2010 GLHHFTS Fish Tissue Data Dictionary for Mercury, PFC, PBDE, and PCBs
September 2014

The Office of Science and Technology (OST) is providing the fish tissue results from the 2010 Great Lakes Human Health Fish Tissue Study (GLHHFTS). The specific analyses include:

- Mercury
- Polybrominated diphenyl ethers (PBDEs)
- Polychlorinated biphenyls (PCBs)
- Perfluorinated compounds (PFCs)

This document includes the "data dictionary" for each type of contaminant analysis. The field names and descriptions for the analytical results are similar for each type of analysis, but some analyses include additional information that may not apply to all analysis types. OST is also providing information on the fish composite samples collected during the study and used to create the fillet tissue samples that were analyzed. The sample information for each file is identical, so only one version of the dictionary for the sample information is provided after the dictionary for the results for each type of analysis.

Data Tabs for Mercury, PBDEs, PCBs, and Perfluorinated Compounds	
Field Name	**Description**
EPA Region	The EPA Region in which the sample was collected.
State	USPS 2-letter abbreviation for the state in which the sample was collected.
Lake Name	Name of the Great Lake from which the sample was collected.
Site ID	The identifier assigned by EPA to the site. The first six characters are "NCCAGL," for National Coastal Condition Assessment in the Great Lakes (of which the GLHHFTS is a part), the next two are the site selection year (10), followed by either the 4-digit site location, or for sites in Illinois, a 9-character site location that begins with "QLM."
EPA Sample ID	Unique 6-digit number assigned by EPA.
% Lipids	Applies only to the PBDE and PCB results. The percentage of lipids in the sample determined by the sample processing laboratory.
Analyte	Common name or abbreviation for the analyte. For the PBDEs, the abbreviation "BDE" (for brominated diphenyl ether) is followed by the congener number (i.e., "BDE-7"). It is not practical to completely separate all of the target PBDE congeners from one another, so congeners that elute from the gas chromatograph together are listed with a forward slash between each congener, in increasing congener number order, e.g., BDE-12/BDE-13. "Summed PBDEs (52)" is the name given to the sum of the results for the 52 congeners and coeluting congener groups reported in the sample. This value was calculated by OST, using zero for any congener result that was "not detected" at the method detection limit. The PBDE data also include two other brominated analytes: HBB = Hexabromobenzene and PBEB = Pentabromoethylbenzene. For the PCBs, the abbreviation "PCB" is followed by the congener number (i.e., "PCB-7"). It is not practical to completely separate all 209 PCB congeners from one another, so congeners that elute from the gas chromatograph together are listed with a forward slash between each congener, in increasing congener number order, e.g., PCB-12/PCB-13. "Total PCBs" is the name given to the sum of the results for all 209 of the congeners (which includes the coeluting congener groups) reported in the sample. This value was calculated by OST, using zero for any congener result that was "not detected" at the method detection limit. For the PFCs, the analyte names are those of the anion form of the analyte (e.g., the "ate" form).
CAS Number	Chemical Abstracts Service Registry Number assigned by CAS to the analyte. Seven of the PBDE congeners do not have CAS Numbers at this time, and are listed as "NA" for "not available." CAS Numbers also do not exist for the groups of coeluting PBDE congeners and the groups of coeluting PCB congeners. For the PFCs, this is the CAS Number of the parent acid or amide form, since the anions do not have separate CAS Numbers.

