026				
48	0.028				
50	0.015				
52	0.080	Outlier,ND			
53	0.014				
55	0.022	ND			
56	0.18	Outlier,ND			
57	0.015	ND			
58	0.011	ND			
59	0.026				
60	0.024	ND			
61	0.015				

Consensus median, pg/g	0.016
Median all values pg/g	0.018
Consensus mean, pg/g	0.017
Standard deviation, pg/g	0.0054
Relative standard deviation, %	33
No. of values reported	71
No. of values removed	14
No. of reported non-detects	17

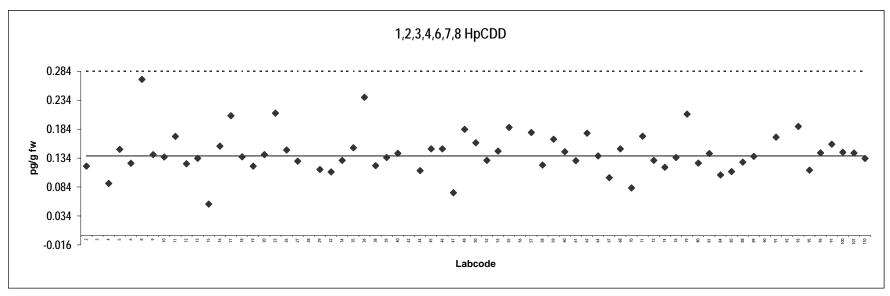


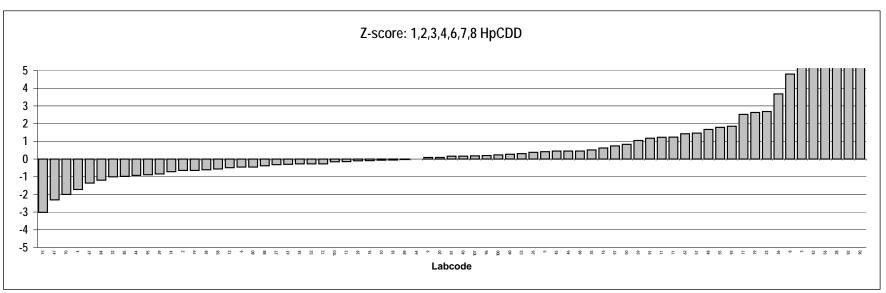


Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.12		62	0.18	
3	0.30	Outlier	64	0.14	
4	0.090		67	0.10	
5	0.15		68	0.15	
6	0.13		70	0.083	
8	0.27		71	0.17	
9	0.14		72	0.13	
10	0.14		74	0.12	
11	0.17		76	0.13	
12	0.12		79	0.21	
13	0.13		80	0.13	
15	0.055		81	0.14	
16	0.15		84	0.10	
17	0.21	ND	85	0.11	
18	0.14		88	0.13	
19	0.12		89	0.14	
20	0.14		90	1.8	Outlier
23	0.21		91	0.17	
26	0.15		92	0.54	Outlier
27	0.13		93	0.19	
28	0.31	Outlier	95	0.11	
29	0.11		96	0.14	
32	0.11		97	0.16	
34	0.13		100	0.14	
35	0.15		107	0.14	
36	0.24		110	0.13	
38	0.12				
39	0.13				
40	0.14				
42	0.30	Outlier,ND			
44	0.11				
45	0.15				
46	0.15				
47	0.074				
48	0.18				
50	0.16				
52	0.13				
53	0.15				
55	0.19				
56	0.31	Outlier,ND			
57	0.18				
58	0.12				
59	0.17				
60	0.15				
61	0.13				

Consenus statistics				
Consensus median, pg/g	0.14			
Median all values pg/g	0.14			
Consensus mean, pg/g	0.14			
Standard deviation, pg/g	0.036			
Relative standard deviation, %	25			
No. of values reported	71			
No. of values removed	6			
No. of reported non-detects	3			





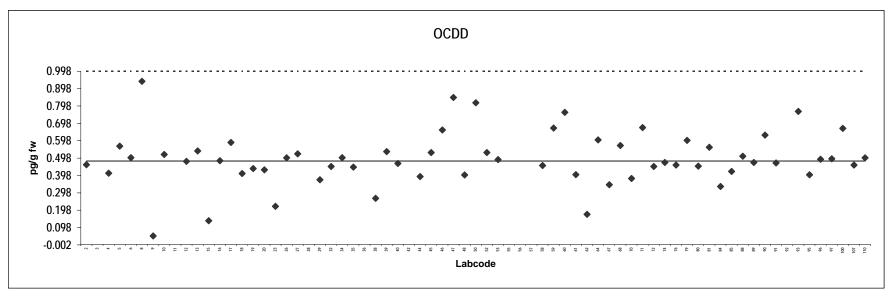
**Congener: OCDD** 

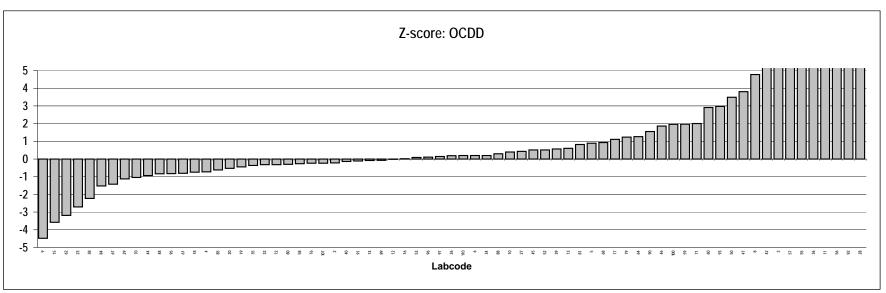
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.46		62	0.17	ND
3	1.1	Outlier	64	0.60	
4	0.41		67	0.34	
5	0.57		68	0.57	
6	0.50		70	0.38	
8	0.94		71	0.67	
9	0.050	ND	72	0.45	
10	0.52		74	0.47	
11	1.5	Outlier	76	0.46	
12	0.48		79	0.60	
13	0.54		80	0.45	
15	0.14		81	0.56	
16	0.48		84	0.33	
17	0.59		85	0.42	
18	0.41		88	0.51	
19	0.44		89	0.47	
20	0.43		90	0.63	
23	0.22		91	0.47	
26	0.50		92	1.8	Outlier
27	0.52		93	0.77	
28	2.4	Outlier	95	0.40	
29	0.37		96	0.49	
32	0.45		97	0.49	
34	0.50		100	0.67	
35	0.45		107	0.46	
36	1.4	Outlier	110	0.50	
38	0.27				
39	0.54				
40	0.47				
42	1.0	Outlier,ND			
44	0.39				
45	0.53				
46	0.66				
47	0.85				
48	0.40				
50	0.82				
52	0.53				
53	0.49	0.41			
55	1.2	Outlier			
56	1.7	Outlier,ND			
57	1.1	Outlier			
58	0.46				
59	0.67				
60	0.76				
61	0.40				

Consensus median, pg/g	0.48
Median all values pg/g	0.50
Consensus mean, pg/g	0.49
Standard deviation, pg/g	0.16
Relative standard deviation, %	32
No. of values reported	71
No. of values removed	9

Consenus statistics

No. of reported non-detects

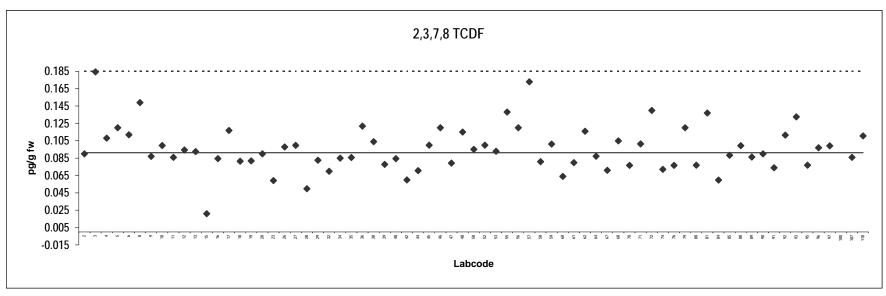


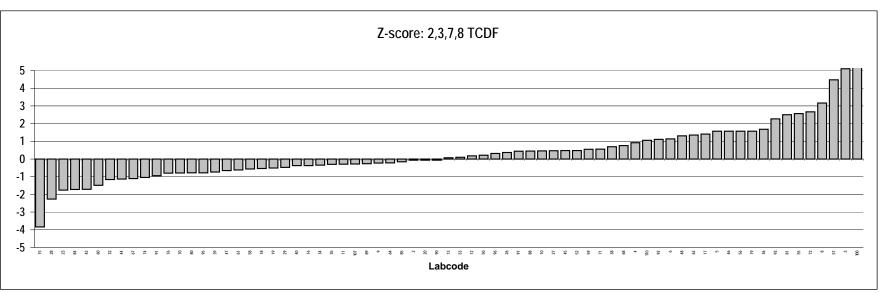


Congener: 2,3,7,8 TCDF

					Congen
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.090		62	0.12	
3	0.18		64	0.087	
4	0.11		67	0.071	
5	0.12		68	0.11	
6	0.11		70	0.077	
8	0.15		71	0.10	
9	0.087		72	0.14	
10	0.100		74	0.072	
11	0.086		76	0.077	
12	0.095		79	0.12	
13	0.093		80	0.077	
15	0.021		81	0.14	
16	0.084		84	0.060	
17	0.12		85	0.088	
18	0.082		88	0.100	
19	0.082		89	0.086	
20	0.090		90	0.090	
23	0.059		91	0.074	
26	0.098		92	0.11	
27	0.100		93	0.13	
28	0.050		95	0.077	
29	0.083		96	0.097	
32	0.070		97	0.099	0.41
34	0.085		100	0.22	Outlier
35	0.086		107	0.086	
36	0.12		110	0.11	
38 39	0.10				
40	0.078 0.084				
40					
44	0.060 0.071				
44	0.071				
46	0.10				
47	0.079				
48	0.079				
50	0.095				
52	0.10				
53	0.093				
55	0.093				
56	0.12	ND			
57	0.12	1112			
58	0.081				
59	0.10				
60	0.064				
61	0.080				

Consensus median, pg/g	0.09
Median all values pg/g	0.09
Consensus mean, pg/g	0.10
Standard deviation, pg/g	0.027
Relative standard deviation, %	28
No. of values reported	71
No. of values removed	1
No. of reported non-detects	1



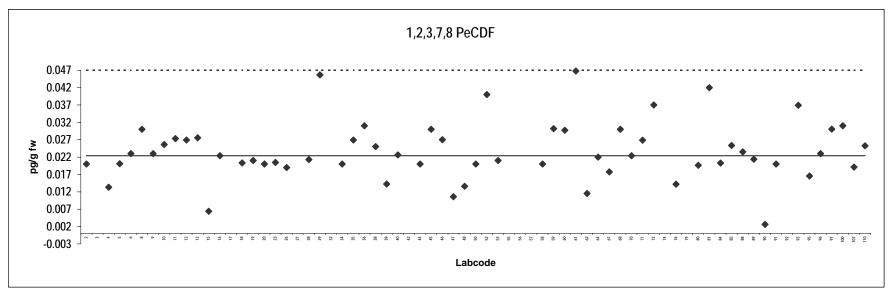


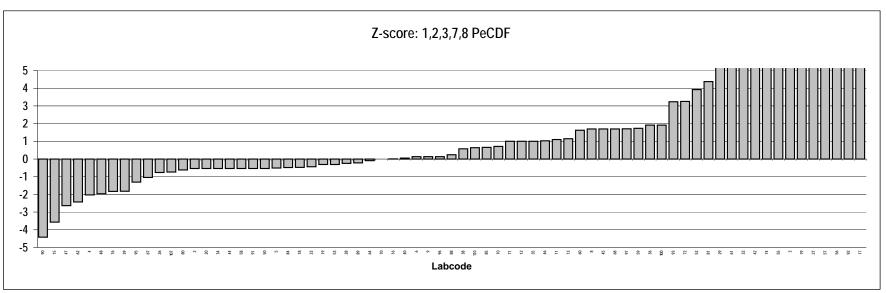
**Congener: 1,2,3,7,8 PeCDF** 

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.020		62	0.012	ND
3	0.078	Outlier	64	0.022	
4	0.013	ND	67	0.018	
5	0.020		68	0.030	
6	0.023		70	0.022	
8	0.030	ND	71	0.027	
9	0.023		72	0.037	
10	0.026		74	0.050	Outlier,ND
11	0.027		76	0.014	ND
12	0.027		79	0.087	Outlier
13	0.028		80	0.020	
15	0.0064		81	0.042	
16	0.022		84	0.020	
17	0.67	Outlier	85	0.025	
18	0.020		88	0.024	
19	0.021		89	0.021	
20	0.020		90	0.0026	ND
23	0.020		91	0.020	
26	0.019		92	0.19	Outlier
27	0.10	Outlier,ND	93	0.037	
28	0.021		95	0.017	
29	0.046		96	0.023	
32	0.050	Outlier,ND	97	0.030	
34	0.020		100	0.031	ND
35	0.027		107	0.019	
36	0.031		110	0.025	
38	0.025				
39	0.014				
40	0.023				
42	0.050	Outlier,ND			
44	0.020				
45	0.030				
46	0.027				
47	0.011				
48	0.014				
50	0.020				
52	0.040	ND			
53	0.021				
55	0.067	Outlier			
56	0.13	Outlier,ND			
57	0.13	Outlier			
58	0.020				
59	0.030				
60	0.030				
61	0.047				

Consenus	statistics	

Consensus median, pg/g	0.022
Median all values pg/g	0.024
Consensus mean, pg/g	0.024
Standard deviation, pg/g	0.0084
Relative standard deviation, %	36
No. of values reported	71
No. of values removed	11
No. of reported non-detects	12



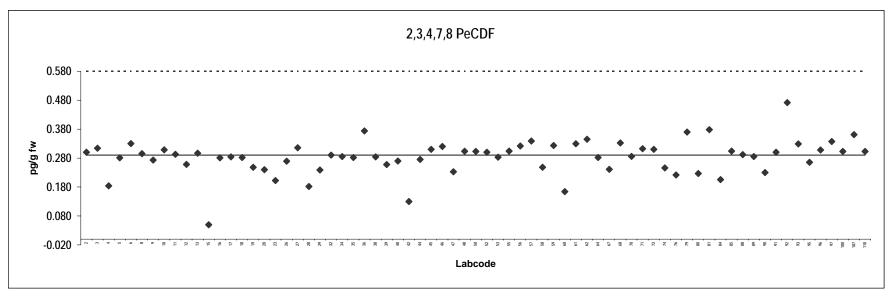


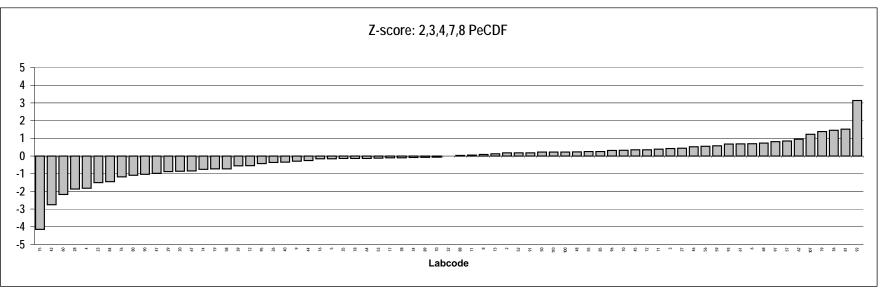
Congener: 2,3,4,7,8 PeCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.30		62	0.35	
3	0.31		64	0.28	
4	0.18		67	0.24	
5	0.28		68	0.33	
6	0.33		70	0.29	
8	0.30		71	0.31	
9	0.27		72	0.31	
10	0.31		74	0.25	
11	0.29		76	0.22	
12	0.26		79	0.37	
13	0.30		80	0.23	
15	0.050		81	0.38	
16	0.28		84	0.21	
17	0.28		85	0.30	
18	0.28		88	0.29	
19	0.25		89	0.29	
20	0.24		90	0.23	
23	0.20		91	0.30	
26	0.27		92	0.47	
27	0.32		93	0.33	
28	0.18		95	0.27	
29	0.24		96	0.31	
32	0.29		97	0.34	
34	0.29		100	0.30	
35	0.28		107	0.36	
36	0.37		110	0.30	
38	0.28				
39	0.26				
40	0.27				
42	0.13				
44	0.28				
45	0.31				
46	0.32				
47	0.23				
48	0.30				
50	0.30				
52	0.30				
53	0.28				
55	0.30				
56	0.32				
57	0.34				
58	0.25				
59	0.32				
60	0.16				
61	0.33				

Consenus	statistics

Constitus statistics	
Consensus median, pg/g Median all values pg/g Consensus mean, pg/g	0.29 0.29 0.28
Standard deviation, pg/g Relative standard deviation, %	0.060 21
No. of values reported No. of values removed	71 0
No. of reported non-detects	U

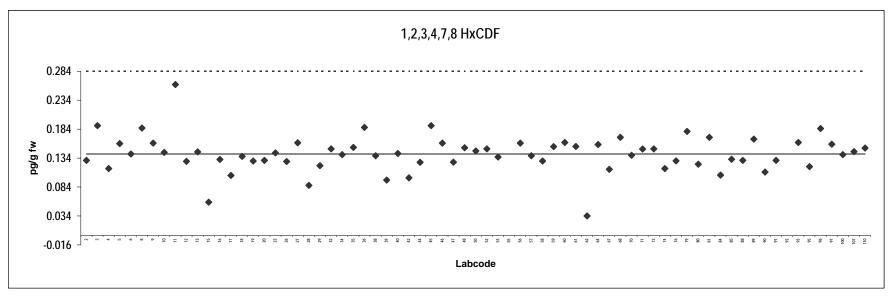


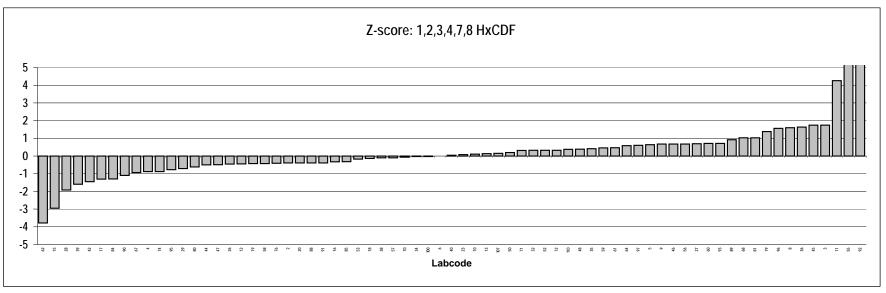


**Congener: 1,2,3,4,7,8 HxCDF** 

				•	ongener:
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.13		62	0.034	ND
3	0.19		64	0.16	
4	0.12		67	0.11	
5	0.16		68	0.17	
6	0.14		70	0.14	
8	0.19		71	0.15	
9	0.16		72	0.15	
10	0.14		74	0.12	
11	0.26		76	0.13	
12	0.13		79	0.18	
13	0.14		80	0.12	
15	0.058		81	0.17	
16	0.13		84	0.10	
17	0.10		85	0.13	
18	0.14		88	0.13	
19	0.13		89	0.17	
20	0.13		90	0.11	
23	0.14		91	0.13	
26	0.13		92	0.33	Outlier
27	0.16		93	0.16	
28	0.087		95	0.12	
29	0.12		96	0.19	
32	0.15		97	0.16	
34	0.14		100	0.14	
35	0.15		107	0.15	
36	0.19		110	0.15	
38	0.14				
39	0.096				
40	0.14				
42	0.10	ND			
44	0.13				
45	0.19				
46	0.16				
47	0.13				
48	0.15				
50	0.15				
52	0.15				
53	0.14				
55	0.31	Outlier			
56	0.16	ND			
57	0.14				
58	0.13				
59	0.15				
60	0.16				
61	0.15				

Consensus median, pg/g	0.14
Median all values pg/g	0.14
Consensus mean, pg/g	0.14
Standard deviation, pg/g	0.031
Relative standard deviation, %	22
No. of values reported	71
No. of values removed	2
No. of reported non-detects	3



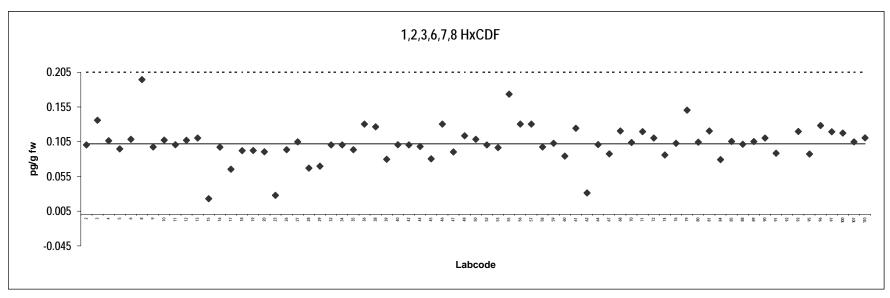


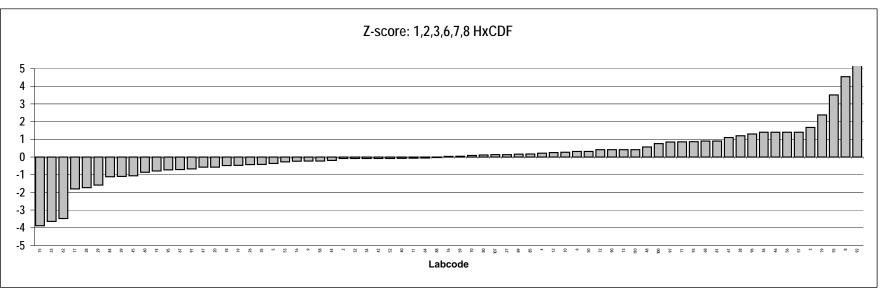
**Congener: 1,2,3,6,7,8 HxCDF** 

				•	ongener:
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.10		62	0.031	ND
3	0.14		64	0.10	
4	0.11		67	0.087	
5	0.094		68	0.12	
6	0.11		70	0.10	
8	0.19		71	0.12	
9	0.097		72	0.11	
10	0.11		74	0.086	
11	0.10		76	0.10	
12	0.11		79	0.15	
13	0.11		80	0.10	
15	0.023		81	0.12	
16	0.097		84	0.079	
17	0.065	ND	85	0.11	
18	0.092		88	0.10	
19	0.092		89	0.10	
20	0.090		90	0.11	
23	0.028		91	0.088	
26	0.093		92	0.30	Outlier
27	0.10		93	0.12	
28	0.067		95	0.087	
29	0.069		96	0.13	
32	0.10		97	0.12	
34	0.10		100	0.12	
35	0.093		107	0.10	
36	0.13		110	0.11	
38	0.13				
39	0.079				
40	0.10				
42	0.10	ND			
44	0.098				
45	0.080				
46	0.13				
47	0.090				
48	0.11				
50	0.11				
52	0.10				
53	0.096				
55	0.17				
56	0.13	ND			
57	0.13				
58	0.097				
59	0.10				
60	0.084				
61	0.12				

Cons	enus	statistics	

Consensus median, pg/g	0.10
Median all values pg/g	0.10
Consensus mean, pg/g	0.10
Standard deviation, pg/g	0.026
Relative standard deviation, %	26
No. of values reported	71
No. of values removed	1
No. of reported non-detects	4





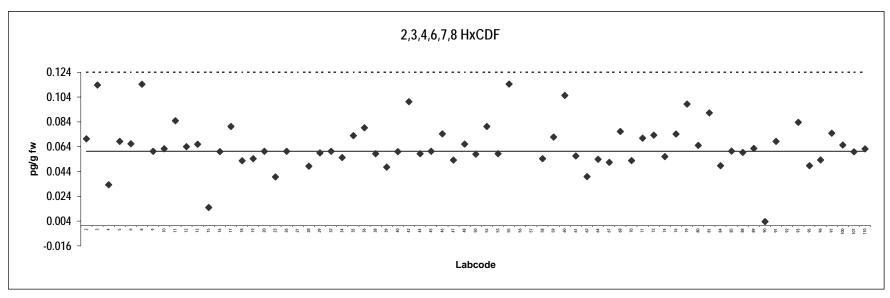
**Congener: 2,3,4,6,7,8 HxCDF** 

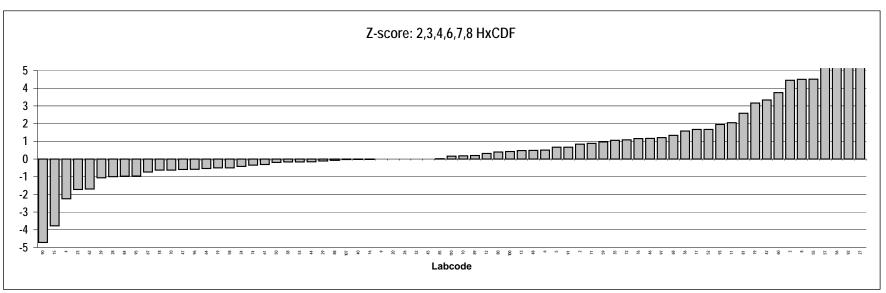
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.070	1,000	62	0.040	ND
3	0.11		64	0.054	112
4	0.033		67	0.051	
5	0.068		68	0.076	
6	0.066		70	0.052	
8	0.11		71	0.071	
9	0.060		72	0.073	
10	0.062		74	0.056	
11	0.085		76	0.074	
12	0.064		79	0.098	
13	0.066		80	0.065	
15	0.015		81	0.091	
16	0.060		84	0.048	
17	0.080	ND	85	0.060	
18	0.052	112	88	0.059	
19	0.054		89	0.062	
20	0.060		90	0.0034	ND
23	0.039		91	0.068	112
26	0.060		92	0.25	Outlier
27	808	Outlier	93	0.083	outher
28	0.048	Guiller	95	0.048	
29	0.059		96	0.053	
32	0.060		97	0.075	
34	0.055		100	0.065	ND
35	0.073		107	0.060	1,12
36	0.079		110	0.062	
38	0.058		110	0.002	
39	0.047				
40	0.060				
42	0.10	ND			
44	0.058				
45	0.060				
46	0.074				
47	0.053				
48	0.066				
50	0.058				
52	0.080	ND			
53	0.058				
55	0.11				
56	0.17	Outlier,ND			
57	0.13	Outlier			
58	0.054				
59	0.072				
60	0.11				
61	0.056				

Consensus median, pg/g	0.06
Median all values pg/g	0.06
Consensus mean, pg/g	0.06
Standard deviation, pg/g	0.020
Relative standard deviation, %	31
No. of values reported	71
No. of values removed	4

Consenus statistics

No. of reported non-detects

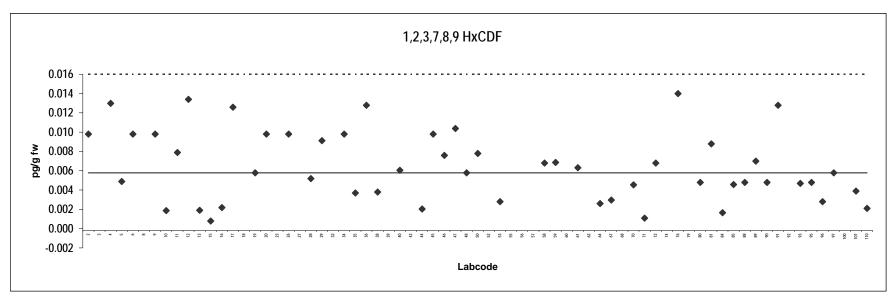


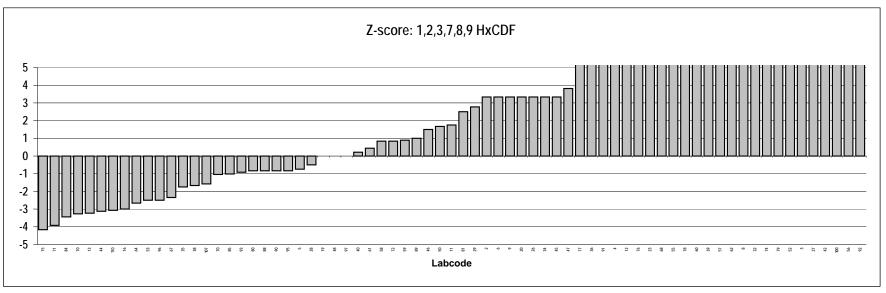


**Congener: 1,2,3,7,8,9 HxCDF** 

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010	ND	62	0.040	Outlier,ND
3	0.081	Outlier	64	0.0028	
4	0.013	ND	67	0.0032	ND
5	0.0051	ND	68	0.020	Outlier,ND
6	0.010	ND	70	0.0047	ND
8	0.050	Outlier,ND	71	0.0013	ND
9	0.010	ND	72	0.0070	
10	0.0021		74	0.050	Outlier,ND
11	0.0081	ND	76	0.014	ND
12	0.014	ND	79	0.058	Outlier
13	0.0021		80	0.0050	ND
15	0.0010	ND	81	0.0090	
16	0.0024	ND	84	0.0019	
17	0.013	ND	85	0.0048	
18	0.022	Outlier	88	0.0050	ND
19	0.0060	ND	89	0.0072	ND
20	0.010	ND	90	0.0050	ND
23	0.018	Outlier	91	0.013	
26	0.010	ND	92	0.21	Outlier
27	0.10	Outlier,ND	93	0.0049	
28	0.0054		95	0.0050	ND
29	0.0093		96	0.0030	ND
32	0.050	Outlier,ND	97	0.0060	ND
34	0.010	ND	100	0.12	Outlier,ND
35	0.0039	ND	107	0.0041	ND
36	0.013		110	0.0023	
38	0.0040				
39	0.030	Outlier,ND			
40	0.0063	ND			
42	0.10	Outlier,ND			
44	0.0023				
45	0.010	ND			
46	0.0078				
47	0.011				
48	0.0060	ND			
50	0.0080	ND			
52	0.080	Outlier,ND			
53	0.0030	ND			
55	0.021	Outlier,ND			
56	0.15	Outlier,ND			
57	0.032	Outlier			
58	0.0070	ND			
59	0.0071				
60	0.023	Outlier,ND			
61	0.0065				

Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported	0.0060 0.0081 0.0067 0.0036 54 71
No. of values removed No. of reported non-detects	19 46

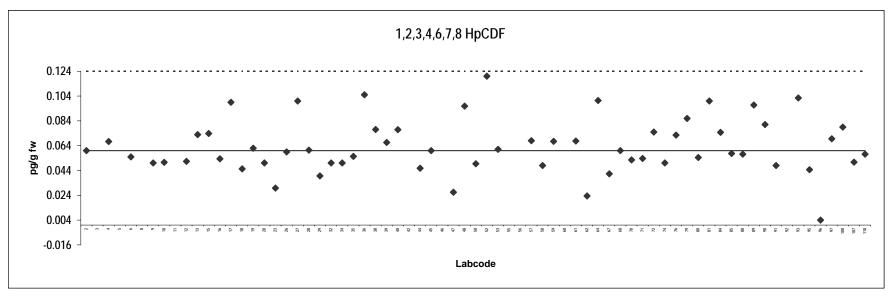


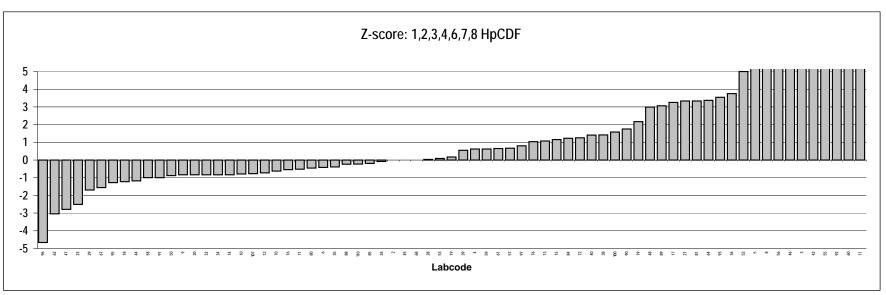


Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.060		62	0.023	ND
3	0.24	Outlier	64	0.10	
4	0.067		67	0.041	
5	0.14	Outlier	68	0.060	
6	0.055		70	0.052	
8	0.15	Outlier	71	0.054	
9	0.050		72	0.075	
10	0.051		74	0.050	ND
11	1.3	Outlier	76	0.072	
12	0.051		79	0.086	
13	0.073		80	0.054	
15	0.074		81	0.10	
16	0.053		84	0.075	
17	0.099	ND	85	0.058	
18	0.045		88	0.057	
19	0.062		89	0.097	
20	0.050		90	0.081	
23	0.030		91	0.048	
26	0.059		92	0.31	Outlier
27	0.10	ND	93	0.10	
28	0.060		95	0.045	
29	0.040		96	0.0040	ND
32	0.050	ND	97	0.070	
34	0.050		100	0.079	
35	0.055		107	0.051	
36	0.11		110	0.057	
38	0.077				
39	0.067				
40	0.077				
42	0.30	Outlier,ND			
44	0.046				
45	0.060				
46	0.19	Outlier			
47	0.026				
48	0.096				
50	0.049				
52	0.12	ND			
53	0.061				
55	0.31	Outlier			
56	0.18	Outlier,ND			
57	0.068				
58	0.048				
59	0.067				
60	0.51	Outlier			
61	0.068				

Consenus statistics				
Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported No. of values removed	0.060 0.062 0.063 0.022 34 71 10			
No. of reported non-detects	9			



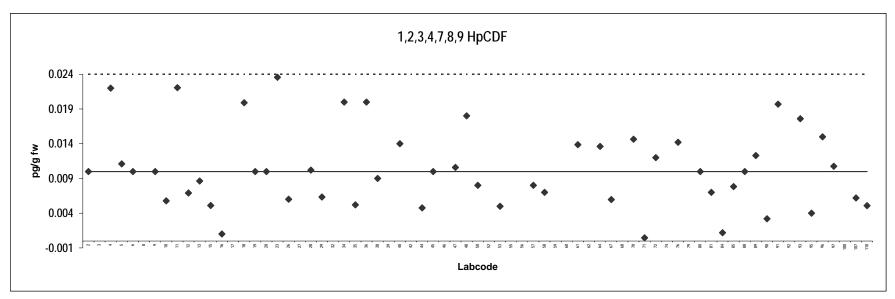


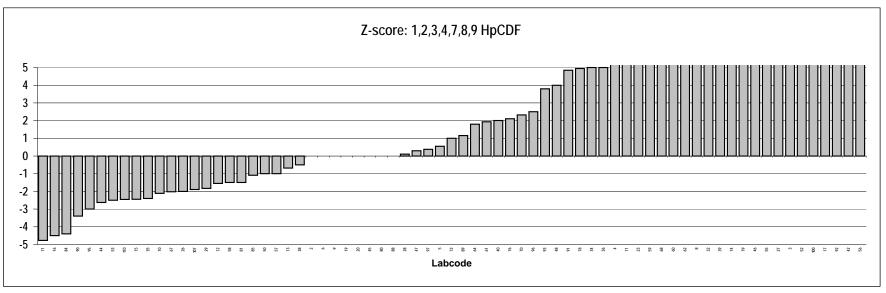
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010	ND	62	0.050	Outlier,ND
3	0.11	Outlier	64	0.014	
4	0.022		67	0.0060	
5	0.011		68	0.030	Outlier,ND
6	0.010	ND	70	0.015	ND
8	0.050	Outlier,ND	71	0.00046	ND
9	0.010	ND	72	0.012	
10	0.0058	·	74	0.050	Outlier,ND
11	0.022		76	0.014	ND
12	0.0069		79	0.055	Outlier
13	0.0086		80	0.010	ND
15	0.0051		81	0.0070	
16	0.0010	ND	84	0.0012	ND
17	0.18	Outlier,ND	85	0.0078	
18	0.020	ND	88	0.010	ND
19	0.010		89	0.012	
20	0.010	ND	90	0.0032	ND
23	0.024	·	91	0.020	ND
26	0.0060		92	0.23	Outlier
27	0.10	Outlier,ND	93	0.018	
28	0.010	,	95	0.0040	ND
29	0.0063		96	0.015	
32	0.050	Outlier,ND	97	0.011	
34	0.020	ND	100	0.16	Outlier,ND
35	0.0052		107	0.0062	ND
36	0.020		110	0.0051	
38	0.0090				
39	0.050	Outlier,ND			
40	0.014				
42	0.30	Outlier,ND			
44	0.0048				
45	0.010	ND			
46	0.066	Outlier			
47	0.011				
48	0.018	ND			
50	0.0080	ND			
52	0.12	Outlier,ND			
53	0.0050	ND			
55	0.083	Outlier			
56	0.34	Outlier,ND			
57	0.0080				
58	0.0070	ND			
59	0.025	Outlier			
60	0.041	Outlier,ND			
61	0.014				

Consenus	statis	tics
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Consensus median, pg/g	0.010
Median all values pg/g	0.012
Consensus mean, pg/g	0.010
Standard deviation, pg/g	0.0057
Relative standard deviation, %	55
No. of values reported	71
No. of values removed	19
No. of reported non-detects	35

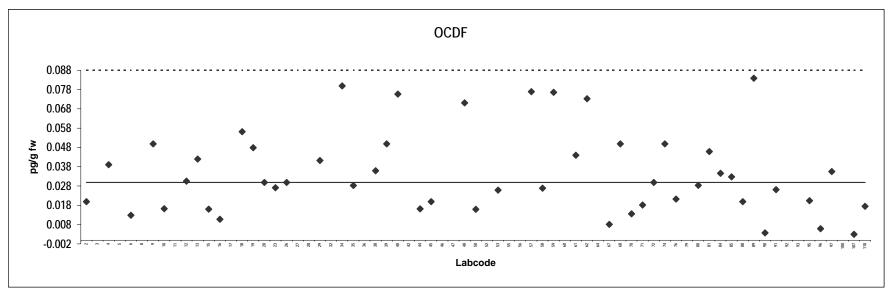


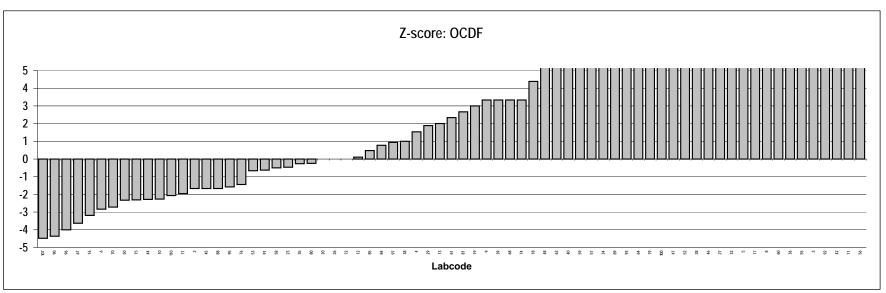


**Congener: OCDF** 

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.020		62	0.073	ND
3	0.44	Outlier	64	0.090	Outlier
4	0.039	ND	67	0.0082	
5	0.21	Outlier	68	0.050	ND
6	0.013		70	0.014	ND
8	0.28	Outlier	71	0.018	
9	0.050	ND	72	0.030	
10	0.016		74	0.050	ND
11	1.1	Outlier	76	0.021	ND
12	0.031		79	0.14	Outlier
13	0.042		80	0.029	
15	0.016		81	0.046	
16	0.011		84	0.035	
17	0.25	Outlier,ND	85	0.033	
18	0.056	ND	88	0.020	ND
19	0.048		89	0.084	
20	0.030	ND	90	0.0038	ND
23	0.027		91	0.026	ND
26	0.030	ND	92	0.54	Outlier
27	0.20	Outlier,ND	93	0.089	Outlier
28	0.17	Outlier	95	0.021	
29	0.041		96	0.0060	ND
32	0.20	Outlier,ND	97	0.036	
34	0.080	ND	100	0.15	Outlier,ND
35	0.028		107	0.0031	ND
36	0.37	Outlier	110	0.018	
38	0.036				
39	0.050	ND			
40	0.076				
42	1.0	Outlier,ND			
44	0.016				
45	0.020	0.41			
46	0.18	Outlier			
47	0.15	Outlier			
48	0.071	MD			
50	0.016	ND			
52	0.16	Outlier,ND			
53	0.026	O/1'			
55	0.37	Outlier			
56	1.2 0.077	Outlier,ND			
57 59					
58 59	0.027				
	0.077 0.34	Outlier			
60	0.34	Outilei			
61	0.044				

Relative standard deviation, % 62 No. of values reported 71 No. of values removed 21	Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g	0.030 0.044 0.035 0.022
No of reported non-detects 25	Relative standard deviation, % No. of values reported	71





Congener: PCB 77

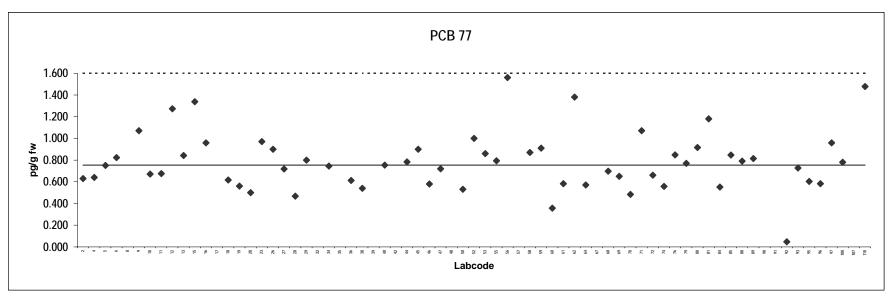
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.63		64	0.57	
4	0.64		67	8.1	Outlier,ND
5	0.75		68	0.70	
6	0.82		69	0.65	
8	5.0	Outlier,ND	70	0.48	
9	1.1		71	1.1	
10	0.67		72	0.66	
11	0.68		74	0.56	
12	1.3		76	0.85	
13	0.84		79	0.77	
15	1.3		80	0.92	
16	0.96		81	1.2	
17	2.9	Outlier	84	0.55	
18	0.62		85	0.85	
19	0.56		88	0.79	
20	0.50		89	0.81	0.41
23	0.97		90	1.8	Outlier
26	0.90		91	3.7	Outlier
27	0.72		92	0.047	
28	0.47		93	0.73	
29	0.80	0 41 170	95	0.60	
32	2.0	Outlier,ND	96	0.58	
34	0.75	Outlier	97	0.96	
35	2.0	Outher	100	0.78 33	Outlier
36 38	0.61 0.54		107 110	1.5	Outner
38	10	Outlier,ND	110	1.5	
40	0.75	Outlier,ND			
42	2.0	Outlier,ND			
44	0.78	Outlief,ND			
45	0.78				
46	0.58				
47	0.72				
48	2.2	Outlier			
50	0.53	Outilei			
52	1.0	ND			
53	0.86	T\D			
55	0.79				
56	1.6				
57	1.8	Outlier			
58	0.87	0 444101			
59	0.91				
60	0.36				
61	0.58				
62	1.4				

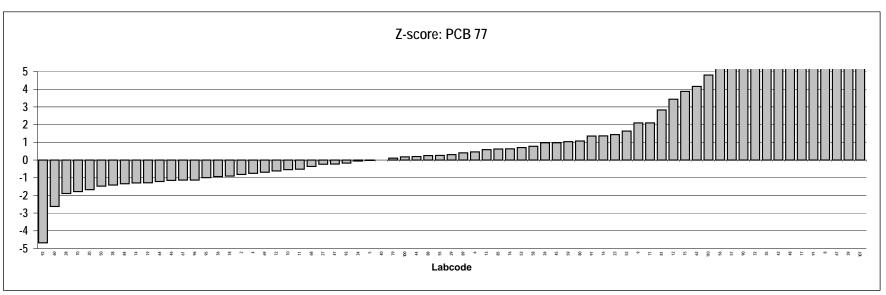
Consensus median, pg/g	0.75
Median all values pg/g	0.80
Consensus mean, pg/g	0.78
Standard deviation, pg/g	0.27
Relative standard deviation, %	34
No. of values reported	71
No. of values removed	12

6

Consenus statistics

No. of reported non-detects

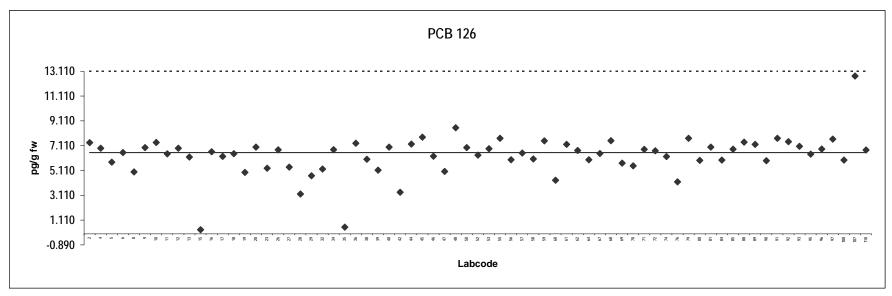


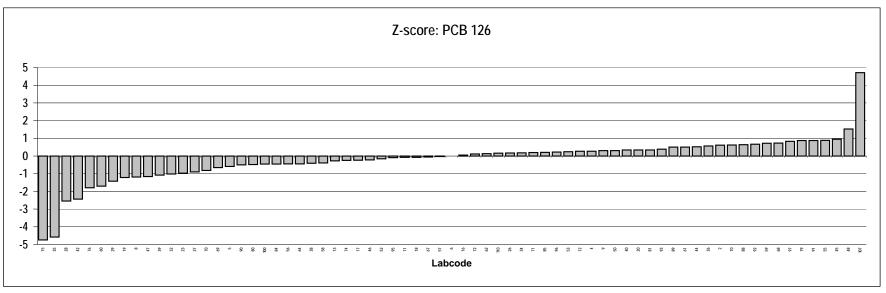


Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	7.4		64	6.0	
4	6.9		67	6.5	
5	5.8		68	7.5	
6	6.6		69	5.7	
8	5.0	ND	70	5.5	
9	7.0		71	6.8	
10	7.4		72	6.7	
11	6.5		74	6.2	
12	6.9		76	4.2	
13	6.2		79	7.7	
15	0.34		80	5.9	
16	6.6		81	7.0	
17	6.2		84	6.0	
18	6.5		85	6.8	
19	5.0		88	7.4	
20	7.0		89	7.2	
23	5.3		90	5.9	
26	6.8		91	7.7	
27	5.4		92	7.4	
28	3.2		93	7.1	
29	4.7		95	6.4	
32	5.2		96	6.8	
34	6.8		97	7.6	
35	0.54		100	6.0	
36	7.3		107	13	
38	6.0		110	6.8	
39	5.1				
40	7.0				
42	3.4				
44	7.2				
45	7.8				
46	6.3				
47	5.0				
48	8.6				
50	7.0				
52	6.4				
53	6.9				
55	7.7				
56	6.0				
57 59	6.5				
58	6.0				
59	7.5				
60	4.3 7.2				
61					
62	6.7				

Consensus median, pg/g	6.6
Median all values pg/g	6.6
Consensus mean, pg/g	6.3
Standard deviation, pg/g	1.6
Relative standard deviation, %	26
No. of values reported	71
No. of values removed	0
No. of reported non-detects	1



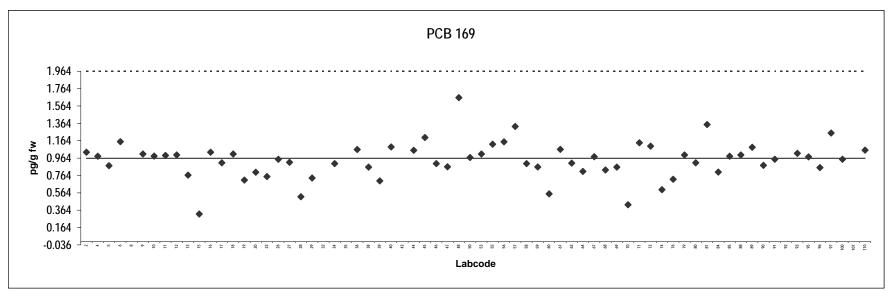


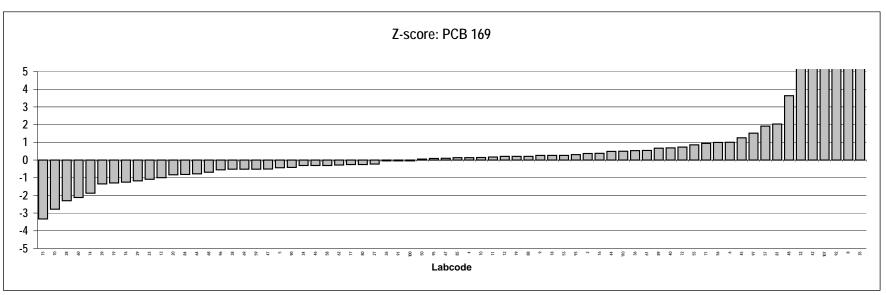
Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	1.0		67	0.98	
4	0.99		68	0.83	
5	0.88		69	0.86	
6	1.2		70	0.43	
8	5.0	Outlier,ND	71	1.1	
9	1.0		72	1.1	
10	0.99		74	0.60	
11	0.99		76	0.72	
12	1.00		79	1.0	
13	0.77		80	0.91	
15	0.32		81	1.4	
16	1.0		84	0.80	
17	0.91		85	0.98	
18	1.0		88	1.0	
19	0.71		89	1.1	
20	0.80		90	0.88	
23	0.75		91	0.95	
26	0.95		92	4.5	Outlier,ND
27	0.92		93	1.0	
28	0.52		95	0.98	
29	0.73		96	0.85	
32	2.0	Outlier,ND	97	1.3	
34	0.90		100	0.95	
35	6.9	Outlier	107	3.1	Outlier,ND
36	1.1		110	1.1	
38	0.86				
39	0.70				
40	1.1				
42	2.0	Outlier,ND			
44	1.1				
45	1.2				
46	0.90				
47	0.86				
48	1.7				
50	0.97				
53	1.0				
55	1.1				
56	1.2				
57	1.3				
58	0.90				
59	0.86				
60	0.55				
61	1.1				
62	0.91				
64	0.81				

Consenus statistics	
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Consensus median, pg/g	0.96
Median all values pg/g	0.98
Consensus mean, pg/g	0.94
Standard deviation, pg/g	0.21
Relative standard deviation, %	23
No. of values reported	70
No. of values removed	6
No. of reported non-detects	5



