**NCCA 2015 GLHHFFTS Fish Fillet Tissue Data Dictionary for Mercury, PCBs, PFAS, and PCDDs/PCDFs**
**November 2021**

The U.S. Environmental Protection Agency (EPA) Office of Science and Technology (OST) is providing the fish tissue results from the 2015 Great Lakes Human Health Fish Fillet Tissue Study (GLHHFFTS) conducted under the agency's National Coastal Condition Assessment (NCCA). The specific analyses include:

- Mercury
- Polychlorinated biphenyls (PCBs)
- Per- and polyfluoroalkyl substances (PFAS)
- Polychlorinated dibenzo-*p*-dioxins (PCDDs) and Polychlorinated dibenzofurans (PCDFs), also referred to as dioxins and furans

This file 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 samples collected during the study and used to prepare the fillet tissue samples that were analyzed. The fish sample information for each contaminant data file is identical, so only one version of the dictionary for the fish sample information is provided after the dictionary for the results for each type of contaminant analysis.

| **"Results" Tabs for Mercury, PCBs, PFAS, and PCDDs/PCDFs (also referred to as dioxins and furans)** | |
|---|---|
| **Field Name** | **Description** |
| EPA Region | The EPA Region in which the fish sample was collected. |
| State | USPS 2-letter abbreviation for the state in which the fish sample was collected. |
| Lake | Name of the Great Lake from which the fish sample was collected. |
| Site ID | The identifier assigned by EPA to the fish sample collection site. The first four characters are "GLNS," the next two are the site selection year (15), followed by the 4-digit site location. |
| EPA Sample ID | Unique 6-digit number assigned by EPA. |
| % Lipids | Data that is provided in the PCB and PCDD/PCDF (dioxin and furan) results tabs. The percentage of lipids measured in the fillet tissue sample. |
| Analyte (Chemical) | Common name or abbreviation for the analyte (or chemical).<br><br>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 fillet tissue sample. This value was calculated by OST, using zero for any congener that was "not detected" at the method detection limit.<br><br>For the PFAS, the analyte (or chemical) names are those of the anion form of the analyte (e.g., the "ate" form).<br><br>For PCDDs/PCDFs (dioxins and furans), the analyte (or chemical) names use the common abbreviations, such as "TCDD" for tetrachloro-dibenzo-*p*-dioxin. In addition, OST calculated the sum of the "toxic equivalents" (TEQ) for the 17 analytes, plus the TEQ attributable to the 12 World Health Organization (WHO) "toxic" (dioxin-like) PCB congeners, and the sum of those two TEQs as "Total TEQ." The three TEQ values are listed as separate analytes. |
| CAS Number | Chemical Abstracts Service (CAS) Registry Number assigned by CAS to the analyte.<br><br>CAS Numbers do not exist for the groups of coeluting PCB congeners.<br><br>For the PFAS, this is the CAS Number of the parent acid or amide form, since the anions do not have separate CAS Numbers.<br><br>For PCDDs/PCDFs (dioxins and furans), there are no CAS numbers for the TEQ values. |

| **"Results" Tabs for Mercury, PCBs, PFAS, and PCDDs/PCDFs (also referred to as dioxins and furans)** | |
|---|---|
| **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.<br><br>For mercury, the amount field is presented to one decimal place.<br>For PCBs, the amount field is presented to 6 decimal places.<br>For PFAS, the amount field is presented to 2 decimal places.<br>For PCDDs/PCDFs, the amount field is presented to 3 decimal places.<br><br>However, these results have at most 3 significant figures, regardless of the number of decimal places (e.g., a PFAS value of 19.00 does not imply 4 significant figures). |
| TEF | Toxicity Equivalency Factor that applies only to PCDDs/PCDFs and relates the toxicity of a given PCDD or PCDF to the toxicity of 2,3,7,8-TCDD, the most toxic congener. OST used the 2005 WHO TEF values to calculate TEQs. |
| Congener TEQ | The TEQ contribution for each PCDD/PCDF congener was calculated by OST as the product of the congener amount and the congener-specific TEF value. |
| Unit 1 | The weight/weight units, ng/g (Mercury, PCBs, and PFAS) or pg/g (PCDDs/PCDFs only). |
| Unit 2 | The "parts per billion" notation ppb, which is equivalent to ng/g, or the "parts per trillion" notation ppt, which is equivalent to pg/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.<br><br>For mercury, MDLs are reported to 2 decimal places (1 more place than the amount).<br>For PCBs, MDLs are reported to 6 decimal places (the same number of decimal places as the amount).<br>For PFAS, MDLs are reported to 2 decimal places (the same number of decimal places as the amount).<br>For PCDDs/PCDFs, MDLs are reported to 4 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. |
| Lab Qualifier Flag | The data qualifier flag(s) applied by the laboratory.<br><br>**For mercury, no lab qualifier flags were required.**<br><br>For the other analytes, the following flags were used, either singly or in combination:<br>U = Not detected<br>B = Analyte also present in the method blank<br>J = Estimated value (between the MDL and QL values)<br><br>For the PCBs and PCDDs/PCDFs, the following additional flags were used, either singly or in combination:<br>C = Analyte is a coeluting group of congeners<br>D = Result is from a diluted analysis<br>E = Original result exceeded the calibration range; reported result is from a dilution<br>G = Evidence of a disturbance with the lock-mass used during the analysis<br>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 providing analytical support to OST programs during data validation. **For the mercury data, no SCC codes were required.**<br><br>The individual SCC codes applied to the other results (PCBs, PFAS, and PCDDs/PCDFs) are identified and defined in the table of SCC codes below. |