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Field Name	**Description**
Amount	Concentration of the analyte, if detected. If this field is blank, then the analyte was not detected in the sample. In order to accommodate the range of concentrations in these samples, all of the results are presented with the same number of decimal places for an analyte class. For mercury, the amount field is presented to one decimal place. For the PBDEs and PCBs, the amount fields are presented to 5 decimal places. For PFCs, the amount field is presented to 2 decimal places. However, these results have at most 3 significant figures, regardless of the number of decimal places (e.g., a PBDE value of 1.84000 does not imply 6 significant figures and a PFC value of 19.00 does not imply 4 significant figures).
EPA HH Screening Value or HH Screening Value	The human health (HH) screening value (SV) used by OST for interpretation of the results. When the value comes from an EPA source, it is labeled as the EPA HH Screening Value. When the value is from a non-EPA source, it is labeled as the HH Screening Value. The sources of all of the screening values are described below. • For mercury, OST used a screening value of 300 ng/g, which is EPA's tissue-based Water Quality Criterion for methylmercury. • For the PBDEs, OST used a screening value of 210 ng/g for Summed PBDEs (52), derived by the California Environmental Protection Agency. • For the PCBs, OST used a screening value of 12 ng/g for Total PCBs, derived from the EPA Guidance for Assessing Chemical Contaminant Data for Use in Fish Advisories, Volume 2 (2000). • For the PFC data, OST used a screening value of 40 ng/g for PFOS, derived by the Minnesota Department of Health.
Over HH SV?	OST's assessment of the results for the analyte relative to the HH screening value, as either "Exceeds SV" or "Does not exceed SV".
GL HH 1 Meal/Mo Screening Value	Applies only to mercury and PCBs. The Great Lakes Sport Fish Advisory Task Force (1993) human health screening value for consumption of 1 meal per month (1 Meal/Mo) for mercury is 220 ng/g, and for Total PCBs is 210 ng/g.
Over GL HH 1 Meal/Mo SV?	Applies only to mercury and PCBs. OST's assessment of the results for the analyte relative to the GL 1 Meal/Mo human health screening value, as either "Exceeds SV" or "Does not exceed SV".
GL HH 1 Meal/Wk Screening Value	Applies only to mercury and PCBs. The Great Lakes Sport Fish Advisory Task Force (1993) human health screening value for consumption of 1 meal per week (1 Meal/Wk) for mercury is 110 ng/g, and for Total PCBs is 60 ng/g.
Over GL HH 1 Meal/Wk SV?	Applies only to mercury and PCBs. OST's assessment of the results for the analyte relative to the GL 1 Meal/Wk human health screening value, as either "Exceeds SV" or "Does not exceed SV".
Unit 1	The weight/weight units, ng/g.
Unit 2	The "parts per billion" notation ppb, which is equivalent to ng/g.
MDL	The nominal method detection limit for the analyte, based on the procedure in 40 CFR part 136, not adjusted for actual sample size, in the units shown in the Units column. For mercury, MDLs are reported to 2 decimal places (1 more place than the amount). For PBDEs and PCBs, MDLs are reported to 6 decimal places (1 more place than the amount). For PFCs, MDLs are reported to 3 decimal places (1 more place than the amount).
QL	The nominal quantitation limit (QL) or "Minimum Level" for the analyte, based on the lowest calibration standard analyzed, not adjusted for sample size, in the units shown in the Units column. QLs are presented to the same number of decimal places as the MDL values.

Data Tabs for Mercury, PBDEs, PCBs, and Perfluorinated Compounds	
Field Name	**Description**
Lab Qualifier Flag	The data qualifier flag(s) applied by the laboratory. For mercury, no lab qualifier flags were applied. For the other analytes, the following flags were used, either singly or in combination: U = Not detected B = Analyte also present in the method blank J = Estimated value (between the MDL and QL values) For the PBDEs, the following additional flags were used, either singly or in combination: E = Original result exceeded the calibration range; reported result is from a dilution. M = Manual integration of the instrument response. R = Ion abundance ratio is outside of the acceptance limits, but the analyte meets all the other identification criteria. For the PCBs, the following additional flags were used, either singly or in combination: C = Analyte is a coeluting group of congeners. D = Result is from a diluted analysis. G = Evidence of a disturbance with the lock-mass used during the analysis K = Ion abundance ratio is outside of the acceptance limits, but the analyte meets all the other identification criteria.
SCC Code	Qualifiers applied by the Sample Control Center staff at CSC during data validation. *For mercury, no SCC codes were applied.* The individual SCC codes applied to the other results (PBDEs, PCBs, and PFCs) are identified and defined in the table of SCC codes below.
Comments	A text translation of the SCC code combinations applied to each result. *For mercury, no SCC codes were applied, so no comments were needed.*
Sort Order	Applies only to PBDEs, PCBs, and PFCs. A field used to sort the analyte names in a consistent order within each analyte class. For the PBDEs, the values range from 1 to 49. For PCBs, the values in this field range from 1 to 160. For PFCs, the values in this field range from 1 to 13.