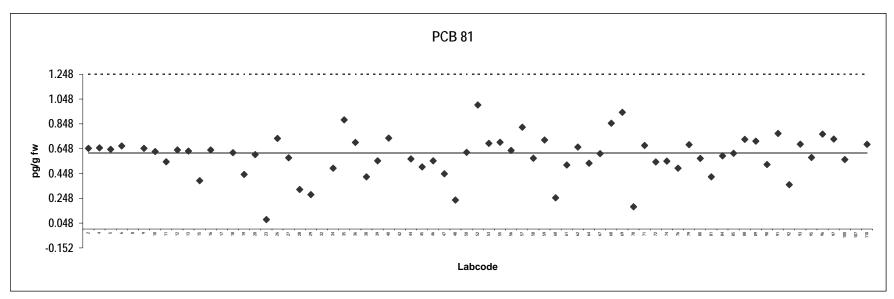


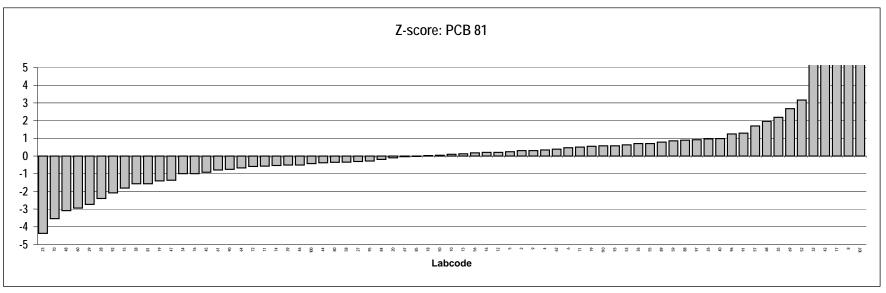
Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.65		64	0.53	
4	0.65		67	0.61	
5	0.64		68	0.85	
6	0.67		69	0.94	
8	5.0	Outlier,ND	70	0.18	
9	0.65		71	0.67	
10	0.62		72	0.54	
11	0.54		74	0.55	
12	0.64		76	0.49	
13	0.63		79	0.68	
15	0.39	ND	80	0.57	
16	0.64		81	0.42	
17	2.2	Outlier	84	0.59	
18	0.62		85	0.61	
19	0.44		88	0.72	
20	0.60		89	0.71	
23	0.076		90	0.52	
26	0.73		91	0.77	
27	0.57		92	0.36	
28	0.32		93	0.68	
29	0.28		95	0.58	
32	2.0	Outlier,ND	96	0.77	
34	0.49		97	0.72	
35	0.88		100	0.56	
36	0.70		107	44	Outlier
38	0.42		110	0.68	
39	0.55				
40	0.73				
42	2.0	Outlier,ND			
44	0.57				
45	0.50				
46	0.55				
47	0.44				
48	0.23				
50	0.62				
52	1.0	ND			
53	0.69				
55	0.70				
56	0.63				
57	0.82	ND			
58	0.57				
59	0.72				
60	0.25				
61	0.52				
62	0.66				

Consensus median, pg/g	0.61
Median all values pg/g	0.62
Consensus mean, pg/g	0.59
Standard deviation, pg/g	0.17
Relative standard deviation, %	29
No. of values reported	71
No. of values removed	5

No. of reported non-detects

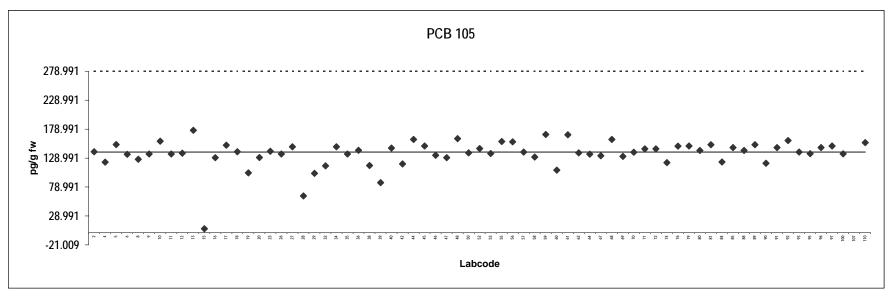


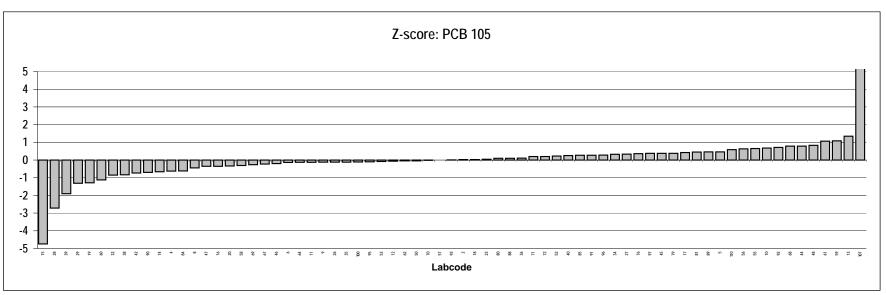


Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	140		64	136	
4	122		67	133	
5	152		68	161	
6	135		69	132	
8	127		70	139	
9	136		71	145	
10	158		72	145	
11	136		74	121	
12	138		76	150	
13	177		79	150	
15	7.0		80	142	
16	130		81	152	
17	151		84	122	
18	140		85	147	
19	104		88	142	
20	130		89	152	
23	141		90	120	
26	136		91	147	
27	149		92	159	
28	64		93	139	
29	103		95	137	
32	116		96	147	
34	149		97	150	
35	136		100	136	
36	142		107	644	Outlier
38	116		110	156	
39	86				
40	146				
42	119				
44	161				
45	150				
46	134				
47	130				
48	162				
50	138				
52	146				
53	137				
55	158				
56	157				
57	139				
58	131				
59	170				
60	108				
61	169				
62	138				

Consensus median, pg/g	139
Median all values pg/g	139
Consensus mean, pg/g	137
Standard deviation, pg/g	24
Relative standard deviation, %	18
No. of values reported	71
No. of values removed	1
No. of reported non-detects	0

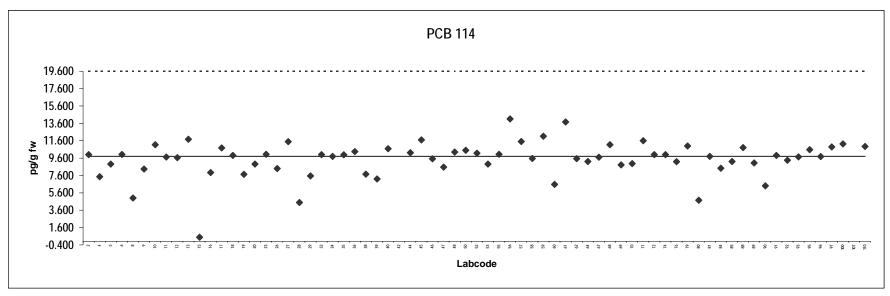


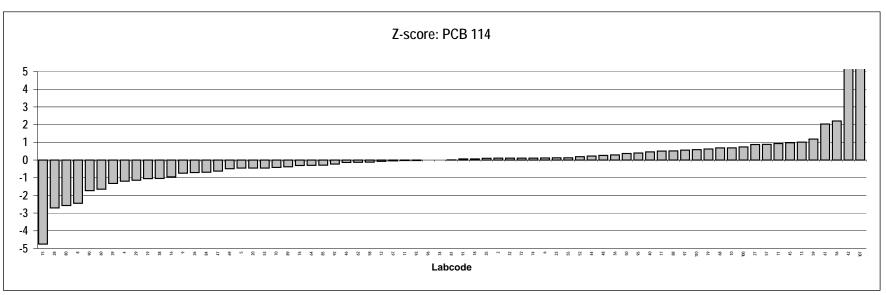


Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	10		64	9.2	
4	7.5		67	9.7	
5	8.9		68	11	
6	10		69	8.8	
8	5.0	ND	70	9.0	
9	8.3		71	12	
10	11		72	10	
11	9.7		74	10	ND
12	9.6		76	9.2	
13	12		79	11	
15	0.48		80	4.7	
16	7.9		81	9.8	
17	11		84	8.4	
18	9.9		85	9.2	
19	7.7		88	11	
20	8.9		89	9.0	
23	10		90	6.4	
26	8.4		91	9.9	
27	11		92	9.3	
28	4.5		93	9.7	
29	7.5		95	11	
32	10	ND	96	9.8	
34	9.8		97	11	
35	10.0		100	11	
36	10		107	34	Outlier
38	7.8		110	11	
39	7.2				
40	11				
42	20	Outlier,ND			
44	10				
45	12				
46	9.5				
47	8.6				
48	10				
50	11				
52	10				
53	8.9				
55	10				
56	14				
57	12				
58	9.6 12				
59					
60	6.6 14				
61					
62	9.5				

# Consenus statistics Consensus median, pg/g 9.8 Median all values pg/g 9.8 Consensus mean, pg/g 9.5 Standard deviation, pg/g 2.1 Relative standard deviation, % 22 No. of values reported 71 No. of values removed 2 No. of reported non-detects 4

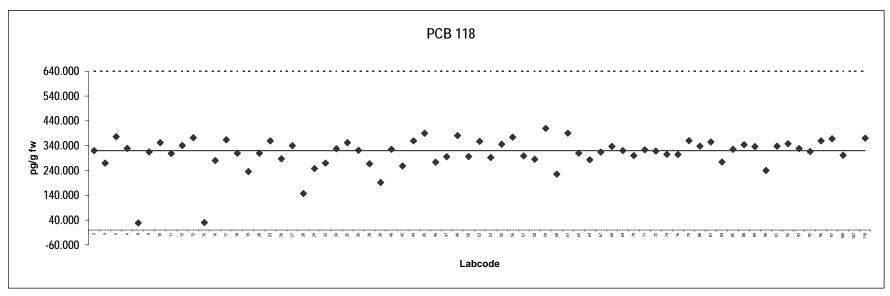


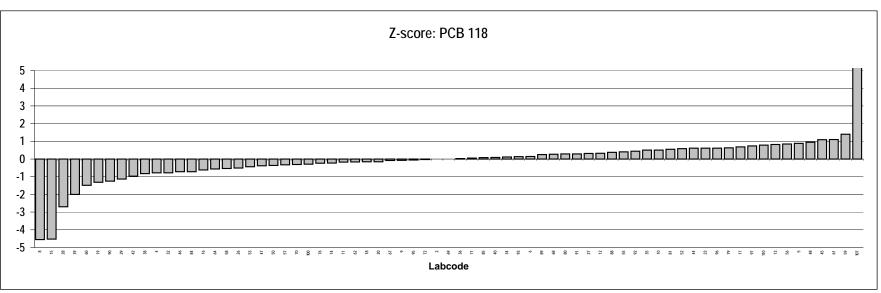


Congener: PCB 118

			1	T	Conge
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	320		64	284	
4	270		67	314	
5	376		68	337	
6	329		69	320	
8	28		70	300	
9	315		71	323	
10	352		72	318	
11	309		74	305	
12	340		76	305	
13	372		79	360	
15	30		80	338	
16	280		81	355	
17	364		84	274	
18	310		85	325	
19	235		88	344	
20	310		89	336	
23	359		90	240	
26	287		91	338	
27	340		92	348	
28	147		93	329	
29	248		95	316	
32	270		96	359	
34	328		97	367	
35	352		100	301	
36	321		107	1329	Outlier
38	267		110	370	
39	192				
40	325				
42	258				
44	359				
45	390				
46	274				
47	295				
48	381				
50	296				
52	357				
53	292				
55	346				
56	374				
57	299				
58	285				
59	410				
60	225				
61	390				
62	310			1	

Consensus median, pg/g Median all values pg/g Consensus mean, pg/g	320 320 309
Standard deviation, pg/g	67
Relative standard deviation, %	22
No. of values reported	71
No. of values removed	1
No. of reported non-detects	0

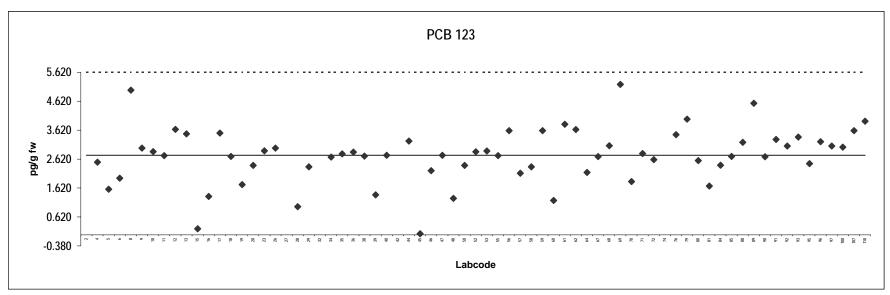


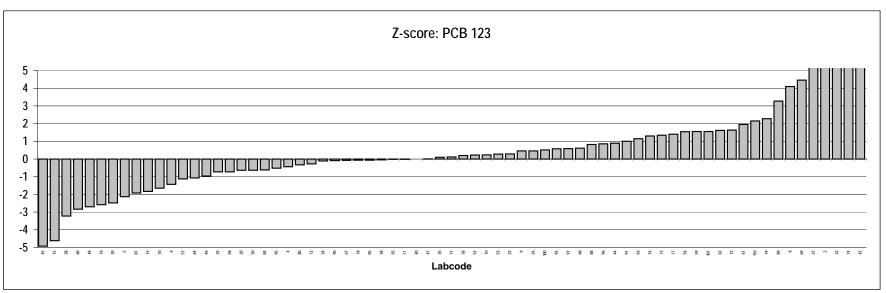


Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	10	Outlier,ND	64	2.2	
4	2.5	ND	67	2.7	
5	1.6		68	3.1	
6	2.0		69	5.2	
8	5.0	ND	70	1.8	
9	3.0		71	2.8	
10	2.9		72	2.6	
11	2.7		74	10	Outlier,ND
12	3.6		76	3.5	
13	3.5		79	4.0	
15	0.21	ND	80	2.6	
16	1.3		81	1.7	
17	3.5		84	2.4	
18	2.7		85	2.7	
19	1.7		88	3.2	
20	2.4		89	4.5	
23	2.9		90	2.7	
26	3.0		91	3.3	
27	5.7	Outlier	92	3.1	
28	0.98		93	3.4	
29	2.4		95	2.5	
32	10	Outlier,ND	96	3.2	
34	2.7		97	3.1	
35	2.8		100	3.0	
36	2.9		107	3.6	ND
38	2.7		110	3.9	
39	1.4				
40	2.7				
42	20	Outlier,ND			
44	3.2				
45	0.040	ND			
46	2.2				
47	2.8				
48	1.3				
50	2.4				
52	2.9				
53	2.9				
55	2.7				
56	3.6				
57	2.1				
58	2.4				
59	3.6				
60	1.2				
61	3.8				
62	3.6				

# Consensus median, pg/g Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported No. of values removed No. of reported non-detects Page 2.7 Standard deviation, % 35 No. of values reported No. of values 9



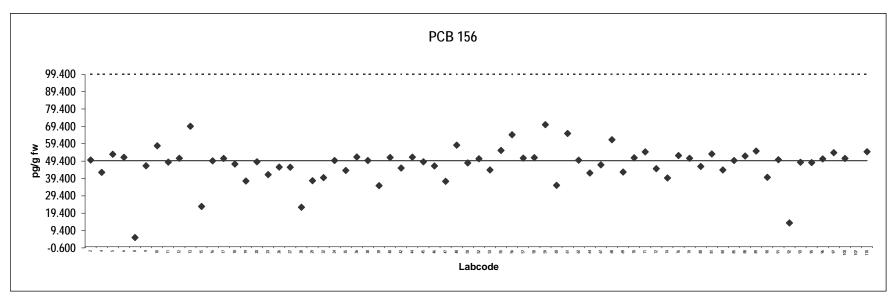


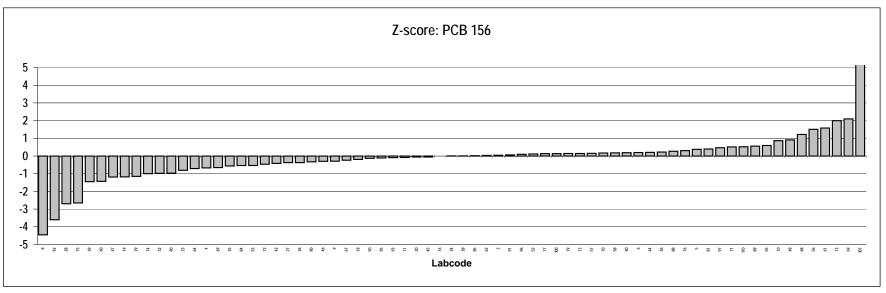
Congener: PCB 156

					Conge
Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
2	50		64	43	
4	43		67	47	
5	53		68	62	
6	52		69	43	
8	5.4		70	51	
9	47		71	55	
10	58		72	45	
11	49		74	40	
12	51		76	53	
13	69		79	51	
15	23		80	46	
16	50		81	54	
17	51		84	44	
18	48		85	50	
19	38		88	52 5.5	
20	49		89	55	
23	42		90	40	
26	46		91	50	
27	46 23		92 93	14 49	
28 29	38		93 95	49 49	
	40				
32 34	50		96 97	51 54	
35	44		100	51	
36	52		107	168	Outlier
38	50		110	55	Outlief
39	35		110	33	
40	51				
42	45				
44	52				
45	49				
46	47				
47	38				
48	59				
50	48				
52	51				
53	44				
55	56				
56	65				
57	51				
58	51				
59	70				
60	35				
61	65				
62	50				

# Consensus median, pg/g 50 Median all values pg/g 50 Consensus mean pg/g 48

Consensus mean, pg/g	48
Standard deviation, pg/g	11
Relative standard deviation, %	22
No. of values reported	71
No. of values removed	1
No. of reported non-detects	0

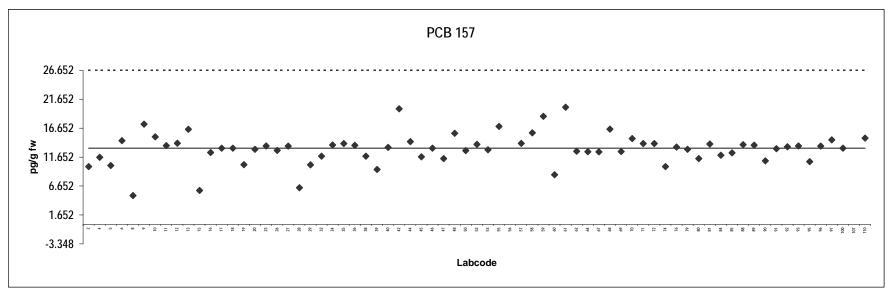


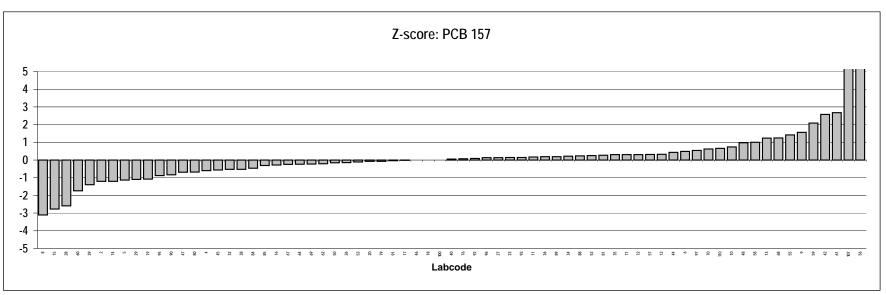


Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	10		64	13	
4	12		67	13	
5	10		68	16	
6	14		69	13	
8	5.0	ND	70	15	
9	17		71	14	
10	15		72	14	
11	14		74	10	
12	14		76	13	
13	16		79	13	
15	5.9		80	11	
16	12		81	14	
17	13		84	12	
18	13		85	12	
19	10		88	14	
20	13		89	14	
23	14		90	11	
26	13		91	13	
27	14		92	13	
28	6.3		93	14	
29	10		95	11	
32	12		96	14	
34	14		97	15	
35	14		100	13	
36	14		107	49	Outlier
38	12		110	15	
39	9.5				
40	13				
42	20	ND			
44	14				
45	12				
46	13				
47	11				
48	16				
50	13				
52	14				
53	13				
55	17	O-41:			
56	65	Outlier			
57	14				
58	16				
59	19				
60	8.6 20				
61					
62	13				

# Consensus median, pg/g 13 Median all values pg/g 13 Consensus mean, pg/g 13 Standard deviation, pg/g 2.7 Relative standard deviation, % 21 No. of values reported 71 No. of values removed 2 No. of reported non-detects 2

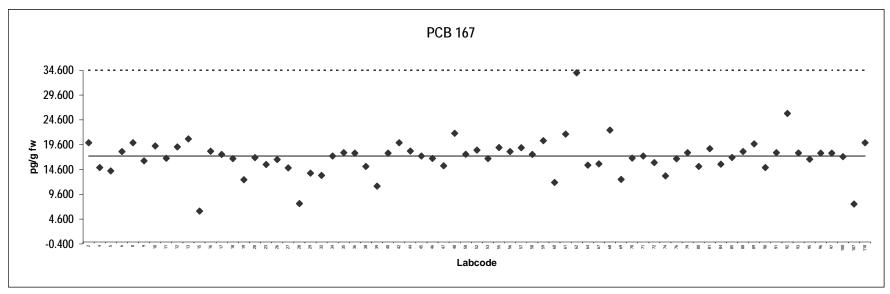


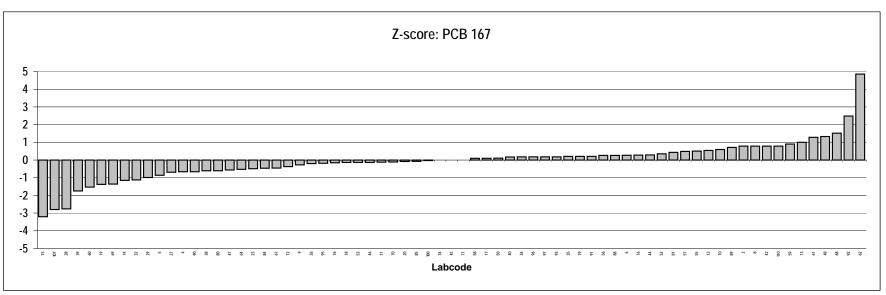


Congener: PCB 167

2 20 64 15 4 15 67 16 5 14 68 23 6 18 69 13 8 20 70 17	
5 14 68 23 6 18 69 13 8 20 70 17	
6 18 69 13 8 20 70 17	
8 20 70 17	
8 20 70 17	
0 16 71 17	
9 16 71 17	
10 19 72 16	
11 17 74 13	
12 19 76 17	
13 21 79 18	
15 6.2 80 15	
16 18 81 19	
17 18 84 16	
18 17 85 17	
19 13 88 18	
20 17 89 20	
23 16 90 15	
26 17 91 18	
27 15 92 26	
28 7.7 93 18	
29 14 95 17	
32 13 96 18	
34 17 97 18	
35 18 100 17	
36 18 107 7.6	ND
38 15 110 20	
39 11	
40 18	
42 20 ND	
44 18	
45 17	
46 17	
47 15	
48 22	
50 18	
52 19	
53 17	
55 19	
56 18	
57 19	
58 18	
59 20	
60 12	
61 22	
62 34	

Consensus median, pg/g	17
Median all values pg/g	17
Consensus mean, pg/g	17
Standard deviation, pg/g	3.8
Relative standard deviation, %	22
No. of values reported	71
No. of values removed	0
No. of reported non-detects	2

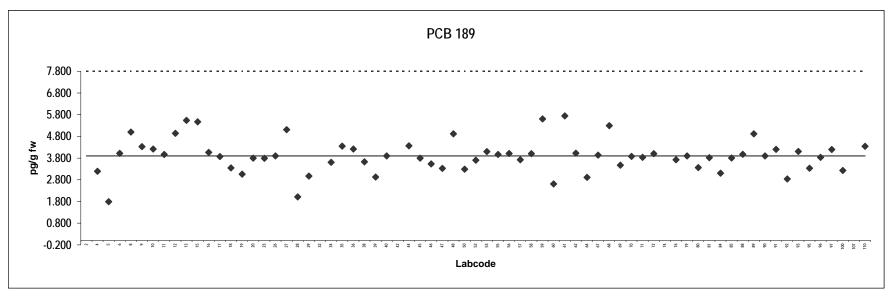


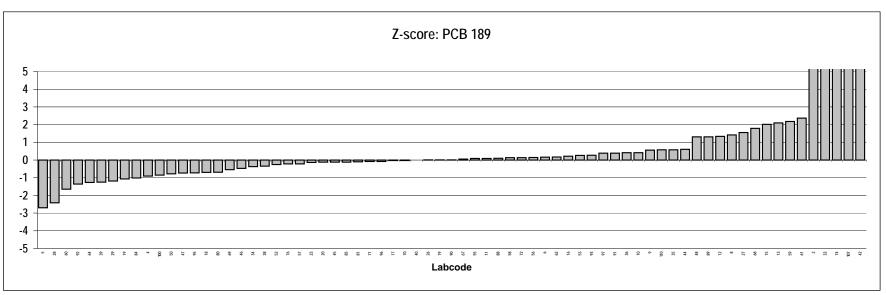


Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	10	Outlier,ND	64	2.9	
4	3.2		67	3.9	
5	1.8		68	5.3	
6	4.0		69	3.5	
8	5.0	ND	70	3.9	
9	4.3		71	3.8	
10	4.2		72	4.0	
11	4.0		74	10	Outlier,ND
12	4.9		76	3.7	
13	5.5		79	3.9	
15	5.5		80	3.4	
16	4.1		81	3.8	
17	3.9		84	3.1	
18	3.4		85	3.8	
19	3.1		88	4.0	
20	3.8		89	4.9	
23	3.8		90	3.9	
26	3.9		91	4.2	
27	5.1		92	2.8	
28	2.0		93	4.1	
29	3.0		95	3.3	
32	10	Outlier,ND	96	3.8	
34	3.6		97	4.2	
35	4.4		100	3.2	
36	4.2		107	14	Outlier
38	3.6		110	4.3	
39	2.9				
40	3.9				
42	20	Outlier,ND			
44	4.4				
45	3.8				
46	3.5				
47	3.3				
48	4.9				
50	3.3				
52	3.7				
53	4.1				
55	4.0				
56	4.0				
57	3.7				
58	4.0				
59	5.6				
60	2.6				
61	5.7				
62	4.0				

# Consensus median, pg/g Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported No. of values removed No. of reported non-detects 5





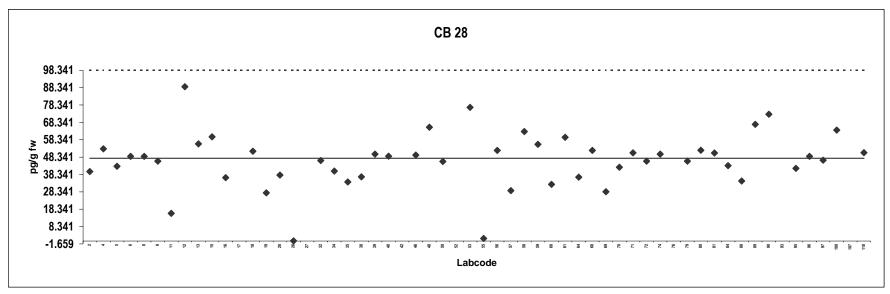
Congener: CB 28

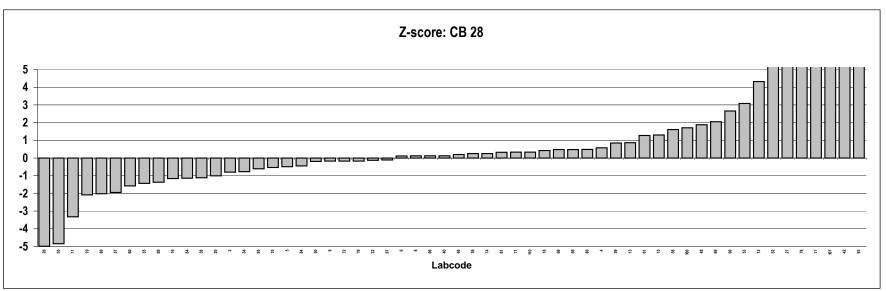
					Con
Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
2	40		80	52	
4	53		81	51	
5	43		84	43	
6	49		88	35	
8	49		89	67	
9	46		90	73	
11	16		93	1155	Outlier
12	89		95	42	
13	56		96	49	
15	60		97	47	
16	37		100	64	
17	199	Outlier	107	480	Outlier
18	52		110	51	
19	28				
20	38				
26	0.061				
27	128	Outlier,ND			
32	46	,			
34	40				
35	34				
38	37				
39	50	ND			
40	49				
42	1000	Outlier,ND			
46	50	, .			
48	66				
50	46				
52	100	Outlier,ND			
53	77				
55	1.5	ND			
56	52				
57	29				
58	63				
59	56				
60	33				
61	60				
64	37				
68	52				
69	28				
70	43				
71	51				
72	46				
74	50	ND			
76	138	Outlier			
79	46	Outilei			
17	70				

# Consensus median, pg/g 48 Median all values pg/g 49 Consensus mean, pg/g 46 Standard deviation, pg/g 16 Relative standard deviation, % 34 No. of values reported 58 No. of values removed 7

6

No. of reported non-detects

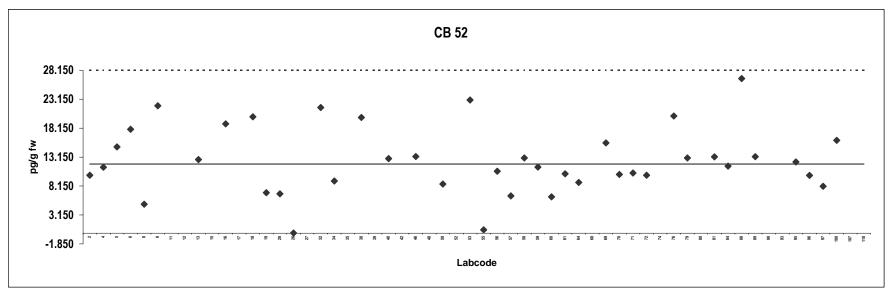


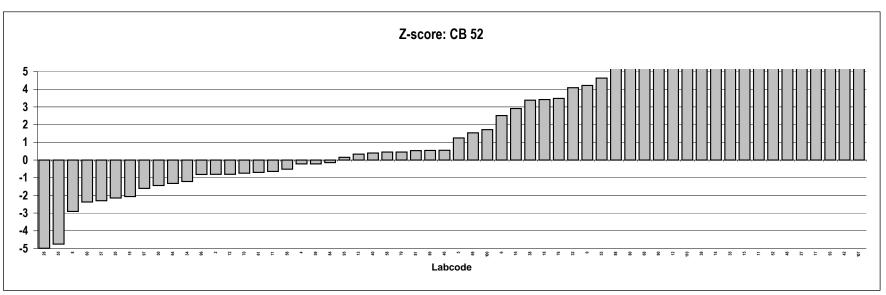


Congener: CB 52

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	10		80	30	Outlier
4	11		81	13	
5	15		84	12	
6	18		88	27	
8	5.0	ND	89	13	
9	22		90	35	Outlier
11	62	Outlier	93	555	Outlier
12	35	Outlier	95	12	
13	13		96	10.0	
15	60	Outlier	97	8.1	
16	19		100	16	
17	253	Outlier	107	1221	Outlier
18	20		110	47	Outlier
19	7.0				
20	6.8				
26	0.018				
27	128	Outlier,ND			
32	22				
34	9.0				
35	56	Outlier			
38	20	ND			
39	50	Outlier,ND			
40	13				
42	1000	Outlier,ND			
46	13				
48	107	Outlier			
50	8.5				
52	100	Outlier,ND			
53	23				
55	0.57	ND			
56	11				
57	6.5				
58	13				
59	11				
60	6.3				
61	10				
64	8.8	Outlier			
68 69	31 16	Outher			
70	10				
70	10				
71 72	10				
74	50	Outlier,ND			
76	20	Junet, ND			
79	13				
17	13				

# Consensus median, pg/g Median all values pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported No. of values removed No. of reported non-detects 8





Congener: CB 101

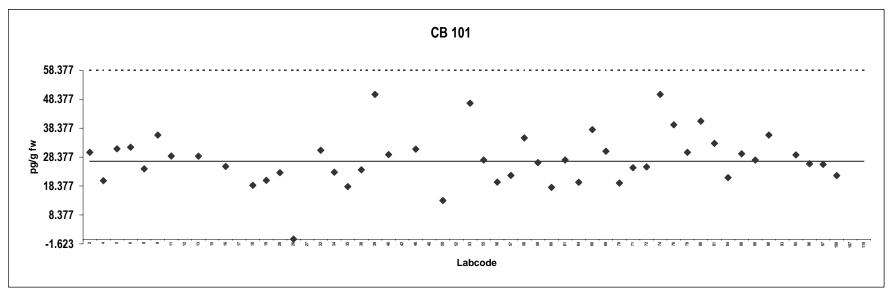
		** .		~	Cong
Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
2	30		80	41	
4	20		81	33	
5	31		84	21	
6	32		88	30	
8	24		89	27	
9	36		90	36	
11	29		93	803	Outlier
12	68	Outlier	95	29	
13	29		96	26	
15	60	Outlier	97	26	
16	25		100	22	
17	103	Outlier	107	1815	Outlier
18	19		110	96	Outlier
19	20				
20	23				
26	0.034				
27	141	Outlier			
32	31				
34	23				
35	18				
38	24				
39	50	ND			
40	29				
42	1000	Outlier,ND			
46	31	· ·			
48	81	Outlier			
50	13				
52	100	Outlier,ND			
53	47				
55	27				
56	20				
57	22				
58	35				
59	26				
60	18				
61	27				
64	20				
68	38				
69	30				
70	19				
71	25				
72	25				
74	50	ND			
76	40	עא			
76 79	30				
79	30				

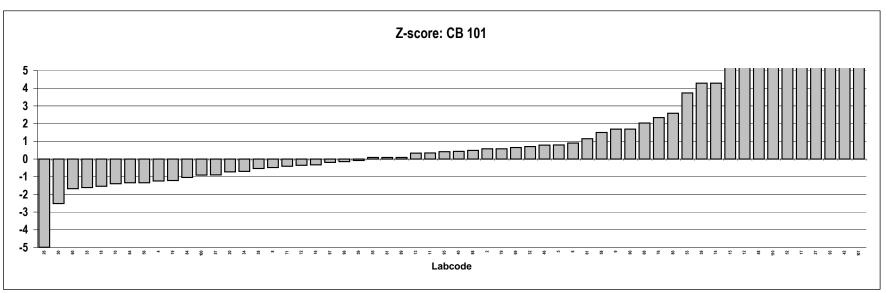
### 

Consenus statistics

Consensus mean, pg/g
Standard deviation, pg/g
Relative standard deviation, %
No. of values reported
No. of values removed
No. of reported non-detects

4

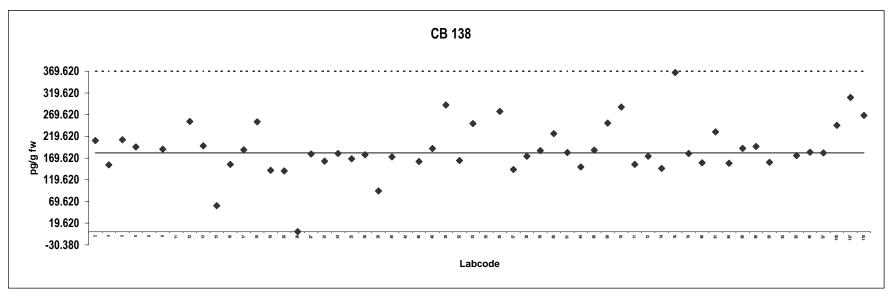


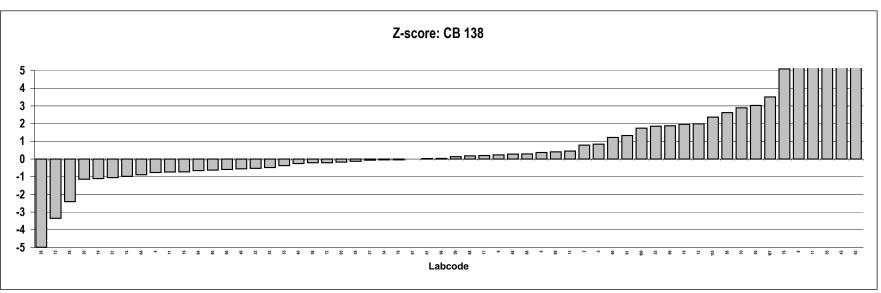


Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	210		80	159	
4	154		81	230	
5	212		84	158	
6	195		88	192	
8	396	Outlier	89	196	
9	190		90	160	
11	403	Outlier	93	3089	Outlier
12	254		95	175	
13	198		96	183	
15	60		97	182	
16	155		100	245	
17	189		107	309	
18	253		110	268	
19	141				
20	140				
26	0.22				
27	179				
32	162				
34	180				
35	168				
38	177				
39	94				
40	172				
42	1000	Outlier,ND			
46	162				
48	192				
50	292				
52	164				
53	249				
55	497	Outlier			
56	277				
57	143				
58	174				
59	187				
60	226				
61	182				
64	149				
68	188				
69	250				
70	287				
71	155				
72	174				
74	146				
76	367				
79	180				

Consensus median, pg/g	182
Median all values pg/g	185
Consensus mean, pg/g	190
Standard deviation, pg/g	60
Relative standard deviation, %	31
No. of values reported	58
No. of values removed	5
No. of reported non-detects	1

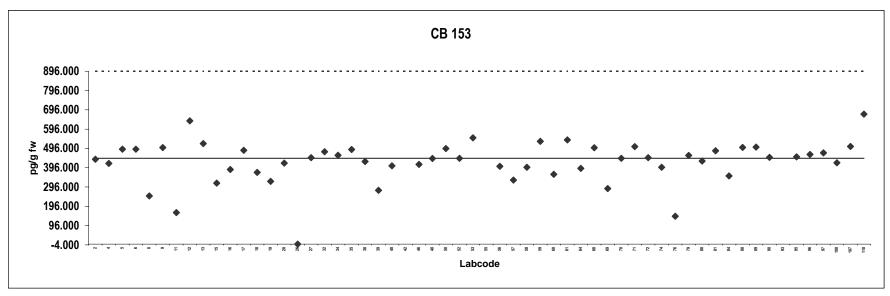


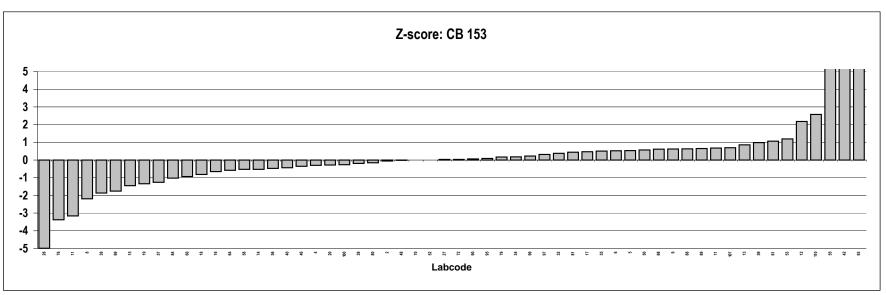


Congener: CB 153

					Cong
Lab code		Notes	Lab code		Notes
2	440		80	431	
4	418		81	484	
5	492		84	353	
6	492		88	501	
8	250		89	503	
9	500		90	450	
11	164		93	6986	Outlier
12	639		95	452	
13	521		96	465	
15	316		97	473	
16	386		100	421	
17	486		107	506	
18	372		110	674	
19	326				
20	420				
26	0.51				
27	448				
32	479				
34	461				
35	490				
38	428				
39	279 406				
40 42	1000	Outlier,ND			
46	413	Outlier,ND			
48	413				
50	495				
52	445				
53	551				
55	935	Outlier			
56	403	Outilei			
57	332				
58	398				
59	533				
60	362				
61	540				
64	393				
68	500				
69	288				
70	444				
71	505				
72	448				
74	398				
76	144				
79	460				

Consents statistics	
Consensus median, pg/g	445
Median all values pg/g	448
Consensus mean, pg/g	426
Standard deviation, pg/g	112
Relative standard deviation, %	26
No. of values reported	58
No. of values removed	3
No. of reported non-detects	1

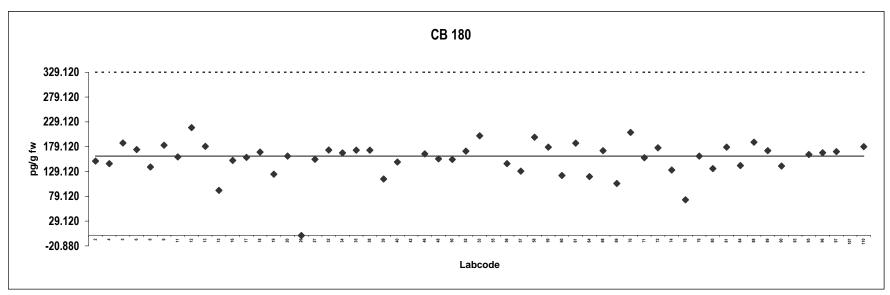


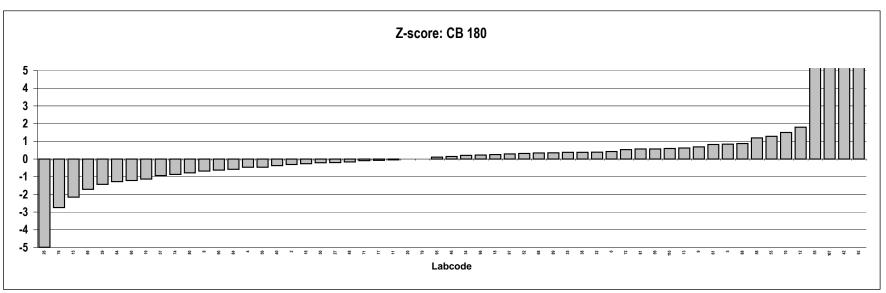


Congener: CB 180

					Cong
Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
2	150		80	135	
4	145		81	178	
5	187		84	141	
6	173		88	188	
8	138		89	171	
9	182		90	140	
11	158		93	3192	Outlier
12	217		95	163	
13	180		96	167	
15	91		97	169	
16	151		107	831	Outlier
17	157		110	179	
18	168				
19	124				
20	160				
26	0.19				
27	154				
32	172				
34	167				
35	172				
38	172				
39	114				
40	148				
42	1000	Outlier,ND			
46	165	Guiller, TE			
48	155				
50	153				
52	170				
53	201				
55	354	Outlier			
56	145	Outher			
57	130				
58	198				
59	178				
60	121				
61	186				
64	119				
68	171				
69	105				
70	208				
71	157				
72	177				
74	132				
76	72				
79	160				
19	100			I I	

Consensus median, pg/g	160
Median all values pg/g	165
Consensus mean, pg/g	155
Standard deviation, pg/g	35
Relative standard deviation, %	23
No. of values reported	57
No. of values removed	4
No. of reported non-detects	1
	1

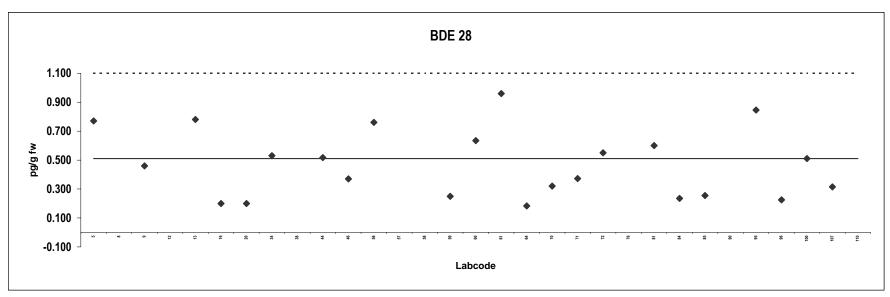


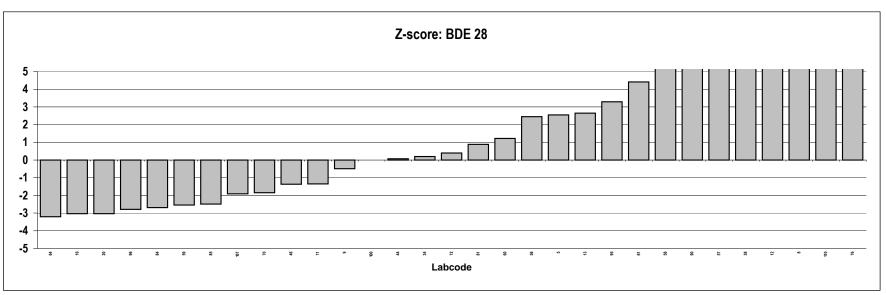


Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
5	0.77				
8	5.0	Outlier,ND			
9	0.46				
12	3.2	Outlier			
13	0.78				
16	0.20	ND			
20	0.20	ND			
34	0.53				
38	1.6	Outlier			
44	0.52				
46	0.37				
56	0.76	ND			
57	1.4	Outlier			
58	1.3	Outlier			
59	0.25				
60	0.63				
61	0.96				
64	0.18				
70	0.32				
71	0.37	ND			
72	0.55				
76	7.1	Outlier,ND			
81	0.60				
84	0.24				
85	0.26				
90	1.4	Outlier			
95	0.85				
96	0.23				
100	0.51				
107	0.31				
110	5.5	Outlier			
1					

Consensus median, pg/g	0.51
Median all values pg/g	0.55
Consensus mean, pg/g	0.47
Standard deviation, pg/g	0.23
Relative standard deviation, %	50
No. of values reported	31
No. of values removed	8
No. of reported non-detects	6

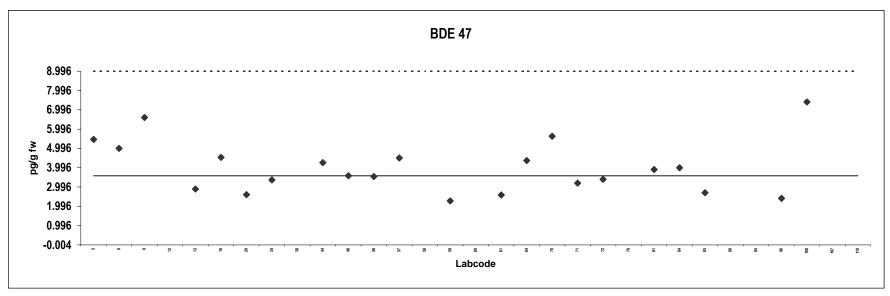


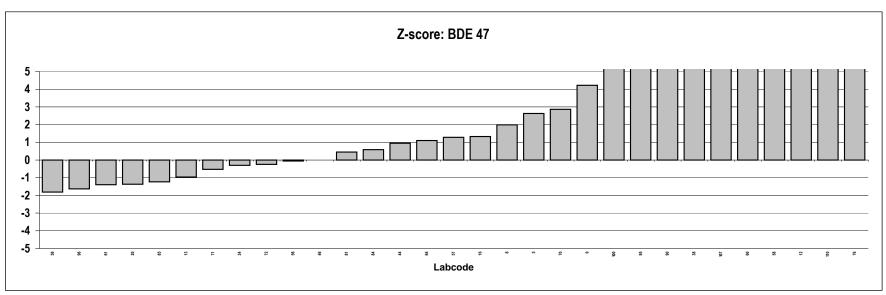


Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
5	5.5				
8	5.0	ND			
9	6.6				
12	38	Outlier			
13	2.9				
16	4.5				
20	2.6				
34	3.4	0.41			
38	17	Outlier			
44	4.3				
46	3.6				
56	3.5				
57	4.5	0.41			
58	36	Outlier			
59	2.3	0.41			
60	20	Outlier			
61 64	2.6 4.4				
70	5.6				
70	3.0				
72	3.4				
76	704	Outlier			
81	3.9	Outilei			
84	4.0				
85	2.7				
90	15	Outlier			
95	9.1	Outlier			
96	2.4	Guiller			
100	7.4				
107	19	Outlier			
110	99	Outlier			
110		Guiller			

Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported No. of values removed	3.6 4.5 4.0 1.4 34 31 9
No. of reported non-detects	1





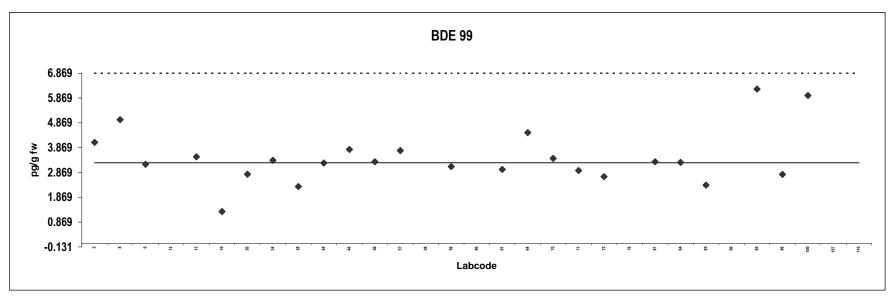
Congener: BDE 99

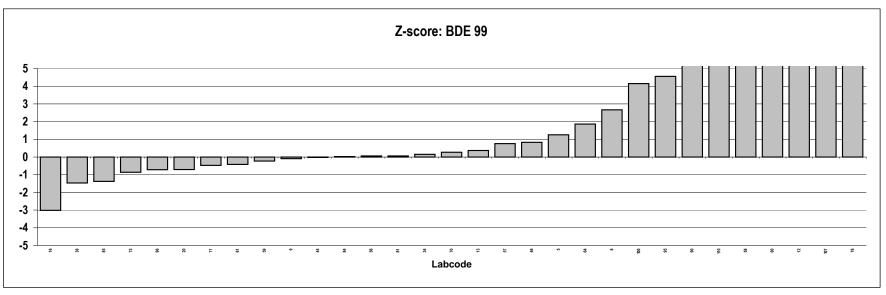
Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
5	4.1				
8	5.0	ND			
9	3.2				
12	22	Outlier			
13	3.5				
16	1.3				
20	2.8				
34	3.4				
38	2.3				
44 46	3.2				
	3.8 3.3	ND			
56 57	3.3	ND			
58	3.8 12	Outlier			
59	3.1	Outlief			
60	21	Outlier			
61	3.0	Outlief			
64	4.5				
70	3.4				
71	3.0				
72	2.7				
76	1195	Outlier			
81	3.3	Outher			
84	3.3				
85	2.4				
90	8.3	Outlier			
95	6.2	Guiner			
96	2.8				
100	6.0				
107	23	Outlier			
110	9.8	Outlier			

# Consensus median, pg/g 3.3 Median all values pg/g 3.4 Consensus mean, pg/g 3.5 Standard deviation, pg/g 1.1 Relative standard deviation, % 32 No. of values removed 7