| **"Results" Tabs for Mercury, PCBs, PFAS, and PCDDs/PCDFs (also referred to as dioxins and furans)** | |
|---|---|
| **Field Name** | **Description** |
| Comments | A text translation of the SCC code combinations applied to each applicable result. For mercury, no SCC codes were applied, so no comments were needed. |
| Sort Order | Applies only to PCBs, PFAS, and PCDDs/PCFDs. A field used to sort the analyte names in a consistent order within each analyte class.<br><br>For PCBs, the values in this field range from 1 to 163.<br><br>For PFAS, the values in this field range from 1 to 13.<br><br>For PCDDs/PCDFs, the values in this field range from 1 to 20. |

| **"Sample Information" Tab for All Analytes** | |
|---|---|
| **Field Name** | **Description** |
| EPA Region | The EPA Region in which the fish sample was collected. |
| State | USPS 2-letter abbreviation for the state in which the fish sample was collected. |
| Lake Name | Name of the Great Lake from which the fish sample was collected. |
| Site ID | The identifier assigned by EPA to the fish sample collection site. The first four characters are "GLNS," the next two are the site selection year (15), followed by the 4-digit site location. |
| EPA Sample ID | Unique 6-digit number assigned by EPA. |
| Latitude | Latitude, in decimal format, to 5 decimal places. |
| Longitude | Longitude, in decimal format, to 5 decimal places. |
| Sample Collection Date | Actual sampling date, in MM/DD/YYYY format. |
| Sample 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 | Scientific 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 | Scientific name of the Family based on Nelson *et al.* (2004). |
| Tissue Type | The type of fish tissue used to prepare the tissue sample for analysis. For the 2015 GLHHFFTS, all of the samples were prepared from fillet tissue. |
| Total Length (mm) | Length of each individual fish specimen in millimeters (mm). |
| Included in Composite? | This field indicates if the fish specimen was included in the fillet tissue composite 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 fish species as either:<br>P = Predator species, or<br>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). |
| Fillet Sample Preparation Instructions | Instructions from OST to the fish tissue sample preparation laboratory regarding which fish specimens to include in the fillet composite sample for analysis, based on specimen length and species. |

| **Individual SCC Codes Applied to the 2015 GLHHFFTS 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. |
| CONF | Result confirmed on method-specified second GC column | This code only applies to 2,3,7,8-TCDF, where the GC column used for the initial analysis of the sample may not separate this congener from other TCDF congeners. Therefore, the method directs the laboratory to analyze the sample extract for 2,3,7,8-TCDF on a second GC column to confirm any positive results. Non-detects do not require confirmation. |
| 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 | High Labeled Compound Recovery | 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. |
| HLBL, J | High Labeled Compound Recovery, Estimated | 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. |
| 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 fillet 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 fillet tissue 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 fillet tissue sample, so there was no high bias concern for the specific sample and the RNAF flag was applied. |

| **Individual SCC Codes Applied to the 2015 GLHHFFTS Results** | | |
|---|---|---|
| **SCC Code** | **Comments** | **Implication** |
| 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 fillet tissue sample, so there is no high bias concern and the RNAF flag is applied. |
| 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 fillet tissue 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 fillet tissue samples in the batch with the matrix spike sample. |
| REXC, J | Result exceeded calibration range, but further dilution not practical, Estimated | The results for the analyte exceeded the calibration range of the instrument, but dilution of the extract to bring the result in range was not practical because it would dilute out the labeled compounds in the sample to the point that they could not be used for quantitation. Therefore, the result also is flagged as an estimated value. |

**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).