Sample Information Tab for All Analytes	
Field Name	**Description**
EPA Region	The EPA Region in which the sample was collected.
State	USPS 2-letter abbreviation for the state in which the sample was collected.
Lake Name	Name of the Great Lake from which the sample was collected.
Latitude	Latitude, in decimal format, to 5 decimal places.
Longitude	Longitude, in decimal format, to 5 decimal places.
Sample Date	Actual sampling date, in MM/DD/YYYY format.
Site ID	The identifier assigned by EPA to the site. The first six characters are "NCCAGL," for National Coastal Condition Assessment in the Great Lakes (of which the GLHHFTS is a part), the next two are the site selection year (10), followed by either the 4-digit site location, or for sites in Illinois, a 9-character site location that begins with "QLM."
EPA Sample ID	Unique 6-digit number assigned by EPA.
Specimen ID	The 6-digit EPA Sample ID, followed by a decimal point and a value between 1 and 10. The decimal portion identifies the number assigned to the individual fish specimen in the composite sample.
Spec Sort	A specimen sorting field designed to account for the fact that samples with more than 9 specimens do not sort properly (i.e., XX.10 sorts before XX.2).
Species - Scientific Name	Latin name (Genus and species) based on Nelson *et al.* (2004), *Common and Scientific Names of Fishes from the United States, Canada, and Mexico*, Sixth Edition.
Species - Common Name	Generally accepted common name based on Nelson *et al.* (2004).
Family	Latin name of the Family based on Nelson *et al.* (2004).
Tissue Type	The type of fish tissue used to prepare the sample. For the GLHHFTS, all of the samples were prepared from fillet tissue.
Total Length (mm)	Length of each individual specimen in millimeters (mm).
Included in composite?	This field indicates if the specimen was included in the tissue sample for analysis or not. The options are either "Yes" or "No" and the rationale is explained in the "Instructions" field to the far right.
Predator or Bottom Dweller	Classification of the species as either: P = Predator species, or BD = Bottom-dweller species
Composite Classification	Routine vs. Non-routine composite, based on the fish composite sample criteria specified in the human health fish sampling procedures.
Deviation	For non-routine composites, the nature of the deviation from the criteria (e.g., number of fish, fish length, or both).
Instructions	Instructions from EPA/OW/OST to the sample preparation laboratory regarding which specimens to include in the fillet composite sample for analysis, based on specimen length, species, etc.