2

No. of reported non-detects

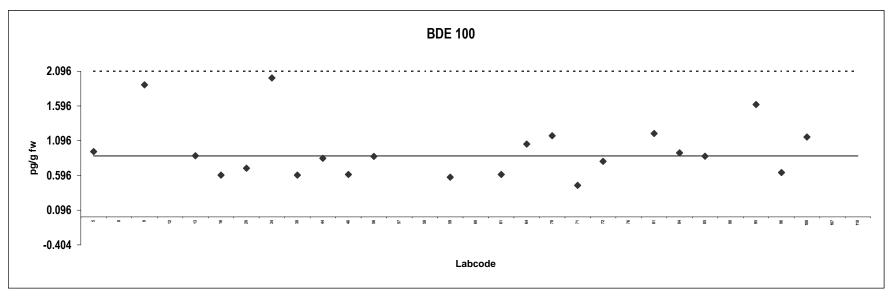


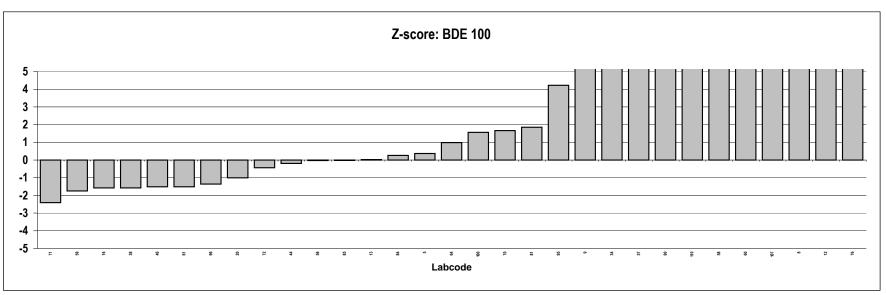


Congener: BDE 100

Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
5	0.94				
8	5.0	Outlier,ND			
9	1.9				
12	5.8	Outlier			
13	0.88				
16	0.60	ND			
20	0.70	MD			
34	2.0	ND			
38	0.60				
44	0.84				
46	0.61	ND			
56	0.87				
57	2.1 3.5	Outlier			
58	3.5	Outlier			
59	0.57 4.1	Outlier			
60 61	4.1 0.61	Outher			
64	1.0				
70	1.0				
70	0.45	ND			
72	0.43	ND			
76	242	Outlier			
81	1.2	Outilei			
84	0.92				
85	0.87				
90	2.6	Outlier			
95	1.6	Guiner			
96	0.64				
100	1.2				
107	4.9	Outlier			
110	3.1	Outlier			

Consensus median, pg/g	0.88
Median all values pg/g	1.05
Consensus mean, pg/g	0.95
Standard deviation, pg/g	0.42
Relative standard deviation, %	44
No. of values reported	31
No. of values removed	9
No. of reported non-detects	5

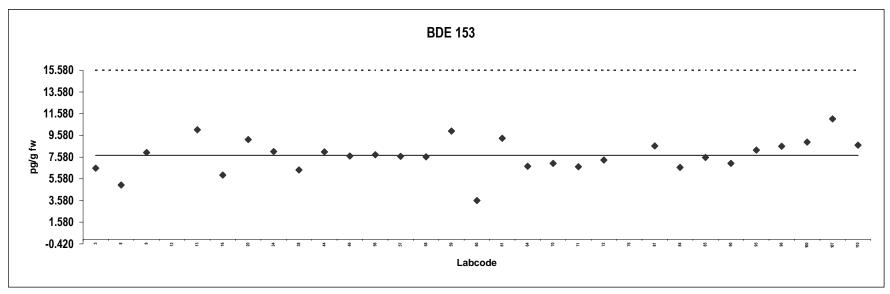


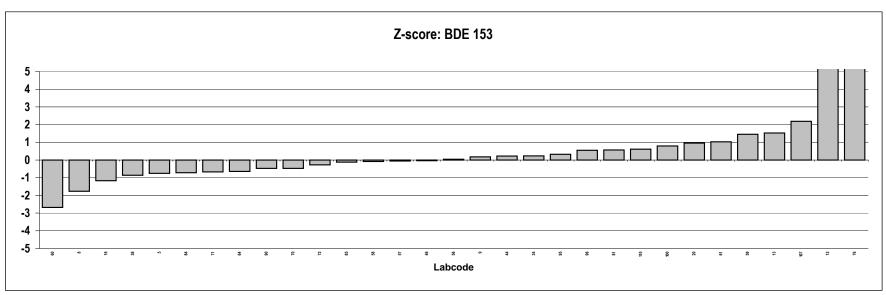


Congener: BDE 153

Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
5	6.6				
8	5.0	ND			
9	8.0				
12	46	Outlier			
13	10				
16	5.9				
20	9.2				
34	8.1				
38	6.4				
44	8.1				
46	7.7				
56	7.8				
57	7.6				
58	7.6				
59	10.0				
60	3.6				
61	9.3				
64	6.7				
70	7.0				
71	6.7				
72	7.3				
76	132	Outlier			
81	8.6				
84	6.6				
85	7.5				
90	7.0				
95	8.2				
96	8.6				
100	9.0				
107	11				
110	8.7				

# Consensus median, pg/g 7.7 Median all values pg/g 7.8 Consensus mean, pg/g 7.7 Standard deviation, pg/g 1.5 Relative standard deviation, % 20 No. of values reported 31 No. of values removed 2 No. of reported non-detects 1

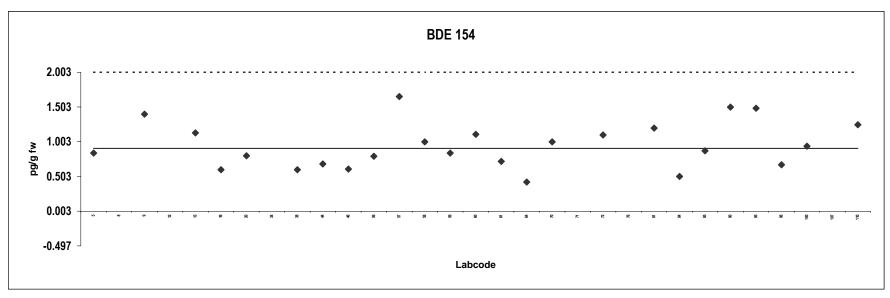


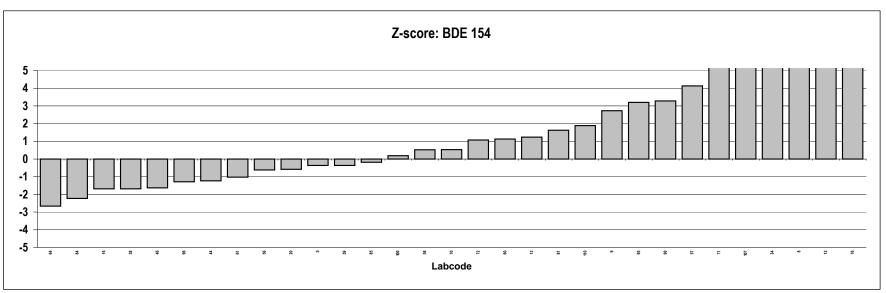


Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
5	0.84				
8	8.5	Outlier			
9	1.4				
12	14	Outlier			
13	1.1				
16	0.60	ND			
20	0.80				
34	3.0	Outlier,ND			
38	0.60				
44	0.68				
46	0.61				
56	0.79				
57	1.7				
58	1.0				
59	0.84				
60	1.1				
61	0.72				
64	0.42				
70	1.0				
71	2.4	Outlier,ND			
72	1.1				
76	104	Outlier			
81	1.2				
84	0.50				
85	0.87				
90	1.5				
95	1.5				
96	0.67				
100	0.94				
107	2.8	Outlier			
110	1.2				

Consensus median, pg/g	0.91
Median all values pg/g	1.0
Consensus mean, pg/g	0.95
Standard deviation, pg/g	0.33
Relative standard deviation, %	35
No. of values reported	31
No. of values removed	6
No. of reported non-detects	3

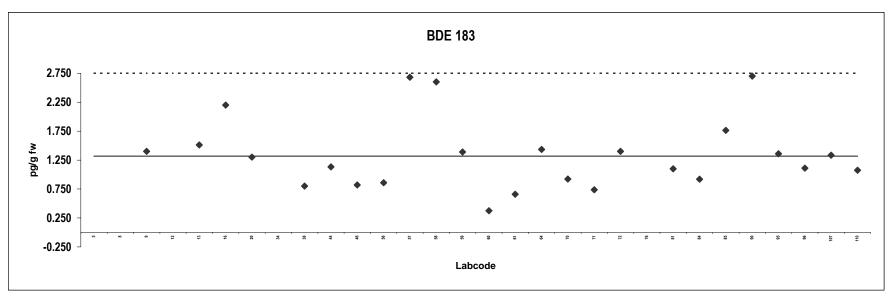


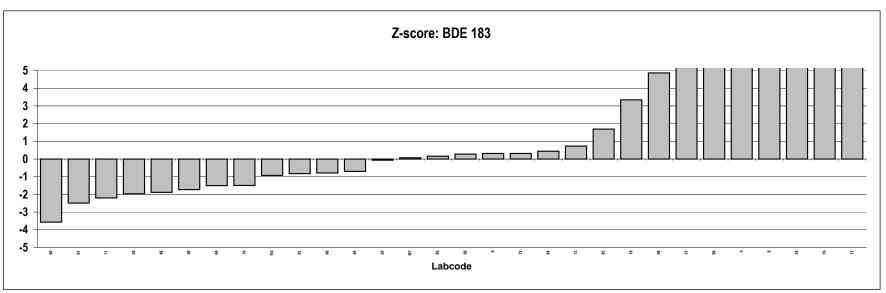


Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
5	3.2	Outlier,ND			
8	5.0	Outlier,ND			
9	1.4				
12	61	Outlier			
13	1.5				
16	2.2	ND			
20	1.3				
34	5.0	Outlier,ND			
38	0.80	o delitor, r 12			
44	1.1				
46	0.82				
56	0.86	ND			
57	2.7	ND			
58	2.6				
59	1.4				
60	0.38				
61	0.66				
64	1.4				
	0.92				
70 71	0.92	ND			
71	0.74	ND			
72	1.4	O di ND			
76	7.1	Outlier,ND			
81	1.1				
84	0.92				
85	1.8				
90	2.7				
95	1.4				
96	1.1				
107	1.3				
110	1.1				

# Consensus median, pg/g Median all values pg/g Consensus mean, pg/g 1.3 Median all values pg/g 1.4 Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported No. of values removed No. of reported non-detects 7

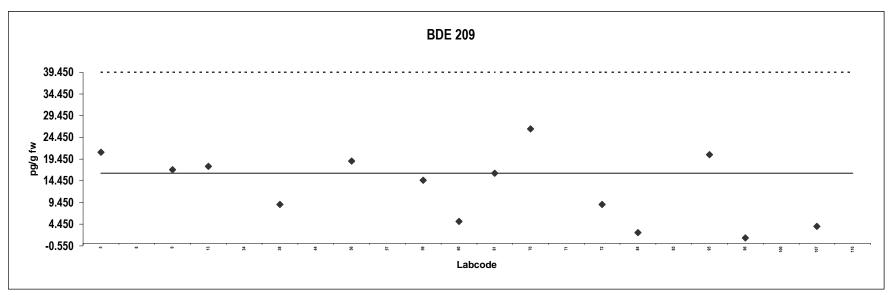


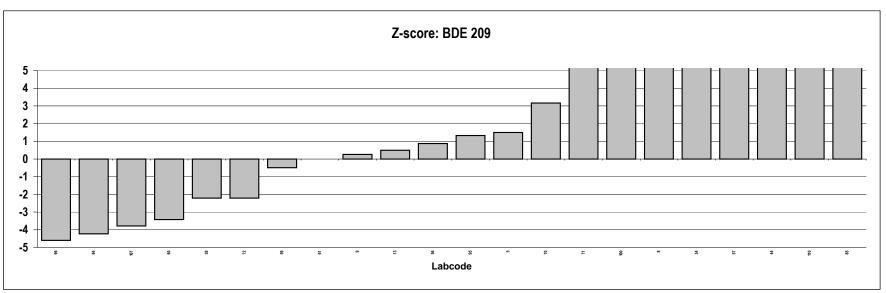


Congener: BDE 209

					Conge
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
5	21	ND			
8	67	Outlier			
9	17				
13	18				
34	75	Outlier			
38	9.0				
44	91	Outlier			
56	19				
57	82	Outlier			
59	15				
60	5.1				
61	16				
70	26				
71	44	Outlier			
72	9.0				
84	2.5	ND			
85	280	Outlier			
95	20				
96	1.3	ND			
100	46	Outlier			
107	3.9				
110	125	Outlier			
1					

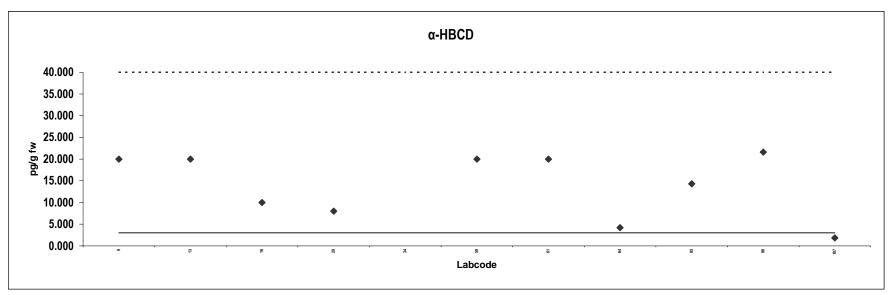
Consensus median, pg/g	16
Median all values pg/g	20
Consensus mean, pg/g	13
Standard deviation, pg/g	7.9
Relative standard deviation, %	60
No. of values reported	22
No. of values removed	8
No. of reported non-detects	3

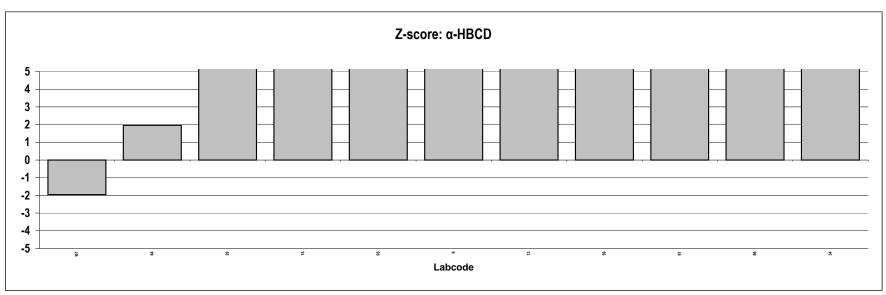




Congener: α-HBCD

Consensus median, pg/g	3.03
Median all values pg/g	20
Consensus mean, pg/g	14
Standard deviation, pg/g	7.4
Relative standard deviation, %	53
No. of values reported	11
No. of values removed	1
No. of reported non-detects	9
110. of reported non detects	



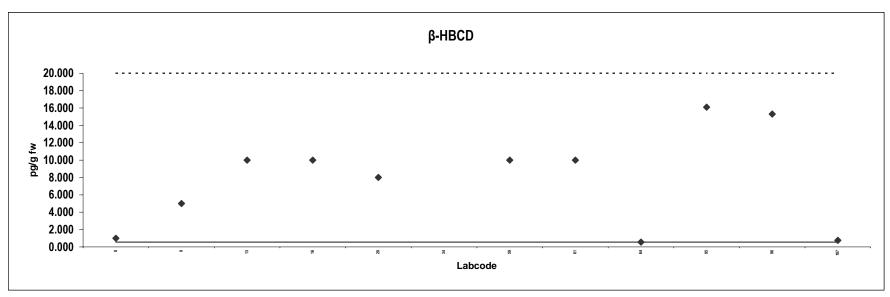


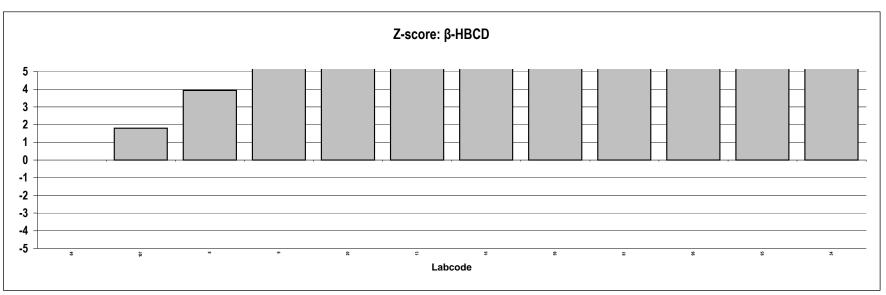
### Reindeer meat

Congener: β-HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
8 9 13	1.0	ND		_	
9	5.0	ND			
13	10	ND			
16 20	10 8.0	ND ND			
34	50	Outlier,ND			
59	10	ND			
61	10	ND			
64	0.56	1,2			
64 95	16	ND			
96	15	ND			
96 107	0.76	ND			

Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, %	0.56 10 7.9 5.5 70
No. of values reported No. of values removed No. of reported non-detects	70 12 1 11



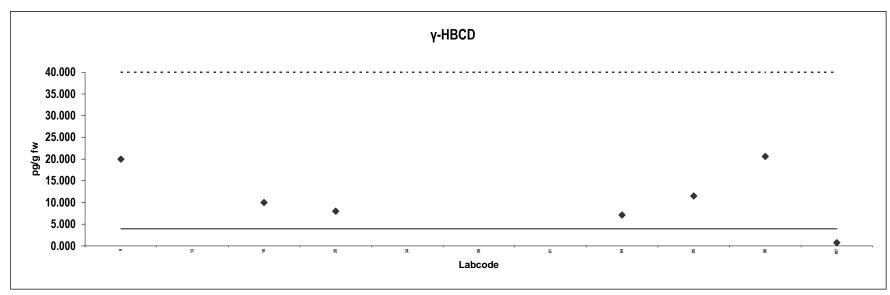


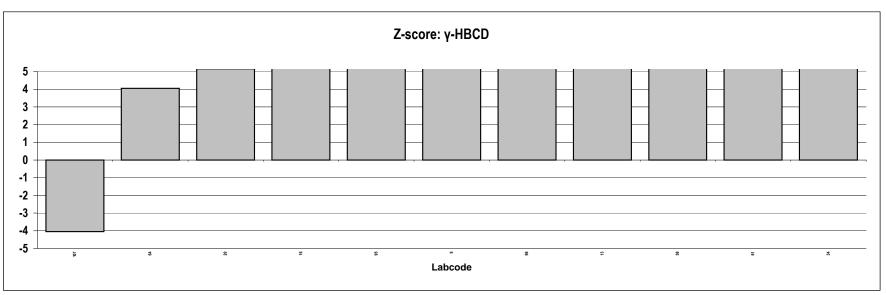
### Reindeer meat

Congener: γ-HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
9 13 16 20 34 59 61 64 95 96 107	Conc. pg/g fw.  20 60 10 8.0 176 60 60 7.1 12 21 0.75	Notes  ND Outlier,ND ND Outlier Outlier,ND Outlier,ND ND N	Lab code	Conc. pg/g fw.	Notes

Consensus median, pg/g	3.9
Median all values pg/g	20
Consensus mean, pg/g	11
Standard deviation, pg/g	7.1
Relative standard deviation, %	64
No. of values reported	11
No. of values removed	4
No. of reported non-detects	8
-	



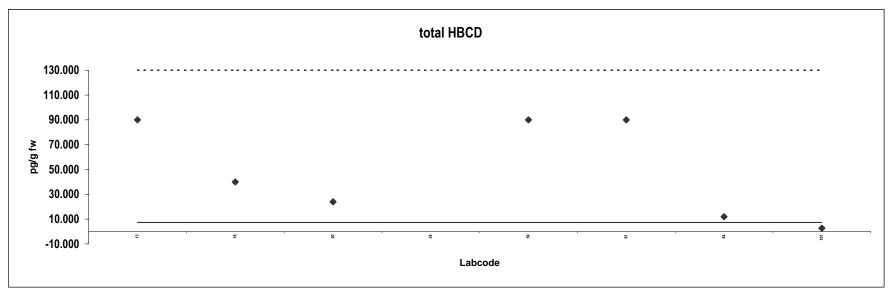


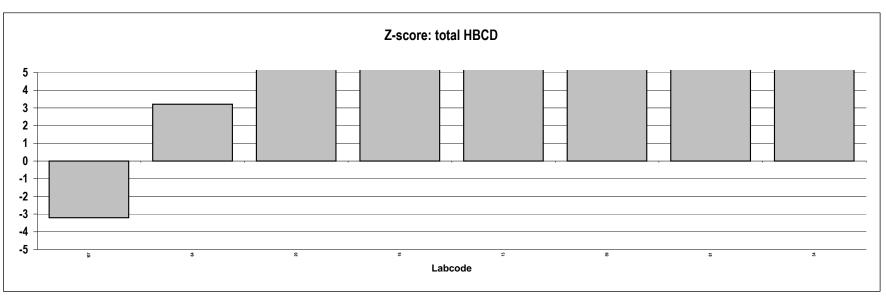
### Reindeer meat

**Congener: total HBCD** 

					Congen
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
13	90	ND			
16 20	40	ND			
20	24	ND			
34	176	Outlier			
59 61	90 90	ND ND			
64	12	ND			
64 107	2.6				
107	2.0				

Consensus median, pg/g	7.2
Median all values pg/g	65
Consensus mean, pg/g	50
Standard deviation, pg/g	39
Relative standard deviation, %	79
No. of values reported	8
No. of values removed	1
No. of reported non-detects	5





# Appendix 3:

Presentation of results for halibut filet

### **Appendix 3: Presentation of results: Halibut filet**

#### Statistic calculations for PCDDs, PCDFs and dioxin-like PCBs

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

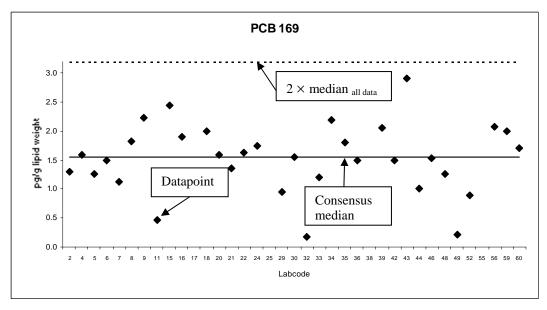
- 1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
- 2. Values exceeding  $2 \times$  this median, were defined as outliers and removed from the data set.
- 3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.

#### Statistic calculations for indicator PCBs, PBDEs and HBCD

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

- 1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners (NDs).
- 2. Values exceeding  $2 \times$  this median, were defined as outliers and removed from the data set. The NDs were also removed.
- 3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.
- 4. For comparison, median, mean and standard deviation were also calculated without removing NDs.

The diagram shows the reported data up to approximately the limit for outliers ( $2 \times$  the first median).



### **Z-Scores of individual congeners**

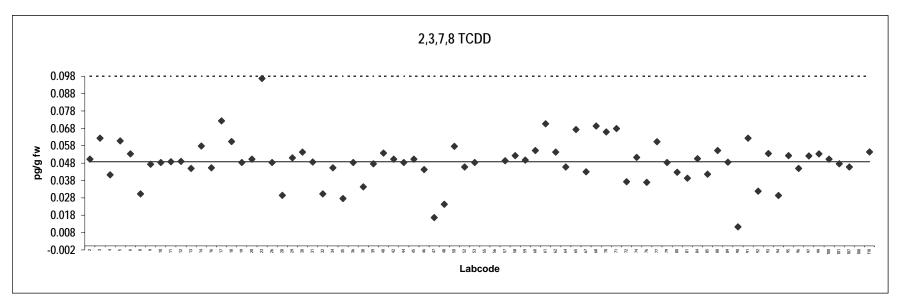
Z-scores of each congener were calculated for each laboratory according to the following equation:

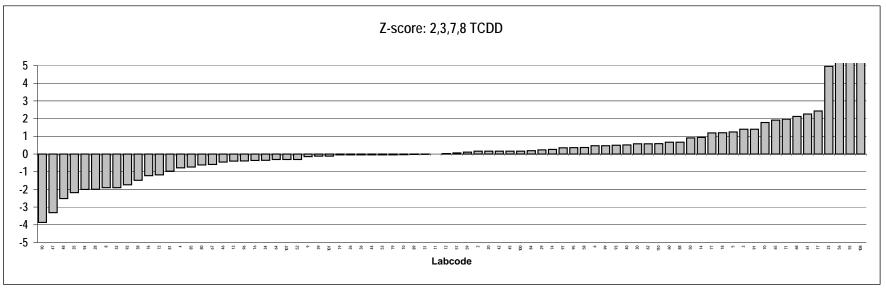
$$z = (x - X)/\sigma$$

where x = reported value; X = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm$  20% from the consensus value.

Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.050		61	0.070	
3	0.062		62	0.054	
4	0.041		64	0.045	
5	0.061		65	0.067	
6	0.053		67	0.043	
8	0.030	ND	68	0.069	
9	0.047		70	0.066	
10	0.048		71	0.068	
11	0.048		72	0.037	
12	0.049		74	0.051	
13	0.045		76	0.037	
14	0.058		77	0.060	
16	0.045		79	0.048	
17	0.072	ND	80	0.042	
18	0.060		81	0.039	
19	0.048		84	0.050	
20	0.050		85	0.041	
23	0.096		88	0.055	
26	0.048		89	0.048	
28	0.029		90	0.011	ND
29	0.051		91	0.062	
30	0.054		92	0.032	
31	0.048		93	0.053	
32	0.030		94	0.029	
34	0.045		95	0.052	
35	0.027		96	0.045	
36	0.048		97	0.052	
38	0.034		99	0.053	
39	0.047		100	0.050	
40	0.053		101	0.047	
42	0.050		107	0.045	
44	0.048		108	0.23	Outlier
45	0.050		110	0.054	
46	0.044				
47	0.016				
48	0.024				
50	0.057				
52	0.045				
53	0.048				
55	0.12	Outlier			
56	0.11	Outlier,ND			
57	0.049				
58	0.052				
59	0.049				
60	0.055				



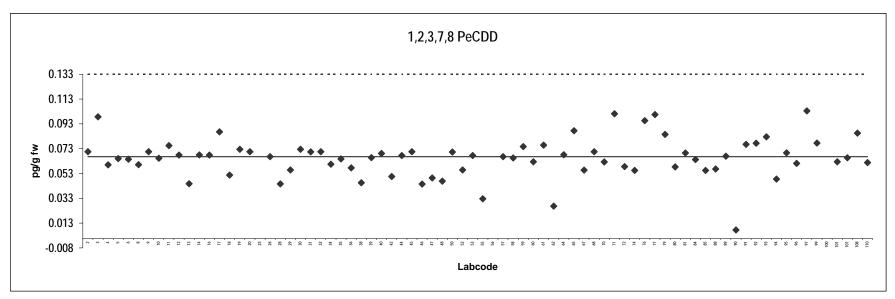


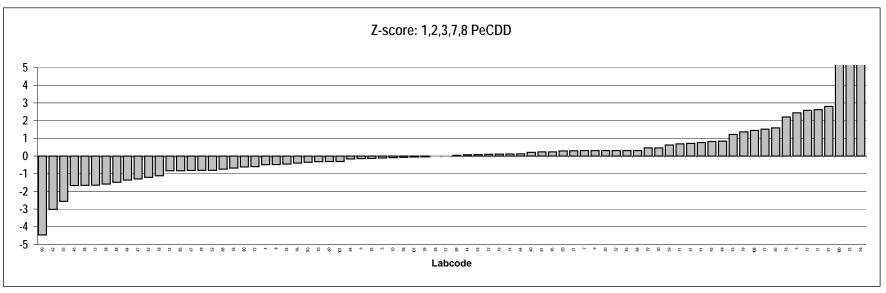
**Congener: 1,2,3,7,8 PeCDD** 

					Congener
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.070		61	0.075	
3	0.098		62	0.026	ND
4	0.060		64	0.068	
5	0.065		65	0.087	
6	0.064		67	0.055	
8	0.060		68	0.070	
9	0.070		70	0.062	
10	0.065		71	0.10	
11	0.075		72	0.058	
12	0.067		74	0.055	
13	0.044		76	0.095	
14	0.068		77	0.10	
16	0.067		79	0.084	
17	0.086	ND	80	0.058	
18	0.051		81	0.069	
19	0.072		84	0.064	
20	0.070		85	0.055	
23	0.15	Outlier	88	0.056	
26	0.066		89	0.067	
28	0.044		90	0.0070	ND
29	0.055		91	0.076	
30	0.072		92	0.077	
31 32	0.070		93 94	0.082	
34	0.070 0.060		94 95	0.048	
35	0.064		95 96	0.069 0.061	
36	0.057		90 97	0.10	
38	0.037		99	0.077	
39	0.045		100	0.077	Outlier
40	0.069		101	0.062	Outlief
42	0.050		107	0.065	
44	0.067		108	0.085	
45	0.070		110	0.061	
46	0.044				
47	0.049				
48	0.046				
50	0.070				
52	0.055				
53	0.067				
55	0.032	ND			
56	0.17	Outlier			
57	0.066				
58	0.065				
59	0.074				
60	0.062				

Consenus	statistics

Consensus median, pg/g	0.066
Median all values pg/g	0.066
Consensus mean, pg/g	0.065
Standard deviation, pg/g	0.016
Relative standard deviation, %	25
No. of values reported	78
No. of values removed	3
No. of reported non-detects	4

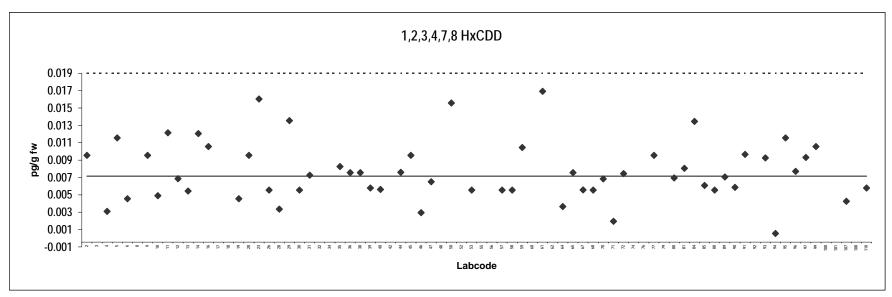


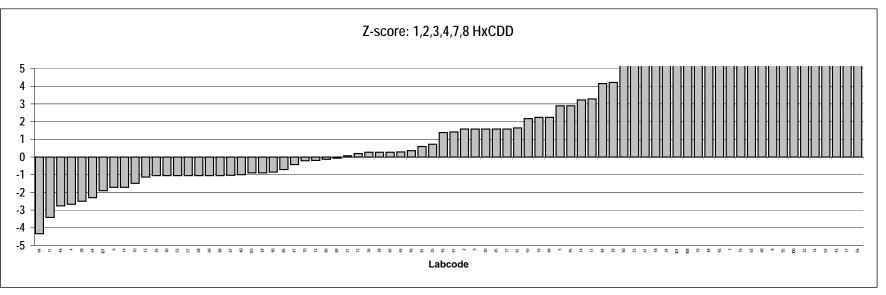


**Congener: 1,2,3,4,7,8 HxCDD** 

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes Notes
2	0.010	ND	61	0.017	
3	0.027	Outlier	62	0.033	Outlier,ND
4	0.0035	ND	64	0.0041	
5	0.012	ND	65	0.0080	ND
6	0.0050		67	0.0060	
8	0.040	Outlier	68	0.0060	
9	0.010	ND	70	0.0073	ND
10	0.0053		71	0.0024	ND
11	0.013		72	0.0079	
12	0.0073	ND	74	0.050	Outlier,ND
13	0.0059		76	0.029	Outlier
14	0.013	ND	77	0.010	
16	0.011		79	0.023	Outlier
17	0.10	Outlier,ND	80	0.0074	
18	0.020	Outlier,ND	81	0.0085	
19	0.0050	ND	84	0.014	
20	0.010	ND	85	0.0065	
23	0.016		88	0.0060	ND
26	0.0060		89	0.0075	
28	0.0038		90	0.0063	ND
29	0.014		91	0.010	ND
30	0.0060		92	0.024	Outlier
31	0.0077		93	0.0097	
32	0.050	Outlier,ND	94	0.0010	
34	0.020	Outlier,ND	95	0.012	ND
35	0.0087		96	0.0081	
36	0.0080		97	0.0098	
38	0.0080		99	0.011	
39	0.0062		100	0.048	Outlier
40	0.0061		101	0.020	Outlier,ND
42	0.10	Outlier,ND	107	0.0047	
44	0.0080		108	0.021	Outlier
45	0.010	ND	110	0.0062	
46	0.0034	NE			
47	0.0069	ND			
48	0.023	Outlier			
50	0.016	O di MB			
52	0.080	Outlier,ND			
53	0.0060	O-dian ND			
55	0.043	Outlier,ND			
56 57	0.16	Outlier,ND			
57 59	0.0060	ND			
58 59	0.0060	ND			
	0.011	Outlies			
60	0.036	Outlier			

Consensus median, pg/g Median all values pg/g	0.0076 0.010
Consensus mean, pg/g	0.0081
Standard deviation, pg/g	0.0034
Relative standard deviation, %	42
No. of values reported	78
No. of values removed	20
No. of reported non-detects	29

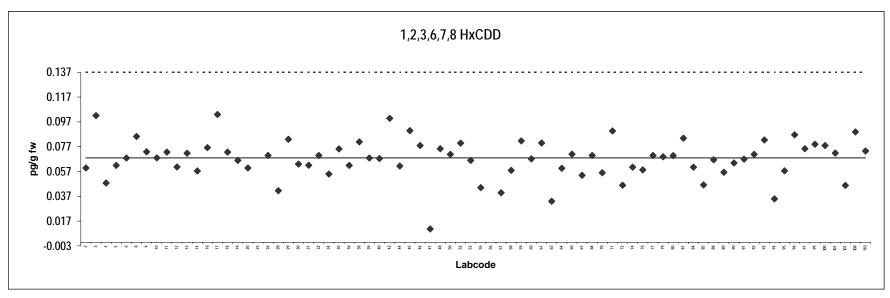


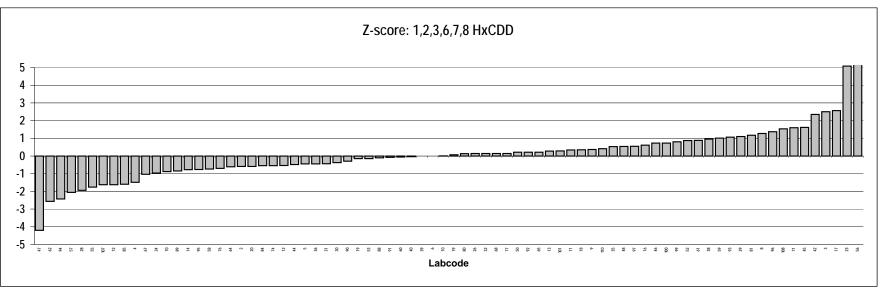


Congener: 1,2,3,6,7,8 HxCDD

				•	ongener:
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.060		61	0.080	
3	0.10		62	0.033	ND
4	0.048		64	0.060	
5	0.062		65	0.071	
6	0.068		67	0.054	
8	0.085		68	0.070	
9	0.073		70	0.056	
10	0.068		71	0.090	
11	0.073		72	0.046	
12	0.061		74	0.061	
13	0.072		76	0.058	
14	0.058		77	0.070	
16	0.076		79	0.069	
17	0.10	ND	80	0.070	
18	0.073		81	0.084	
19	0.066		84	0.061	
20	0.060		85	0.046	
23	0.14	Outlier	88	0.067	
26	0.070		89	0.057	
28	0.042		90	0.064	
29	0.083		91	0.067	
30	0.063		92	0.071	
31	0.062		93	0.083	
32	0.070		94	0.035	
34	0.055		95	0.058	
35	0.075		96	0.087	
36	0.062		97	0.076	
38	0.081		99	0.079	
39	0.068		100	0.078	
40	0.068		101	0.072	
42	0.10	ND	107	0.046	
44	0.061		108	0.089	
45	0.090		110	0.074	
46	0.078				
47	0.011				
48	0.075				
50	0.071	MD			
52	0.080	ND			
53	0.066	MD			
55	0.044	ND O di ND			
56	0.15	Outlier,ND			
57	0.040				
58	0.058				
59	0.082				
60	0.067				

Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported	0.068 0.069 0.067 0.016 23 78
No. of values removed	2
No. of reported non-detects	6



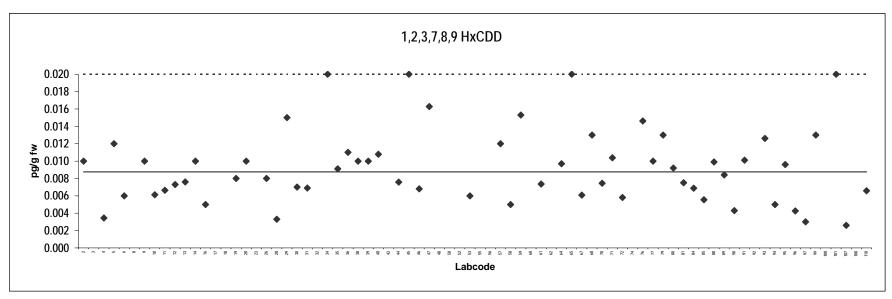


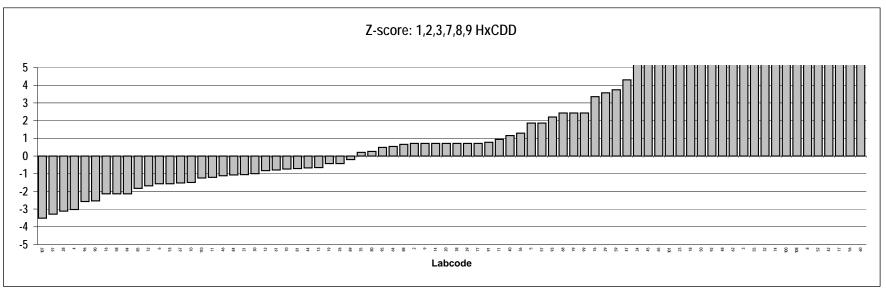
Congener: 1,2,3,7,8,9 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010	ND	61	0.0074	
3	0.036	Outlier	62	0.036	Outlier,ND
4	0.0035	ND	64	0.0097	
5	0.012	ND	65	0.020	ND
6	0.0060		67	0.0061	
8	0.077	Outlier	68	0.013	
9	0.010	ND	70	0.0075	ND
10	0.0061		71	0.010	
11	0.0066	ND	72	0.0058	
12	0.0073	ND	74	0.050	Outlier,ND
13	0.0076		76	0.015	ND
14	0.010	ND	77	0.010	
16	0.0050		79	0.013	
17	0.15	Outlier,ND	80	0.0092	
18	0.022	Outlier,ND	81	0.0075	
19	0.0080		84	0.0069	
20	0.010	ND	85	0.0056	
23	0.021	Outlier	88	0.0099	
26	0.0080	ND	89	0.0084	
28	0.0033		90	0.0043	ND
29	0.015		91	0.010	ND
30	0.0070		92	0.032	Outlier
31	0.0069		93	0.013	
32	0.050	Outlier,ND	94	0.0050	
34	0.020	ND	95	0.0096	
35	0.0091		96	0.0043	
36	0.011		97	0.0030	ND
38	0.010	ND	99	0.013	
39	0.010	ND	100	0.052	Outlier,ND
40	0.011		101	0.020	ND
42	0.10	Outlier,ND	107	0.0026	ND
44	0.0076	MD	108	0.073	Outlier
45	0.020	ND	110	0.0066	
46	0.0068				
47	0.016	0.41			
48	0.034	Outlier			
50	0.030	Outlier			
52	0.080	Outlier,ND			
53	0.0060	ND Oti ND			
55	0.045	Outlier,ND			
56 57	0.16	Outlier,ND			
	0.012	ND			
58 59	0.0050	ND			
60	0.015	Outlier			
00	0.20	Outlier			

Consenus st	atistics
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Consensus median, pg/g	0.0088
Median all values pg/g	0.010
Consensus mean, pg/g	0.0093
Standard deviation, pg/g	0.0043
Relative standard deviation, %	46
No. of values reported	78
No. of values removed	18
No. of reported non-detects	33



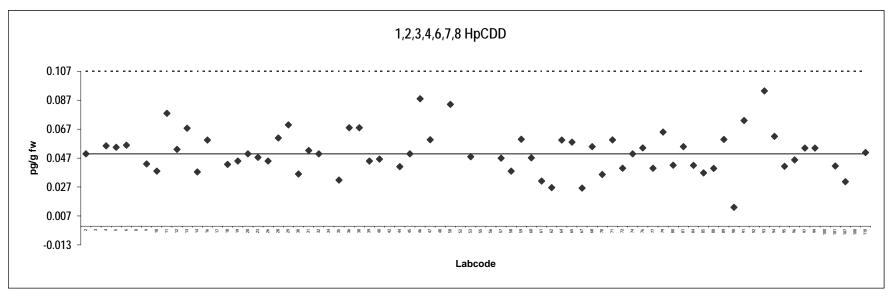


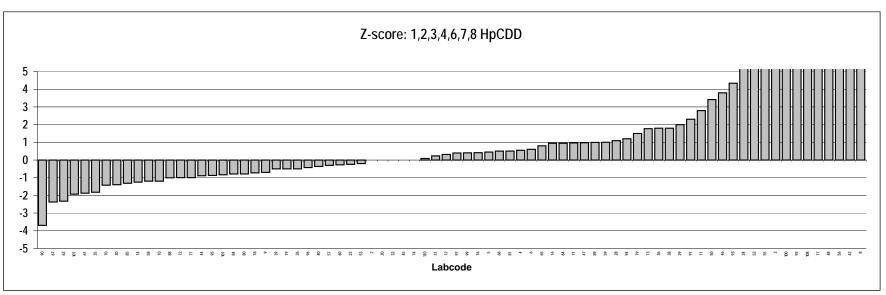
Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.050		61	0.031	
3	0.14	Outlier	62	0.027	ND
4	0.056		64	0.060	
5	0.055		65	0.058	
6	0.056		67	0.026	
8	0.40	Outlier	68	0.055	
9	0.043		70	0.036	
10	0.038		71	0.060	
11	0.078		72	0.040	
12	0.053		74	0.050	ND
13	0.068		76	0.054	
14	0.038		77	0.040	
16	0.059		79	0.065	
17	0.17	Outlier,ND	80	0.042	
18	0.043		81	0.055	
19	0.045		84	0.042	
20	0.050		85	0.037	
23	0.048		88	0.040	
26	0.045		89	0.060	
28	0.061		90	0.013	ND
29	0.070		91	0.073	
30	0.036		92	0.15	Outlier
31	0.052		93	0.093	
32	0.050	ND	94	0.062	
34	0.12	Outlier,ND	95	0.041	
35	0.032		96	0.046	
36	0.068		97	0.054	
38	0.068		99	0.054	ND
39	0.045		100	0.14	Outlier,ND
40	0.046		101	0.042	
42	0.30	Outlier,ND	107	0.031	
44	0.041		108	0.16	Outlier
45	0.050		110	0.051	
46	0.088				
47	0.060				
48	0.21	Outlier			
50	0.084				
52	0.12	Outlier,ND			
53	0.048				
55	0.13	Outlier			
56	0.26	Outlier,ND			
57	0.047				
58	0.038				
59	0.060				
60	0.047				

Cons	senus s	statistics	

Consensus median, pg/g	0.050
Median all values pg/g	0.054
Consensus mean, pg/g	0.051
Standard deviation, pg/g	0.0146
Relative standard deviation, %	29
No. of values reported	78
No. of values removed	12
No. of reported non-detects	11

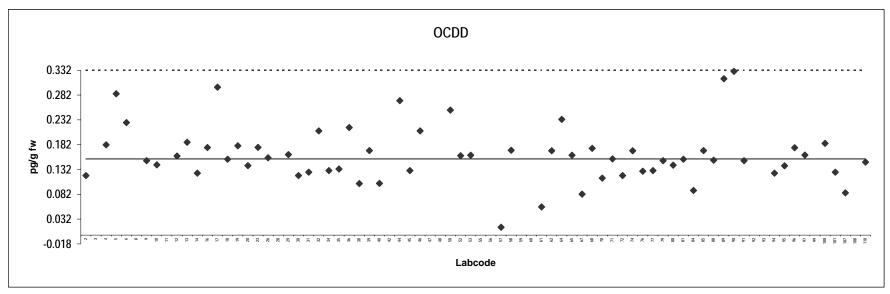


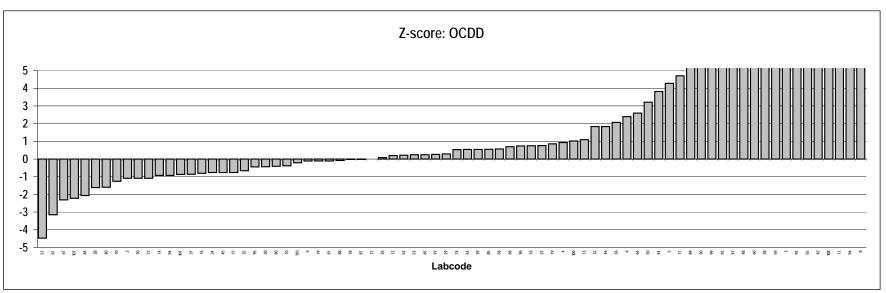


Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.12		61	0.057	
3	0.55	Outlier	62	0.17	ND
4	0.18		64	0.23	
5	0.29	ND	65	0.16	
6	0.23		67	0.083	ND
8	4.3	Outlier	68	0.18	
9	0.15		70	0.11	
10	0.14		71	0.15	
11	1.1	Outlier	72	0.12	
12	0.16		74	0.17	
13	0.19		76	0.13	
14	0.13		77	0.13	
16	0.18		79	0.15	
17	0.30	ND	80	0.14	
18	0.15		81	0.15	
19	0.18		84	0.090	
20	0.14		85	0.17	
23	0.18		88	0.15	
26	0.16		89	0.32	
28	0.45	Outlier	90	0.33	
29	0.16		91	0.15	
30	0.12		92	0.56	Outlier
31	0.13		93	0.36	Outlier
32	0.21		94	0.13	
34	0.13	ND	95	0.14	
35	0.13		96	0.18	
36	0.22		97	0.16	
38	0.10		99	0.34	Outlier,ND
39	0.17		100	0.19	ND
40	0.10		101	0.13	
42	1.0	Outlier,ND	107	0.085	0 11
44	0.27		108	1.0	Outlier
45	0.13		110	0.15	
46	0.21	0.41			
47	0.37	Outlier			
48	0.38	Outlier			
50	0.25	ND			
52	0.16	ND			
53 55	0.16	Outlier			
55 56	0.67 1.3	Outlier,ND			
57	0.016	ND			
58	0.016	ND			
59	0.17	Outlier			
60	0.48	Outlier			
OU	0.40	Outilei			

Consensus median, pg/g	0.15
Median all values pg/g	0.17
Consensus mean, pg/g	0.16
Standard deviation, pg/g	0.057
Relative standard deviation, %	35
No. of values reported	78
No. of values removed	15
No. of reported non-detects	11



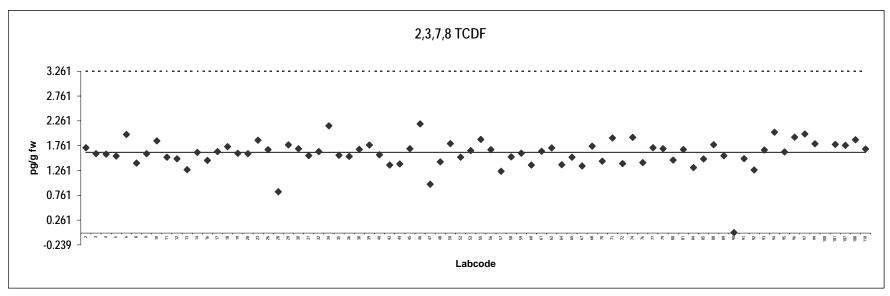


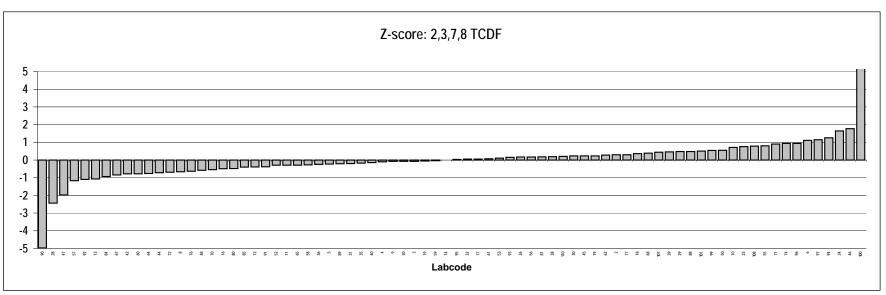
Congener: 2,3,7,8 TCDF

					Congene
Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
2	1.7		61	1.6	
3	1.6		62	1.7	
4	1.6		64	1.4	
5	1.6		65	1.5	
6	2.0		67	1.4	
8	1.4		68	1.8	
9	1.6		70	1.4	
10	1.9		71	1.9	
11	1.5		72	1.4	
12	1.5		74	1.9	
13	1.3		76	1.4	
14	1.6		77	1.7	
16	1.5		79	1.7	
17	1.6		80	1.5	
18	1.7		81	1.7	
19	1.6		84	1.3	
20 23	1.6		85 88	1.5	
26	1.9 1.7		88 89	1.8 1.6	
28	0.83		90	0.0093	ND
29	1.8		91	1.5	ND
30	1.7		92	1.3	
31	1.6		93	1.7	
32	1.6		94	2.0	
34	2.2		95	1.6	
35	1.6		96	1.9	
36	1.5		97	2.0	
38	1.7		99	1.8	
39	1.8		100	12	Outlier
40	1.6		101	1.8	
42	1.4		107	1.8	
44	1.4		108	1.9	
45	1.7		110	1.7	
46	2.2				
47	0.98				
48	1.4				
50	1.8				
52	1.5				
53	1.7				
55	1.9				
56	1.7				
57	1.2				
58	1.5				
59	1.6				
60	1.4				

Consensus median, pg/g	1.6
Median all values pg/g	1.6
Consensus mean, pg/g	1.6

Consensus mean, pg/g	1.6
Standard deviation, pg/g	0.30
Relative standard deviation, %	18
No. of values reported	78
No. of values removed	1
No. of reported non-detects	1





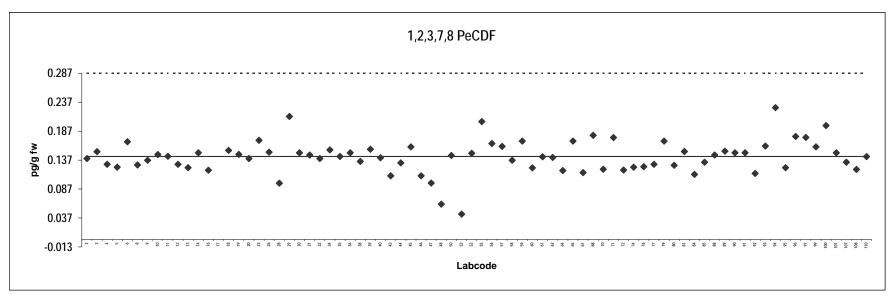
**Congener: 1,2,3,7,8 PeCDF** 

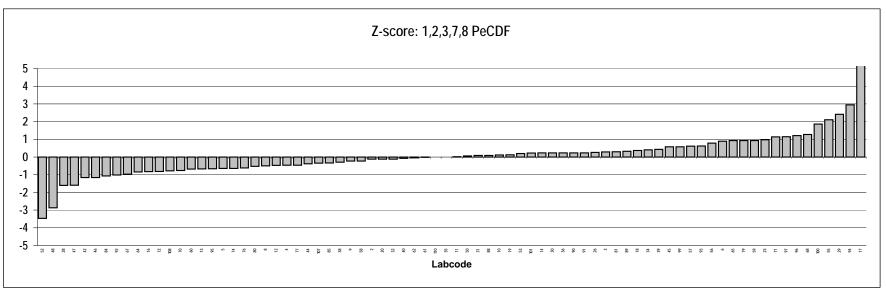
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.14		61	0.14	
3	0.15		62	0.14	
4	0.13		64	0.12	
5	0.13		65	0.17	
5 6	0.17		67	0.12	
8	0.13		68	0.18	
9	0.14		70	0.12	
10	0.15		71	0.18	
11	0.14		72	0.12	
12	0.13		74	0.13	
13	0.12		76	0.13	
14	0.15		77	0.13	
16	0.12		79	0.17	
17	0.48	Outlier	80	0.13	
18	0.15		81	0.15	
19	0.15		84	0.11	
20	0.14		85	0.13	
23	0.17		88	0.15	
26	0.15		89	0.15	
28	0.097		90	0.15	
29	0.21		91	0.15	
30	0.15		92	0.11	
31	0.15		93	0.16	
32	0.14		94	0.23	
34	0.16		95	0.12	
35	0.14		96	0.18	
36	0.15		97	0.18	
38	0.14		99	0.16	
39	0.16		100	0.20	
40	0.14		101	0.15	
42	0.11		107	0.13	
44	0.13		108	0.12	
45	0.16		110	0.14	
46	0.11				
47	0.098				
48	0.061				
50	0.15				
52	0.044				
53	0.15				
55	0.20				
56	0.17				
57	0.16				
58	0.14				
59	0.17				
60	0.12				

Consensus median, pg/g	0.14
Median all values pg/g	0.14
Consensus mean, pg/g	0.14
Standard deviation, pg/g	0.028
Relative standard deviation, %	20
No. of values reported	78
No. of values removed	1

Consenus statistics

No. of reported non-detects



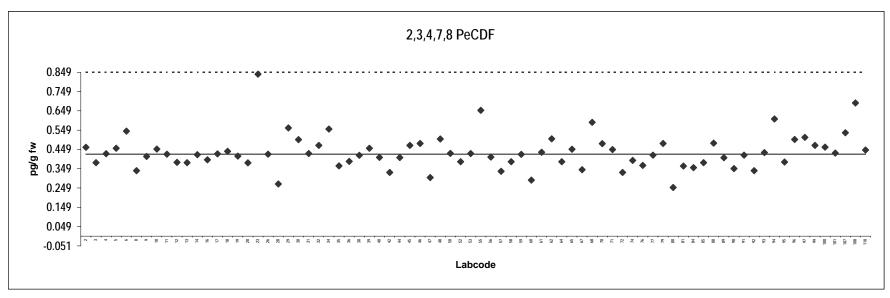


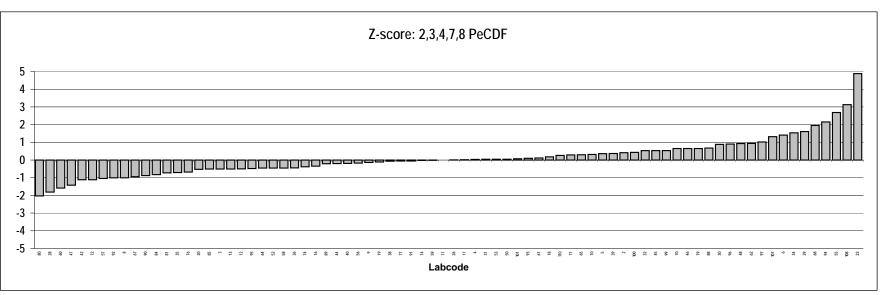
Congener: 2,3,4,7,8 PeCDF

					Congener
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2 3	0.46		61	0.43	
3	0.38		62	0.50	
4	0.43		64	0.39	
5	0.46		65	0.45	
6	0.54		67	0.34	
8	0.34		68	0.59	
9	0.41		70	0.48	
10	0.45		71	0.45	
11	0.42		72	0.33	
12	0.38		74	0.39	
13	0.38		76	0.37	
14	0.42		77	0.42	
16	0.40		79	0.48	
17	0.43		80	0.25	
18	0.44		81	0.36	
19	0.42		84	0.35	
20	0.38		85	0.38	
23	0.84		88	0.48	
26	0.43		89	0.41	
28 29	0.27 0.56		90 91	0.35 0.42	
30	0.50		91	0.42	
31	0.30		92	0.43	
32	0.43		93	0.43	
34	0.56		95	0.38	
35	0.36		96	0.50	
36	0.39		97	0.51	
38	0.42		99	0.47	
39	0.46		100	0.46	
40	0.41		101	0.43	
42	0.33		107	0.54	
44	0.41		108	0.69	
45	0.47		110	0.45	
46	0.48				
47	0.30				
48	0.50				
50	0.43				
52	0.39				
53	0.43				
55	0.65				
56	0.41				
57	0.34				
58	0.39				
59	0.42				
60	0.29				

Consenus	statistics

Consensus median, pg/g	0.42
Median all values pg/g	0.42
Consensus mean, pg/g	0.42
Standard deviation, pg/g	0.43
Relative standard deviation, %	2.1
No. of values reported	78
No. of values removed	0
No. of reported non-detects	0
No. of reported non-detects	U



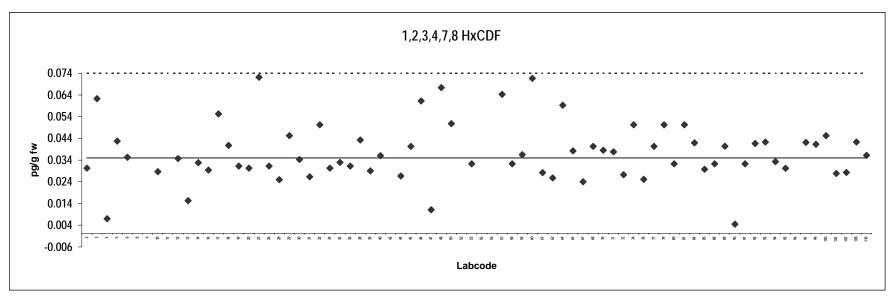


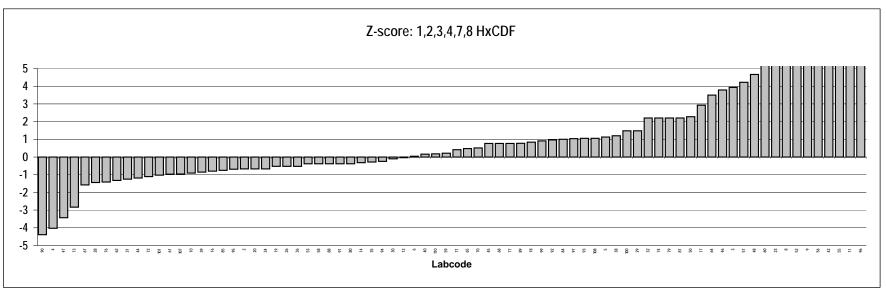
**Congener: 1,2,3,4,7,8 HxCDF** 

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.030	110165	61	0.028	110165
3	0.062		62	0.026	ND
4	0.0067	ND	64	0.059	ND
5	0.043	ND	65	0.038	
6	0.035	ND	67	0.024	
8	0.074	Outlier	68	0.040	
9	0.087	Outlier	70	0.038	
10	0.028	Outilei	71	0.038	
11	0.15	Outlier	72	0.027	
12	0.034	Guiner	74	0.050	ND
13	0.015		76	0.025	112
14	0.033		77	0.040	
16	0.029		79	0.050	
17	0.055	ND	80	0.032	
18	0.041	1,12	81	0.050	
19	0.031		84	0.042	
20	0.030		85	0.029	
23	0.072		88	0.032	
26	0.031		89	0.040	
28	0.025		90	0.0042	ND
29	0.045		91	0.032	
30	0.034		92	0.041	
31	0.026		93	0.042	
32	0.050	ND	94	0.033	
34	0.030		95	0.030	
35	0.033		96	0.15	Outlier
36	0.031		97	0.042	
38	0.043		99	0.041	
39	0.029		100	0.045	ND
40	0.036		101	0.028	
42	0.10	Outlier,ND	107	0.028	
44	0.026		108	0.042	
45	0.040		110	0.036	
46	0.061				
47	0.011				
48	0.067				
50	0.050				
52	0.080	Outlier,ND			
53	0.032				
55	0.14	Outlier			
56	0.091	Outlier,ND			
57	0.064				
58	0.032				
59	0.036				
60	0.071				

Consenus sta	atisi	tics
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Consensus median, pg/g	0.035
Median all values pg/g	0.037
Consensus mean, pg/g	0.037
Standard deviation, pg/g	0.013
Relative standard deviation, %	36
No. of values reported	78
No. of values removed	8
No. of reported non-detects	11



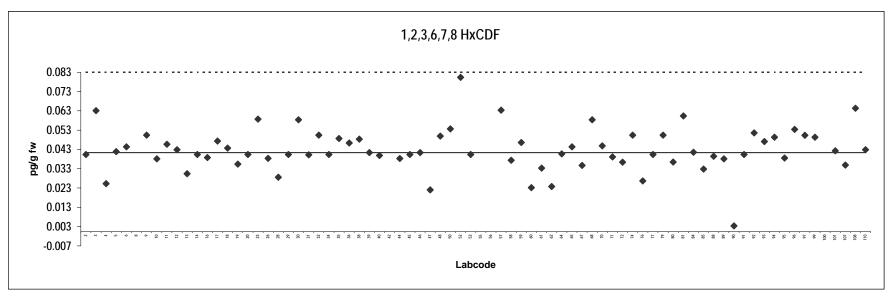


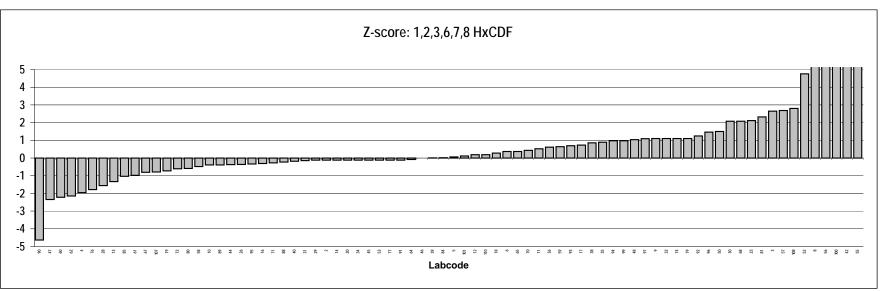
Congener: 1,2,3,6,7,8 HxCDF

				•	ongener:
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.040		61	0.033	
3	0.063		62	0.023	ND
4	0.025		64	0.040	
5	0.042		65	0.044	
6	0.044		67	0.034	
8	0.085	Outlier	68	0.058	
9	0.050		70	0.044	
10	0.038		71	0.039	
11	0.045		72	0.036	
12	0.043		74	0.050	ND
13	0.030		76	0.026	
14	0.040		77	0.040	
16	0.038		79	0.050	
17	0.047	ND	80	0.036	
18	0.043		81	0.060	
19	0.035		84	0.041	
20	0.040		85	0.032	
23	0.058		88	0.039	
26	0.038		89	0.038	
28	0.028		90	0.0030	ND
29	0.040		91	0.040	
30	0.058		92	0.051	
31	0.040		93	0.047	
32	0.050	ND	94	0.049	
34	0.040		95	0.038	
35	0.048		96	0.053	
36	0.046		97	0.050	
38	0.048		99	0.049	
39	0.041		100	0.088	Outlier
40	0.039		101	0.042	
42	0.10	Outlier,ND	107	0.035	
44	0.038		108	0.064	
45	0.040		110	0.043	
46	0.041				
47	0.022				
48	0.050				
50	0.053	MD			
52	0.080	ND			
53	0.040	0.41			
55	0.12	Outlier			
56	0.086	Outlier,ND			
57	0.063				
58	0.037				
59	0.046				
60	0.023				

Constitus statistics	Consenus	sta	tist	tics
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Consensus median, pg/g	0.041
Median all values pg/g	0.041
Consensus mean, pg/g	0.042
Standard deviation, pg/g	0.011
Relative standard deviation, %	26
No. of values reported	78
No. of values removed	5
No. of reported non-detects	8



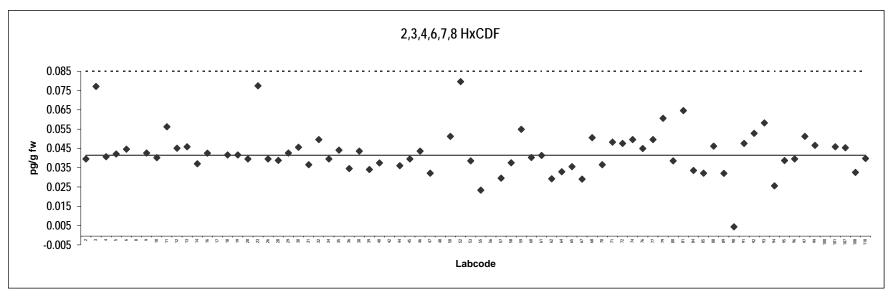


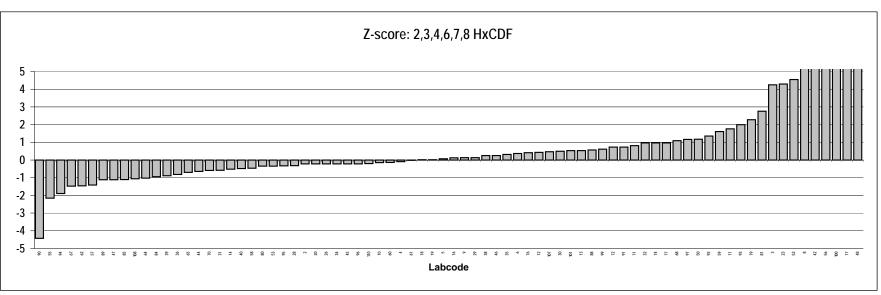
Congener: 2,3,4,6,7,8 HxCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.040		61	0.042	
3	0.078		62	0.030	ND
4	0.041		64	0.033	
5	0.043		65	0.036	
6	0.045		67	0.030	
8	0.089	Outlier	68	0.051	
9	0.043		70	0.037	
10	0.041		71	0.049	
11	0.057		72	0.048	
12	0.046		74	0.050	ND
13	0.046		76	0.045	
14	0.038		77	0.050	
16	0.043		79	0.061	
17	0.11	Outlier,ND	80	0.039	
18	0.042		81	0.065	
19	0.042		84	0.034	
20	0.040		85	0.033	
23	0.078		88	0.047	
26	0.040		89	0.033	
28	0.039		90	0.0048	ND
29	0.043		91	0.048	
30	0.046		92	0.053	
31	0.037		93	0.059	
32	0.050	ND	94	0.026	
34	0.040		95	0.039	
35	0.045		96	0.040	
36	0.035		97	0.052	
38	0.044		99	0.047	
39	0.034		100	0.10	Outlier
40	0.038		101	0.046	
42	0.10	Outlier,ND	107	0.046	
44	0.036		108	0.033	
45	0.040		110	0.040	
46	0.044				
47	0.033				
48	0.13	Outlier			
50	0.052				
52	0.080	ND			
53	0.039				
55	0.024	ND O di ND			
56	0.10	Outlier,ND			
57	0.030				
58	0.038				
59	0.055				
60	0.041				

Consenus	statistics

Consensus median, pg/g	0.042
Median all values pg/g	0.043
Consensus mean, pg/g	0.043
Standard deviation, pg/g	0.012
Relative standard deviation, %	27
No. of values reported	78
No. of values removed	6
No. of reported non-detects	9



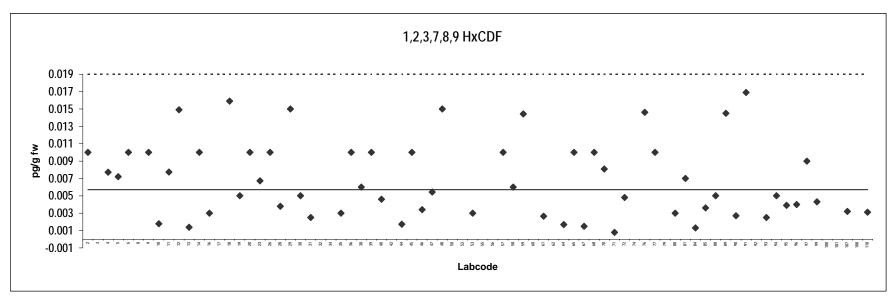


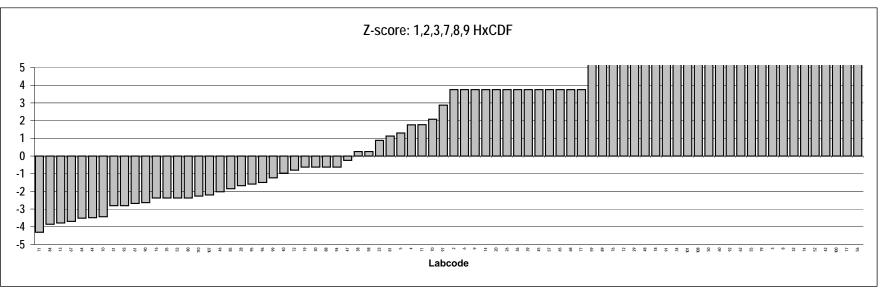
**Congener: 1,2,3,7,8,9 HxCDF** 

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010	ND	61	0.0026	
3	0.043	Outlier	62	0.030	Outlier,ND
4	0.0077	ND	64	0.0017	
5	0.0072	ND	65	0.010	ND
6	0.010	ND	67	0.0015	ND
8	0.050	Outlier,ND	68	0.010	ND
9	0.010	ND	70	0.0081	ND
10	0.0018		71	0.00078	ND
11	0.0077	ND	72	0.0048	
12	0.015	ND	74	0.050	Outlier,ND
13	0.0014		76	0.015	ND
14	0.010	ND	77	0.010	ND
16	0.0030		79	0.034	Outlier
17	0.12	Outlier,ND	80	0.0030	ND
18	0.016		81	0.0070	
19	0.0050	ND	84	0.0013	ND
20	0.010	ND	85	0.0036	
23	0.0067		88	0.0050	ND
26	0.010	ND	89	0.015	ND
28	0.0038	ND	90	0.0027	ND
29	0.015	ND	91	0.017	ND
30	0.0050	ND	92	0.024	Outlier
31	0.0025	ND	93	0.0025	
32	0.050	Outlier,ND	94	0.0050	
34	0.020	Outlier,ND	95	0.0039	ND
35	0.0030	ND	96	0.0040	ND
36	0.010		97	0.0090	ND
38	0.0060		99	0.0043	ND
39	0.010	ND	100	0.12	Outlier,ND
40	0.0046	ND	101	0.020	Outlier,ND
42	0.10	Outlier,ND	107	0.0032	ND
44	0.0017		108	0.020	Outlier,ND
45	0.010	ND	110	0.0031	ND
46	0.0034				
47	0.0054				
48	0.015	ND			
50	0.020	Outlier			
52	0.080	Outlier,ND			
53	0.0030	ND			
55	0.033	Outlier,ND			
56	0.14	Outlier,ND			
57	0.010	ND			
58	0.0060	ND			
59	0.014				
60	0.021	Outlier,ND			

Consenus	statis	tics
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Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported	0.0057 0.010 0.0069 0.0044 64 78
No. of values removed	18
No. of reported non-detects	56

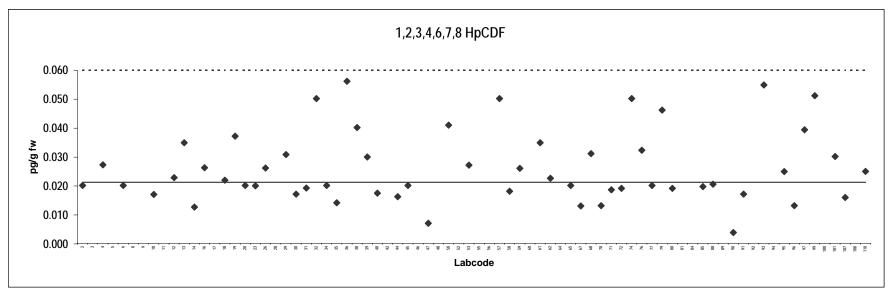


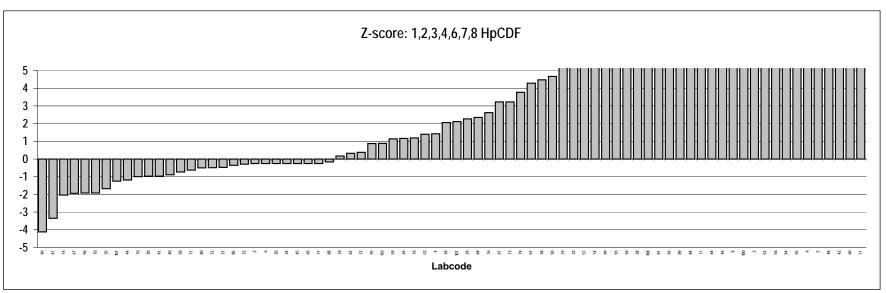


Congener: 1,2,3,4,6,7,8 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.020		61	0.035	
3	0.12	Outlier	62	0.022	ND
4	0.027		64	0.094	Outlier
5	0.21	Outlier,ND	65	0.020	ND
6	0.020		67	0.013	
8	0.096	Outlier	68	0.031	
9	0.13	Outlier	70	0.013	
10	0.017		71	0.018	
11	1.2	Outlier	72	0.019	
12	0.023		74	0.050	ND
13	0.035		76	0.032	
14	0.013		77	0.020	
16	0.026		79	0.046	
17	0.076	Outlier,ND	80	0.019	
18	0.022	ND	81	0.065	Outlier
19	0.037		84	0.075	Outlier
20	0.020		85	0.020	
23	0.020		88	0.020	
26	0.026		89	0.071	Outlier
28	0.060	Outlier	90	0.0037	ND
29	0.031		91	0.017	
30	0.017		92	0.069	Outlier
31	0.019		93	0.055	
32	0.050	ND	94	0.13	Outlier
34	0.020	ND	95	0.025	
35	0.014		96	0.013	ND
36	0.056		97	0.039	
38	0.040		99	0.051	ND
39	0.030		100	0.098	Outlier,ND
40	0.017		101	0.030	ND
42	0.30	Outlier,ND	107	0.016	
44	0.016		108	0.062	Outlier
45	0.020		110	0.025	
46	0.095	Outlier			
47	0.0069	ND			
48	0.24	Outlier			
50	0.041				
52	0.12	Outlier,ND			
53	0.027				
55	0.13	Outlier			
56	0.12	Outlier,ND			
57	0.050				
58	0.018				
59	0.026				
60	0.52	Outlier			

Consensus median, pg/g	0.021
Median all values pg/g	0.030
Consensus mean, pg/g	0.026
Standard deviation, pg/g	0.012
Relative standard deviation, %	47
No. of values reported	78
No. of values removed	22
No. of reported non-detects	17



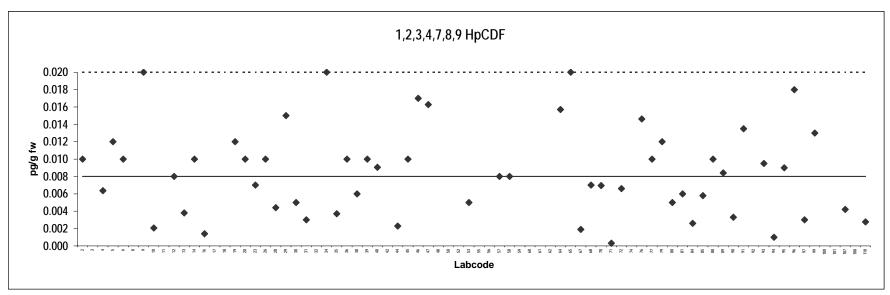


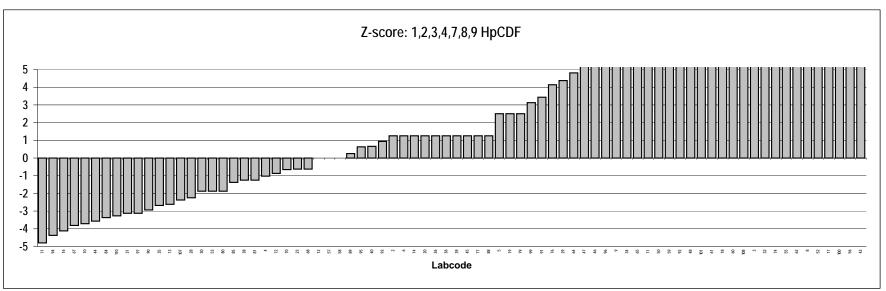
Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes Notes
2	0.010	ND	61	0.030	Outlier
3	0.042	Outlier	62	0.052	Outlier,ND
4	0.0064	ND	64	0.016	
5	0.012	ND	65	0.020	ND
6	0.010	ND	67	0.0019	1.2
8	0.054	Outlier	68	0.0070	
9	0.020		70	0.0069	ND
10	0.0021		71	0.00031	ND
11	0.020	Outlier	72	0.0066	
12	0.0080	ND	74	0.050	Outlier,ND
13	0.0038		76	0.015	ND
14	0.010	ND	77	0.010	ND
16	0.0014	ND	79	0.012	ND
17	0.13	Outlier,ND	80	0.0050	ND
18	0.034	Outlier,ND	81	0.0060	ND
19	0.012		84	0.0026	ND
20	0.010	ND	85	0.0058	
23	0.0070		88	0.010	ND
26	0.010	ND	89	0.0084	ND
28	0.0044		90	0.0033	ND
29	0.015	ND	91	0.014	ND
30	0.0050	ND	92	0.028	Outlier
31	0.0030	ND	93	0.0095	
32	0.050	Outlier,ND	94	0.0010	
34	0.020	ND	95	0.0090	ND
35	0.0037		96	0.018	ND
36	0.010		97	0.0030	ND
38	0.0060		99	0.013	ND
39	0.010	ND	100	0.19	Outlier,ND
40	0.0091	ND	101	0.030	Outlier,ND
42	0.30	Outlier,ND	107	0.0042	ND
44	0.0023		108	0.040	Outlier,ND
45	0.010	ND	110	0.0028	
46	0.017				
47	0.016				
48	0.028	Outlier,ND			
50	0.022	Outlier			
52	0.12	Outlier,ND			
53	0.0050	ND ND			
55	0.050	Outlier,ND			
56	0.23	Outlier,ND			
57 59	0.0080	ND			
58	0.0080	ND Outlier			
59 60	0.025	Outlier ND			
60	0.035	Outlier,ND			

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Consenus	STATISTICS

Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, %	0.0080 0.010 0.0085 0.0051 60
100	
No. of values reported No. of values removed No. of reported non-detects	78 21 51

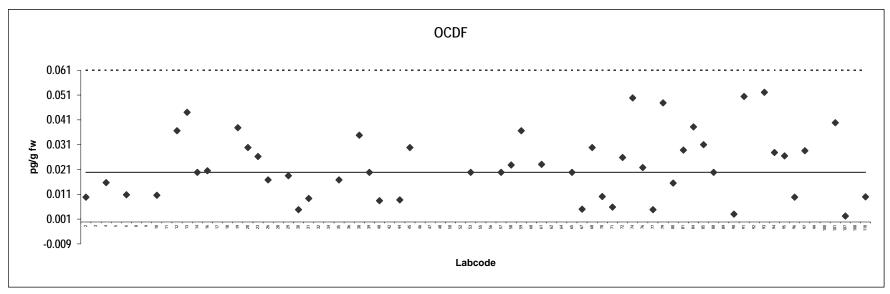


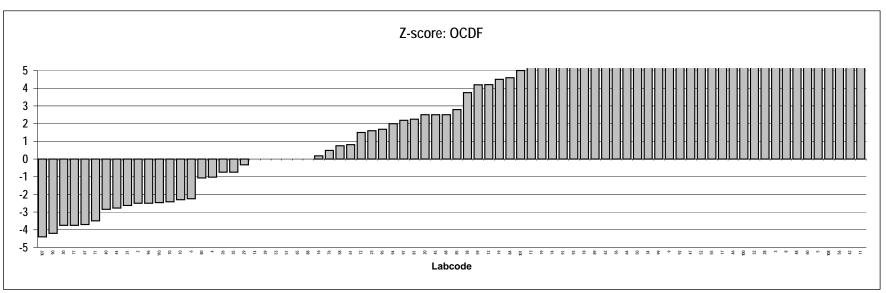


**Congener: OCDF** 

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.010	ND	61	0.023	- 1000
3	0.24	Outlier	62	0.073	Outlier,ND
4	0.016	ND	64	0.096	Outlier
5	0.40	Outlier,ND	65	0.020	ND
6	0.011		67	0.0052	ND
8	0.25	Outlier	68	0.030	ND
9	0.14	Outlier	70	0.010	ND
10	0.011		71	0.0060	
11	1.0	Outlier	72	0.026	
12	0.037		74	0.050	ND
13	0.044		76	0.022	ND
14	0.020	ND	77	0.0050	ND
16	0.021		79	0.048	
17	0.19	Outlier,ND	80	0.016	
18	0.063	Outlier,ND	81	0.029	
19	0.038		84	0.038	
20	0.030	ND	85	0.031	
23	0.026		88	0.020	ND
26	0.017	ND	89	0.068	Outlier
28	0.22	Outlier	90	0.0032	ND
29	0.019		91	0.051	ND
30	0.0050		92	0.14	Outlier
31	0.0095		93	0.052	
32	0.20	Outlier,ND	94	0.028	
34	0.11	Outlier,ND	95	0.027	
35	0.017		96	0.010	ND
36	0.096	Outlier	97	0.029	
38	0.035		99	0.12	Outlier,ND
39	0.020	ND	100	0.20	Outlier,ND
40	0.0086		101	0.040	ND
42	1.0	Outlier,ND	107	0.0024	ND
44	0.0089	MD	108	0.50	Outlier,ND
45	0.030	ND	110	0.010	
46	0.19	Outlier			
47	0.15	Outlier			
48	0.25	Outlier			
50	0.10 0.16	Outlier			
52 53		Outlier,ND			
55 55	0.020 0.17	ND Outlier			
55 56	0.17	Outlier,ND			
50 57	0.78	ND			
58	0.020	עויו			
59	0.023				
60	0.36	Outlier			
00	0.30	Outliel			

Consensus median, pg/g	0.020
Median all values pg/g	0.031
Consensus mean, pg/g	0.023
Standard deviation, pg/g	0.013
Relative standard deviation, %	58
No. of values reported	78
No. of values removed	27
No. of reported non-detects	34

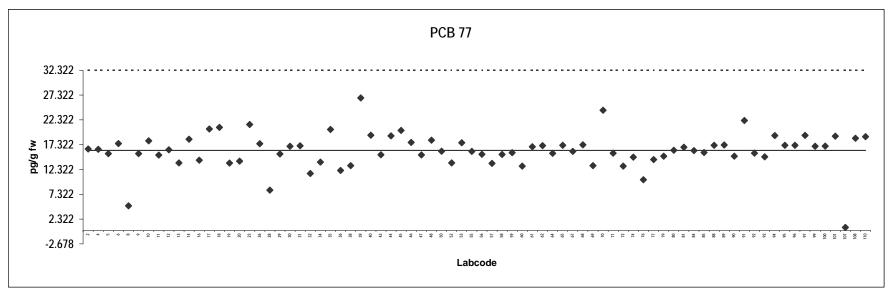


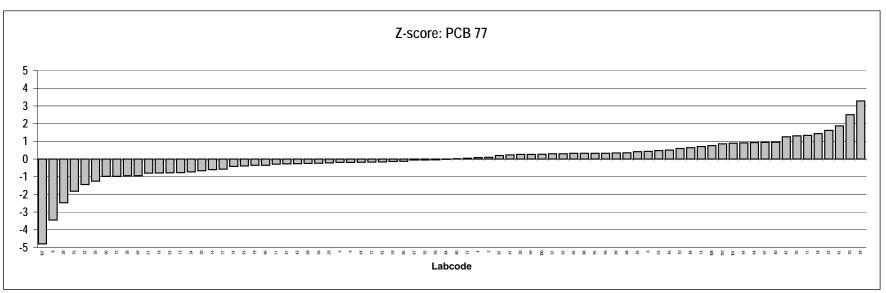


Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
	16	110165	62	17	Hous
2 4	16		64	16	
5	16		65	17	
6	18		67	16	
8	5.0	ND	68	17	
9	16	ND	69	13	
10	18		70	24	
11	15		70	24 16	
12	16		72	13	
13	14		74	15	
13	18		74 76	10	
16	14		77	14	
17	20		79	15	
18	20 21		80	16	
19	14		81	17	
20	14		84	16	
23	21		85	16	
26	18		88	17	
28	8.2		89	17	
29	15		90	15	
30	17		91	22	
31	17		92	16	
32	12		93	15	
34	14		94	19	
35	20		95	17	
36	12		96	17	
38	13		97	19	
39	27		99	17	
40	19		100	17	
42	15		101	19	
44	19		107	0.65	
45	20		108	19	
46	18		110	19	
47	15				
48	18				
50	16				
52	14				
53	18				
55	16				
56	15				
57	14				
58	15				
59	16				
60	13				
61	17				

16
16
16
3.6
22
78
0
1

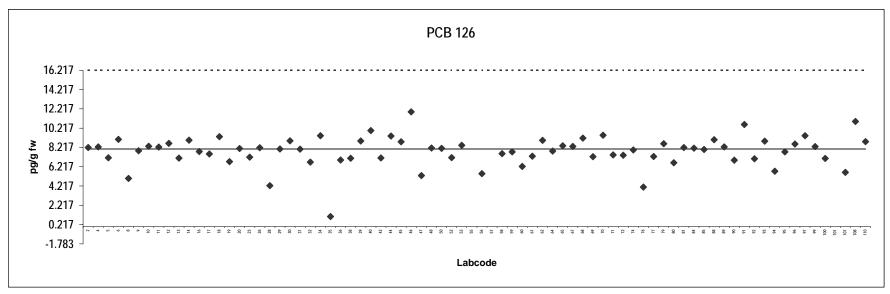


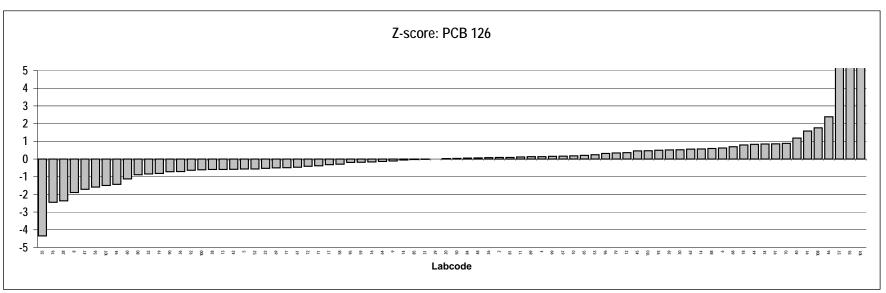


Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	8.2		62	9.0	
4	8.3		64	7.8	
5	7.1		65	8.4	
6	9.1 5.0		67	8.3	
8	5.0	ND	68	9.2	
9	7.9		69	7.3	
10	8.3		70	9.5	
11	8.2		71	7.4	
12	8.6		72	7.4	
13	7.1		74	8.0	
14	9.0		76	4.1	
16	7.8		77	7.3	
17	7.5		79	8.6	
18	9.3		80	6.6	
19	6.7		81	8.2	
20	8.1		84	8.1	
23	7.2		85	8.0	
26	8.2		88	9.0	
28	4.3		89	8.3	
29	8.1		90	6.9	
30	8.9		91	11	
31	8.0		92	7.0	
32	6.7		93	8.9	
34	9.4		94	5.7	
35	1.1		95	7.8	
36	6.9		96	8.6	
38	7.1		97	9.4	
39	8.9		99	8.3	
40	10.0		100	7.1	
42	7.1		101	30	Outlier
44	9.4		107	5.6	
45	8.8		108	11	
46	12		110	8.8	
47	5.3				
48	8.1				
50	8.1				
52	7.2				
53	8.4				
55	22	Outlier			
56	5.5				
57	20	Outlier			
58	7.6				
59	7.8				
60	6.3				
61	7.3				

8.1
8.1
7.8
1.6
20
78
3
1

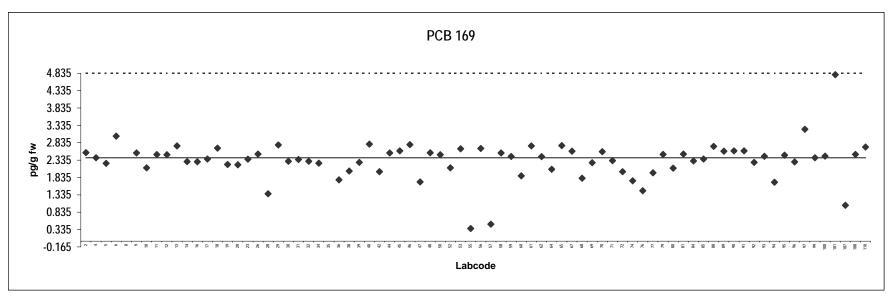


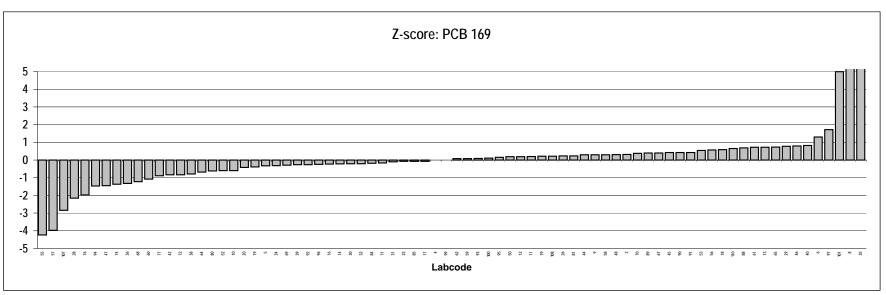


Congener: PCB 169

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	2.6		62	2.4	
4	2.4		64	2.1	
5	2.2		65	2.8	
6	3.0		67	2.6	
8	5.0	Outlier,ND	68	1.8	
9	2.5		69	2.3	
10	2.1		70	2.6	
11	2.5		71	2.3	
12	2.5		72	2.0	
13	2.7		74	1.7	
14	2.3		76	1.5	
16	2.3		77	2.0	
17	2.4		79	2.5	
18	2.7		80	2.1	
19	2.2		81	2.5	
20	2.2		84	2.3	
23	2.4		85	2.4	
26	2.5		88	2.7	
28	1.4		89	2.6	
29	2.8		90	2.6	
30	2.3		91	2.6	
31	2.4		92	2.3	
32	2.3		93	2.4	
34	2.2		94	1.7	
35	8.4	Outlier	95	2.5	
36	1.8		96	2.3	
38	2.0		97	3.2	
39	2.3		99	2.4	
40	2.8		100	2.5	
42	2.0		101	4.8	
44	2.5		107	1.0	
45	2.6		108	2.5	
46	2.8		110	2.7	
47	1.7				
48	2.5				
50	2.5				
52	2.1				
53	2.7				
55	0.36	ND			
56	2.7				
57	0.49	ND			
58	2.5	.=			
59	2.4				
60	1.9				
61	2.7				

Consenus statistics				
Consensus median, pg/g	2.4			
Median all values pg/g	2.4			
Consensus mean, pg/g	2.3			
Standard deviation, pg/g	0.56			
Relative standard deviation, %	24			
No. of values reported	78			
No. of values removed	2			
No. of reported non-detects	3			

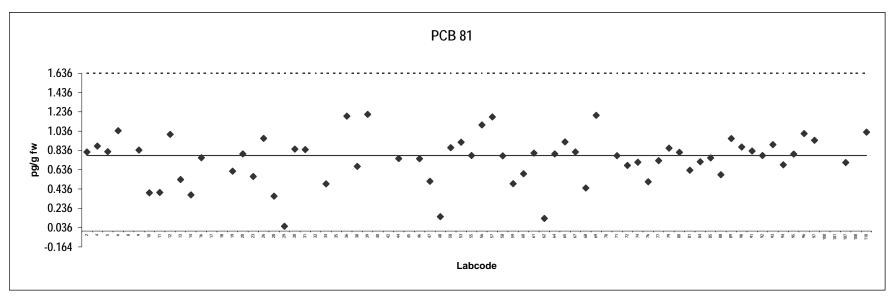


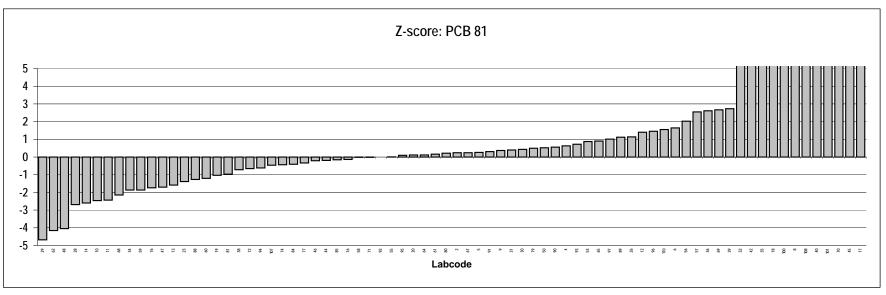


Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	0.82		64	0.80	
4	0.88		65	0.92	
5	0.82		67	0.82	
6	1.0		68	0.45	
8	5.0	Outlier,ND	69	1.2	
9	0.84		70	15	Outlier
10	0.40		71	0.78	
11	0.40		72	0.68	
12	1.0		74	0.71	
13	0.53		76	0.51	
14	0.38		77	0.73	
16	0.76		79	0.86	
17	35	Outlier	80	0.82	
18	2.8	Outlier	81	0.63	
19	0.62		84	0.72	
20	0.80		85	0.76	
23	0.57		88	0.58	
26	0.96		89	0.96	
28	0.36		90	0.87	
29	0.050	ND	91	0.83	
30	0.85		92	0.78	
31	0.84		93	0.90	
32	2.0	Outlier,ND	94	0.69	
34	0.49	ND	95	0.80	
35	2.0	Outlier	96	1.0	
36	1.2		97	0.94	0 11
38	0.67		100	2.9	Outlier
39	1.2	0 4	101	8.9	Outlier
40	7.9	Outlier	107	0.71	0 41 170
42	2.0	Outlier,ND	108	5.0	Outlier,ND
44	0.75	0 41	110	1.0	
45	16	Outlier			
46	0.75				
47	0.52				
48	0.15				
50	0.86				
53	0.92	ND			
55 56	0.78	ND			
56 57	1.1				
57 58	1.2 0.78				
58 59	0.78 0.49				
60	0.49				
61	0.59				
		ND			
62	0.13	ND			

Consensus median, pg/g	0.78
Median all values pg/g	0.82
Consensus mean, pg/g	0.75
Standard deviation, pg/g	0.25
Relative standard deviation, %	33
No. of values reported	76
No. of values removed	12
No. of reported non-detects	8

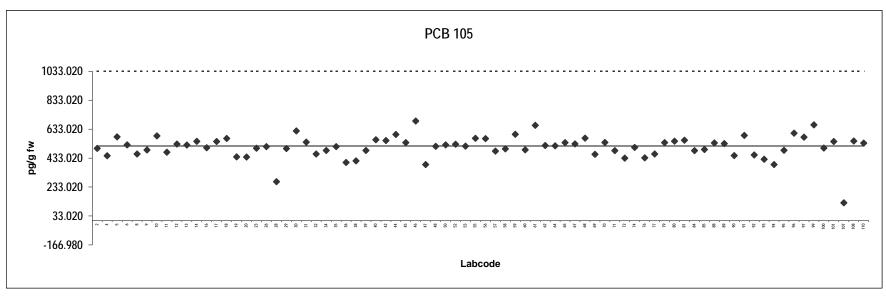


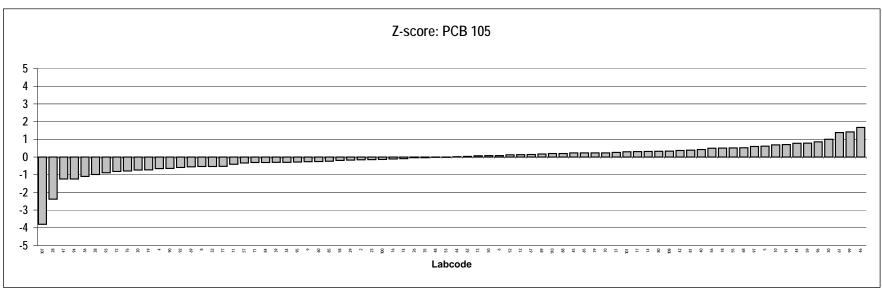


Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	500		62	520	
4	449		64	518	
5	580		65	540	
6	525		67	531	
8	461		68	570	
9	489		69	459	
10	587		70	540	
11	474		71	484	
12	530		72	432	
13	524		74	507	
14	549		76	435	
16	505		77	461	
17	548		79	540	
18	568		80	549	
19	441		81	556	
20	440		84	484	
23	501		85	492	
26	512		88	537	
28	270		89	533	
29	499		90	450	
30	620		91	589	
31	543		92	455	
32	461		93	425	
34	486		94	388	
35	512		95	487	
36	403		96	605	
38	414		97	578	
39	485		99	663	
40	560		100	502	
42	554		101	547	
44	597		107	124	
45	540		108	551	
46	689		110	537	
47	388				
48	515				
50	525				
52	529				
53	515				
55	569				
56	567				
57	482				
58	496				
59	597				
60	490				
61	659				

Consensus median, pg/g	517
Median all values pg/g	517
Consensus mean, pg/g	509
Standard deviation, pg/g	79
Relative standard deviation, %	16
No. of values reported	78
No. of values removed	0
No. of reported non-detects	0

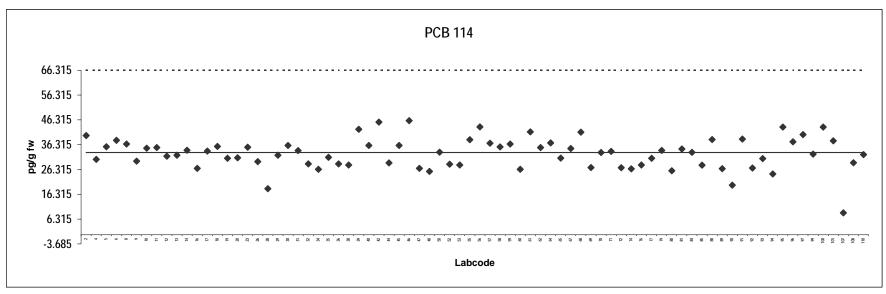


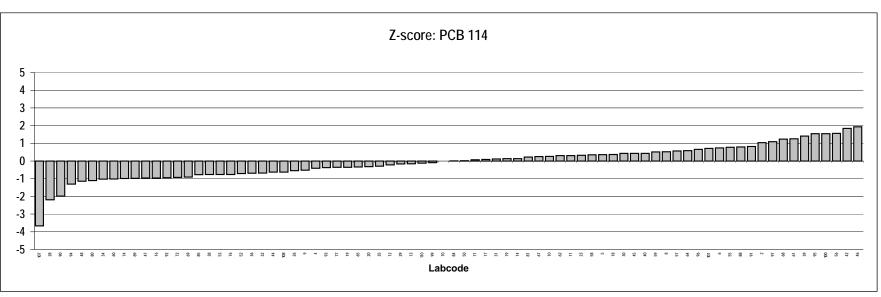


Congener: PCB 114

	•				Conge
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	40		62	35	
2 4 5	30		64	37	
5	36		65	31	
6	38		67	35	
8	37		68	41	
9	30		69	27	
10	35		70	33	
11	35		71	34	
12	32		72	27	
13	32		74	27	
14	34		76	28	
16	27		77	31	
17	34		79	34	
18	36		80	26	
19	31		81	35	
20	31		84	33	
23	35		85	28	
26	30		88	38	
28	19		89	27	
29	32		90	20	
30	36		91	39	
31	34		92	27	
32	29		93	31	
34	26		94	25	
35	31		95	43	
36	29		96	38	
38	28		97	40	
39	42		99	33	
40	36		100	43	
42	45		101	38	
44	29		107	8.8	
45	36		108	29	
46	46		110	32	
47	27				
48	26				
50	33				
52	28				
53	28				
55	38				
56	44				
57	37				
58	35				
59	37				
60	26				
61	41				

Consensus median, pg/g	33
Median all values pg/g	33
Consensus mean, pg/g	33
Standard deviation, pg/g	6.3
Relative standard deviation, %	19
No. of values reported	78
No. of values removed	0
No. of reported non-detects	0



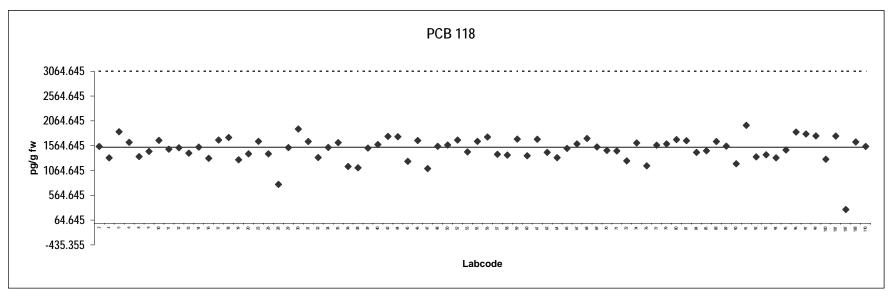


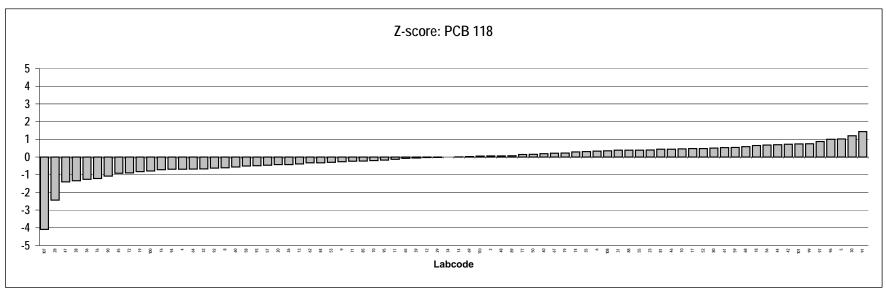
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	1550		62	1430	
4	1320		64	1322	
5	1845		65	1510	
6	1633		67	1599	
8	1345		68	1711	
9	1450		69	1540	
10	1671		70	1469	
11	1493		71	1459	
12	1522		72	1257	
13	1412		74	1620	
14	1535		76	1159	
16	1311		77	1575	
17	1678		79	1600	
18	1730		80	1687	
19	1280		81	1666	
20	1400		84	1430	
23	1652		85	1461	
26	1400		88	1650	
28	785		89	1554	
29	1526		90	1200	
30	1900		91	1973	
31	1650		92	1340	
32	1326		93	1381	
34	1530		94	1319	
35 36	1625 1146		95 96	1477 1838	
38	1120		90 97	1801	
39	1515		99	1760	
40	1515		100	1289	
42	1752		101	1758	
44	1745		107	277	
45	1250		108	1639	
46	1668		110	1548	
47	1102				
48	1550				
50	1578				
52	1678				
53	1440				
55	1651				
56	1740				
57	1389				
58	1375				
59	1698				
60	1360				
61	1694				