Individual SCC Codes Applied to the 2010 GLHHFTS Results		
SCC Code	**Comments**	**Implication**
B, RMAX	Blank Contamination, Result is a Maximum Value	Blank contamination was observed and the target analyte was reported in the sample at a concentration between 5 and 10 times higher than the blank value. The result was considered to be of acceptable quality, but data users are cautioned that it may be a maximum value due to possible influence of contamination.
B, RNAF	Blank Contamination, Result is Not Affected	Blank contamination was present but was not considered to adversely impact the sample result. The presence of the analyte in the blank is not considered to adversely affect the data in cases where the sample results are more than 10 times the associated blank results or where the analyte is not detected in associated samples.
B, RNON	Blank Contamination, Result Reported as a Non-detect	When the sample result is less than five times the blank result, there are no means by which to ascertain whether or not the presence of the analyte may be attributed to contamination. Therefore, the result is reported in the database as a non-detect at the MDL, adjusted for sample size and dilution.
HIAR, J	High Ion Abundance Ratio, Estimated	Each analyte is identified and quantified based on the instrumental response for two specific ions and the ratio of those two ions was above the upper acceptance limit, suggesting a potential interference that may affect the sample result. Therefore, the result also is flagged as an estimated value.
HLBL, RNAF	High Labeled Compound Recovery, Result is Not Affected	The labeled analog of the target analyte was recovered above acceptance criteria, suggesting the possible presence of matrix interferences. Isolated instances of high recovery are not uncommon, and patterns across multiple samples are more of a concern. If the analyte was not detected in a field sample, there is no concern and the RNAF is added to the HLBL flag.
HLCS	High Lab Control Sample Recovery	The lab control sample (LCS) was a clean reference matrix. If recovery in the LCS was high, there may be a high bias for that analyte.
HLCS, RNAF	High Lab Control Sample Recovery, Result is Not Affected	The recovery in the LCS was high, but the analyte was not detected in the associated tissue sample, so there was no high bias concern and the RNAF flag was applied.
HMSR	High Matrix Spike Recovery	High matrix spike (MS) recovery indicated a positive interference or a high bias. Isolated instances of high recovery are not uncommon, and patterns across multiple MS samples are more of a concern. When high matrix spike recovery was observed for an analyte, the results for that analyte were qualified in all of the samples in the batch with the matrix spike sample.
HMSR, RNAF	High Matrix Spike Recovery, Result is Not Affected	High matrix spike (MS) recovery indicated a positive interference or a high bias, but the analyte was not detected in the sample, so there was no high bias concern for the specific sample and the RNAF flag was applied.
HRPD, J	High RPD, Estimated	The relative percent difference (RPD) between the results in the parent sample and the laboratory duplicate is above the acceptance limit. This may be due to inhomogeneity in the bulk sample or analytical variability. When high RPD was observed for an analyte, all the detected results for that analyte in any of the samples in the batch with the duplicate sample were qualified as estimated values.
HRPD, RNAF	High RPD, Result is Not Affected	The relative percent difference (RPD) between the results in the parent sample and the laboratory duplicate is above the acceptance limit. This may be due to inhomogeneity in the bulk sample or analytical variability. However, when high RPD was observed for an analyte, the non-detected results for that analyte were not affected, and the RNAF flag was applied.
HVER, J	High CALVER, Estimated	The results for the calibration verification associated with the analyte were above the acceptance limit, suggesting a possible high bias. Detected analytes also are considered estimated values.
HVER, RNAF	High CALVER, Result is Not Affected	The results for the calibration verification associated with the analyte were above the acceptance limit, suggesting a possible high bias, but the analyte was not detected in the associated tissue sample, so there is no high bias concern and the RNAF flag is applied.

Individual SCC Codes Applied to the 2010 GLHHFTS Results		
SCC Code	**Comments**	**Implication**
J	Estimated	When applied alone, this code indicates that the result is at or above the MDL, but below the QL. This flag also may be applied in conjunction with other flags to indicate the potential for greater uncertainty.
LIAR, J	Low Ion Abundance Ratio, Estimated	Each analyte is identified and quantified based on the instrumental response for two specific ions and the ratio of those two ions was below the lower acceptance limit, suggesting a potential interference that may lower the sample result. Therefore, the result also is flagged as an estimated value.
LLBL	Low Labeled Compound Recovery	The labeled analog of the target analyte was recovered below acceptance criteria, suggesting the possible presence of matrix interferences or incomplete recovery of both the labeled compound and target analyte during the extract cleanup processes used in the analytical procedure. The use of isotope dilution quantitation automatically corrects the results for the target analyte, even when the labeled compound recovery is below expectations.
LLCS	Low LCS result	The lab control sample (LCS) was a clean reference matrix. If recovery in the LCS was low, there may be a low bias for that analyte. When low LCS recovery was observed for an analyte, the results for that analyte were qualified in all of the samples in the batch with the LCS.
LMSR	Low Matrix Spike Recovery	Low recovery in the matrix spike indicated a potential low bias for the analyte, possibly due to poor extraction efficiency in the sample matrix. Isolated instances of low recovery are not uncommon, and patterns across multiple MS samples are more of a concern. When low matrix spike recovery was observed for an analyte, the results for that analyte were qualified in all of the samples in the batch with the matrix spike sample.

Note: Commas are used to separate related parts of a single code (e.g., “B, RNON” is considered one code), while semicolons are used to separate different codes (e.g., “B, RNAF; J” is the combination of two codes).