~	4 4. 4.
Consenus	statistics

Consensus median, pg/g	1532
Median all values pg/g	1532
Consensus mean, pg/g	1499
Standard deviation, pg/g	249
Relative standard deviation, %	17
No. of values reported	78
No. of values removed	0
No. of reported non-detects	0

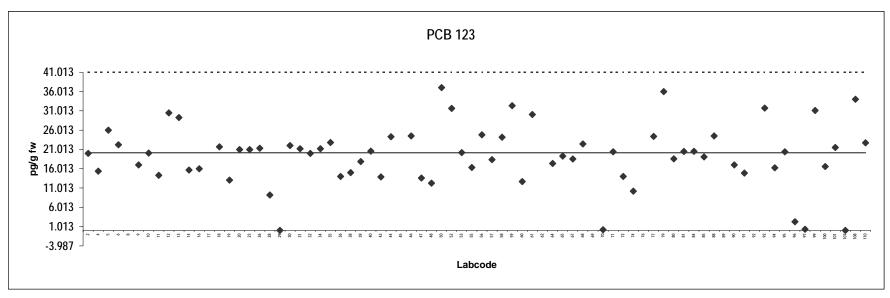


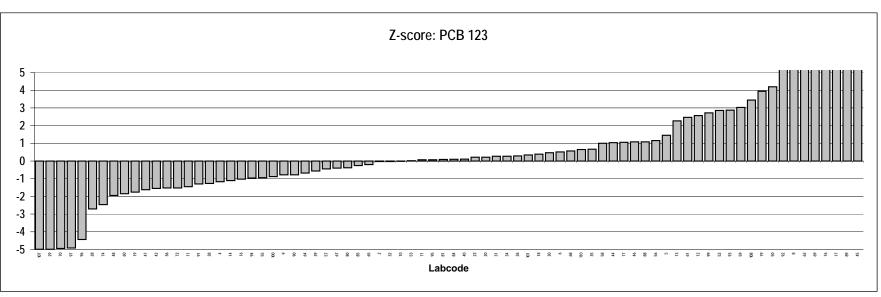


Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	20		62	58	Outlier
4	15		64	17	
5	26		65	19	
6	22		67	19	
8	50	Outlier	68	22	
9	17		69	169	Outlier
10	20		70	0.22	ND
11	14		71	20	
12	30		72	14	
13	29		74	10	
14	16		76	171	Outlier
16	16		77	24	
17	173	Outlier	79	36	
18	22		80	19	
19	13		81	21	
20	21		84	21	
23	21		85	19	
26	21		88	25	
28	9.2		89	176	Outlier
29	0.050	ND	90	17	
30	22		91	15	
31	21		92	42	Outlier
32	20		93	32	
34	21		94	16	
35	23		95	20	
36	14		96	2.3	ND
38	15		97	0.34	ND
39	18		99	31	
40	21		100	17	
42	14		101	22	
44	24		107	0.019	ND
45	190	Outlier	108	34	
46	25		110	23	
47	14				
48	12				
50	37				
52	32				
53	20				
55	16				
56	25				
57	18				
58	24				
59	32				
60	13				
61	30				

Consensus median, pg/g	20
Median all values pg/g	21
Consensus mean, pg/g	19
Standard deviation, pg/g	8.0
Relative standard deviation, %	41
No. of values reported	78
No. of values removed	8
No. of reported non-detects	5

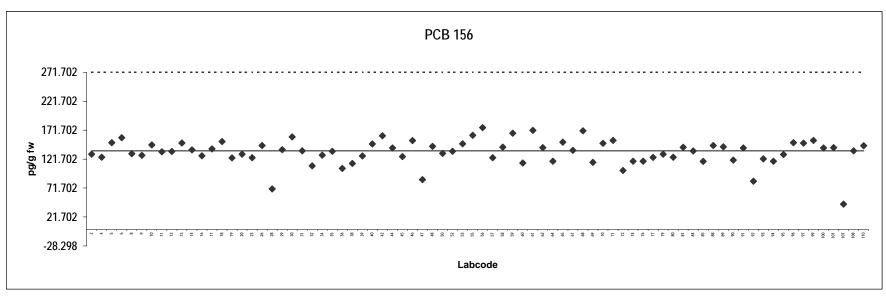


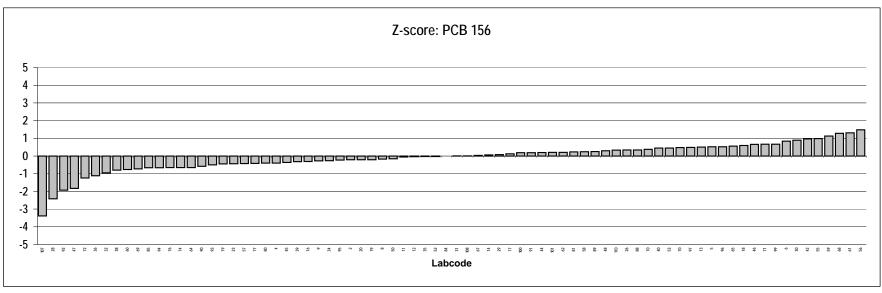


Congener: PCB 156

					Conge
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2 4	130		62	141	
4	125		64	118	
5	150		65	151	
6	159		67	137	
8	131		68	171	
9	128		69	116	
10	146		70	149	
11	134		71	154	
12	135		72	102	
13	150		74	118	
14	138		76	118	
16	127		77	125	
17	139		79	130	
18	152		80	125	
19	124		81	142	
20	130		84	136	
23	124		85	118	
26	145		88	145	
28	70		89	143	
29	138		90	120	
30	160		91	141	
31	136		92	83	
32	110		93	122	
34	129		94	118	
35	135		95	130	
36	105		96	150	
38	114		97	149	
39	127		99	154	
40	148		100	141	
42	162		101	141	
44	141		107	44	
45	126		108	136	
46	154		110	145	
47	86				
48	144				
50	131				
52	135				
53	148				
55	163				
56	176				
57	124				
58	142				
59	166				
60	115				
61	171				

Consensus median, pg/g	136
Median all values pg/g	136
Consensus mean, pg/g	134
Standard deviation, pg/g	22
Relative standard deviation, %	16
No. of values reported	78
No. of values removed	0
No. of reported non-detects	0

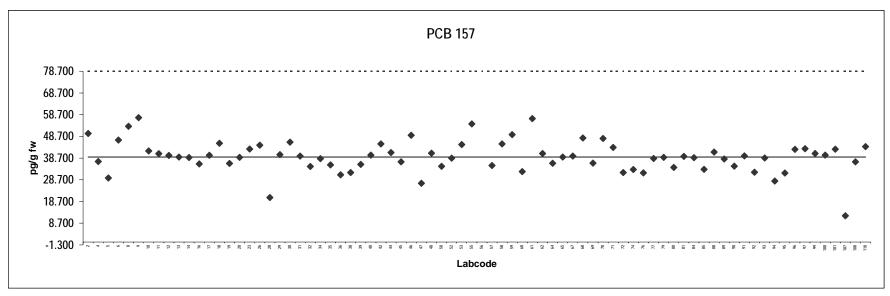


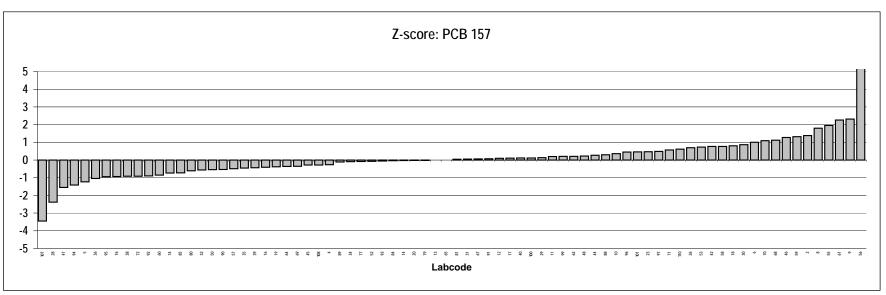


Congener: PCB 157

_		1	m*		Conge
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	50		62	41	
2 4 5	37		64	36	
5	30		65	39	
6	47		67	40	
8	53		68	48	
9	57		69	36	
10	42		70	48	
11	41		71	44	
12	40		72	32	
13	39		74	33	
14	39		76	32	
16	36		77	39	
17	40		79	39	
18	46		80	34	
19	36		81	40	
20	39		84	39	
23	43		85	33	
26	45		88	42	
28	21		89	38	
29	40		90	35	
30	46		91	40	
31	40		92	32	
32	35		93	39	
34	38		94	28	
35	36		95	32	
36	31		96	43	
38	32		97	43	
39	36		99	41	
40	40		100	40	
42	45		101	43	
44	41		107	12	
45	37		108	37	
46	49		110	44	
47	27				
48	41				
50	35				
52	39				
53	45				
55	54				
56	176	Outlier			
57	35				
58	45				
59	50				
60	33				
61	57				

Consenus statistics					
C	20				
Consensus median, pg/g	39				
Median all values pg/g	39				
Consensus mean, pg/g	39				
Standard deviation, pg/g	7.3				
Relative standard deviation, %	18				
No. of values reported	78				
No. of values removed	1				
No. of reported non-detects	0				

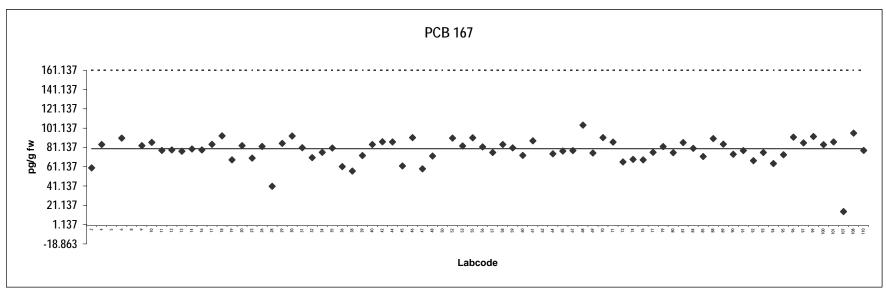


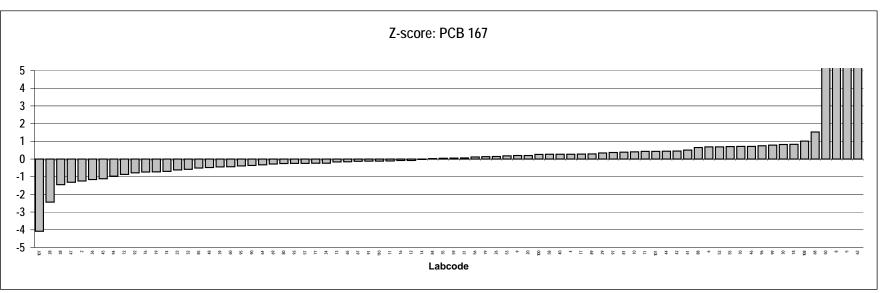


Congener: PCB 167

					Conge
Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
2	60		62	356	Outlier
4	84		64	75	
5	290	Outlier	65	77	
6	91		67	78	
8	210	Outlier	68	104	
9	83		69	75	
10	86		70	91	
11	78		71	87	
12	79		72	66	
13	77		74	69	
14	80		76	68	
16	79		77	76	
17	84		79	82	
18	93		80	76	
19	68		81	86	
20	83		84	80	
23	70		85	72	
26	82		88	90	
28	41		89	84	
29	85		90	74	
30	93		91	78	
31	81		92	67	
32	71		93	76	
34	76		94	64	
35	81		95	74	
36	61		96	92	
38	57		97	86	
39	73		99	92	
40	84		100	84	
42	87		101	87	
44	87		107	15	
45	62		108	96	
46	91		110	78	
47	59		110	70	
48	72				
50	207	Outlier			
52	91	Outilei			
53	83				
55	91				
56	82				
57	76				
58	84				
59	81				
60	73				
61	73 88				
01	00				

Consensus median, pg/g	80
Median all values pg/g	81
Consensus mean, pg/g	78
Standard deviation, pg/g	13
Relative standard deviation, %	16
No. of values reported	78
No. of values removed	4
No. of reported non-detects	0





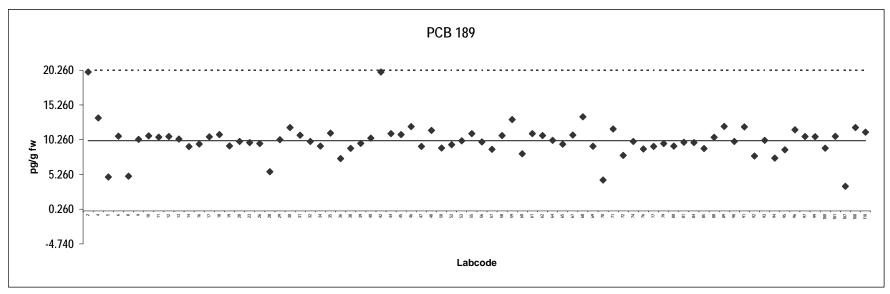
Congener: PCB 189

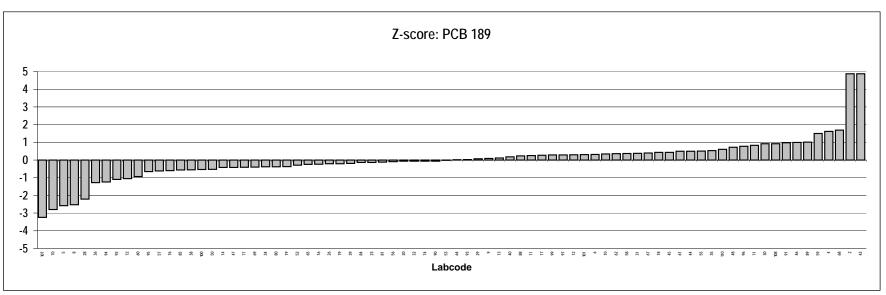
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2 4	20		62	11	
4	13		64	10	
5	4.9		65	9.6	
6	11		67	11	
8	5.0	ND	68	14	
9	10		69	9.3	
10	11		70	4.4	
11	11		71	12	
12	11		72	8.0	
13	10		74	10	ND
14	9.3		76	8.9	
16	9.6		77	9.3	
17	11		79	9.7	
18	11		80	9.3	
19	9.4		81	9.9	
20	10		84	9.8	
23	9.8		85	9.0	
26	9.7		88	11	
28	5.6		89	12	
29	10		90	10	
30	12		91	12	
31	11		92	7.9	
32	10	ND	93	10	
34	9.3		94	7.6	
35	11		95	8.8	
36	7.5		96	12	
38	9.0		97	11	
39	9.7		99	11	
40	10		100	9.0	
42	20	ND	101	11	
44	11		107	3.6	
45	11		108	12	
46	12		110	11	
47	9.3				
48	12				
50	9.1				
52	9.5				
53	10				
55	11				
56	9.9				
57	8.9				
58	11				
59	13				
60	8.2				
61	11				

# Consensus median, pg/g 10 Median all values pg/g 10 Consensus mean, pg/g 10 Standard deviation, pg/g 2.4 Relative standard deviation, % 24 No. of values reported 78 No. of values removed 0

4

No. of reported non-detects

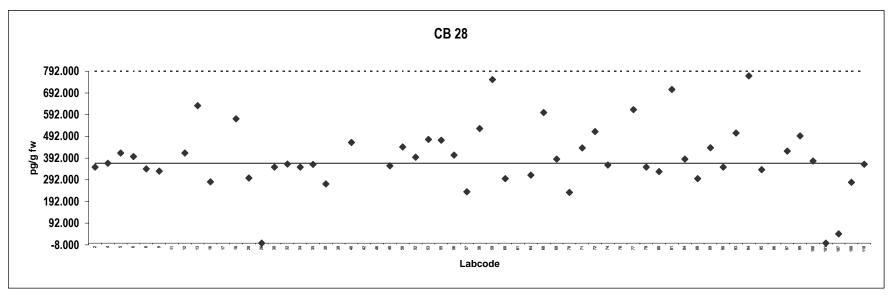


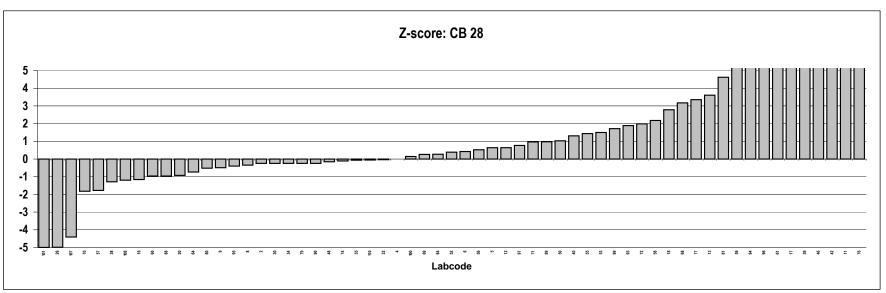


Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	350		81	708	
4	368		84	387	
5	415		88	297	
6	399		89	440	
8	343		90	350	
9	332		93	507	
11	1026	Outlier	94	770	
12	415		95	339	
13	633		96	815	Outlier
16	283		97	424	
17	834	Outlier	99	494	
18	573		100	378	
20	300		101	0.33	
26	0.44		107	43	
30	350		108	280	
32	365		110	364	
34	350				
35	363				
38	273				
39	898	Outlier			
40	464				
42	1000	Outlier,ND			
46	971	Outlier			
48	356				
50	443				
52	396				
53	478				
55	474				
56	406				
57	237				
58	528				
59	754				
60	297				
61	823	Outlier			
64	314				
68	602				
69	387				
70	234				
71	439				
72	514				
74	360				
76	1573	Outlier			
77	615				
79	350				
80	330				

Consensus median, pg/g	368
Median all values pg/g	396
Consensus mean, pg/g	394
Standard deviation, pg/g	153
Relative standard deviation, %	39
No. of values reported	61
No. of values removed	8
No. of reported non-detects	1
	-

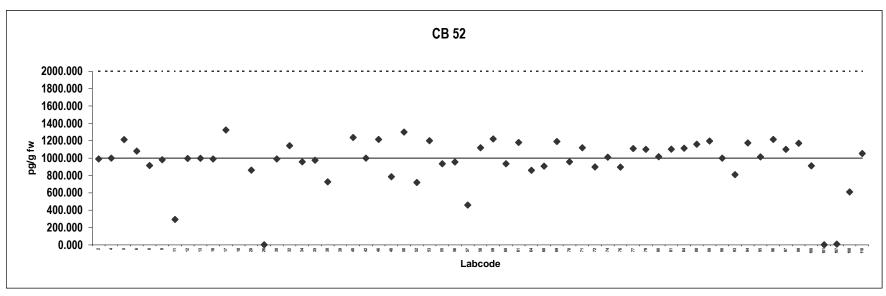


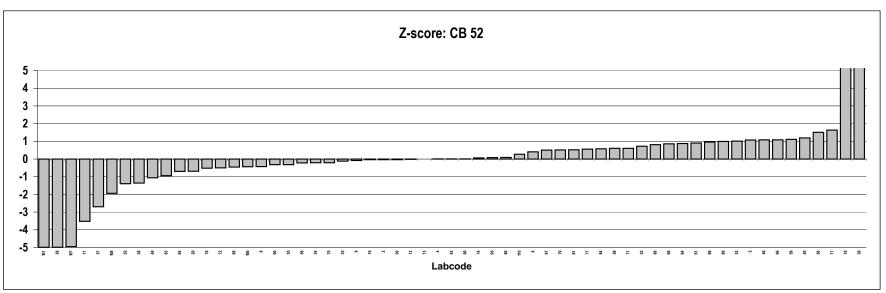


Congener: CB 52

					Con
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	990		81	1102	
4	999		84	1113	
5	1213		88	1160	
6	1080		89	1196	
8	914		90	1000	
9	981		93	809	
11	294		94	1174	
12	996		95	1013	
13	998		96	1215	
16	990		97	1100	
17	1324		99	1170	
18	2680	Outlier	100	911	
20	860		101	1.0	
26	1.2		107	9.9	
30	990		108	610	
32	1142		110	1052	
34	957				
35	975				
38	727				
39	3174	Outlier			
40	1237	Guilei			
42	1000	ND			
46	1215	112			
48	785				
50	1299				
52	719				
53	1200				
55	935				
56	954				
57	458				
58	1118				
59	1220				
60	934				
61	1179				
64	859				
68	906				
69	1190				
70	957				
70	1119				
72	898				
74	1010				
76	895				
77 79	1109				
	1100				
80	1015				

Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported	999 1000 956 291 30 61
No. of values reported	61
No. of values removed No. of reported non-detects	2 1

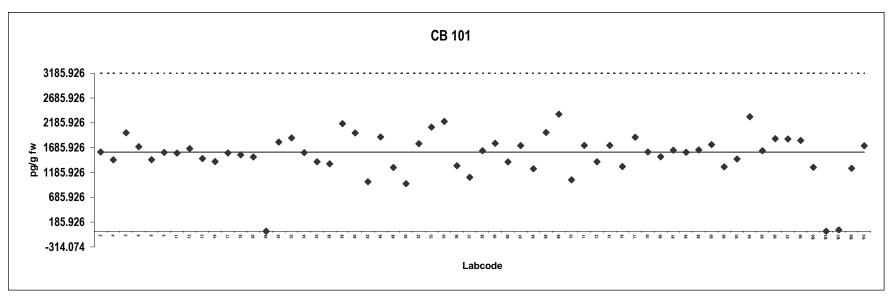


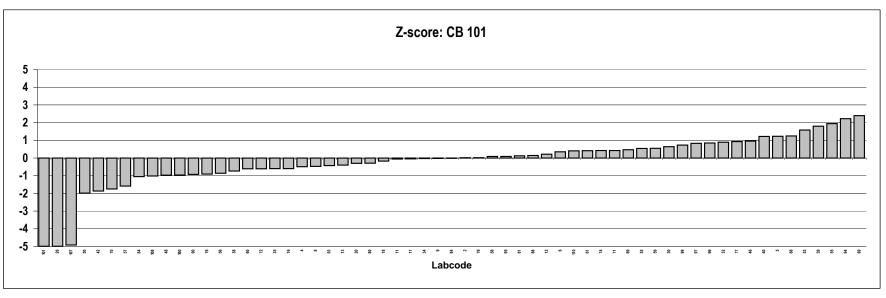


Congener: CB 101

					Cong
Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
2	1600		81	1635	
4	1440		84	1593	
5	1987		88	1640	
6	1706		89	1746	
8	1445		90	1300	
9	1590		93	1458	
11	1576		94	2307	
12	1665		95	1625	
13	1468		96	1867	
16	1405		97	1860	
17	1579		99	1830	
18	1540		100	1290	
20	1500		101	1.8	
26	1.9		107	27	
30	1800		108	1270	
32	1882		110	1725	
34	1585				
35	1403				
38	1360				
39	2171				
40	1984	N.T.			
42	1000	ND			
46	1901				
48	1287				
50 52	962 1767				
53	2100				
55	2216				
56	1320				
57	1088				
58	1624				
59	1772				
60	1400				
61	1729				
64	1259				
68	1994				
69	2360				
70	1038				
71	1732				
72	1401				
74	1730				
76	1307				
77	1894				
79	1600				
80	1503				

Consensus median, pg/g	1596
Median all values pg/g	1593
Consensus mean, pg/g	1538
Standard deviation, pg/g	463
Relative standard deviation, %	30
No. of values reported	61
No. of values removed	0
No. of reported non-detects	1

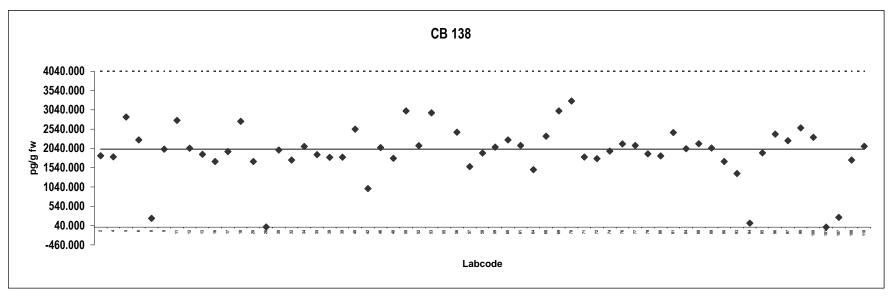


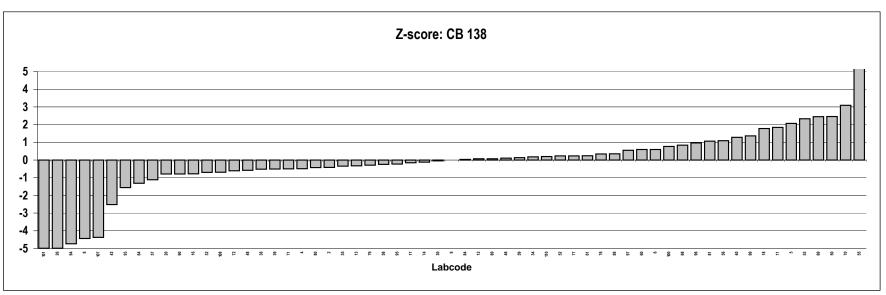


Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	1850		81	2450	
4	1820		84	2034	
5	2854		88	2160	
6	2260		89	2048	
8	229		90	1700	
9	2020		93	1389	
11	2765		94	105	
12	2046		95	1926	
13	1888		96	2409	
16	1703		97	2241	
17	1957		99	2570	
18	2740		100	2328	
20	1700		101	1.9	
26	2.7		107	254	
30	2000		108	1740	
32	1737		110	2097	
34	2090				
35	1881				
38	1810				
39	1814				
40	2538				
42	1000	ND			
46	2063				
48	1784				
50	3011				
52	2112				
53	2960				
55	4394	Outlier			
56	2460				
57	1570				
58	1921				
59	2074				
60	2260				
61	2115				
64	1490				
68	2357				
69	3010				
70	3269				
71	1817				
72	1774				
74	1970				
76	2158				
77	2115				
79	1900				
80	1848				

No. of values reported 61 No. of values removed 1	Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, %	2020 2020 1937 692 36
	No. of values reported	

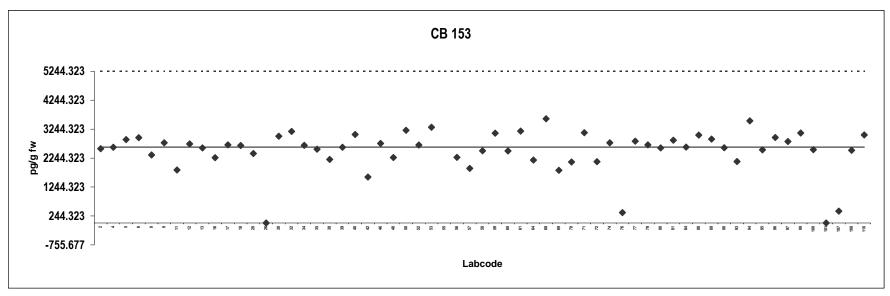


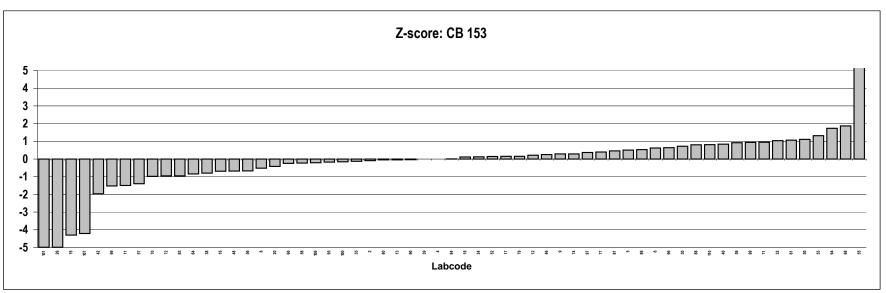


Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	2570		81	2860	
4	2620		84	2622	
5	2885		88	3040	
6	2948		89	2899	
8	2350		90	2600	
9	2770		93	2123	
11	1835		94	3529	
12	2735		95	2529	
13	2595		96	2956	
16	2260		97	2814	
17	2700		99	3110	
18	2680		100	2536	
20	2400		101	2.7	
26	3.1		107	414	
30	3000		108	2510	
32	3163		110	3044	
34	2685				
35	2553				
38	2200				
39	2618				
40	3059				
42	1590				
46	2750				
48	2263				
50	3204				
52	2694				
53	3310				
55	6253	Outlier			
56	2270				
57	1886				
58	2498				
59	3102				
60	2490				
61	3178				
64	2176				
68	3600				
69	1820				
70	2106				
71	3119				
72	2119				
74	2770				
76	364				
77	2826				
79	2700				
80	2593				

Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported	2621 2622 2494 742 30 61
No. of values removed No. of reported non-detects	1 0

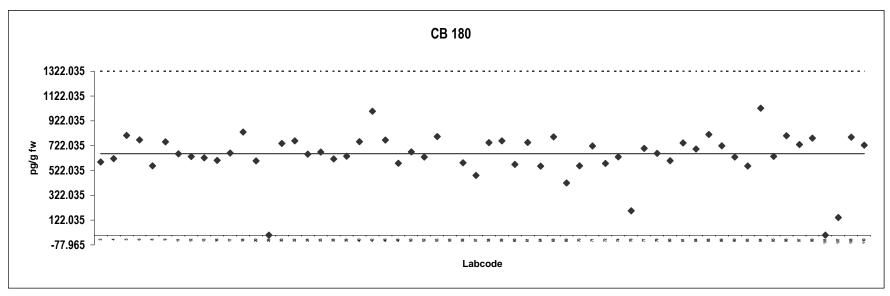


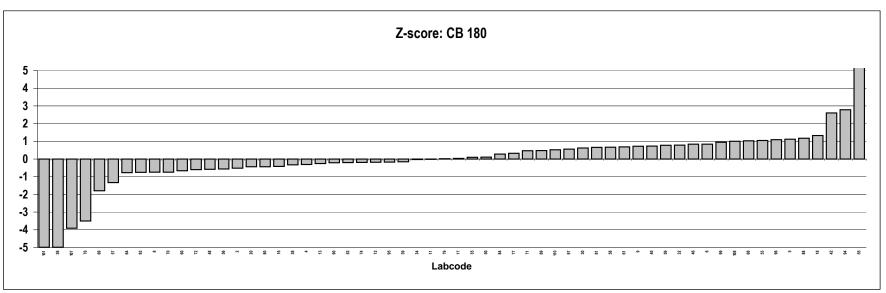


Congener: CB 180

	C / 0	<b>*</b> * .		C / 0	Cong
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	590		81	744	
4	617		84	695	
5	805		88	812	
6	768		89	720	
8	560		90	630	
9	753		93	558	
11	656		94	1024	
12	634		95	635	
13	624		96	802	
16	603		97	731	
17	662		99	783	
18	832		101	0.69	
20	600		107	143	
26	0.78		108	790	
30	740		110	726	
32	761				
34	654				
35	671				
38	615				
39	637				
40	754				
42	1000	ND			
46	768				
48	581				
50	672				
52	631				
53	795				
55	1498	Outlier			
56	584				
57	483				
58	746				
59	760				
60	571				
61	748				
64	556				
68	794				
69	422				
70	560				
71	719				
72	579				
74	632				
76	196				
77	700				
79	660				
80	601				

Consensus median, pg/g	658
Median all values pg/g	661
Consensus mean, pg/g	646
Standard deviation, pg/g	187
Relative standard deviation, %	29
No. of values reported	60
No. of values removed	1
No. of reported non-detects	1

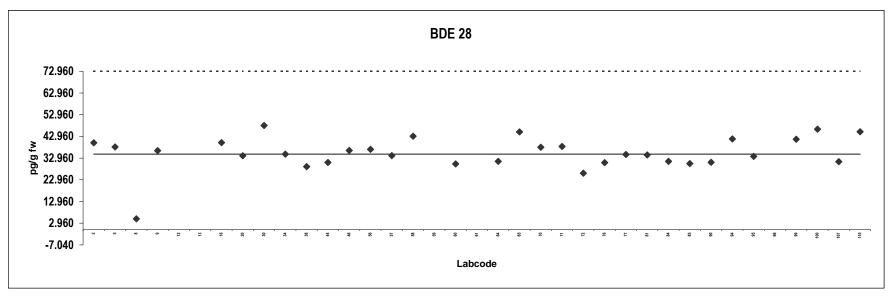


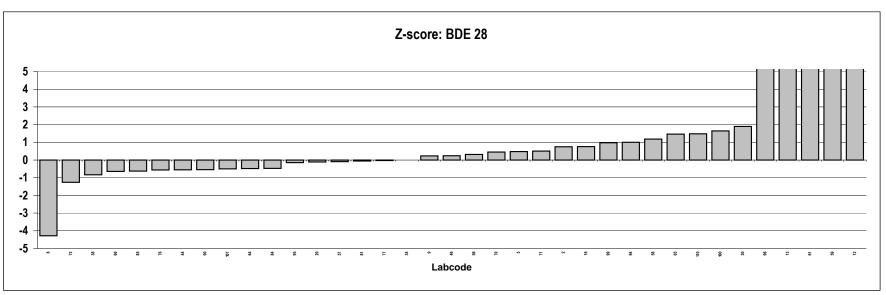


Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	40				
5	38				
8	5.0	ND			
9	36				
12	149	Outlier			
13	89	Outlier			
16	40				
20	34				
30	48				
34	35				
38	29				
44	31				
46	36				
56	37				
57	34				
58	43				
59	115	Outlier			
60	30				
61	100	Outlier			
64	31				
65	45				
70	38				
71	38				
72	26				
76	31				
77	35				
81	34				
84	31				
85	30				
90	31				
94	42				
95	34				
96	83	Outlier			
99	42				
100	46				
107	31				
110	45				
110					

Consensus median, pg/g	35
Median all values pg/g	36
Consensus mean, pg/g	35
Standard deviation, pg/g	7.8
Relative standard deviation, %	22
No. of values reported	37
No. of values removed	5
No. of reported non-detects	1
	-

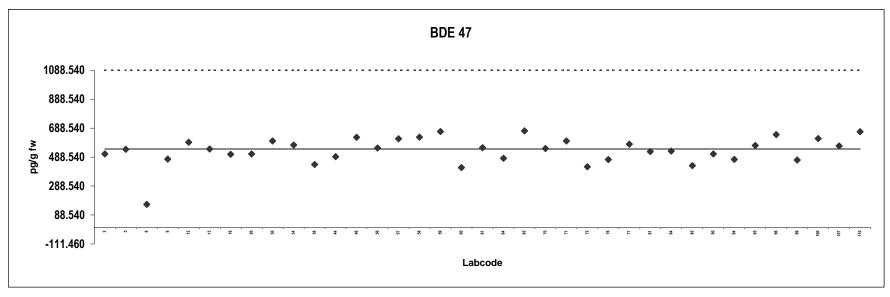


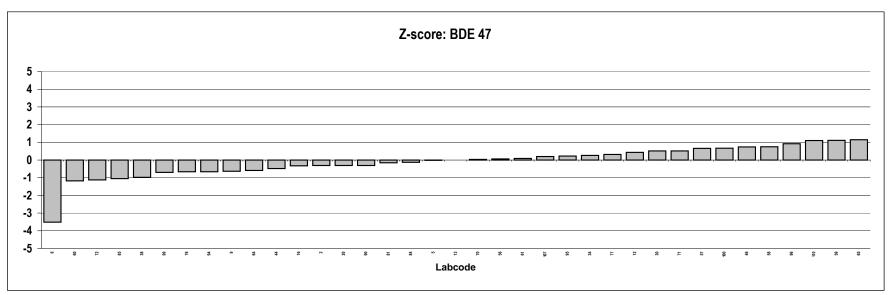


Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2 5 8	510				
5	542				
8	162				
9	475				
12	591				
13	544				
16	508				
20	510				
30	600				
34	573				
38	437				
44	491				
46	625				
56	551				
57	615				
58	626				
59	665				
60	416				
61	554				
64	480				
65	669				
70	548				
71	600				
72	422				
76	472				
77	578				
81	527				
84	530				
85	430				
90	510				
94	472				
95	568				
96	644				
99	468				
100	617				
107	565				
110	664				
1					

Consensus median, pg/g	544
Median all values pg/g	544
Consensus mean, pg/g	534
Standard deviation, pg/g	94
Relative standard deviation, %	18
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0
•	_

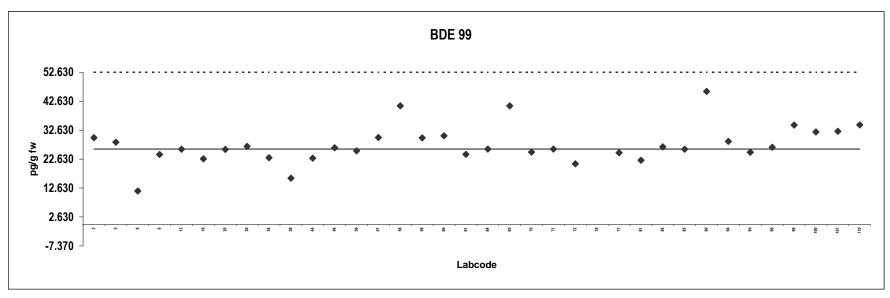


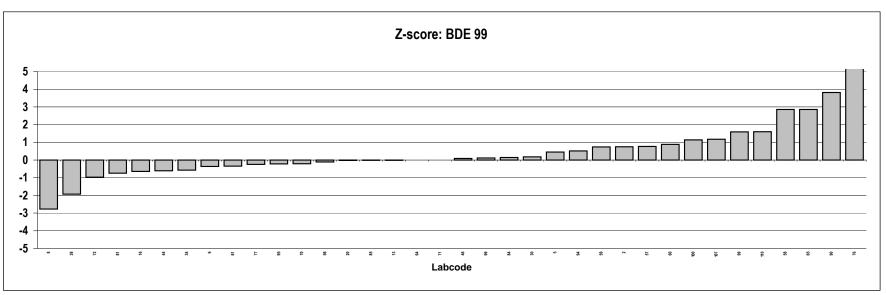


Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2 5 8 9 13 16 20 30 34 38 44 46 56 57 58 59 60 61 64 65 70 71 72 76 77 81 84 85 90 94 95 96 99 100 107 110	30 28 12 24 26 23 26 27 23 16 23 27 26 30 41 30 31 24 26 41 25 26 21 77 25 22 27 26 46 29 25 27 34 32 32 34	Notes	Lab code	Conc. pg/g fw.	Notes

Consensus median, pg/g	26
Median all values pg/g	26
Consensus mean, pg/g	28
Standard deviation, pg/g	6.5
Relative standard deviation, %	24
No. of values reported	36
No. of values removed	1
No. of reported non-detects	0
	-

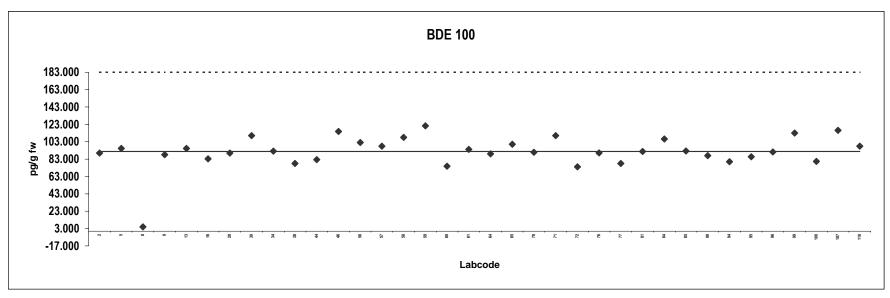


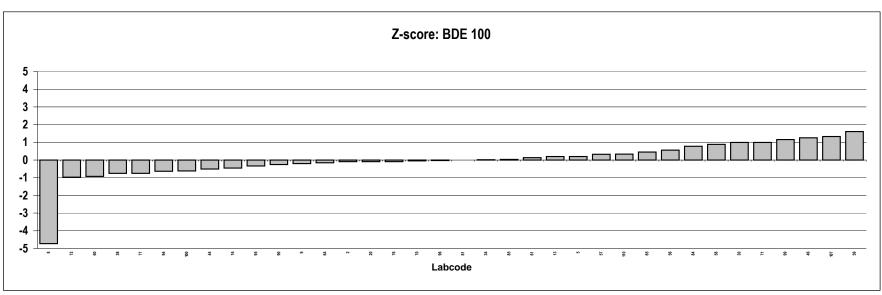


Congener: BDE 100

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
	90			188	
2 5 8	95				
8	5.0	ND			
9	88				
13	95				
16	83				
20	90				
30	110				
34	92				
38	78				
44	82				
46	115				
56	102				
57	98				
58	98 108				
59	121				
60	75				
61	94				
64	89				
65	100				
70	91				
71	110				
72	74				
76	90				
77	78				
81	92				
84	106				
85	92 87				
90	87				
94	80				
95	86				
96	91				
99	113				
100	80				
107	116				
110	98				

Consensus median, pg/g	92
Median all values pg/g	92
Consensus mean, pg/g	92
Standard deviation, pg/g	19
Relative standard deviation, %	21
No. of values reported	36
No. of values removed	0
No. of reported non-detects	1
·	-

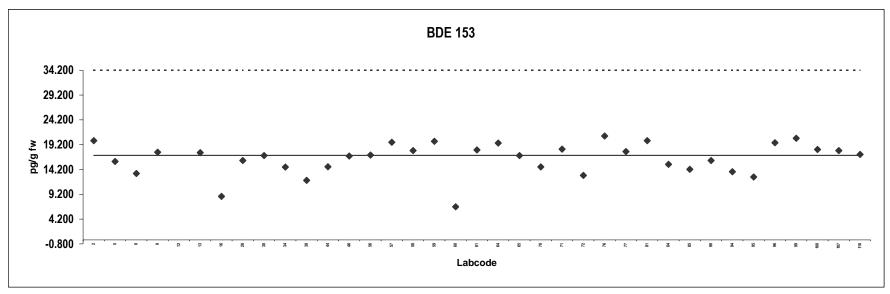


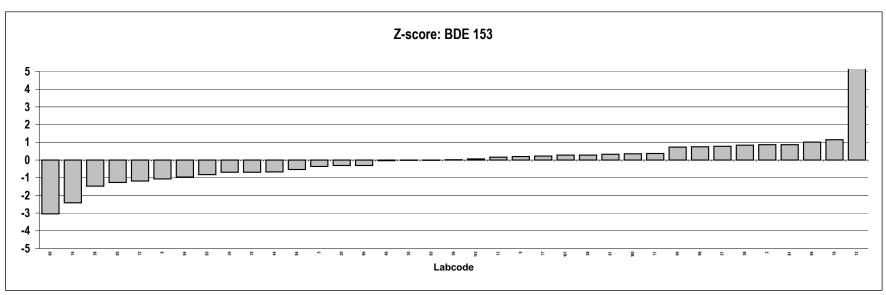


Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
	20	11000	Eus couc	conc. pg/g 1	11000
2 5 8	16				
8	13				
9	18				
12	50	Outlier			
13	18				
16	8.8				
20	16				
30	17				
34	15				
38	12				
44	15				
46	17				
56	17				
57	20				
58	18				
59	20				
60	6.7				
61	18				
64	20				
65	17				
70	15				
71	18				
72	13				
76	21				
77 81	18 20				
84	20 15				
85	13				
90	16				
94	14				
95	13				
96	20				
99	21				
100	18				
107	18				
110	17				

Consensus median, pg/g	17
Median all values pg/g	17
Consensus mean, pg/g	16
Standard deviation, pg/g	3.2
Relative standard deviation, %	19
No. of values reported	37
No. of values removed	1
No. of reported non-detects	0
	-

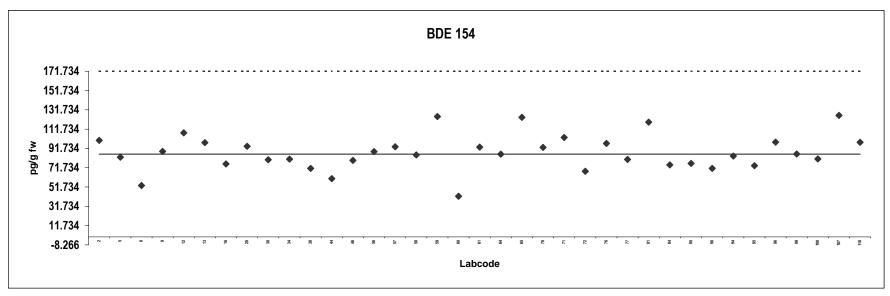


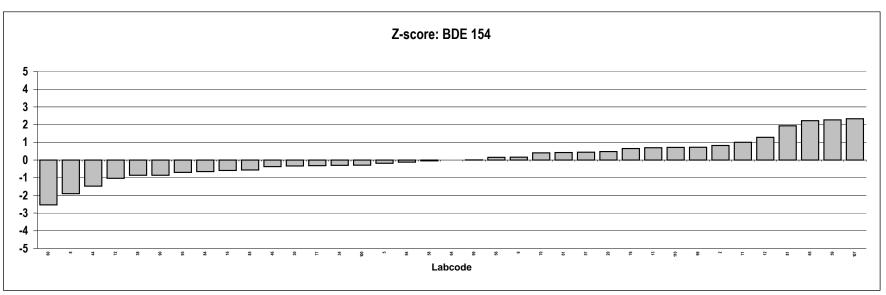


Congener: BDE 154

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
	100	- 10000		real Para	- 10000
2 5 8	83				
8	83 53				
9	89				
12	108				
13	98				
16	76				
20	94				
30	80				
34	81				
38	71				
44	60				
46	79				
56	88				
56 57	93				
58	85				
59	125				
60	42				
61	93				
64	86				
65	124				
70	93				
71	103				
72	68				
76	97				
77	80				
81	119				
84	75 76				
85	76				
90 94	71 84				
94 95	84 74				
95	98				
99	86				
100	81				
107	126				
110	98				
110	90				

0.1
86
86
87
19
21
37
0
0

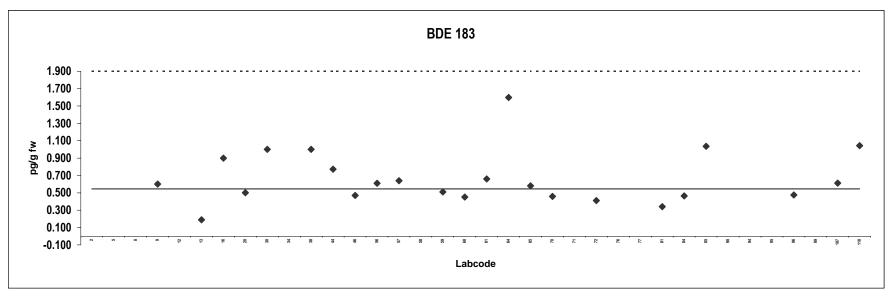


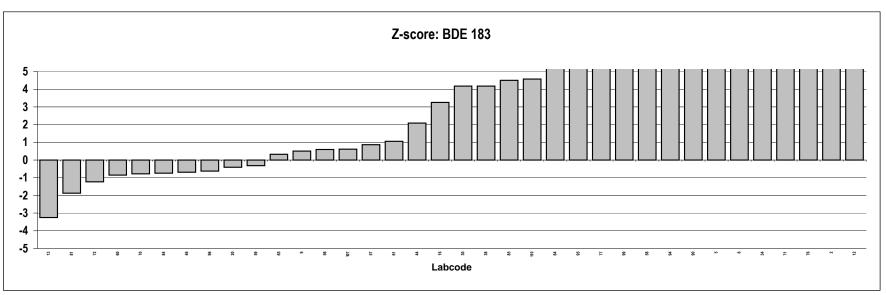


Congener: BDE 183

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	10	Outlier,ND			
5	4.5	Outlier,ND			
8	5.0	Outlier,ND			
9	0.60				
12	33	Outlier			
13	0.19				
16	0.90	ND			
20	0.50	·			
30	1.0	ND			
34	5.0	Outlier,ND			
38	1.0	ND			
44	0.77	1,2			
46	0.47				
56	0.61				
57	0.64				
58	3.2	Outlier			
59	0.51	Outlief			
60	0.45				
61	0.66				
64	1.6				
65	0.58				
70	0.46				
70	6.9	Outlier			
72	0.41	Outlief			
76	7.3	Outlier,ND			
77	2.1	Outlier			
81	0.34	Outlief			
84	0.46				
85					
90	1.0 3.7	Outlier			
90		Outlier			
94	3.4	Outlier			
	2.0	Outlier,ND			
96	0.48	0 41 110			
99	2.6	Outlier,ND			
107	0.61				
110	1.0				

Consensus median, pg/g	0.55
Median all values pg/g	0.95
Consensus mean, pg/g	0.67
Standard deviation, pg/g	0.31
Relative standard deviation, %	46
No. of values reported	36
No. of values removed	13
No. of reported non-detects	10

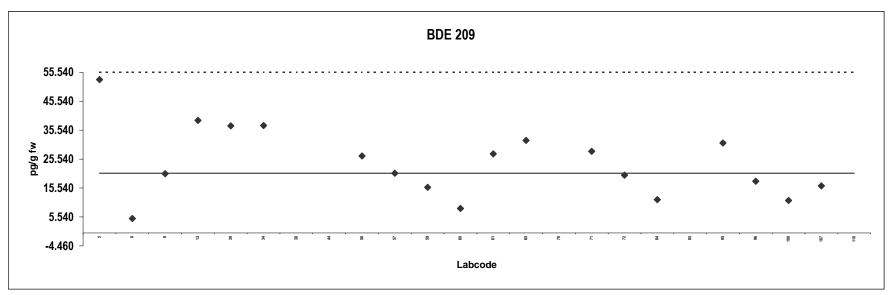


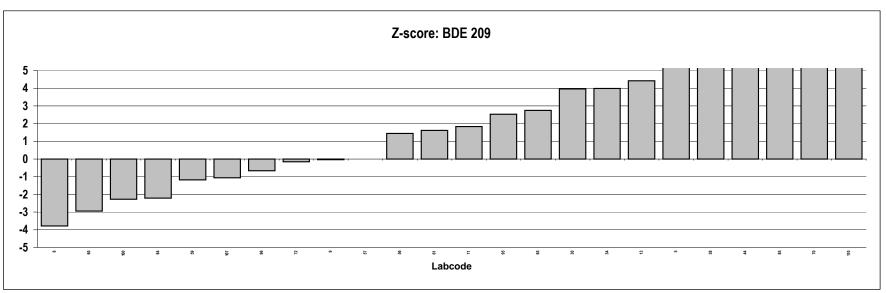


Congener: BDE 209

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
	53	ND			
5 8 9	5.0	ND			
9	21				
13	39				
30	37				
34	37				
38	61	Outlier			
44	116	Outlier			
56	27				
57	21				
59	16				
60	8.5				
61	27				
65 70	32 135	Outlier			
70	28	Outlief			
71 72	20				
84	12				
85	125	Outlier			
95	31	Outilei			
96	18				
100	11				
107	16				
110	194	Outlier			
	-, .				
1					

Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported	21 28 24 12 51 24
No. of values reported	24
No. of values removed	5
No. of reported non-detects	2

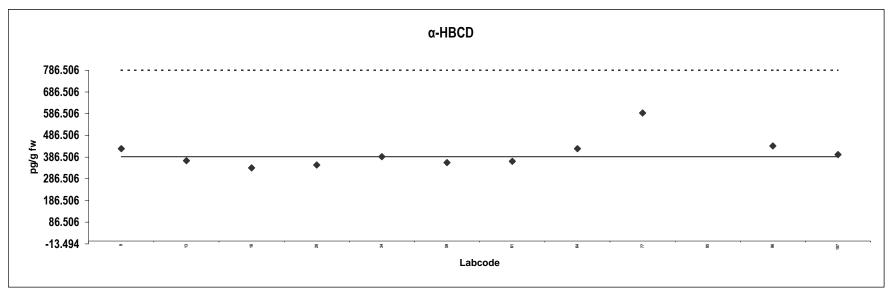


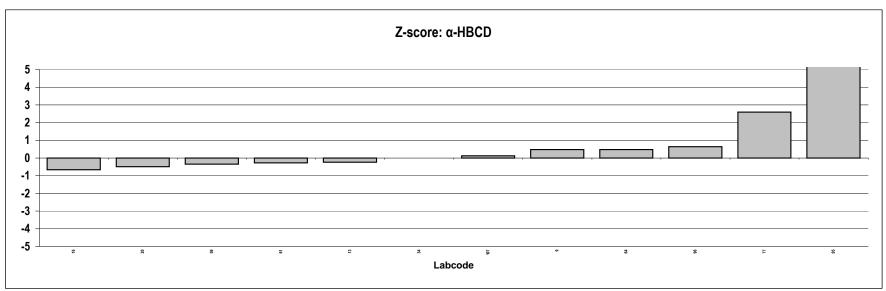


**Congener:** α-HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	
9 13 16 20 34 59 61 64 77 95 96 107	Conc. pg/g fw.  425 370 337 350 388 361 367 425 590 979 438 398	Notes	Lab code	Conc. pg/g fw.	Notes

388
393
405
70
17
12
1
0

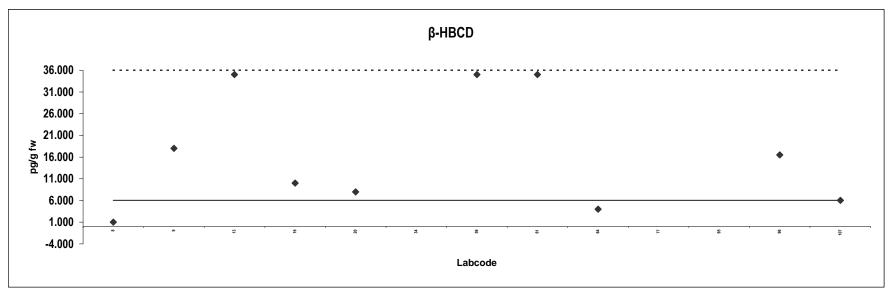


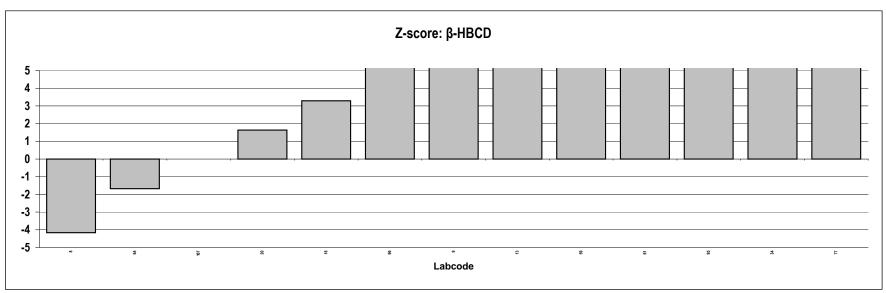


Congener: β-HBCD

	_				Con
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
8 9	1.0	ND			
9	18 35				
13	35	ND			
16	10	ND ND			
20 34	8.0 50	Outlier,ND			
59	35	ND			
61	35	ND			
64	4.0	ND			
77	400	Outlier,ND			
95	36	Outlier,ND ND			
96	17	ND			
107	6.0				
				ı	i

Consensus median, pg/g	6.0
Median all values pg/g	18
Consensus mean, pg/g	17
Standard deviation, pg/g	14
Relative standard deviation, %	80
No. of values reported	13
No. of values removed	3
No. of reported non-detects	10

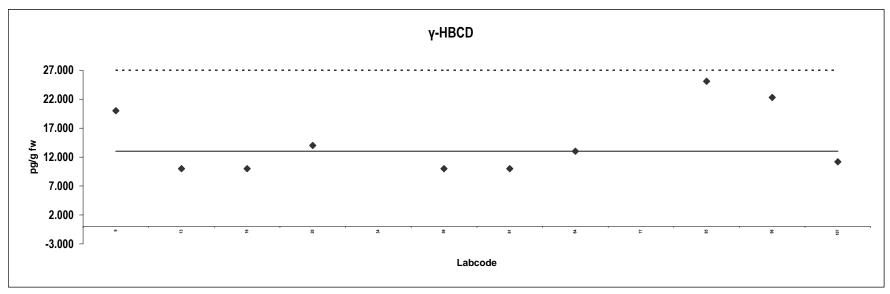


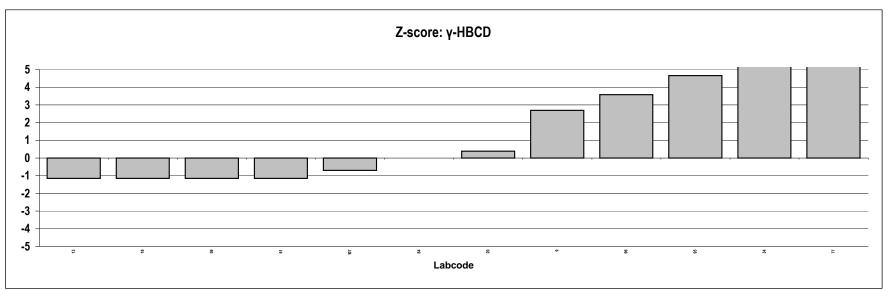


Congener: γ-HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
9	20	ND			
13	10	ND			
16	10	ND			
20	14 50	O 41: NID			
34	50	Outlier,ND			
59	10	ND			
61	10 13	ND			
64 77	400	Outlier,ND			
95	25	ND			
93 96	23	ND ND			
107	11	ND			
107	11				

13
14
15
5.8
40
12
2
9

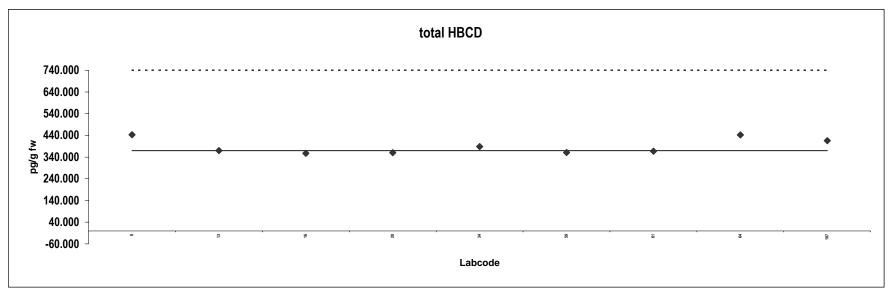


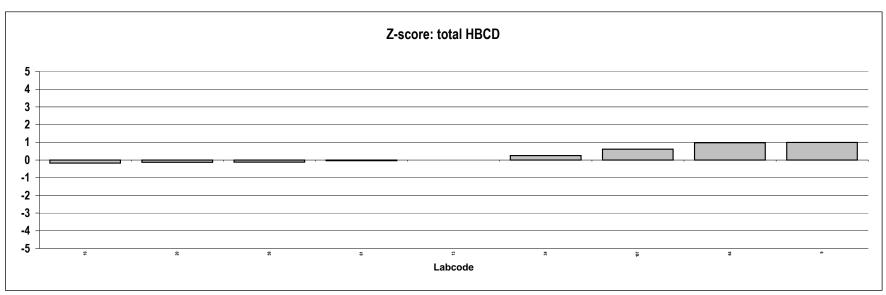


**Congener: total HBCD** 

					Congen
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
9 13	443				
13	370 357				
16 20 34 59	357				
20	360				
34	360 388 361				
59	361				
61	367 442				
61 64 107	415				
107	413				

·	
Consensus median, pg/g	370
Median all values pg/g	370
Consensus mean, pg/g	389
Standard deviation, pg/g	35
Relative standard deviation, %	9
No. of values reported	9
No. of values removed	0
No. of reported non-detects	0
=	•





# Appendix 4:

Presentation of results for cod liver oil

### Appendix 4: Presentation of results: Cod liver oil

### Statistic calculations for PCDDs, PCDFs and dioxin-like PCBs

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

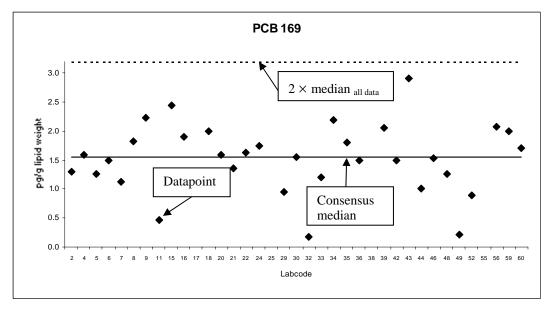
- 1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners.
- 2. Values exceeding  $2 \times$  this median, were defined as outliers and removed from the data set.
- 3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.

### Statistic calculations for indicator PCBs, PBDEs and HBCD

For each congener, the outliers were removed and the consensus calculated according to the following procedure:

- 1. The median was calculated from all the reported data, using the detection limit as concentration for non-detected congeners (NDs).
- 2. Values exceeding  $2 \times$  this median, were defined as outliers and removed from the data set. The NDs were also removed.
- 3. Median, mean and standard deviation were re-calculated from the remaining data. This second median was called consensus.
- 4. For comparison, median, mean and standard deviation were also calculated without removing NDs.

The diagram shows the reported data up to approximately the limit for outliers ( $2 \times$  the first median).



#### **Z-Scores of individual congeners**

Z-scores of each congener were calculated for each laboratory according to the following equation:

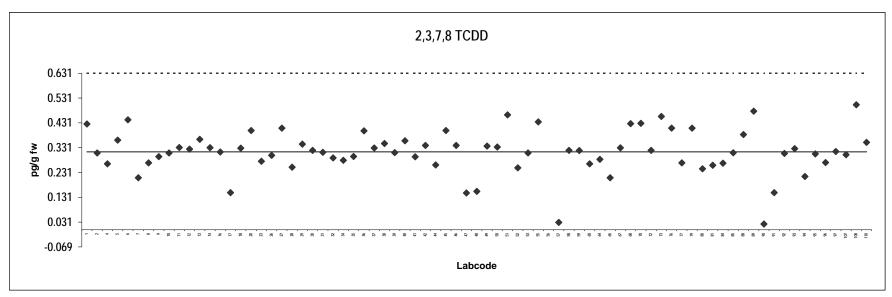
$$z = (x - X)/\sigma$$

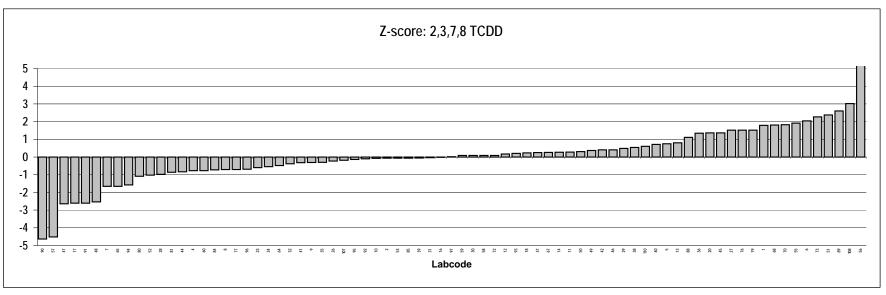
where x = reported value; X = assigned value (consensus);  $\sigma$  = target value for standard deviation. A  $\sigma$  of 20% of the consensus was used, i.e. z-scores between +1 and -1 reflect a deviation of  $\pm$  20% from the consensus value.

Congener: 2,3,7,8 TCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.43		56	1.5	Outlier,ND
2	0.31		57	0.030	ND
4	0.27		58	0.32	
5 6	0.36		59	0.32	
6	0.44		60	0.27	
7	0.21		64	0.28	
8	0.27		65	0.21	
9	0.30		67	0.33	
10	0.31		68	0.43	
11	0.33		70	0.43	
12	0.32		72	0.32	
13	0.36		73	0.46	
14	0.33		76	0.41	
16	0.31		77	0.27	
17	0.15	ND	79	0.41	
18	0.33		80	0.25	
20	0.40		81	0.26	
23	0.28		84	0.27	
26	0.30		85	0.31	
27	0.41		88	0.38	
28	0.25		89	0.48	
29	0.35		90	0.023	ND
30	0.32		91	0.15	
31	0.31		92	0.31	
32	0.29		93	0.33	
34	0.28		94	0.22	
35	0.30		95	0.31	
36	0.40		96	0.27	
37	0.33		97	0.32	
38	0.35		107	0.30	
39	0.31		108	0.50	
40	0.36		110	0.35	
41	0.29				
42	0.34				
44	0.26				
45	0.40				
46	0.34				
47	0.15				
48	0.16				
49	0.34				
50	0.33				
51	0.46				
52	0.25				
53	0.31				
55	0.43	ND			

Consenus statistics					
Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported No. of values removed	0.31 0.32 0.31 0.088 28 77 1				
Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported	0.32 0.31 0.088 28				

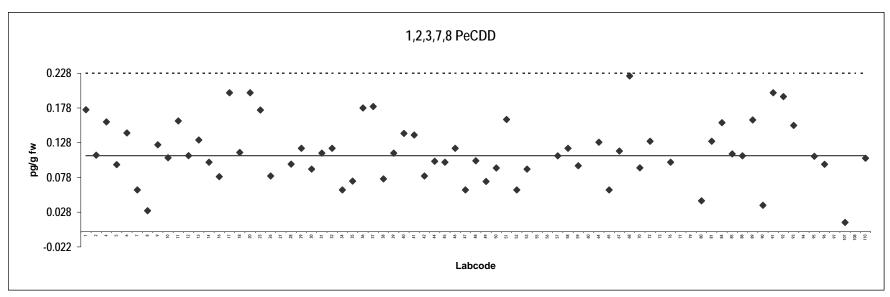


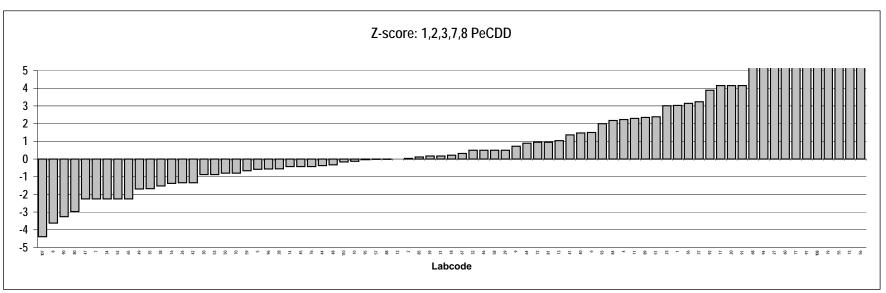


**Congener: 1,2,3,7,8 PeCDD** 

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.18		56	1.6	Outlier,ND
2	0.11		57	0.11	
4	0.16		58	0.12	
5	0.097		59	0.095	
6	0.14		60	0.26	Outlier
7	0.060		64	0.13	
8	0.030	ND	65	0.060	ND
9	0.13		67	0.12	
10	0.11		68	0.22	
11	0.16		70	0.092	
12	0.11		72	0.13	
13	0.13		73	0.57	Outlier
14	0.10		76	0.10	ND
16	0.079		77	0.26	Outlier
17	0.20	ND	79	0.44	Outlier
18	0.11		80	0.044	
20	0.20		81	0.13	
23	0.18		84	0.16	
26	0.080		85	0.11	
27	0.25	Outlier,ND	88	0.11	
28	0.097		89	0.16	
29	0.12		90	0.038	ND
30	0.090		91	0.20	ND
31	0.11		92	0.19	
32	0.12		93	0.15	
34	0.060		94	0.23	Outlier
35	0.073		95	0.11	
36	0.18		96	0.097	
37	0.18		97	0.29	Outlier
38	0.076		107	0.013	ND
39	0.11		108	0.34	Outlier
40	0.14		110	0.11	
41	0.14				
42	0.080				
44	0.10				
45	0.10				
46	0.12				
47	0.060	ND			
48	0.10				
49	0.072	ND			
50	0.092				
51	0.16	ND			
52	0.060				
53	0.090				
55	0.47	Outlier,ND			

Consenus statistics				
Consensus median, pg/g	0.11			
Median all values pg/g	0.11			
Consensus mean, pg/g	0.11			
Standard deviation, pg/g	0.044			
Relative standard deviation, %	38			
No. of values reported	77			
No. of values removed	10			
No. of reported non-detects	13			

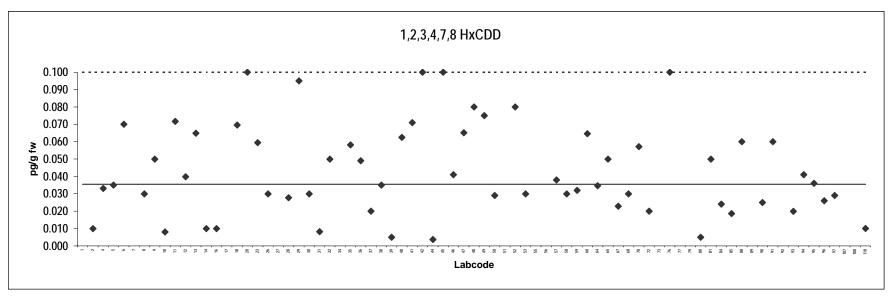


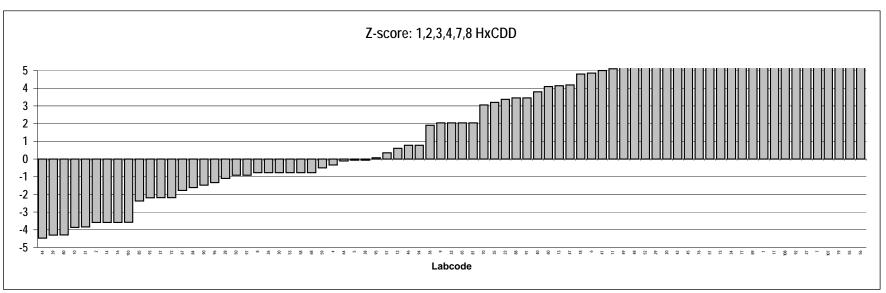


Congener: 1,2,3,4,7,8 HxCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.16	Outlier	56	2.4	Outlier,ND
2	0.010	ND	57	0.038	ND
4	0.033	ND	58	0.030	ND
5	0.035	ND	59	0.032	
6	0.070	ND	60	0.065	ND
7	0.27	Outlier,ND	64	0.035	ND
8	0.030	ND	65	0.050	ND
9	0.050	ND	67	0.023	ND
10	0.0080		68	0.030	ND
11	0.072	ND	70	0.057	ND
12	0.040	ND	72	0.020	
13	0.065		73	0.11	Outlier,ND
14	0.010	ND	76	0.10	ND
16	0.010	ND	77	0.13	Outlier,ND
17	0.20	Outlier,ND	79	0.41	Outlier
18	0.070	ND	80	0.0050	ND
20	0.10	ND	81	0.050	
23	0.059		84	0.024	
26	0.030	ND	85	0.019	
27	0.25	Outlier,ND	88	0.060	ND
28	0.028		89	0.15	Outlier,ND
29	0.095	ND	90	0.025	ND
30	0.030	ND	91	0.060	ND
31	0.0082		92	0.21	Outlier
32	0.050	ND	93	0.020	
34	0.11	Outlier,ND	94	0.041	
35	0.058		95	0.036	ND
36	0.049		96	0.026	ND
37	0.020	ND	97	0.029	ND
38	0.035		107	0.28	Outlier
39	0.0050		108	0.20	Outlier,ND
40	0.062	ND	110	0.010	ND
41	0.071	ND			
42	0.10	ND			
44	0.0037				
45	0.10	ND			
46	0.041	NID			
47	0.065	ND			
48	0.080	ND			
49	0.075	ND			
50	0.029				
51	0.10	Outlier,ND			
52 53	0.080	ND ND			
	0.030				
55	0.54	Outlier,ND			

Consenus statistics	5
Consensus median, pg/g	0.036
Median all values pg/g	0.050
Consensus mean, pg/g	0.043
Standard deviation, pg/g	0.026
Relative standard deviation, %	61
No. of values reported	77
No. of values removed	15
No. of reported non-detects	54





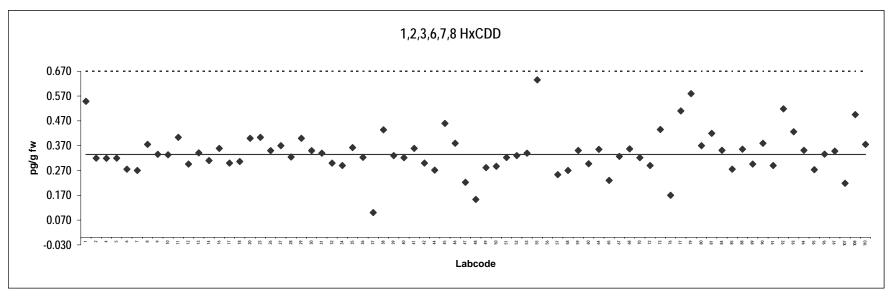
Congener: 1,2,3,6,7,8 HxCDD

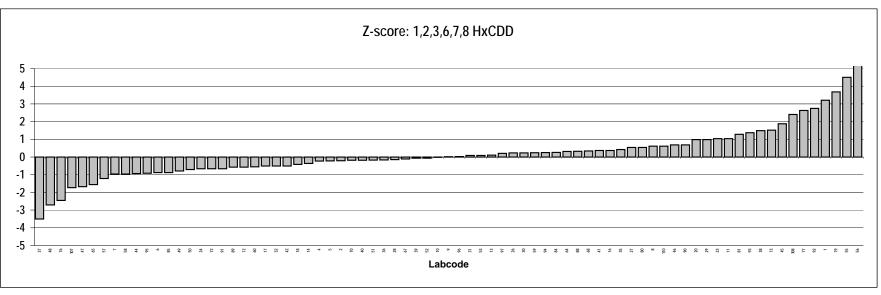
				•	ongener:
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.55		56	2.3	Outlier,ND
2	0.32		57	0.25	
4	0.32		58	0.27	
5	0.32		59	0.35	
6	0.28		60	0.30	
7	0.27	ND	64	0.36	
8	0.38		65	0.23	
9	0.34		67	0.33	
10	0.33		68	0.36	
11	0.40		70	0.32	
12	0.30		72	0.29	
13	0.34		73	0.44	
14	0.31		76	0.17	
16	0.36		77	0.51	
17	0.30	ND	79	0.58	
18	0.31		80	0.37	
20	0.40		81	0.42	
23	0.40		84	0.35	
26	0.35		85	0.28	
27	0.37		88	0.36	
28	0.32		89	0.30	
29	0.40		90	0.38	
30	0.35		91	0.29	
31	0.34		92	0.52	
32	0.30		93	0.43	
34 35	0.29 0.36		94 95	0.35 0.27	
36 37	0.32 0.10		96 97	0.34 0.35	
38	0.43		107	0.33	
39	0.43		107	0.50	
40	0.33		110	0.38	
40	0.36		110	0.36	
42	0.30				
44	0.27				
45	0.46				
46	0.38				
47	0.38				
48	0.15				
49	0.28				
50	0.29				
51	0.32				
52	0.33				
53	0.34				
55	0.64	ND			

Consensus median, pg/g	0.33
Median all values pg/g	0.34
Consensus mean, pg/g	0.34
Standard deviation, pg/g	0.087
Dalativa standard deviation 0/	26

Standard deviation, pg/g
Relative standard deviation, %
No. of values reported
No. of values removed
No. of reported non-detects

26
77
No. of values removed
4

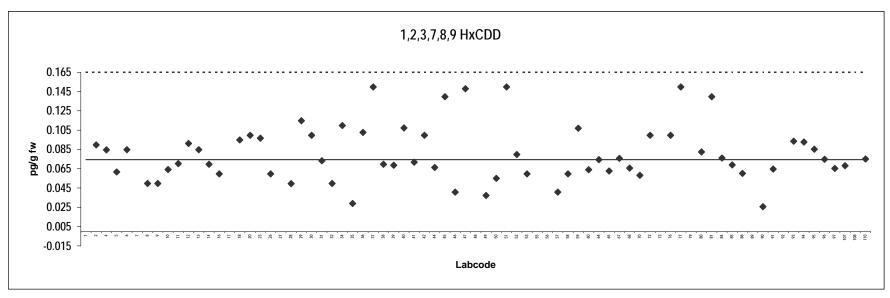


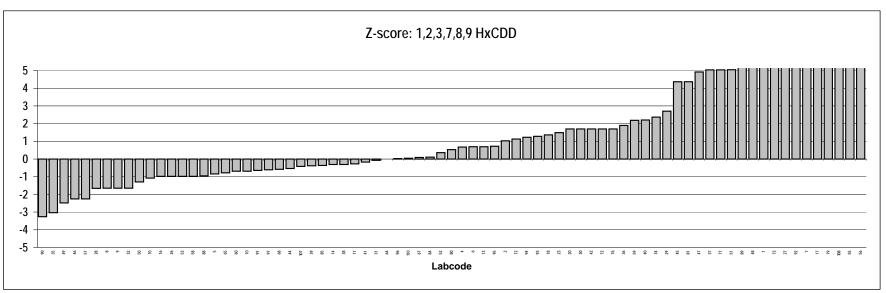


Congener: 1,2,3,7,8,9 HxCDD

					ongener:
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.23	Outlier	56	2.4	Outlier,ND
2	0.090		57	0.041	ND
4	0.085		58	0.060	
5	0.062		59	0.11	
6	0.085		60	0.064	ND
7	0.27	Outlier,ND	64	0.075	
8	0.050	ND	65	0.063	
9	0.050	ND	67	0.076	
10	0.064		68	0.066	
11	0.071	ND	70	0.059	ND
12	0.092		72	0.10	
13	0.085		73	0.23	Outlier
14	0.070		76	0.10	ND
16	0.060		77	0.15	ND
17	0.30	Outlier,ND	79	0.33	Outlier
18	0.095		80	0.083	
20	0.10		81	0.14	
23	0.097		84	0.076	
26	0.060		85	0.069	
27	0.25	Outlier,ND	88	0.061	
28	0.050		89	0.17	Outlier
29	0.12		90	0.026	ND
30	0.10		91	0.065	
31	0.074		92	0.26	Outlier
32	0.050	ND	93	0.094	
34	0.11	ND	94	0.093	
35	0.029		95	0.086	
36	0.10		96	0.075	
37	0.15		97	0.066	
38	0.070		107	0.068	0 41
39	0.069		108	0.51	Outlier
40	0.11		110	0.075	
41	0.072	ND			
42	0.10	ND			
44 45	0.067 0.14	ND			
45 46	0.14 0.041	ND			
46	0.041				
48	0.13	Outlier			
49	0.038	Outilei			
50	0.038				
51	0.055	ND			
52	0.080	ND ND			
53	0.060	ND			
55	0.60	Outlier,ND			
22	0.00	Outher,ND		I	I

0.075
0.083
0.080
0.029
36
77
12
20

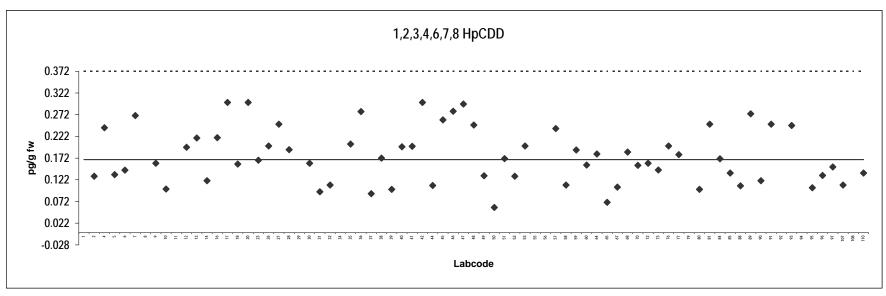


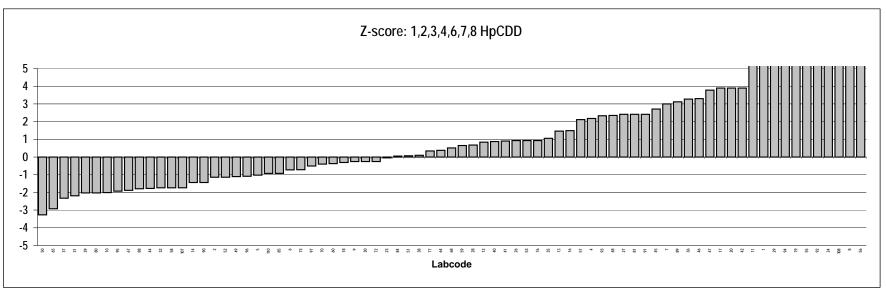


Congener: 1,2,3,4,6,7,8 HpCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.40	Outlier	56	4.9	Outlier,ND
2	0.13		57	0.24	, ,
4	0.24		58	0.11	
5	0.13		59	0.19	
6	0.14		60	0.16	
7	0.27	ND	64	0.18	
8	2.5	Outlier	65	0.070	ND
9	0.16		67	0.11	
10	0.10		68	0.19	
11	0.39	Outlier	70	0.16	ND
12	0.20		72	0.16	
13	0.22		73	0.14	ND
14	0.12		76	0.20	
16	0.22		77	0.18	
17	0.30	ND	79	0.70	Outlier
18	0.16		80	0.10	
20	0.30		81	0.25	
23	0.17		84	0.17	
26	0.20	ND	85	0.14	
27	0.25	ND	88	0.11	
28	0.19		89	0.27	
29	0.43	Outlier	90	0.12	ND
30	0.16		91	0.25	
31	0.095		92	0.73	Outlier
32	0.11		93	0.25	
34	0.78	Outlier,ND	94	0.63	Outlier
35	0.20		95	0.10	
36	0.28		96	0.13	
37	0.090		97	0.15	
38	0.17		107	0.11	
39	0.10	ND	108	1.9	Outlier
40	0.20		110	0.14	
41	0.20				
42	0.30	ND			
44	0.11				
45	0.26				
46	0.28				
47	0.30				
48	0.25				
49	0.13				
50	0.058	NE			
51	0.17	ND			
52	0.13				
53	0.20	ND			
55	0.73	Outlier,ND			

Consenus statistics	
Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g	0.17 0.19 0.18 0.064
Relative standard deviation, %	36
No. of values reported	77
No. of values removed	11
No. of reported non-detects	15

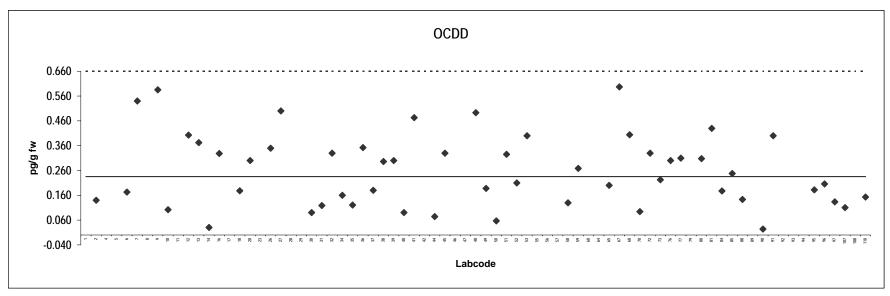


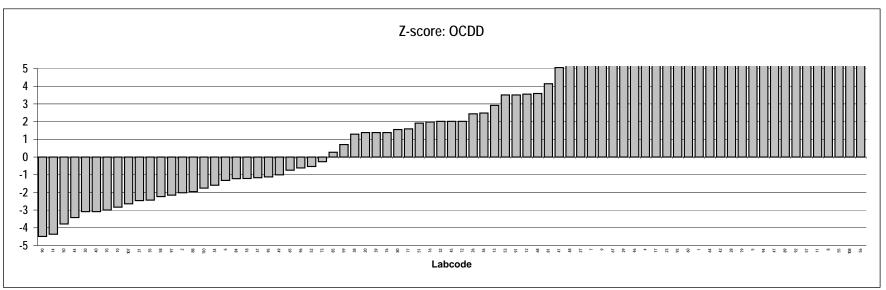


Congener: OCDD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.94	Outlier	56	16	Outlier,ND
2	0.14		57	4.5	Outlier
4	0.77	Outlier,ND	58	0.13	ND
5	1.7	Outlier,ND	59	0.27	
6	0.17		60	0.92	Outlier
7	0.54	ND	64	0.94	Outlier
8	7.3	Outlier	65	0.20	ND
9	0.59		67	0.60	ND
10	0.10		68	0.40	
11	5.0	Outlier	70	0.094	ND
12	0.40		72	0.33	
13	0.37		73	0.22	
14	0.030		76	0.30	
16	0.33		77	0.31	
17	0.80	Outlier,ND	79	1.2	Outlier
18	0.18		80	0.31	
20	0.30	ND	81	0.43	
23	0.86	Outlier	84	0.18	
26	0.35	ND	85	0.25	
27	0.50	ND	88	0.14	
28	1.0	Outlier	89	2.6	Outlier
29	0.70	Outlier	90	0.024	ND
30	0.090		91	0.40	ND
31	0.12		92	2.9	Outlier
32	0.33		93	0.88	Outlier
34	0.16	ND	94	1.8	Outlier
35	0.12		95	0.18	
36	0.35		96	0.21	
37	0.18		97	0.13	
38	0.30	MD	107	0.11	0.41
39	0.30	ND	108	13	Outlier
40	0.090		110	0.15	
41	0.47	Outlies ND			
42 44	1.0 0.074	Outlier,ND			
44	0.074				
45 46	0.33	Outlier			
46 47	1.8	Outlier			
47	0.49	Outilei			
49	0.49				
50	0.19	ND			
51	0.33	ND ND			
52	0.33	ND			
53	0.40	ND			
55	8.8	Outlier			

Consensus median, pg/g	0.24
Median all values pg/g	0.33
Consensus mean, pg/g	0.26
Standard deviation, pg/g	0.15
Relative standard deviation, %	56
No. of values reported	77
No. of values removed	23
No. of reported non-detects	20

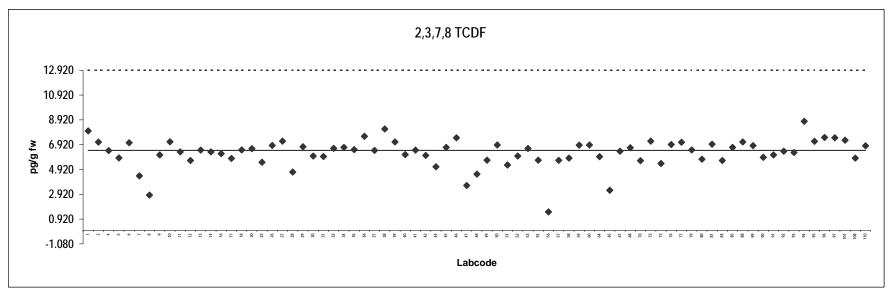


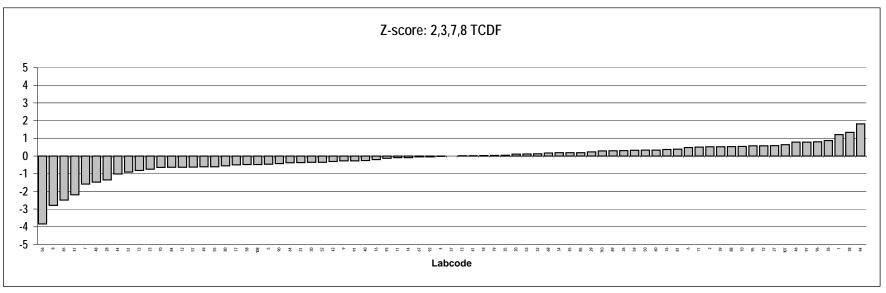


Congener: 2,3,7,8 TCDF

					Congen
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	8.0		56	1.5	ND
2	7.1		57	5.7	
4	6.4		58	5.8	
5	5.9		59	6.9	
6	7.1		60	6.9	
7	4.4		64	6.0	
8	2.9		65	3.2	
9	6.1		67	6.4	
10	7.2		68	6.7	
11	6.3		70	5.6	
12	5.6		72	7.2	
13	6.5		73	5.4	
14	6.3		76	6.9	
16	6.2		77	7.1	
17	5.8		79	6.5	
18	6.5		80	5.7	
20	6.6		81	7.0	
23	5.5		84	5.6	
26	6.9		85	6.7	
27	7.2		88	7.1	
28	4.7		89	6.8	
29	6.8		90	5.9	
30	6.0		91	6.1	
31	6.0		92	6.4	
32	6.6		93	6.3	
34	6.7		94	8.8	
35	6.5		95	7.2	
36	7.6		96	7.5	
37	6.5		97	7.5	
38	8.2		107	7.3	
39	7.1		108	5.8	
40	6.1		110	6.8	
41	6.5				
42	6.1				
44	5.1				
45	6.7				
46	7.5				
47	3.6				
48	4.5				
49	5.7				
50	6.9				
51	5.3				
52	6.0				
53	6.6				
55	5.7				

Consenus statistics				
Consensus median, pg/g	6.5			
Median all values pg/g	6.5			
Consensus mean, pg/g	6.3			
Standard deviation, pg/g	1.1			
Relative standard deviation, %	18			
No. of values reported	77			
No. of values removed	0			
No. of reported non-detects	1			

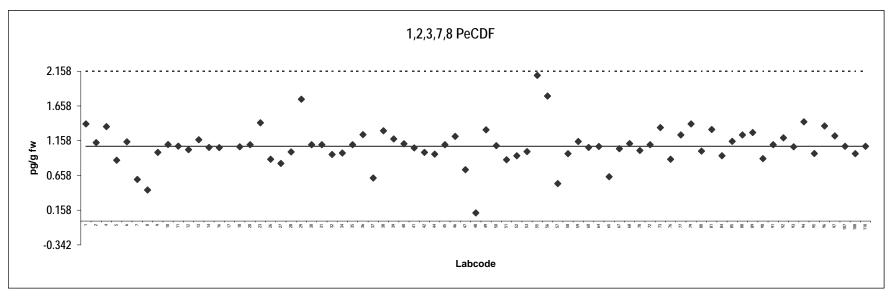


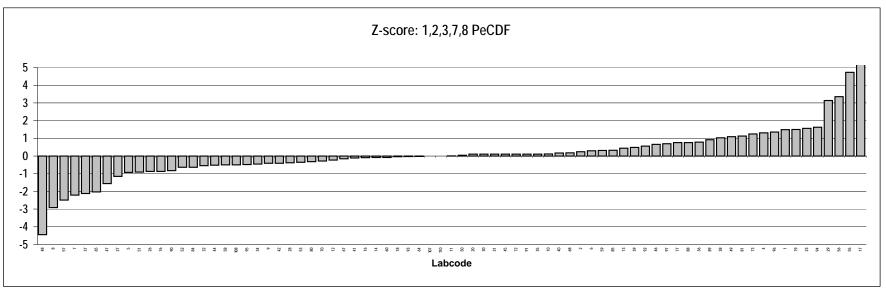


**Congener: 1,2,3,7,8 PeCDF** 

					Congener
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1.4		56	1.8	ND
2	1.1		57	0.54	
4	1.4		58	0.97	
5	0.88		59	1.1	
6	1.1		60	1.1	
7	0.60		64	1.1	
8	0.45		65	0.64	
9	0.99		67	1.0	
10	1.1		68	1.1	
11	1.1		70	1.0	
12	1.0		72	1.1	
13	1.2		73	1.3	
14	1.1		76	0.89	
16	1.1		77	1.2	
17	4.2	Outlier	79	1.4	
18	1.1		80	1.0	
20	1.1		81	1.3	
23	1.4		84	0.94	
26	0.89		85	1.1	
27	0.83		88	1.2	
28	1.00		89	1.3	
29	1.8		90	0.90	
30	1.1		91	1.1	
31	1.1		92	1.2	
32	0.96		93	1.1	
34	0.98		94	1.4	
35	1.1		95	0.97	
36	1.2		96	1.4	
37	0.62		97	1.2	
38	1.3		107	1.1	
39	1.2		108	0.97	
40	1.1		110	1.1	
41	1.1				
42	0.99				
44	0.96				
45	1.1				
46	1.2				
47	0.74				
48	0.12				
49	1.3				
50	1.1				
51	0.88				
52	0.94				
53	1.0				
55	2.1				

Consenus statistics				
Consenus statistics  Consensus median, pg/g  Median all values pg/g  Consensus mean, pg/g  Standard deviation, pg/g  Relative standard deviation, %  No. of values reported	1.1 1.1 1.1 0.28 26 77			
No. of values removed No. of reported non-detects	1 1			

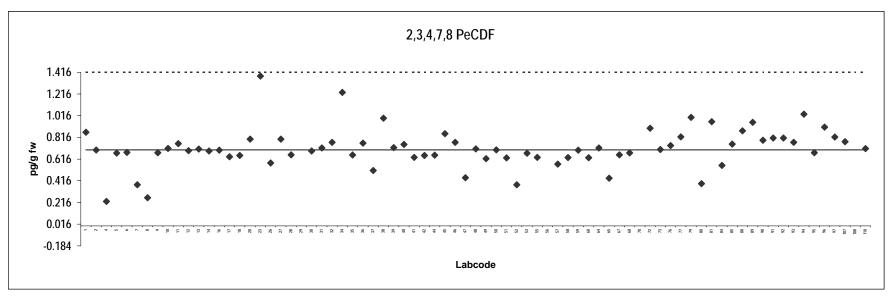


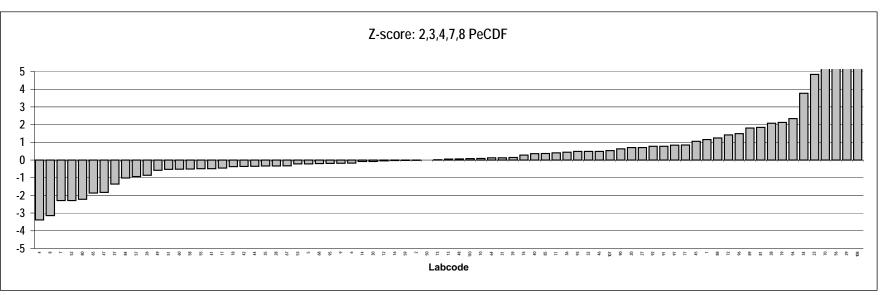


**Congener: 2,3,4,7,8 PeCDF** 

					Congener
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.86		56	1.7	Outlier,ND
2	0.70		57	0.57	
4	0.23		58	0.63	
5	0.67		59	0.70	
6	0.68		60	0.63	
7	0.38		64	0.72	
8	0.26		65	0.44	
9	0.68		67	0.65	
10	0.71		68	0.67	
11	0.76		70	1.5	Outlier
12	0.69		72	0.90	
13	0.71		73	0.70	
14	0.69		76	0.74	
16	0.70		77	0.82	
17	0.64		79	1.0	
18	0.65		80	0.39	
20	0.80		81	0.96	
23	1.4		84	0.56	
26	0.58		85	0.75	
27	0.80		88	0.88	
28	0.65		89	0.95	
29	2.1	Outlier	90	0.79	
30	0.69		91	0.81	
31	0.72		92	0.81	
32	0.77		93	0.77	
34	1.2		94	1.0	
35	0.65		95	0.67	
36	0.76		96	0.91	
37	0.51		97 107	0.82	
38	0.99		107	0.78	O41:
39 40	0.72 0.75		108 110	2.7 0.71	Outlier
40	0.73		110	0.71	
42	0.65				
44	0.65				
45	0.85				
46	0.83				
47	0.77				
48	0.71				
49	0.62				
50	0.70				
51	0.63				
52	0.38				
53	0.67				
55	0.63	ND			

Consenus statistics					
Consensus median, pg/g	0.70				
Median all values pg/g	0.71				
Consensus mean, pg/g	0.71				
Standard deviation, pg/g	0.18				
Relative standard deviation, %	26				
No. of values reported	77				
No. of values removed	4				
No. of reported non-detects	2				

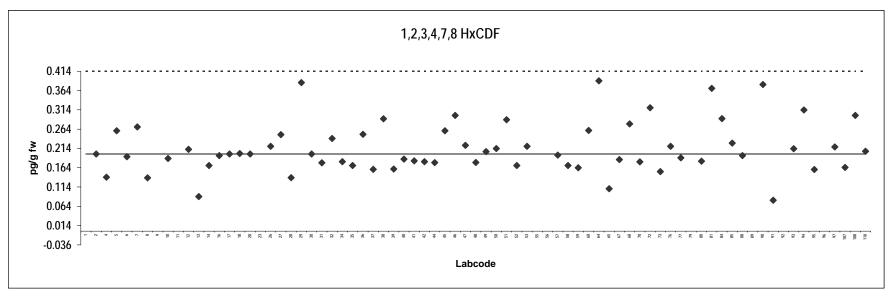


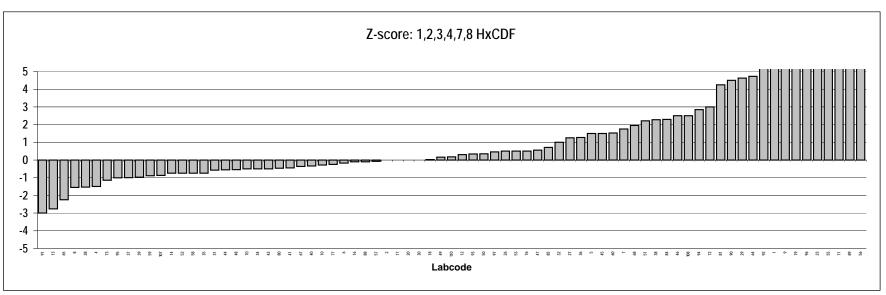


**Congener: 1,2,3,4,7,8 HxCDF** 

					ongener:
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.44	Outlier	56	1.6	Outlier,ND
2	0.20		57	0.20	
4	0.14		58	0.17	
5	0.26	ND	59	0.16	
6	0.19		60	0.26	
7	0.27	ND	64	0.39	
8	0.14		65	0.11	
9	0.45	Outlier	67	0.19	
10	0.19	0.41	68	0.28	
11	0.88	Outlier	70	0.18	
12	0.21		72	0.32	NID
13	0.089		73	0.15	ND
14	0.17		76	0.22	
16 17	0.20	ND	77 79	0.19	Outlier
	0.20	ND	80	0.50	Outner
18 20	0.20 0.20		80 81	0.18 0.37	
23	0.20	Outlier	84	0.37	
26	0.37	Outilei	85	0.23	
27	0.25	ND	88	0.23	
28	0.14	ND	89	0.94	Outlier
29	0.39		90	0.38	Outilei
30	0.20		91	0.080	ND
31	0.18		92	0.42	Outlier
32	0.24		93	0.21	Guiner
34	0.18		94	0.31	
35	0.17		95	0.16	
36	0.25		96	0.55	Outlier
37	0.16		97	0.22	
38	0.29		107	0.17	
39	0.16		108	0.30	
40	0.19		110	0.21	
41	0.18				
42	0.18				
44	0.18				
45	0.26				
46	0.30				
47	0.22				
48	0.18				
49	0.21				
50	0.21				
51	0.29				
52	0.17				
53	0.22	0 11 17			
55	0.64	Outlier,ND			

Consenus statistics					
Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported No. of values removed No. of reported non-detects	0.20 0.21 0.21 0.066 31 77 10 8				
No. of values removed					

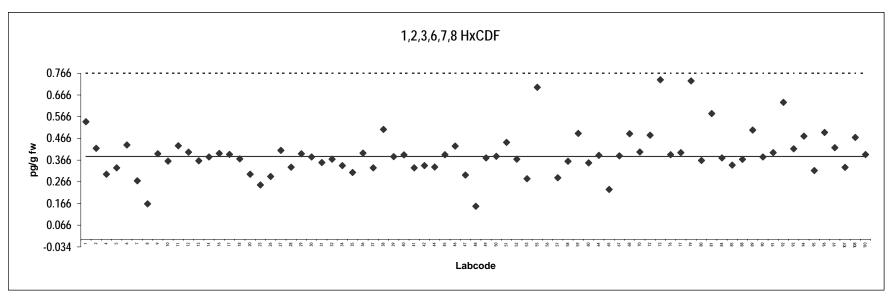


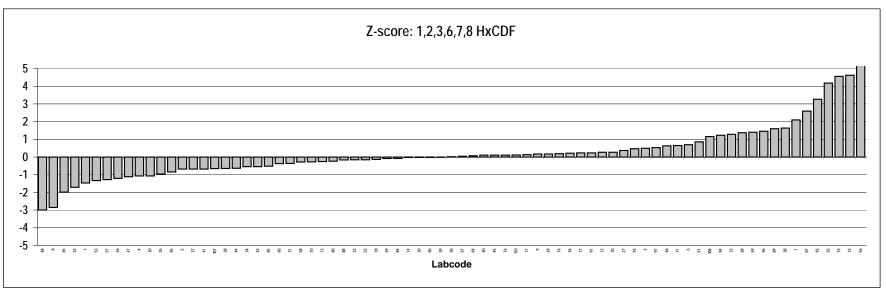


Congener: 1,2,3,6,7,8 HxCDF

				•	ongener:
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.54		56	1.4	Outlier,ND
2	0.42		57	0.28	
4	0.30		58	0.36	
5	0.33		59	0.49	
6	0.44		60	0.35	
7	0.27	ND	64	0.39	
8	0.16		65	0.23	
9	0.40		67	0.38	
10	0.36		68	0.49	
11	0.43		70	0.40	
12	0.40		72	0.48	
13	0.36		73	0.74	
14	0.38		76	0.39	
16	0.40		77	0.40	
17	0.39		79	0.73	
18	0.37		80	0.36	
20	0.30		81	0.58	
23	0.25		84	0.38	
26	0.29		85	0.34	
27	0.41		88	0.37	
28	0.33		89	0.50	
29	0.40		90	0.38	
30	0.38		91	0.40	
31	0.35		92	0.63	
32	0.37		93	0.42	
34	0.34		94	0.48	
35	0.31		95	0.32	
36	0.40		96	0.49	
37	0.33		97	0.42	
38	0.51		107	0.33	
39	0.38		108	0.47	
40	0.39		110	0.39	
41	0.33				
42	0.34				
44	0.33				
45	0.39				
46	0.43				
47	0.30				
48	0.15				
49	0.38				
50	0.38				
51	0.45				
52	0.37				
53	0.28				
55	0.70	ND			

Consenus statistics	
Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g	0.38 0.38 0.39 0.10
Relative standard deviation, %	26
No. of values reported No. of values removed	77 1
No. of reported non-detects	3

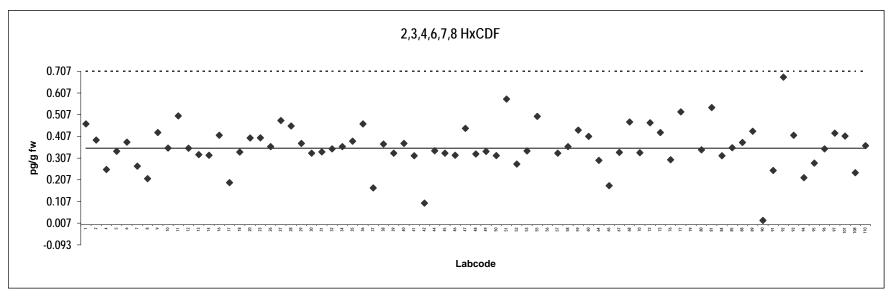


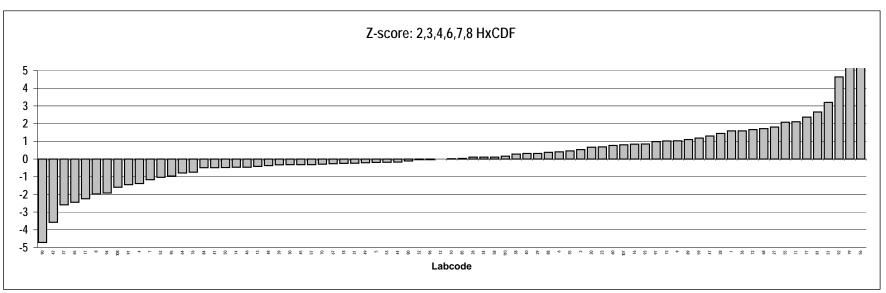


Congener: 2,3,4,6,7,8 HxCDF

	Congener:				
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.46		56	1.8	Outlier,ND
2	0.39		57	0.33	
4	0.26		58	0.36	
5	0.34		59	0.44	
6	0.38		60	0.41	
7	0.27	ND	64	0.30	
8	0.21		65	0.18	
9	0.43		67	0.33	
10	0.35		68	0.47	
11	0.50		70	0.33	
12	0.35		72	0.47	
13	0.32		73	0.42	
14	0.32		76	0.30	
16	0.41		77	0.52	0 11
17	0.19		79	0.87	Outlier
18	0.34		80	0.35	
20	0.40		81 84	0.54	
23	0.40			0.32	
26 27	0.36 0.48		85 88	0.36 0.38	
28	0.45		89	0.38	
29	0.38		90	0.020	ND
30	0.33		91	0.020	ND
31	0.34		92	0.68	
32	0.35		93	0.41	
34	0.36		94	0.22	
35	0.39		95	0.28	
36	0.47		96	0.35	
37	0.17		97	0.42	
38	0.37		107	0.41	
39	0.33		108	0.24	
40	0.37		110	0.36	
41	0.32				
42	0.10	ND			
44	0.34				
45	0.33				
46	0.32				
47	0.44				
48	0.33				
49	0.34				
50	0.32				
51	0.58				
52	0.28				
53	0.34				
55	0.50	ND			

Consenus statistics				
Consensus median, pg/g	0.35			
Median all values pg/g	0.35			
Consensus mean, pg/g	0.36			
Standard deviation, pg/g	0.10			
Relative standard deviation, %	28			
No. of values reported	77			
No. of values removed	2			
No. of reported non-detects	5			

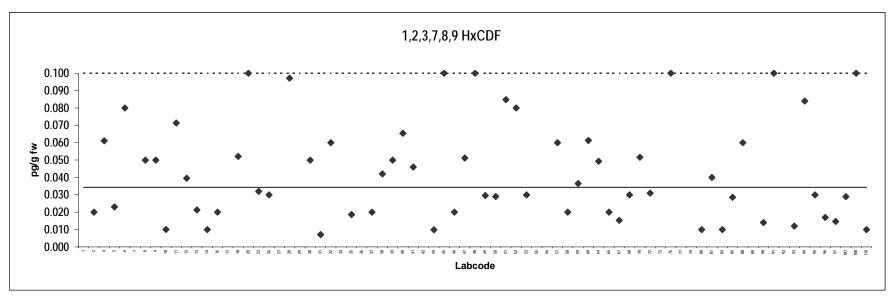


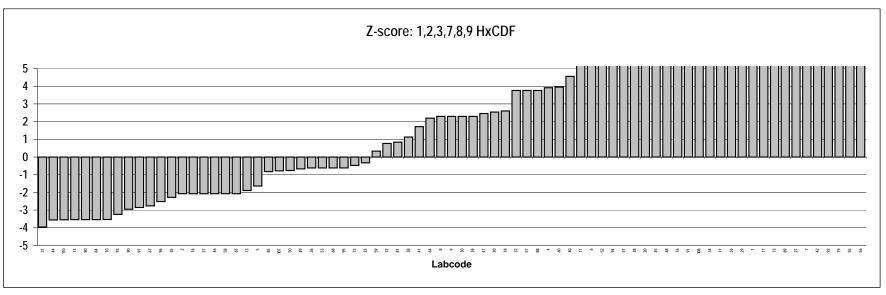


**Congener: 1,2,3,7,8,9 HxCDF** 

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.18	Outlier	56	2.5	Outlier,ND
2	0.020		57	0.060	ND
4	0.061	ND	58	0.020	ND
5	0.023	ND	59	0.037	
6	0.080	ND	60	0.061	ND
7	0.27	Outlier,ND	64	0.049	ND
8	0.050	ND	65	0.020	ND
9	0.050	ND	67	0.015	ND
10	0.010		68	0.030	ND
11	0.071	ND	70	0.052	ND
12	0.040	ND	72	0.031	
13	0.021		73	0.21	Outlier,ND
14	0.010	ND	76	0.10	ND
16	0.020		77	0.12	Outlier,ND
17	0.20	Outlier,ND	79	0.45	Outlier
18	0.052	ND	80	0.010	ND
20	0.10	ND	81	0.040	
23	0.032		84	0.010	ND
26	0.030	ND	85	0.029	
27	0.25	Outlier,ND	88	0.060	ND
28	0.097	ND	89	0.22	Outlier,ND
29	0.14	Outlier	90	0.014	ND
30	0.050	ND	91	0.10	ND
31	0.0071		92	0.34	Outlier
32	0.060		93	0.012	
34	0.11	Outlier,ND	94	0.084	
35	0.019		95	0.030	ND
36	0.13	Outlier	96	0.017	ND
37	0.020	ND	97	0.015	
38	0.042		107	0.029	ND
39	0.050	ND	108	0.10	ND
40	0.065	ND	110	0.0099	
41	0.046	ND			
42	0.33	Outlier			
44	0.0099				
45	0.10	ND			
46	0.020				
47	0.051	ND			
48	0.10	ND			
49	0.030	ND			
50	0.029	ND			
51	0.085	ND			
52	0.080	ND			
53	0.030	ND			
55	0.88	Outlier,ND			

Consensus median, pg/g	0.034
Median all values pg/g	0.050
Consensus mean, pg/g	0.043
Standard deviation, pg/g	0.029
Relative standard deviation, %	66
No. of values reported	77
No. of values removed	15
No. of reported non-detects	52

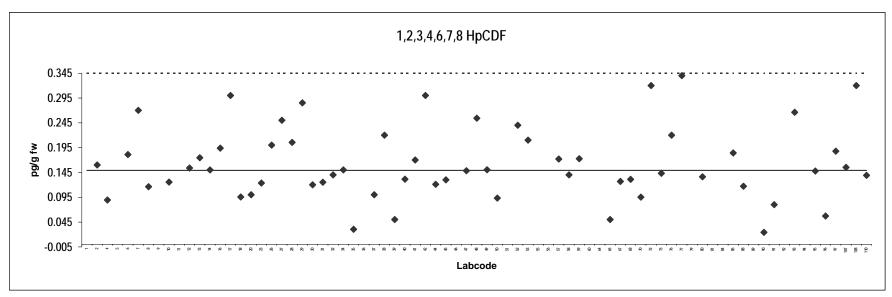


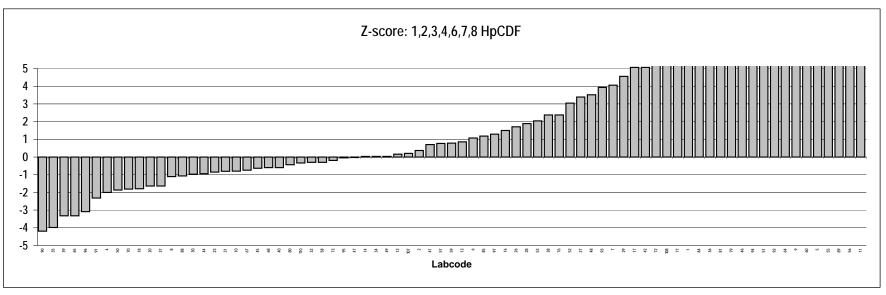


Congener: 1,2,3,4,6,7,8 HpCDF

T 1 1	G / 6	NT 4			ongener.
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.37	Outlier	56	2.4	Outlier,ND
2	0.16		57	0.17	
4	0.089	0 41 170	58	0.14	
5	1.3	Outlier,ND	59	0.17	0 11
6	0.18		60	0.94	Outlier
7	0.27	ND	64	0.69	Outlier
8	0.12	0.41	65	0.050	ND
9	0.72	Outlier	67	0.13	
10	0.13	0.41	68	0.13	
11	6.9	Outlier	70	0.095	ND
12	0.15		72	0.32	
13	0.17		73	0.14	
14	0.15		76	0.22	
16	0.19		77	0.34	0 11
17	0.30	ND	79	0.44	Outlier
18	0.095		80	0.14	0 11
20	0.10		81	0.43	Outlier
23	0.12		84	0.38	Outlier
26	0.20		85	0.18	
27	0.25	ND	88	0.12	0 11
28	0.21		89	2.4	Outlier
29	0.29		90	0.024	ND
30	0.12		91	0.080	ND
31	0.13		92	0.63	Outlier
32	0.14		93	0.27	0 11
34	0.15	ND	94	0.50	Outlier
35	0.030	0 41	95	0.15	
36	0.40	Outlier	96	0.057	ND
37	0.10		97	0.19	
38	0.22	MD	107	0.16	
39	0.050	ND	108	0.32	
40	0.13		110	0.14	
41	0.17	ND			
42	0.30	ND			
44 45	0.12				
	0.13	Out!:			
46	0.45	Outlier			
47 48	0.15				
48 49	0.25 0.15				
50 51	0.093	Outlier,ND			
	0.60	Outlier,ND			
52 53	0.24				
53	0.21	Outline			
55	2.1	Outlier			

Consenus statistics				
Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported	0.15 0.17 0.16 0.074 45			
No. of values removed No. of reported non-detects	17 14			

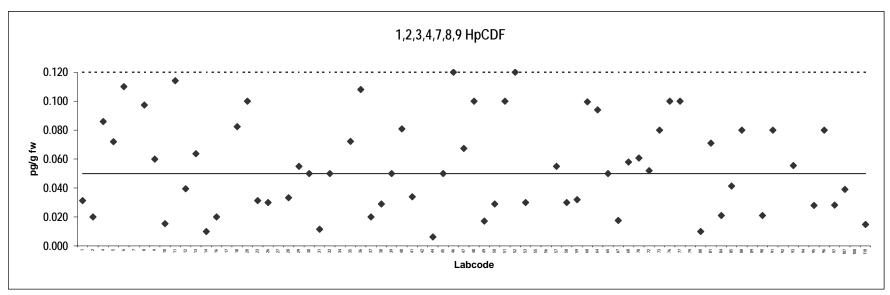


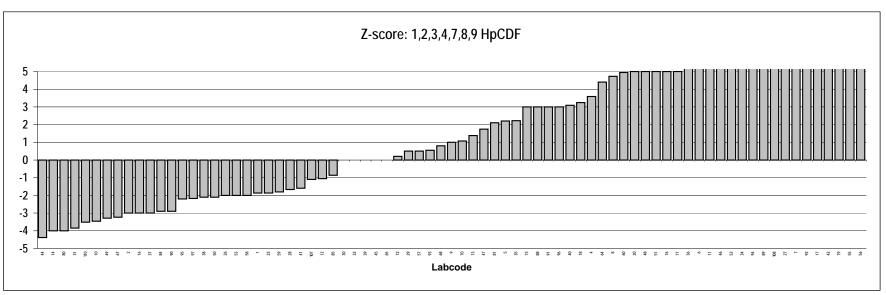


Congener: 1,2,3,4,7,8,9 HpCDF

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.031	11000	56	4.6	Outlier,ND
2	0.020		57	0.055	ND
4	0.086	ND	58	0.030	ND
5	0.072	ND	59	0.032	T\D
6	0.11	ND	60	0.100	ND
7	0.27	Outlier,ND	64	0.094	ND
8	0.097	Outher,11D	65	0.050	ND
9	0.060		67	0.018	ND
10	0.015		68	0.058	
11	0.11	ND	70	0.061	ND
12	0.040	ND	72	0.052	ND
13	0.064		73	0.080	ND
14	0.010	ND	76	0.10	ND
16	0.020	ND	77	0.10	ND ND
17	0.30	Outlier,ND	79	0.55	Outlier
18	0.082	ND	80	0.010	ND
20	0.10	ND	81	0.071	ND
23	0.031	ND	84	0.021	ND
26	0.031	ND	85	0.041	ND
27	0.25	Outlier,ND	88	0.080	ND
28	0.033	ND	89	0.19	Outlier,ND
29	0.055	ND	90	0.021	ND
30	0.050	ND	91	0.080	ND ND
31	0.012	ND	92	0.29	Outlier
32	0.050	ND	93	0.056	Outner
34	0.13	Outlier,ND	94	0.16	Outlier
35	0.072	Guiller, TE	95	0.028	ND
36	0.11		96	0.080	ND
37	0.020	ND	97	0.028	112
38	0.029	T\D	107	0.039	ND
39	0.050	ND	108	0.20	Outlier,ND
40	0.081	ND	110	0.015	Outher, (D
41	0.034	ND	110	0.015	
42	0.30	Outlier,ND			
44	0.0062				
45	0.050	ND			
46	0.12				
47	0.067	ND			
48	0.10	ND			
49	0.017	ND			
50	0.029	ND			
51	0.10	ND			
52	0.12	ND			
53	0.030	ND			
55	1.1	Outlier,ND			

Consenus statistics					
Consensus median, pg/g	0.050				
Median all values pg/g	0.060				
Consensus mean, pg/g	0.056				
Standard deviation, pg/g	0.032				
Relative standard deviation, %	58				
No. of values reported	77				
No. of values removed	12				
No. of reported non-detects	48				

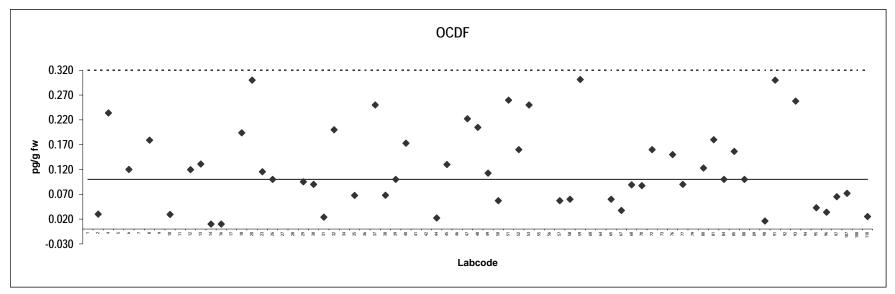


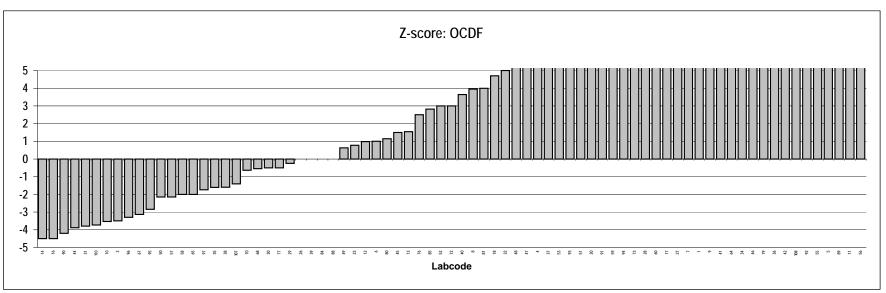


**Congener: OCDF** 

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	0.56	Outlier	56	17	Outlier,ND
2	0.030	ND	57	0.057	ND
4	0.23	ND	58	0.060	ND
5	2.4	Outlier,ND	59	0.30	
6	0.12	ND	60	0.49	Outlier
7	0.54	Outlier,ND	64	0.66	Outlier
8	0.18		65	0.060	ND
9	0.59	Outlier	67	0.037	ND
10	0.029		68	0.089	
11	6.1	Outlier	70	0.087	ND
12	0.12		72	0.16	
13	0.13		73	0.41	Outlier
14	0.010	ND	76	0.15	ND
16	0.010	ND	77	0.090	ND
17	0.50	Outlier,ND	79	0.96	Outlier
18	0.19	ND	80	0.12	
20	0.30	ND	81	0.18	
23	0.12		84	0.10	ND
26	0.10	ND	85	0.16	
27	0.50	Outlier,ND	88	0.10	ND
28	0.43	Outlier	89	2.7	Outlier
29	0.095	ND	90	0.016	ND
30	0.090	ND	91	0.30	ND
31	0.024		92	1.6	Outlier
32	0.20	ND	93	0.26	
34	0.73	Outlier,ND	94	0.37	Outlier
35	0.068		95	0.043	ND
36	0.97	Outlier	96	0.034	ND
37	0.25		97	0.065	
38	0.068		107	0.072	
39	0.10	ND	108	1.0	Outlier,ND
40	0.17	ND	110	0.025	
41	0.61	Outlier			
42	1.0	Outlier,ND			
44	0.022				
45	0.13				
46	0.79	Outlier			
47	0.22				
48	0.21				
49	0.11				
50	0.057	ND			
51	0.26	ND			
52	0.16	ND			
53	0.25	ND			
55	1.7	Outlier,ND			

Consensus median, pg/g	0.10
Median all values pg/g	0.16
Consensus mean, pg/g	0.12
Standard deviation, pg/g	0.082
Relative standard deviation, %	67
No. of values reported	77
No. of values removed	23
No. of reported non-detects	39

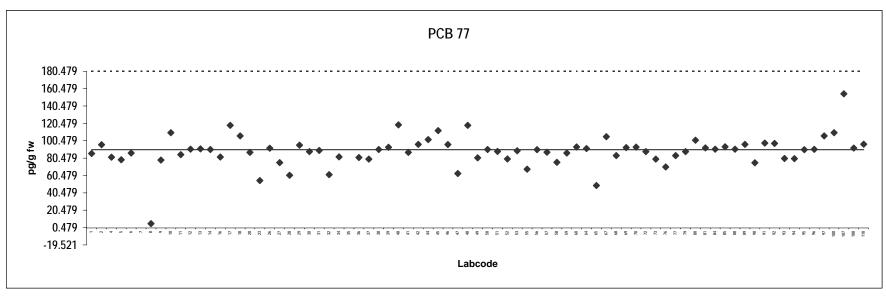


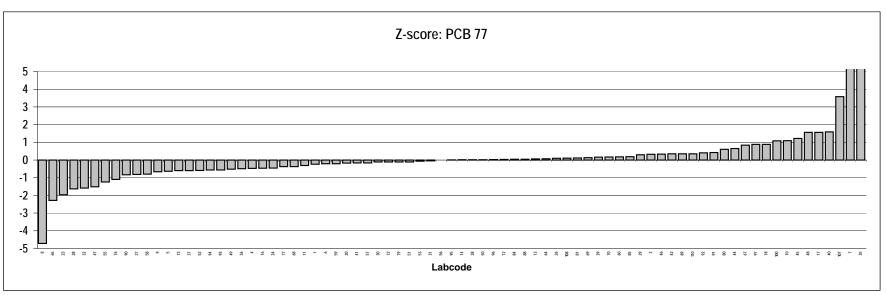


Congener: PCB 77

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	86		56	90	
2	96		57	87	
4	82		58	76	
5 6	79		59	86	
6	86		60	93	
7	252	Outlier	64	91	
8	5.0	ND	65	49	
9	78		67	105	
10	110		68	83	
11	84		69	93	
12	91		70	93	
13	91		72	88	
14	90		73	79	
16	82		76	70	
17	118		77	83	
18	106		79	88	
20	87		80	101	
23	55		81	92	
26	92		84	91	
27	75		85	93	
28	61		88	91	
29	95		89	96	
30	88		90	75	
31	89		91	98	
32	61		92	97	
34	82		93	80	
35	1008	Outlier	94	80	
36	81		95	90	
37	79		96	90	
38	90		97	106	
39	93		100	110	
40	119		107	155	
41	87		108	92	
42	96		110	96	
44	102				
45	112				
46	96				
47	63				
48	118				
49	81				
50	90				
51	88				
52	79				
53	89				
55	68				

Consensus median, pg/g	90
Median all values pg/g	90
Consensus mean, pg/g	88
Standard deviation, pg/g	18
Relative standard deviation, %	20
No. of values reported	79
No. of values removed	2
No. of reported non-detects	1

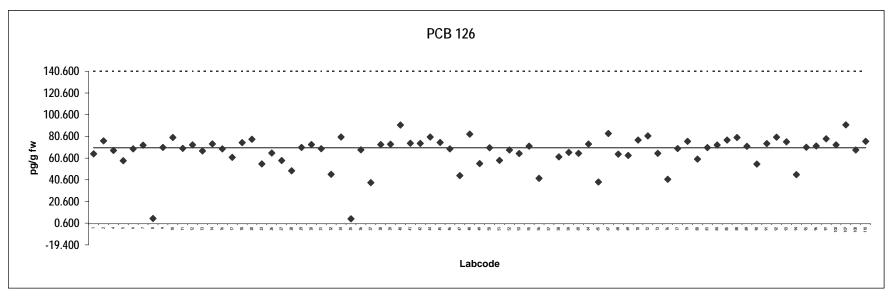


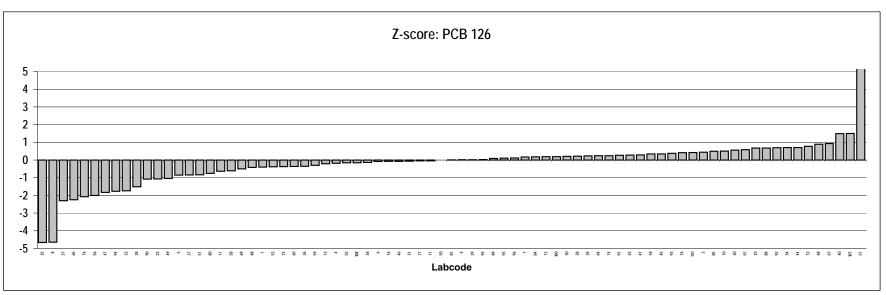


Congener: PCB 126

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	64		56	42	
2	76		57	343	Outlier
4	68		58	62	
5 6	58		59	66	
6	69		60	65	
7	73		64	74	
8	5.0	ND	65	39	
9	70		67	83	
10	80		68	64	
11	69		69	63	
12	73		70	77	
13	67		72	81	
14	74		73	65	
16	69		76	41	
17	61		77	69	
18	75		79	76	
20	78		80	60	
23	55		81	70	
26	65		84	73	
27	58		85	77	
28	49		88	80	
29	70		89	71	
30	73		90	55	
31	69		91	74	
32	46		92	80	
34	80		93	76	
35	4.6		94	45	
36	68		95	71	
37	38		96	72	
38	73		97	78	
39	73		100	73	
40	91 74		107 108	91 68	
41	74 74			08 76	
42 44	80		110	70	
44 45	75				
45	75 69				
46	69 44				
48	83				
49	56				
50	70				
51	58				
52	68				
53	65				
55	72				

Consensus median, pg/g	70
Median all values pg/g	70
Consensus mean, pg/g	67
Standard deviation, pg/g	15
Relative standard deviation, %	23
No. of values reported	79
No. of values removed	1
No. of reported non-detects	1





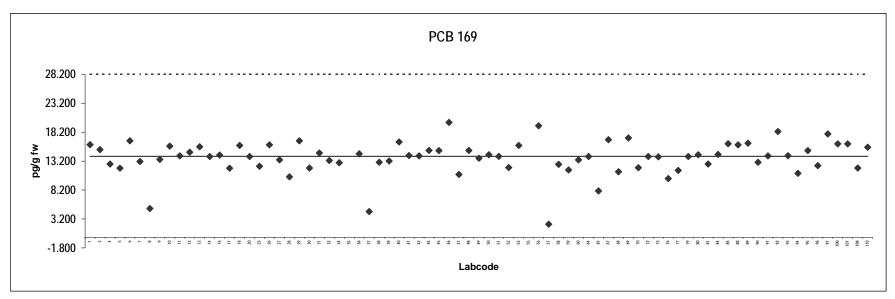
Congener: PCB 169

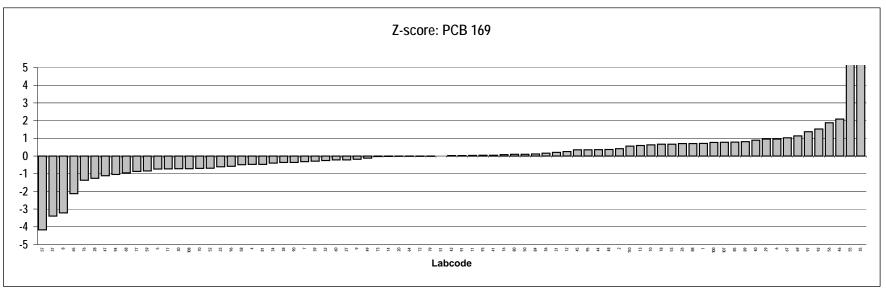
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Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
1	16		56	19	
2 4	15		57	2.3	ND
	13		58	13	
5	12		59	12	
6	17		60	13	
7	13		64	14	
8	5.0	ND	65	8.0	
9	14		67	17	
10	16		68	11	
11	14		69	17	
12	15		70	12	
13	16		72	14	
14	14		73	14	
16	14		76	10	
17	12		77	12	
18	16		79	14	
20	14		80	14	
23	12		81	13	
26	16		84	14	
27	13		85	16	
28	10		88	16	
29	17		89	16	
30	12		90	13	
31	15		91	14	
32	13		92	18	
34	13		93	14	
35	78	Outlier	94	11	
36	14		95	15	
37	4.5		96	12	
38	13		97	18	
39	13		100	16	
40	17		107	16	
41	14		108	12	
42	14		110	16	
44	15				
45	15				
46	20				
47	11				
48	15				
49	14				
50	14				
51	14				
52	12				
53	16				
55	63	Outlier			

# Consenus statistics Consensus median, pg/g 14 Median all values pg/g 14 Consensus mean, pg/g 14 Standard deviation, pg/g 2.9 Relative standard deviation, % 21 No. of values reported 79 No. of values removed 2

2

No. of reported non-detects

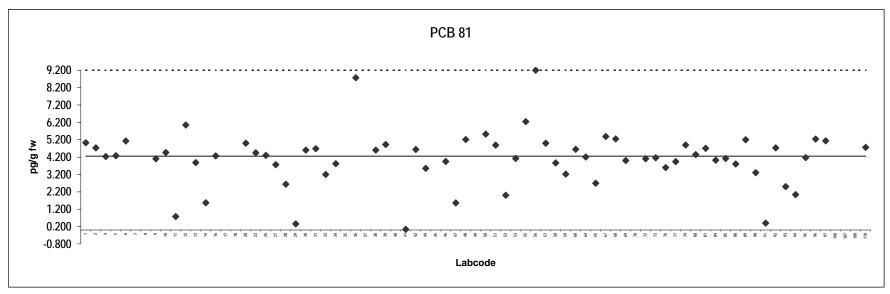


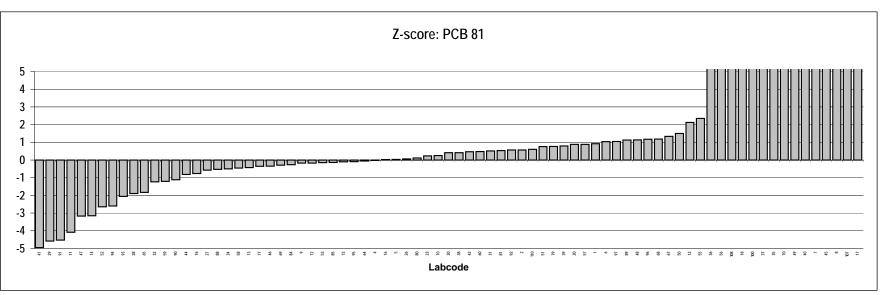


Congener: PCB 81

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	5.0		56	9.2	ND
2	4.7		57	5.0	ND
4	4.2		58	3.9	
5	4.3		59	3.2	
6	5.1		60	4.7	
7	91	Outlier	64	4.2	
8	173	Outlier	65	2.7	
9	4.1		67	5.4	
10	4.5		68	5.2	
11	0.77	ND	69	4.0	ND
12	6.0		70	22	Outlier
13	3.9		72	4.1	
14	1.6		73	4.2	
16	4.3		76	3.6	
17	420	Outlier	77	3.9	
18	15	Outlier	79	4.9	
20	5.0		80	4.3	
23	4.4		81	4.7	
26	4.3		84	4.0	
27	3.8		85	4.1	
28	2.6		88	3.8	
29	0.35	ND	89	5.2	
30	4.6		90	3.3	
31	4.7		91	0.40	ND
32	3.2		92	4.7	
34	3.8	ND	93	2.5	
35	22	Outlier	94	2.0	
36	8.8		95	4.2	
37	18	Outlier	96	5.2	
38	4.6		97	5.1	
39	4.9		100	16	Outlier
40	43	Outlier	107	195	Outlier
41	0.041	ND	108	10	Outlier,ND
42	4.6		110	4.8	
44	3.6				
45	125	Outlier			
46	4.0				
47	1.6				
48	5.2				
49	25	Outlier			
50	5.5				
51	4.9				
52	2.0	ND			
53	4.1				
55	6.2				

# Consenus statistics Consensus median, pg/g 4.2 Median all values pg/g 4.6 Consensus mean, pg/g 4.1 Standard deviation, pg/g 1.6 Relative standard deviation, % 38 No. of values reported 79 No. of values removed 13 No. of reported non-detects 10

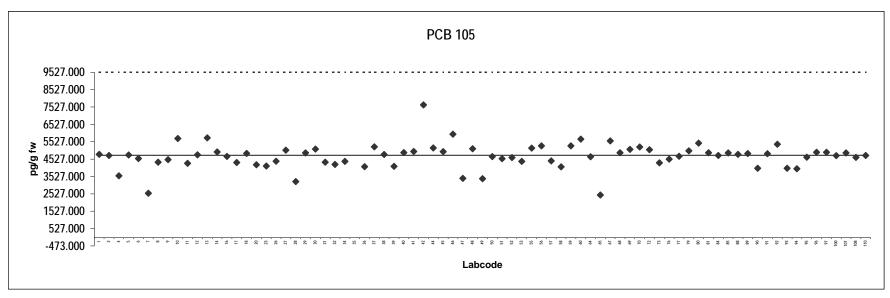


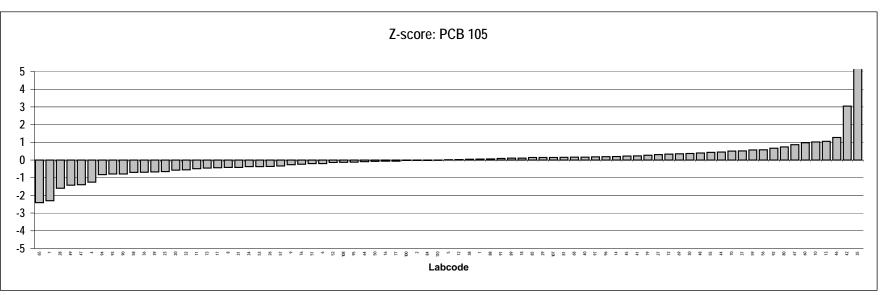


Congener: PCB 105

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	4797		56	5290	
2	4730		57	4422	
4	3560		58	4079	
5	4764		59	5285	
6	4558		60	5670	
7	2563		64	4661	
8	4345		65	2460	
9	4495		67	5571	
10	5716		68	4895	
11	4279		69	5080	
12	4772		70	5221	
13	5751		72	5064	
14	4937		73	4315	
16	4681		76	4524	
17	4332		77	4685	
18	4850		79	5000	
20	4200		80	5448	
23	4123		81	4890	
26	4400		84	4730	
27	5037		85	4882	
28	3234		88	4800	
29	4883		89	4844	
30	5100		90	4000	
31	4350		91	4834	
32	4217		92	5378	
34	4390		93	3994	
35	47805	Outlier	94	3965	
36	4088		95	4634	
37	5235		96	4921	
38	4790		97	4918	
39	4104		100	4728	
40	4896		107	4885	
41	4968		108	4622	
42	7644		110	4733	
44	5172				
45	4960				
46	5958				
47	3419				
48	5121				
49	3398				
50	4671				
51	4551				
52	4615				
53	4390				
55	5157				

Consensus median, pg/g	4748
Median all values pg/g	4764
Consensus mean, pg/g	4688
Standard deviation, pg/g	714
Relative standard deviation, %	15
No. of values reported	79
No. of values removed	1
No. of reported non-detects	0

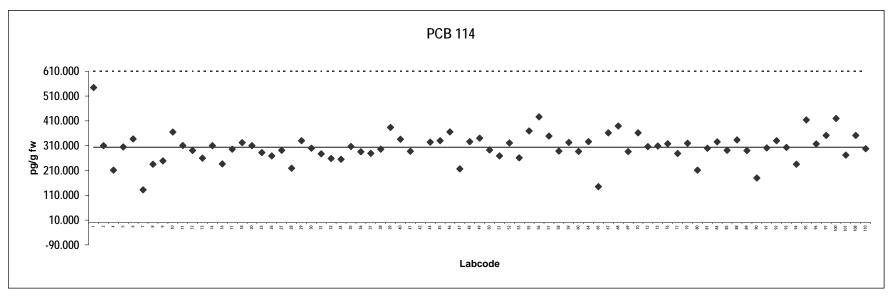


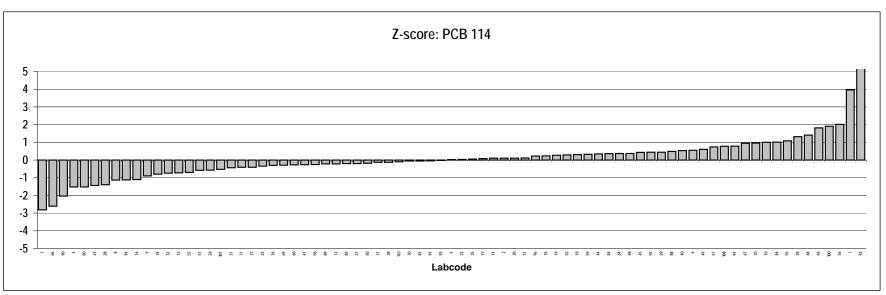


Congener: PCB 114

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	544		56	426	
2	310		57	349	
4	211		58	288	
5 6	305		59	323	
6	337		60	287	
7	132		64	326	
8	235		65	145	
9	249		67	361	
10	365		68	389	
11	311		69	286	
12	290		70	362	
13	260		72	306	
14	310		73	308	
16	237		76	318	
17	296		77	279	
18	322		79	320	
20	310		80	211	
23	282		81	300	
26	269		84	326	
27	291		85	291	
28	219		88	333	
29	330		89	290	
30	300		90	180	
31	277		91	301	
32	259		92	330	
34	255		93	303	
35	307		94	235	
36	286		95	414	
37	279		96	317	
38	296		97	351	
39	384		100	419	
40	336		107	272	
41	287		108	351	
42	774	Outlier	110	297	
44	324				
45	330				
46	365				
47	216				
48	326				
49	340				
50	292				
51	269				
52	321				
53	261				
55	369				

Consensus median, pg/g	304
Median all values pg/g	305
Consensus mean, pg/g	304
Standard deviation, pg/g	61
Relative standard deviation, %	20
No. of values reported	79
No. of values removed	1
No. of reported non-detects	0
	1 0



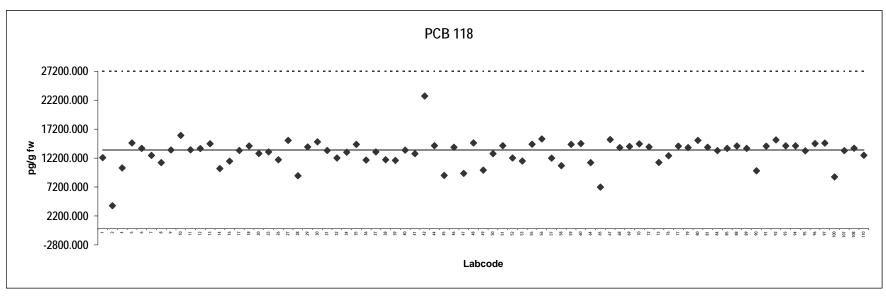


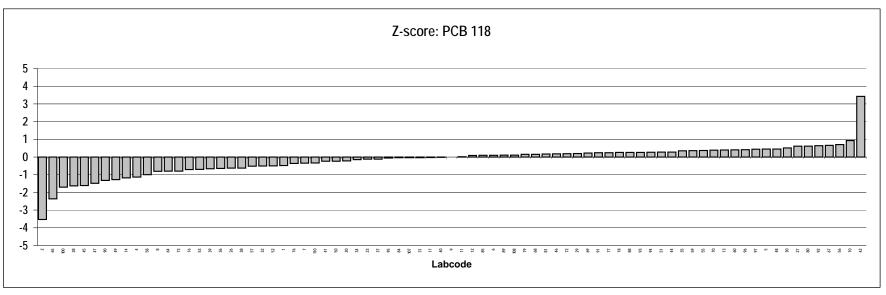
Congener: PCB 118

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	12277		56	15500	
2	3980		57	12190	
4	10500		58	10876	
5	14817		59	14575	
6	13867		60	14700	
7	12652		64	11415	
8	11400		65	7170	
9	13600		67	15384	
10	16121		68	14005	
11	13636		69	14200	
12	13846		70	14656	
13	14676		72	14108	
14	10379		73	11428	
16	11668		76	12612	
17	13508		77	14259	
18	14300		79	14000	
20	13000		80	15263	
23	13256		81	14060	
26	11900		84	13496	
27	15257		85	13867	
28	9149		88	14300	
29	14123		89	13876	
30	15000		90	10000	
31	13500		91	14257	
32	12216		92	15332	
34	13200		93	14309	
35	14555		94	14323	
36	11849		95	13446	
37	13256		96	14710	
38	11900		97	14790	
39	11799		100	8956	
40	13573		107	13496	
41	12947		108	13894	
42	22915		110	12683	
44	14356				
45	9210				
46	14078				
47	9549				
48	14817				
49	10118				
50	12957				
51	14344				
52	12223				
53	11700				
55	14588				

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Consenus	STATISTICS

Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, %	13600 13600 13148 2324 18
No. of values reported No. of values removed No. of reported non-detects	79 0 0

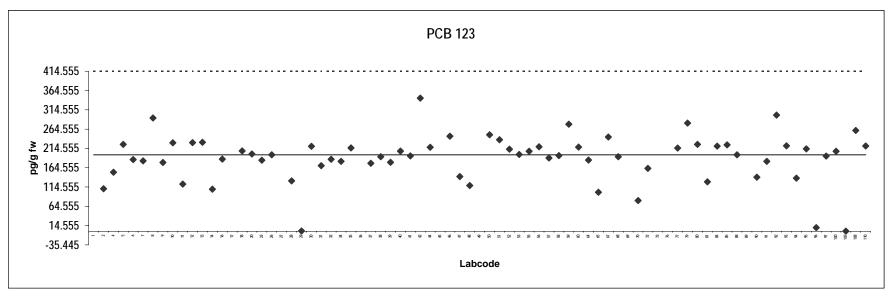


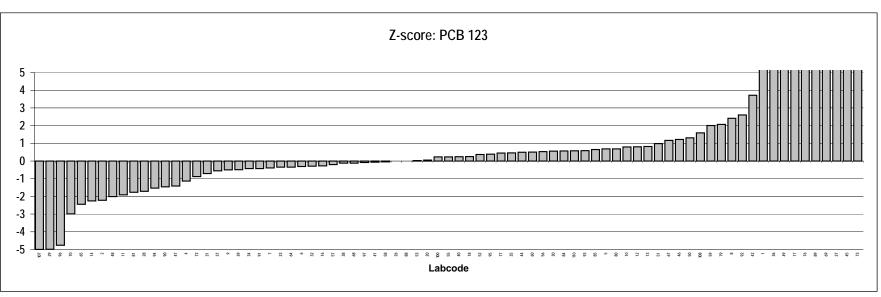


Congener: PCB 123

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	478	Outlier	56	219	
2	110		57	190	
4	153		58	196	
5	225		59	277	
6	186		60	218	
7	182		64	184	
8	294		65	101	
9	178		67	244	
10	229		68	193	
11	122		69	1380	Outlier
12	230		70	80	
13	231		72	163	
14	109		73	1539	Outlier
16	187		76	1365	Outlier
17	1173	Outlier	77	216	
18	208		79	280	
20	200		80	225	
23	184		81	128	
26	198		84	221	
27	1409	Outlier	85	224	
28	130		88	198	
29	0.50	ND	89	1378	Outlier
30	220		90	140	
31	170		91	181	
32	186		92	301	
34	181		93	221	
35	216		94	137	
36	614	Outlier	95	213	
37	176		96	9.4	ND
38	193		97	195	
39	178		100	207	
40	208		107	0.10	ND
41	195		108	261	
42	345		110	221	
44	217				
45	1460	Outlier			
46	246				
47	142				
48	118				
49	1033	Outlier			
50	250				
51	237				
52	212				
53	199				
55	207				

Consensus median, pg/g	198
Median all values pg/g	207
Consensus mean, pg/g	190
Standard deviation, pg/g	62
Relative standard deviation, %	33
No. of values reported	79
No. of values removed	10
No. of reported non-detects	3

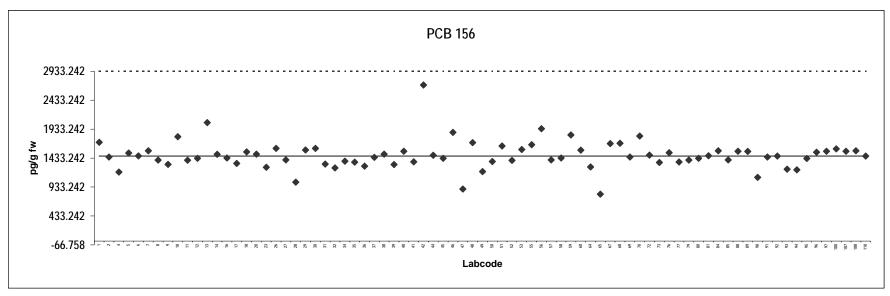


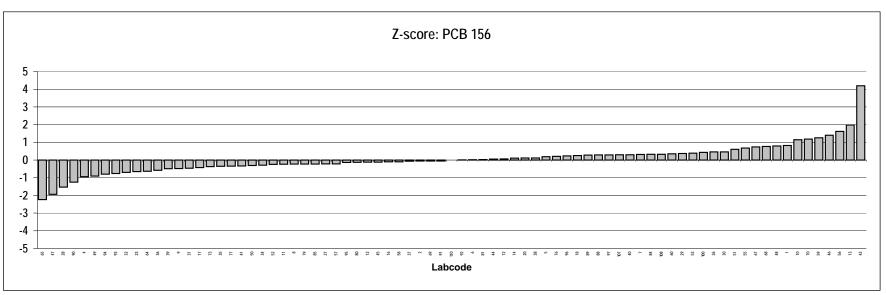


Congener: PCB 156

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	1707		56	1940	
2	1450		57	1402	
4	1190		58	1435	
5	1521		59	1833	
6	1470		60	1570	
7	1558		64	1279	
8	1400		65	810	
9	1325		67	1684	
10	1802		68	1690	
11	1396		69	1450	
12	1430		70	1813	
13	2045		72	1484	
14	1498		73	1356	
16	1435		76	1527	
17	1342		77	1366	
18	1540		79	1400	
20	1500		80	1428	
23	1273		81	1474	
26	1600		84	1560	
27	1401		85	1400	
28	1017		88	1550	
29	1574		89	1548	
30	1600		90	1100	
31	1330		91	1450	
32	1262		92	1468	
34	1380		93	1242	
35	1363		94	1231	
36	1295		95	1426	
37	1447		96	1535	
38	1500		97	1550	
39	1322		100	1593	
40	1552		107	1552	
41	1368		108	1560	
42	2696		110	1467	
44	1482				
45	1430				
46	1877				
47	898				
48	1700				
49	1201				
50	1375				
51	1642				
52	1392				
53	1580				
55	1665				

Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard deviation, % No. of values reported	1467 1467 1481 245 17 79
No. of values removed	ő
No. of reported non-detects	Ö
•	-



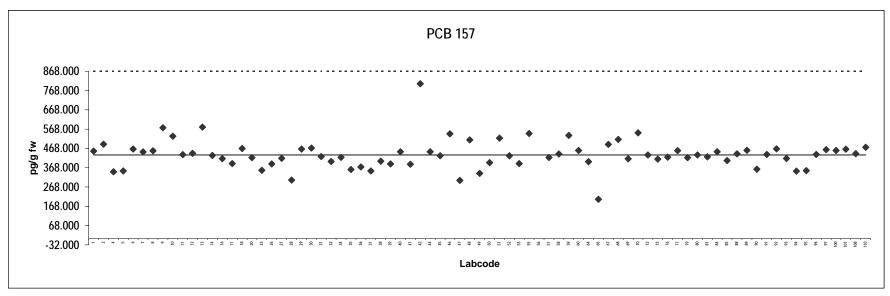


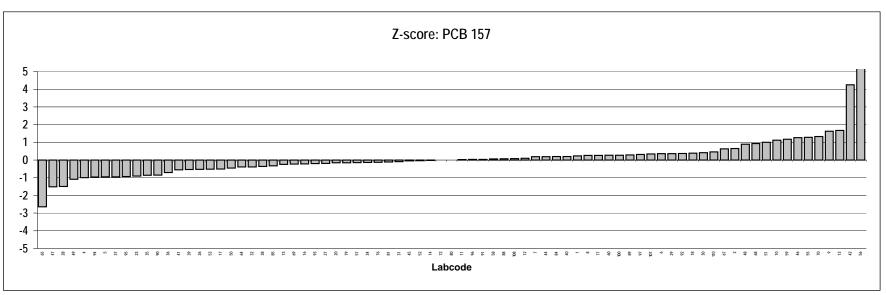
Congener: PCB 157

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	454		56	1940	Outlier
2	490		57	421	
4	347		58	439	
5	351		59	536	
6	465		60	457	
7	450		64	399	
8	456		65	204	
9	575		67	489	
10	531		68	514	
11	436		69	414	
12	442		70	549	
13	579		72	434	
14	432		73	413	
16	415		76	423	
17	389		77	456	
18	467		79	420	
20	420		80	434	
23	355		81	424	
26	388		84	450	
27	417		85	406	
28	304		88	440	
29	465		89	459	
30	470		90	360	
31	426		91	437	
32	400		92	466	
34	422		93	416	
35	359		94	350	
36	372		95	353	
37	351		96	437	
38	402		97	461	
39	388		100	457	
40	451		107	464	
41	386		108	441	
42	803		110	474	
44	450				
45	430				
46	544				
47	302				
48	512				
49	339				
50	394				
51	521				
52	430				
53	389				
55	545				

### Consenus statistics Consensus median, pg/g Median all values pg/g Consensus mean, pg/g Standard deviation, pg/g Relative standard eviation, % 434 434 436 76 17 No. of values reported 79 No. of values removed 1 No. of reported non-detects

0



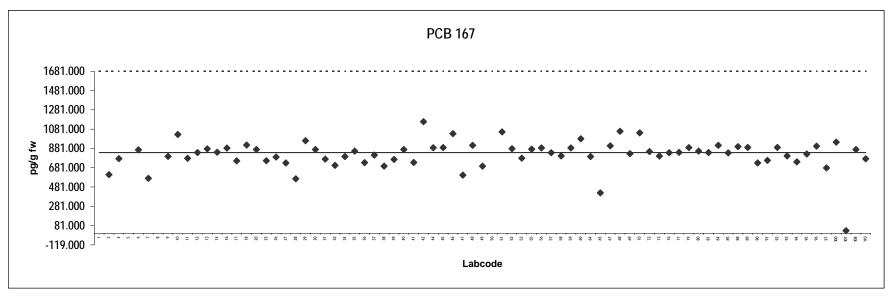


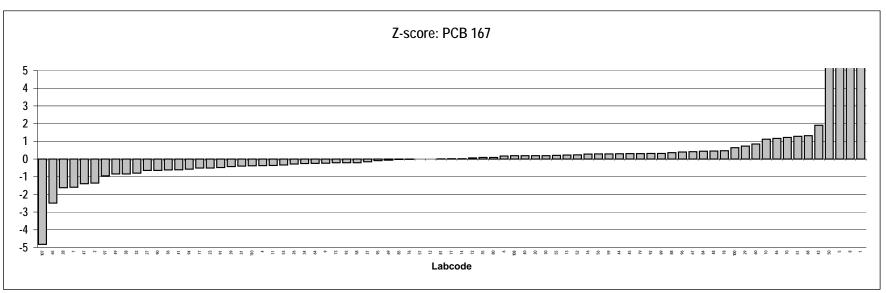
Congener: PCB 167

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	3536	Outlier	56	886	
2	610		57	837	
4	776		58	803	
5	2973	Outlier	59	886	
6	867		60	981	
7	571		64	797	
8	3000	Outlier	65	420	
9	799		67	908	
10	1026		68	1059	
11	778		69	827	
12	839		70	1042	
13	876		72	848	
14	841		73	802	
16	884		76	837	
17	752		77	841	
18	917		79	890	
20	870		80	853	
23	753		81	839	
26	791		84	913	
27	730		85	835	
28	567		88	899	
29	961		89	892	
30	870		90	730	
31	771		91	757	
32	705		92	892	
34	796		93	803	
35	853		94	742	
36	735		95	823	
37	812		96	904	
38	697		97	678	
39	767		100	945	
40	869		107	28	ND
41	736		108	869	
42	1158		110	773	
44	888				
45	890				
46	1033				
47	605				
48	914				
49	697				
50	2569	Outlier			
51	1053				
52	878				
53	781				
55	873				

Consenus	statistics

Consensus median, pg/g	839
Median all values pg/g	841
Consensus mean, pg/g	819
Standard deviation, pg/g	150
Relative standard deviation, %	18
No. of values reported	79
No. of values removed	4
No. of reported non-detects	1

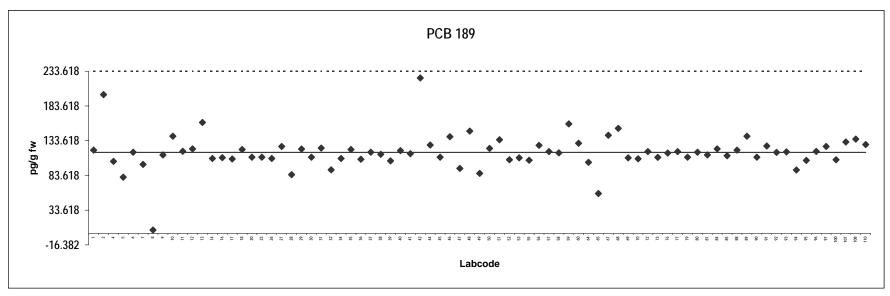


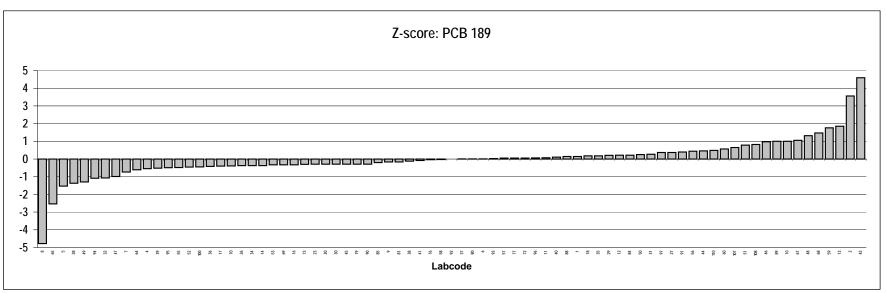


Congener: PCB 189

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
1	120		56	127	
2	200		57	118	
4	104		58	116	
5	81		59	158	
6	117		60	130	
7	100		64	103	
8	5.0	ND	65	58	
9	113		67	141	
10	140		68	151	
11	118		69	109	
12	122		70	108	
13	160		72	118	
14	108		73	110	
16	109		76	116	
17	107		77	118	
18	121		79	110	
20	110		80	117	
23	110		81	113	
26	108		84	122	
27	125		85	112	
28	85		88	120	
29	122		89	140	
30	110		90	110	
31	123 92		91 92	126	
32 34	108		92	117 117	
35	121		93	91	
36	107		95	105	
37	117		96	118	
38	114		97	125	
39	105		100	106	
40	119		107	132	
41	115		108	136	
42	224		110	128	
44	127				
45	110				
46	139				
47	94				
48	148				
49	87				
50	123				
51	135				
52	106				
53	109				
55	106				

117
117
117
26
22
79
0
1

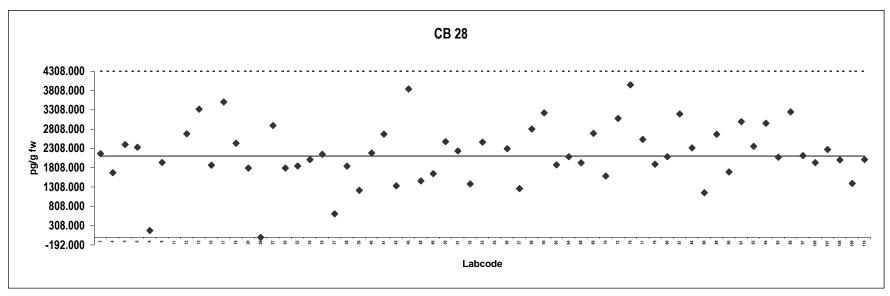


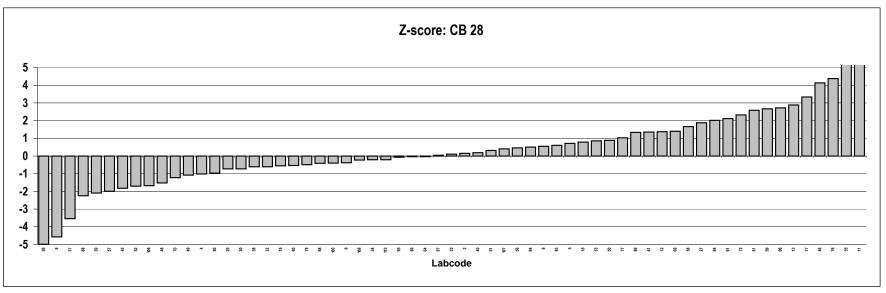


Congener: CB 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	2170		79	1900	
4	1680		80	2093	
5	2409		81	3200	
6	2338		84	2321	
8	180		88	1160	
9	1945		89	2672	
11	5591	Outlier	90	1700	
12	2685		91	3000	ND
13	3325		93	2361	
16	1875		94	2959	
17	3514		95	2081	
18	2440		96	3255	
20	1800		97	2124	
26	2.5		100	1938	
27	2900		107	2279	
30	1800		108	2010	
32	1852		109	1400	
34	2020		110	2021	
35	2154				
37	614				
38	1850				
39	1224				
40	2187				
41	2680				
42	1340				
46	3850				
48	1467				
49	1652				
50	2482				
51	2241				
52	1390				
53	2470				
55	4660	Outlier			
56	2300				
57	1268				
58	2809				
59	3231				
60	1880				
64	2093				
68	1936				
69	2700				
70	1592				
72	3086				
76	3955				
77	2541				

Consensus median, pg/g	2109
Median all values pg/g	2154
Consensus mean, pg/g	2171
Standard deviation, pg/g	769
Relative standard deviation, %	35
No. of values reported	63
No. of values removed	2
No. of reported non-detects	1

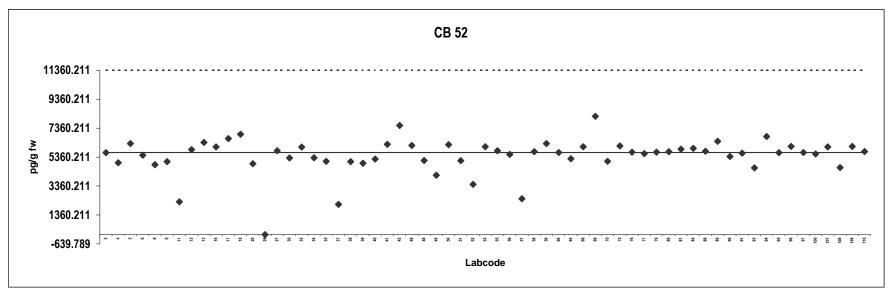


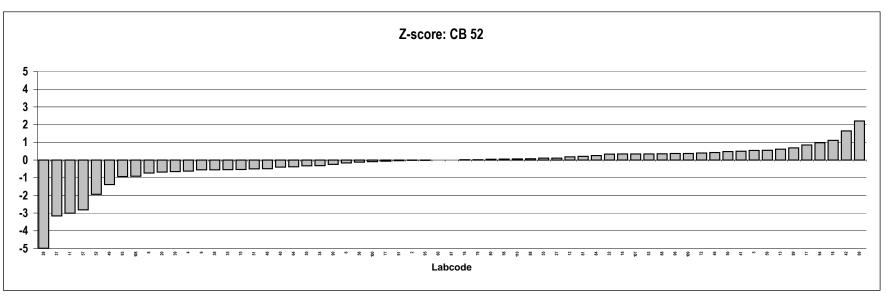


Congener: CB 52

	T				Con
Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	5660		79	5700	
4	4970		80	5730	
5	6295		81	5913	
6	5489		84	5959	
8	4840		88	5760	
9	5045		89	6455	
11	2266		90	5400	
12	5878		91	5635	
13	6371		93	4612	
16	6061		94	6783	
17	6639		95	5662	
18	6940		96	6098	
20	4900		97	5680	
26	6.3		100	5572	
27	5800		107	6061	
30	5300		108	4640	
32	6054		109	6100	
34	5310		110	5746	
35	5063				
37	2092				
38	5050				
39	4930				
40	5227				
41	6240				
42	7550				
46	6160				
48	5123				
49	4102				
50	6221				
51	5114				
52	3470				
53	6070				
55	5796				
56	5540				
57	2475				
58	5734				
59	6300				
60	5680				
64	5247				
68	6071				
69	8180				
70	5066				
72	6125				
76	5693				
77	5599				

5680
5680
5448
1246
23
63
0
0

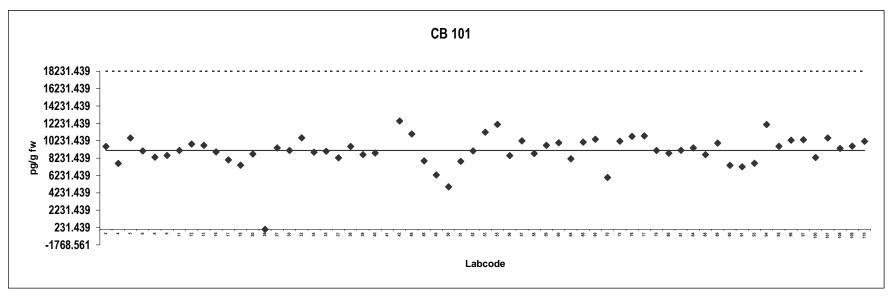


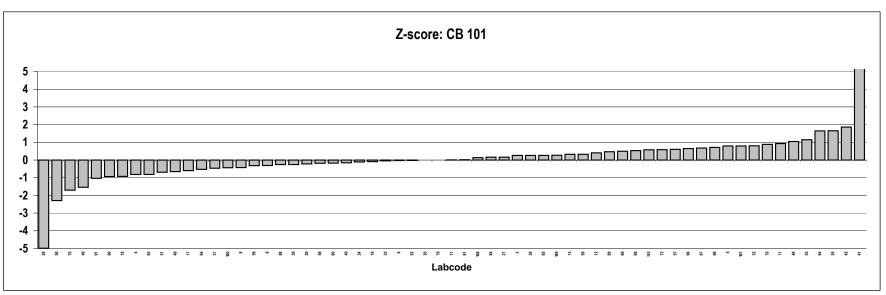


Congener: CB 101

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	9570		79	9100	
4	7610		80	8794	
5	10551		81	9132	
6	9058		84	9399	
8	8330		88	8630	
9	8540		89	9953	
11	9116		90	7400	
12	9835		91	7225	
13	9688		93	7624	
16	8941		94	12101	
17	8018		95	9579	
18	7410		96	10280	
20	8700		97	10342	
26	10		100	8301	
27	9400		107	10552	
30	9100		108	9340	
32	10567		109	9600	
34	8900		110	10157	
35	9016				
37	8264				
38	9570				
39	8636				
40	8819				
41	28280	Outlier			
42	12500				
46	11008				
48	7913				
49	6291				
50	4926				
51	7853				
52	9060				
53	11200				
55	12116				
56	8520				
57	10210				
58	8765				
59	9694				
60	10000				
64	8140				
68	10068				
69	10400				
70	5996				
72	10175				
76	10723				
77	10792				

Consensus median, pg/g	9108
Median all values pg/g	9116
Consensus mean, pg/g	9057
Standard deviation, pg/g	1821
Relative standard deviation, %	20
No. of values reported	63
No. of values removed	1
No. of reported non-detects	0

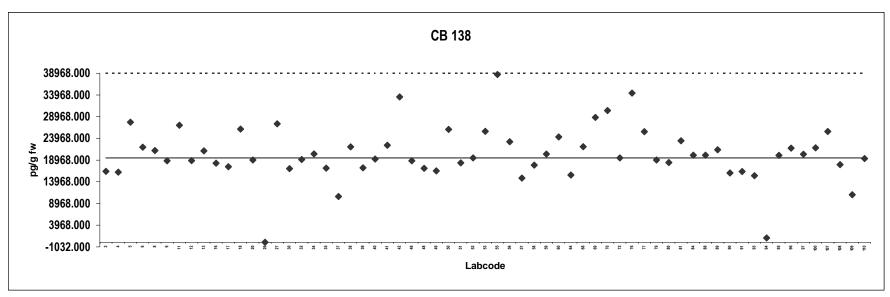


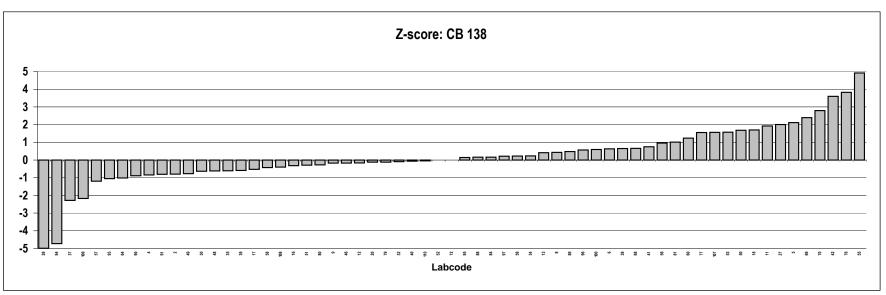


Congener: CB 138

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	16360		79	19000	
4	16200		80	18410	
5	27704		81	23412	
6	21950		84	20106	
8	21150		88	20100	
9	18800		89	21345	
11	26989		90	16000	
12	18839		91	16320	
13	21103		93	15390	
16	18248		94	1042	
17	17437		95	20042	
18	26100		96	21700	
20	19000		97	20329	
26	24		100	21791	
27	27300		107	25565	
30	17000		108	17900	
32	19112		109	11000	
34	20400		110	19305	
35	17100				
37	10573				
38	22000				
39	17180				
40	19213				
41	22390				
42	33500				
46	18814				
48	17065				
49	16480				
50	26010				
51	18337				
52	19460				
53	25600				
55	38661				
56	23200				
57	14810				
58	17810				
59	20364				
60	24300				
64	15523				
68	22041				
69	28800				
70	30378				
72	19484				
76	34387				
77	25517				

Consensus median, pg/g	19484
Median all values pg/g	19484
Consensus mean, pg/g	20341
Standard deviation, pg/g	6279
Relative standard deviation, %	31
No. of values reported	63
No. of values removed	0
No. of reported non-detects	0



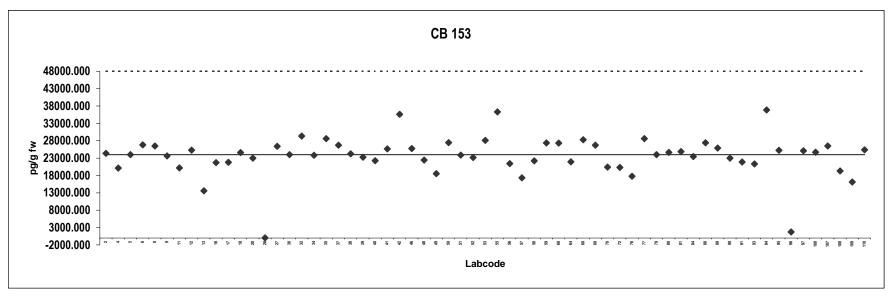


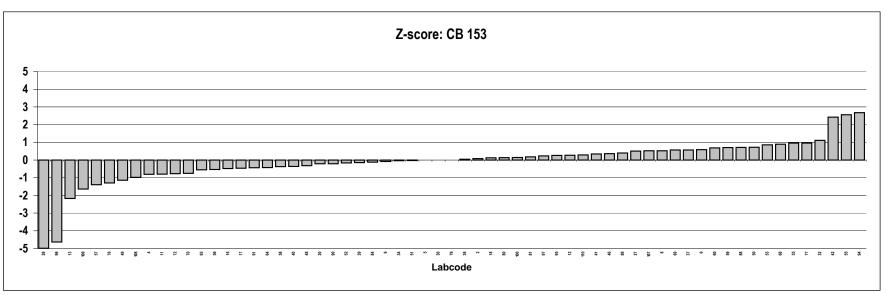
Congener: CB 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	24350		79	24000	
4	20100		80	24630	
5	23968		81	24850	
6	26822		84	23416	
8	26500		88	27400	
9	23600		89	25901	
11	20150		90	23000	
12	25294		91	21890	
13	13574		93	21333	
16	21672		94	36832	
17	21763		95	25238	
18	24600		96	1744	
20	23000		97	25117	
26	28		100	24686	
27	26400		107	26478	
30	24000		108	19300	
32	29341		109	16100	
34	23800		110	25376	
35	28600				
37	26713				
38	24200				
39	23265				
40	22227				
41	25640				
42	35600				
46	25721				
48	22440				
49	18506				
50	27436				
51	23830				
52	23180				
53	28100				
55	36292				
56	21400				
57	17290				
58	22176				
59	27364				
60	27300				
64	21934				
68	28266				
69	26700				
70	20387				
72	20300				
76	17773				
77	28601				

	(	Cor	isen	us	sta	tis	tics
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	24000
Consensus median, pg/g	24000
Median all values pg/g	24000
Consensus mean, pg/g	23611
Standard deviation, pg/g	5862
Relative standard deviation, %	25
No. of values reported	63
No. of values removed	0
No. of reported non-detects	0

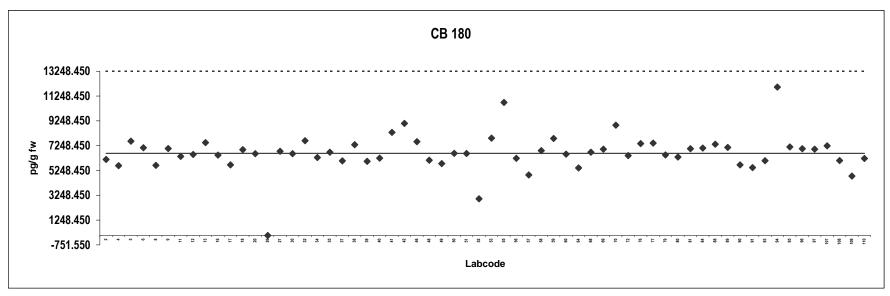


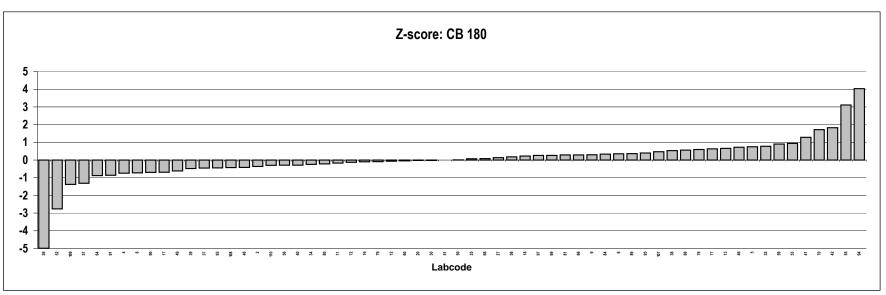


Congener: CB 180

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	6140		79	6500	
4	5630		80	6329	
5	7616		81	7002	
6	7086		84	7057	
8	5665		88	7360	
9	7010		89	7101	
11	6390		90	5700	
12	6533		91	5475	
13	7491		93	6031	
16	6485		94	11965	
17	5705		95	7145	
18	6920		96	7006	
20	6600		97	6962	
26	7.8		107	7236	
27	6800		108	6050	
30	6600		109	4800	
32	7652		110	6217	
34	6290				
35	6720				
37	6021				
38	7320				
39	5986				
40	6236				
41	8320				
42	9040				
46	7577				
48	6072				
49	5807				
50	6628				
51	6621				
52	2960				
53	7860				
55	10737				
56	6230				
57	4881				
58	6854				
59	7823				
60	6560				
64	5459				
68	6725				
69	6970				
70	8895				
72	6454				
76	7415				
77	7456				

Consensus median, pg/g	6624
Median all values pg/g	6624
Consensus mean, pg/g	6680
Standard deviation, pg/g	1534
Relative standard deviation, %	23
No. of values reported	62
No. of values removed	0
No. of reported non-detects	0

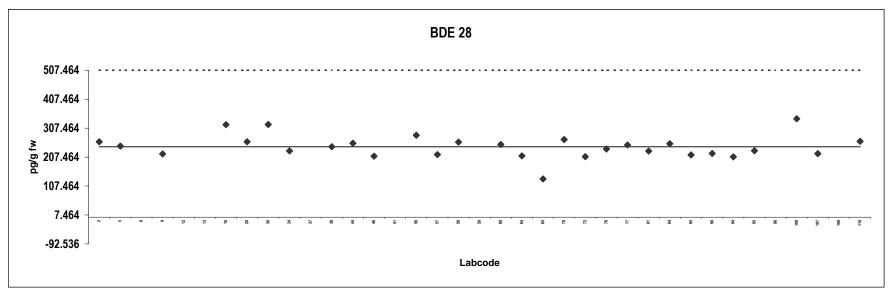


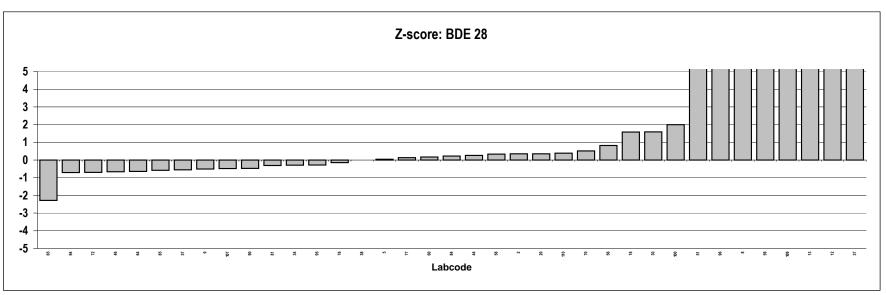


Congener: BDE 28

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
	260	Notes	Lab code	Conc. pg/g iw.	Notes
2 5	245				
8	610	Outlier			
9	218	Outlief			
12	838	Outlier			
13	816	Outlier			
	320	Outlief			
16	320				
20	260				
30	320				
34	229	0.41			
37	893	Outlier			
38	243				
44	255				
46	211	0 41			
51	510	Outlier			
56	283				
57	216				
58	259				
59	641	Outlier			
60	251				
64	211				
65	132				
70	268				
72	209				
76	236				
77	249				
81	228				
84	254				
85	215				
90	220				
94	208				
95	229				
96	552	Outlier			
100	340				
107	220				
109	650	Outlier,ND			
110	262				
1					

243
254
243
40
17
37
8
1

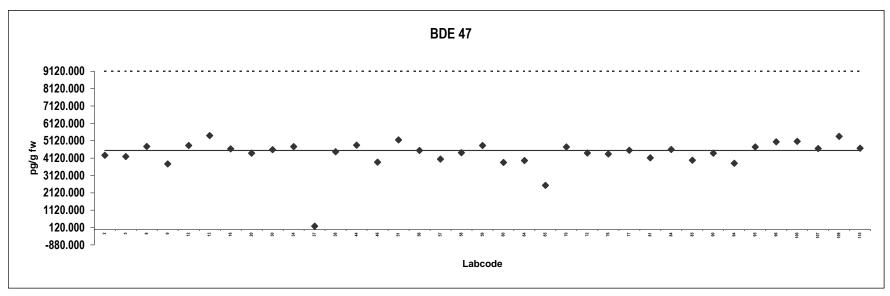


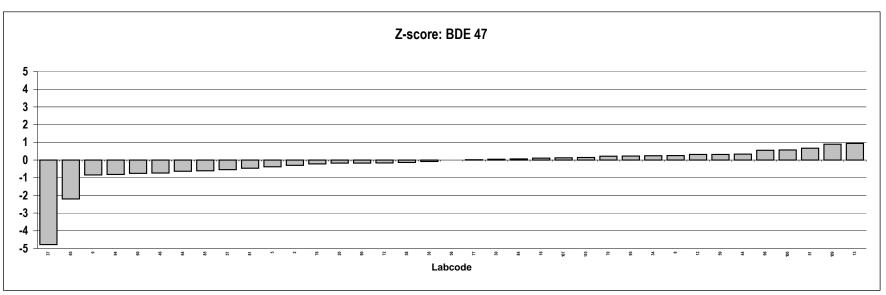


Congener: BDE 47

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
2	4280				
5	4209				
8	4790				
9	3785				
12	4841				
13	5416				
16	4651				
20	4400				
30	4600				
34	4775				
37	197				
38	4480				
44	4859				
46	3884				
51	5164				
56	4560				
57	4064				
58	4432				
59	4847				
60	3870				
64	3981				
65	2550				
70	4756				
72	4410				
76	4355				
77	4569				
81	4131				
84	4616				
85	3999				
90	4400				
94	3817				
95	4758				
96	5058				
100	5079				
107	4668				
109	5370				
110	4689				

Consensus median, pg/g	4560
Median all values pg/g	4560
Consensus mean, pg/g	4360
Standard deviation, pg/g	879
Relative standard deviation, %	20
No. of values reported	37
No. of values removed	0
No. of reported non-detects	0

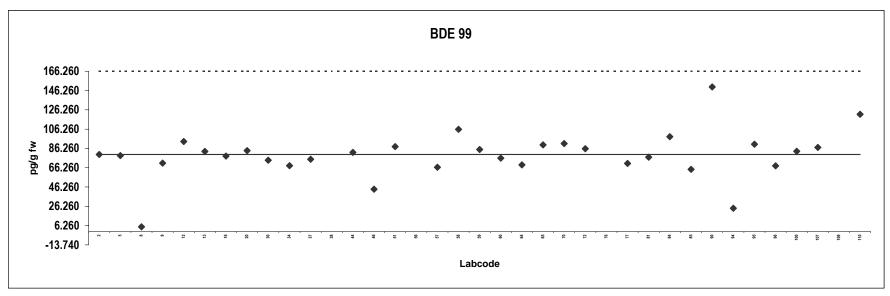


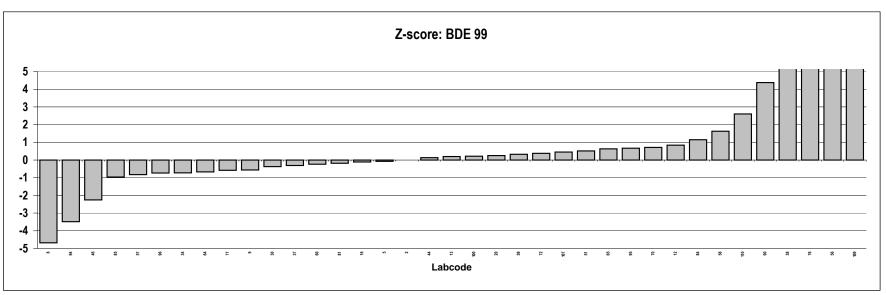


Congener: BDE 99

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
	80				
2 5 8	79				
8	5.0	ND			
9	71				
12	93				
13	83				
16	78				
20	84				
30	74				
34	68				
37	75				
38	174	Outlier			
44	82				
46	44				
51	88				
56	455	Outlier			
57	67				
58	106				
59	85				
60	76				
64	69				
65	90	ND			
70	91				
72	86				
76	244	Outlier			
77	71				
81	77				
84	98				
85	65				
90	150				
94	24				
95	91				
96	68				
100	83				
107	87				
109	650	Outlier,ND			
110	122				
1					
1					

Consensus median, pg/g	80
Median all values pg/g	83
Consensus mean, pg/g	79
Standard deviation, pg/g	25
Relative standard deviation, %	31
No. of values reported	37
No. of values removed	4
No. of reported non-detects	3

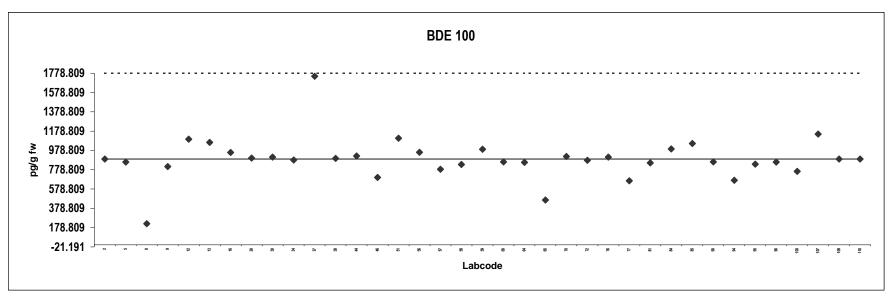


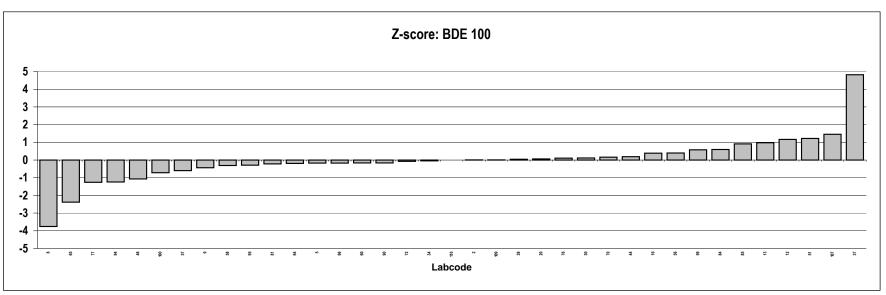


Congener: BDE 100

Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
2	890				
5 8	858				
8	220				
9	812				
12	1096				
13	1062				
16	957				
20	900				
30	910				
34	880				
37	1747				
38	897				
44	922				
46	699				
51	1105				
56	960				
57	783				
58	834				
59	991				
60	860				
64	854				
65	465				
70	917				
72	876				
76	909				
77	664				
81	850				
84	995				
85	1050				
90	860				
94	669				
95	837				
96	858				
100	761				
107	1148				
109	890				
110	889				
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889
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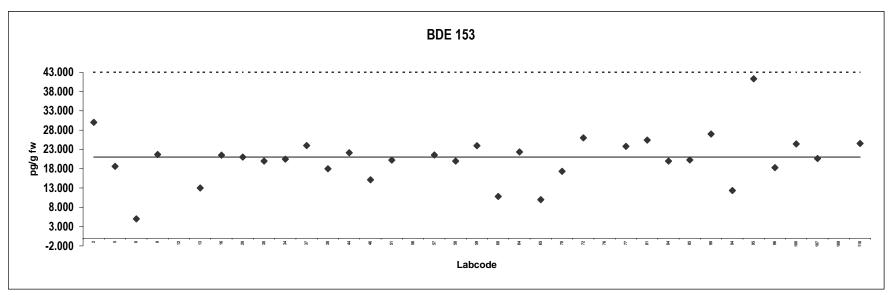


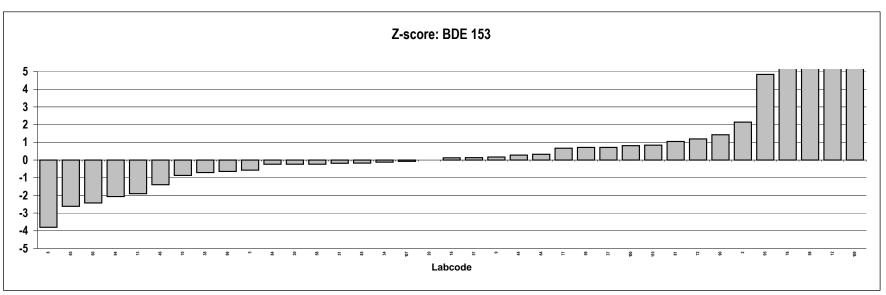


Congener: BDE 153

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
	30	11000	Eus couc	conc. pg/g 1	11000
2 5 8	19				
8	5.0	ND			
9	22	·			
12	70	Outlier			
13	13				
16	22				
20	21				
30	20				
34	21				
37	24				
38	18				
44	22				
46	15				
51	20				
56	57	Outlier			
57	22				
58	20				
59	24				
60	11				
64	22				
65	10	ND			
70	17				
72	26	0 11 170			
76	50	Outlier,ND			
77	24				
81	25				
84 85	20 20				
90	20 27				
90	12				
95	41				
96	18				
100	24				
107	21				
109	650	Outlier,ND			
110	25	Outlier,14D			
110	23				
1					
1					

21
22
21
6.4
31
37
4
4

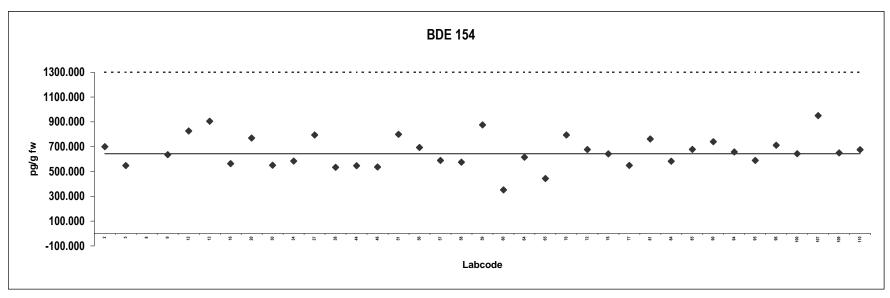


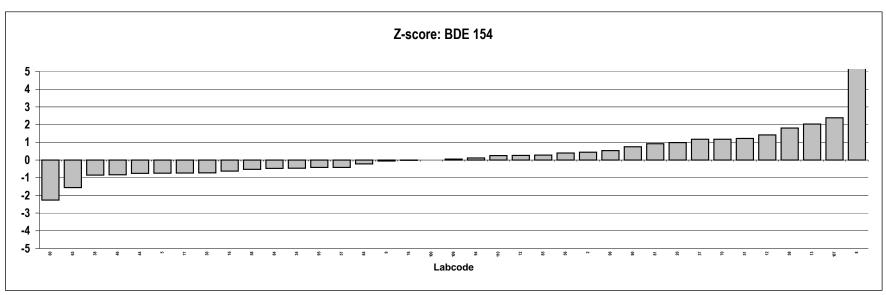


Congener: BDE 154

Total Content   Figure   Figure   Total Content   Figure   F	Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
8	2		Tiotes	Lab couc	Conc. pg/g iw.	110105
8   1570   Outlier   9   636   12   826   13   905   16   563   20   770   30   550   34   584   37   794   38   533   44   546   46   536   51   800   56   694   57   589   58   575   59   876   60   352   64   615   65   443   70   795   72   677   76   642   77   549   81   762   84   582   85   679   90   740   94   658   95   589   96   712   100   643   107   950   109   650   ND	5					
9 636 12 826 13 905 16 563 20 770 30 550 34 584 37 794 38 533 44 546 46 536 51 800 56 694 57 589 58 575 59 876 60 352 64 615 65 443 70 795 72 677 76 642 77 549 81 762 84 582 85 679 90 740 94 658 95 589 96 712 100 643 107 955 109 650 ND	8	1570	Outlier			
12	9	636				
13	12	826				
16	13	905				
20		563				
30	20	770				
34	30	550				
37		584				
38	37	794				
46	38	533				
51       800         56       694         57       589         58       575         59       876         60       352         64       615         65       443         70       795         72       677         76       642         77       549         81       762         84       582         85       679         90       740         94       658         95       589         96       712         100       643         107       950         109       650       ND	44	546				
56 694 57 589 58 575 59 876 60 352 64 615 65 443 70 795 72 677 76 642 77 549 81 762 84 582 85 679 90 740 94 658 95 589 96 712 100 643 107 950 109 650 ND		536				
57	51	800				
58	56	694				
59       876         60       352         64       615         65       443         70       795         72       677         76       642         77       549         81       762         84       582         85       679         90       740         94       658         95       589         96       712         100       643         107       950         109       650       ND	57	589				
60 352 64 615 65 443 70 795 72 677 76 642 77 549 81 762 84 582 85 679 90 740 94 658 95 589 96 712 100 643 107 950 109 650 ND		575				
64 615 65 443 70 795 72 677 76 642 77 549 81 762 84 582 85 679 90 740 94 658 95 589 96 712 100 643 107 950 109 650 ND	59	876				
65 443 70 795 72 677 76 642 77 549 81 762 84 582 85 679 90 740 94 658 95 589 96 712 100 643 107 950 109 650 ND	60	352				
70		615				
72 677 76 642 77 549 81 762 84 582 85 679 90 740 94 658 95 589 96 712 100 643 107 950 109 650 ND	65	443				
76 642 77 549 81 762 84 582 85 679 90 740 94 658 95 589 96 712 100 643 107 950 109 650 ND	70	795				
77	72	677				
81 762 84 582 85 679 90 740 94 658 95 589 96 712 100 643 107 950 109 650 ND	76	642				
84 582 85 679 90 740 94 658 95 589 96 712 100 643 107 950 109 650 ND	77	549				
85 679 90 740 94 658 95 589 96 712 100 643 107 950 109 650 ND		762				
90 740 94 658 95 589 96 712 100 643 107 950 109 650 ND	84	582				
94 658 95 589 96 712 100 643 107 950 109 650 ND	85	6/9				
95 589 96 712 100 643 107 950 109 650 ND		/40				
96 712 100 643 107 950 109 650 ND		658				
100 643 107 950 109 650 ND	95	589 712				
107 950 109 650 ND	100	712				
109 650 ND	100	043				
110 676 ND	107	930 650	ND			
		630	ND			
	110	070				

Consensus median, pg/g	643
Median all values pg/g	650
Consensus mean, pg/g	659
Standard deviation, pg/g	128
Relative standard deviation, %	19
No. of values reported	37
No. of values removed	1
No. of reported non-detects	1





Congener: BDE 183

ſ	Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
ŀ	2	10	ND	Lab couc	Conc. pg/g iw.	110103
	5	20	Outlier,ND			
	8	5.0	ND			
	9	4.6	1,12			
	12	133	Outlier			
	13	2.1				
	16	6.0	ND			
	20	5.9				
	30	9.0				
	34	7.5				
	37	2.0				
	38	7.9				
	44	5.0				
	46	11				
	51	6.2	ND			
	56	7.9				
	57	7.2				
	58	5.5				
	59	3.7				
	60	4.0	ND			
	64	9.6				
	65	2.6				
	70	3.6				
	72	4.0				
	76	50	Outlier,ND			
	77	5.5				
	81	7.7				
	84	5.8				
	85	5.6				
	90	8.2	ND			
	94	1.6				
	95	34	Outlier			
	96	3.7				
	107	4.9				
	109	1300	Outlier,ND			
	110	7.0				
I						
1						
1						
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L			li .			

# Consensus median, pg/g 5.5 Median all values pg/g 6.0 Consensus mean, pg/g 5.8 Standard deviation, pg/g 2.4 Relative standard deviation, % 41 No. of values reported 36

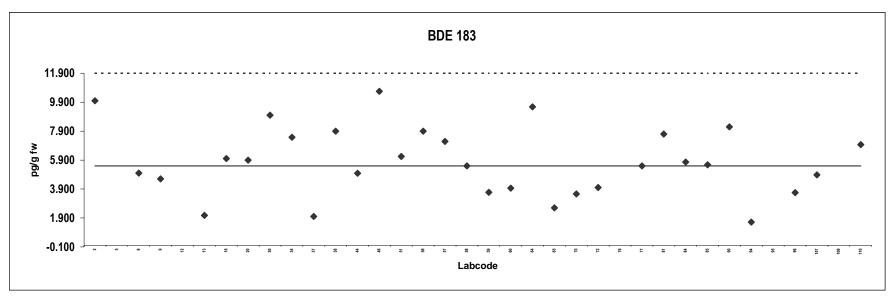
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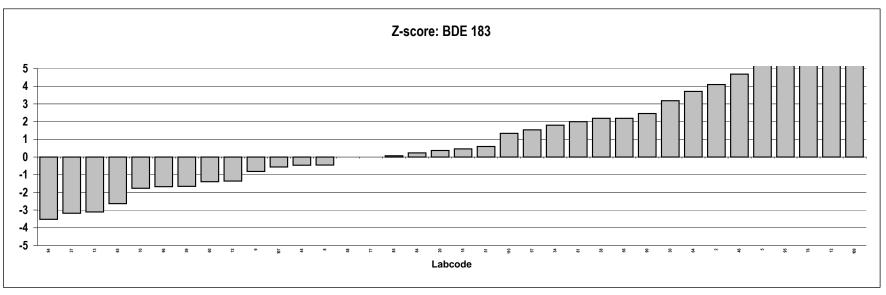
9

Consenus statistics

No. of values removed

No. of reported non-detects

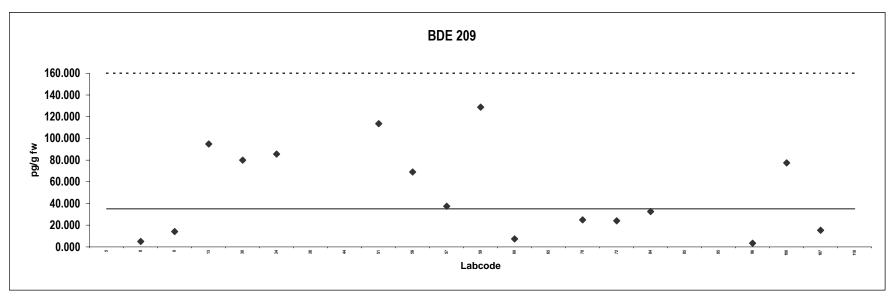


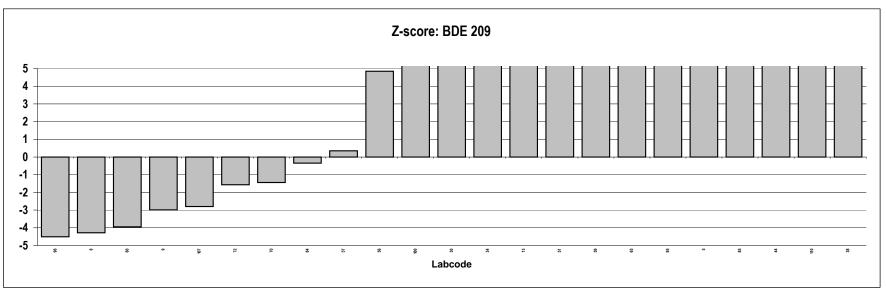


Cod liver oil Congener: BDE 209

Lab code		Notes	Lab code	Conc. pg/g fw.	Notes
5	320	Outlier,ND			
8	5.0	ND			
9	14				
13	95				
30	80	ND			
34	86				
38	1150	Outlier			
44	635	Outlier			
51	114	ND			
56	69	ND			
57	37	ND			
59	129				
60	7.4	ND			
60	7.4	ND ND			
65	200	Outlier,ND			
70	25				
72	24				
84	33				
85	349	Outlier			
95	250	Outlier			
96	3.4	ND			
100	77				
107	15				
110	1087	Outlier			
1					
1					
1					

G " '	25
Consensus median, pg/g	35
Median all values pg/g	80
Consensus mean, pg/g	51
Standard deviation, pg/g	41
Relative standard deviation, %	82
No. of values reported	23
No. of values removed	7
No. of reported non-detects	8

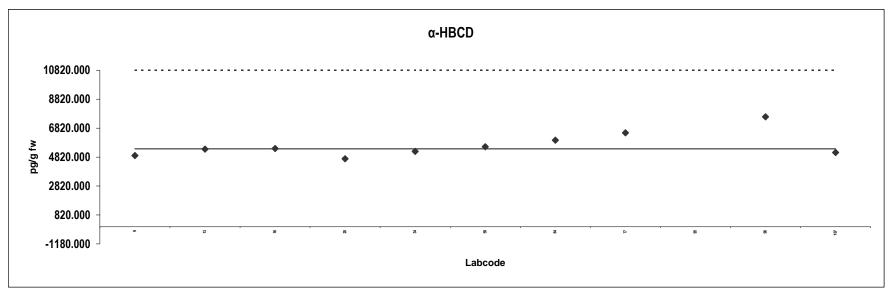


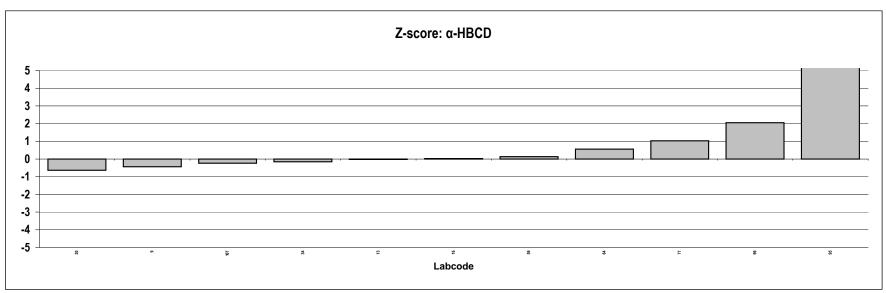


Congener: α-HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
9 13 16 20 34 59 64 77 95 96 107	4921 5369 5410 4700 5215 5530 5991 6500 12274 7597 5132	Outlier			

Consensus median, pg/g	5390
Median all values pg/g	5410
Consensus mean, pg/g	5637
Standard deviation, pg/g	861
Relative standard deviation, %	15
No. of values reported	11
No. of values removed	1
No. of reported non-detects	0

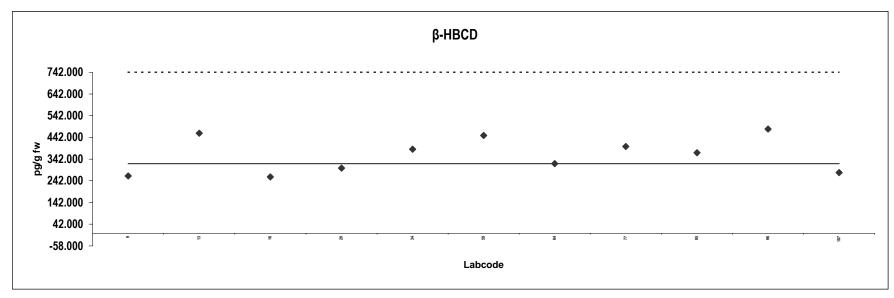


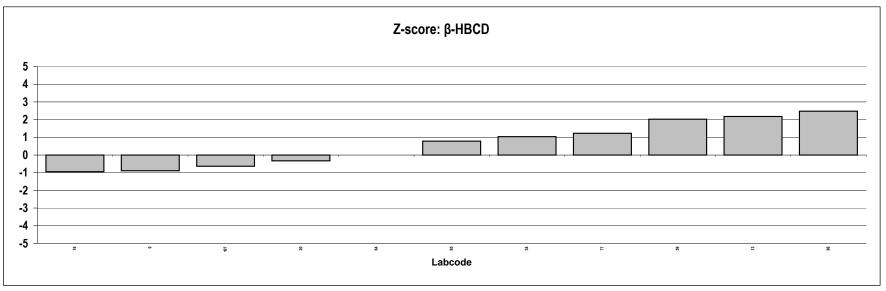


# Cod liver oil Congener: β-HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
9 13 16 20 34	264				
13	461				
20	200 300				
34	461 260 300 388				
59	451 321				
64 77	321				
77	400	ND			
95 96 107	400 371 480 280	ND			
96 107	480 280				
107	200				

Consensus median, pg/g	321
Median all values pg/g	371
Consensus mean, pg/g	361
Standard deviation, pg/g	81
Relative standard deviation, %	22
No. of values reported	11
No. of values removed	0
No. of reported non-detects	2

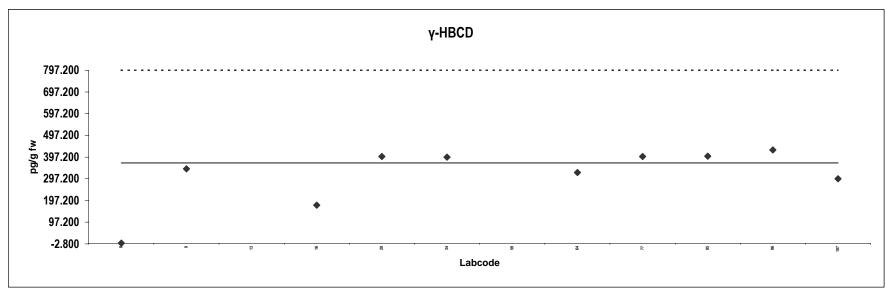


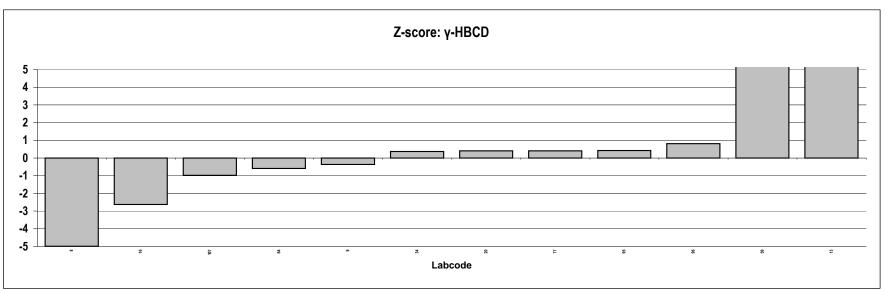


**Congener:** γ-HBCD

Lab code	Conc. pg/g fw.	Notes	Lab code	Conc. pg/g fw.	Notes
8	1.0	ND		reserve	- 10 10 1
8 9	343				
13	1610	Outlier			
16 20	176 400				
34	397				
59	1401	Outlier			
64	326				
77	400	ND			
95	401				
96 107	430 297				
107	291				

Consensus median, pg/g Median all values pg/g	370 399
Consensus mean, pg/g Standard deviation, pg/g	317 134
Relative standard deviation, % No. of values reported No. of values removed	42 12 2
No. of reported non-detects	2

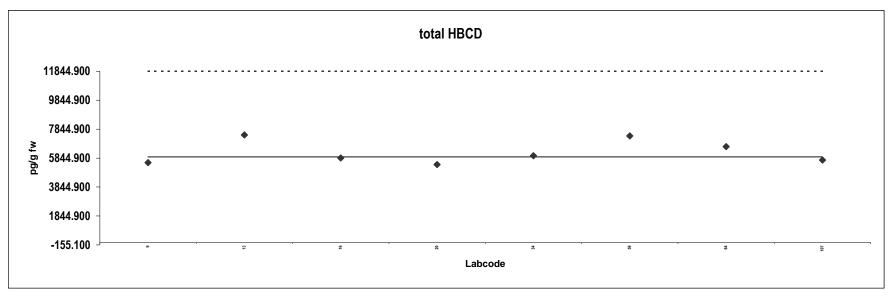


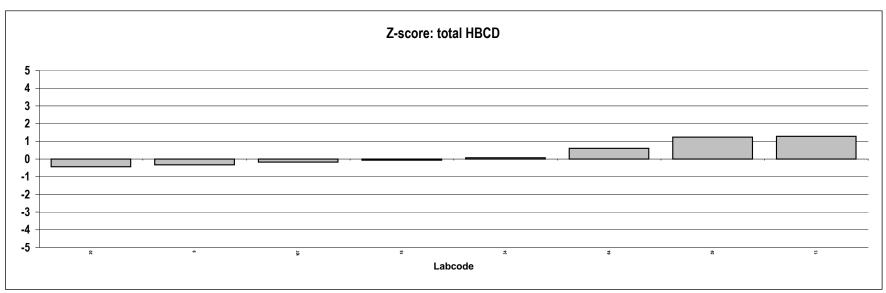


**Congener: total HBCD** 

					Conge
Lab code	Conc. pg/g fw. 5528	Notes	Lab code	Conc. pg/g fw.	Notes
9 13	5528				
13	7440				
16	5845				
20 34 59	5400				
34 50	6000				
59	7382				
64 107	6638 5710				
107	3/10				

Consensus median, pg/g	5922
Median all values pg/g	5922
Consensus mean, pg/g	6243
Standard deviation, pg/g	812
Relative standard deviation, % No. of values reported No. of values removed No. of reported non-detects	13 8 0 0





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