

**2018-19 NRSA Fish Fillet Tissue Data Dictionary for Mercury, PCBs, and PFAS  
October 2022**

The U.S. Environmental Protection Agency (EPA) Office of Science and Technology (OST) within the Office of Water (OW) is providing the fish fillet tissue results from the 2018-19 National Rivers and Streams Assessment (NRSA). The specific chemical analyses include:

- Mercury (total)
- Polychlorinated biphenyls (PCBs) (all 209 congeners)
- Per- and polyfluoroalkyl substances (PFAS) (33 compounds)

This file includes the “data dictionary” for each type of chemical contaminant analysis. The field names and descriptions for the analytical results are similar for each type of chemical analysis, but results from 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 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 sample information is provided after the dictionary for the results for each type of contaminant analysis.

<b>Results Tabs for Mercury, PCBs, and PFAS</b>	
<b>Field Name</b>	<b>Description</b>
EPA Region (Column A)	The EPA Region in which the fish composite sample was collected.
State (Column B)	U.S. Postal Service 2-letter abbreviation for the state in which the fish composite sample was collected.
Site ID (Column C)	The identifier assigned by EPA to each river sampling site.
EPA Sample ID (Column D)	Unique 6-digit number assigned by EPA to each fish composite sample.
Tissue Type (Column E)	The type of fish tissue used to prepare samples for analysis. For the 2018-19 NRSA Fish Tissue Study, fillet tissue samples were analyzed for all the chemical contaminants.
% Lipids (Column F)	The percentage of lipids in the fillet tissue sample. (Please note that the lipid results were <i>not</i> used to normalize the mercury, PCB, or PFAS results.)
Method (Column G)	<p>An identifier for the analytical method used for each chemical. For the mercury and PCB results, the identifiers refer to the following standardized EPA methods: <u>EPA Method 1631E, Mercury in Water by Oxidation, Purge and Trap, and Cold Vapor Atomic Fluorescence Spectrometry</u>, EPA-821-R-02-019, August 2002.</p> <p><u>EPA Method 1668C, Chlorinated Biphenyl Congeners in Water, Soil, Sediment, Biosolids, and Tissue by HRGC/HRMS</u>, EPA-820-R-10-005, April 2010.</p> <p>For the PFAS results, there were no EPA methods for analysis of fish tissue at the time of the study, so fillet samples were analyzed by an in-house procedure developed by the commercial laboratory, utilizing liquid chromatography with tandem mass spectrometric detection (LC/MS/MS).</p>
Chemical (Column H)	<p>Common name or abbreviation for the chemical.</p> <p>For 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 during analysis, 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 sample. This value was calculated by OST, using zero for any congener result that was “not detected” at the method detection limit.</p> <p>For PFAS, the chemical names are those of the anion form of the chemical (e.g., the “ate” form).</p>
CAS Number (Column I)	<p>Chemical Abstracts Service (CAS) Registry Number assigned by CAS to the chemical.</p> <p>CAS Numbers do not exist for the groups of coeluting PCB congeners.</p> <p>For PFAS, this is the CAS Number of the parent acid or amide form, because the anions do not have separate CAS Numbers.</p>

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<b>Field Name</b>	<b>Description</b>
Amount (Column J)	<p>Concentration of the chemical, if detected. If this field is blank, then the chemical was not detected in the fillet sample. In order to accommodate the range of concentrations in these samples, all the results are presented with the same number of decimal places for a chemical (mercury) or chemical class (PCBs and PFAS).</p> <p>For mercury, the amount field is presented to 1 decimal place. For the PCBs, the amount fields are presented to 5 decimal places. For PFAS, the amount field is presented to 3 decimal places.</p> <p>However, these results have at most 3 significant figures, regardless of the number of decimal places (for example, a PFAS value of 19.000 does not imply 5 significant figures).</p>
MDL (Column K)	<p>The nominal method detection limit (MDL) for the chemical, based on the procedure in 40 CFR part 136, not adjusted for actual sample size, in the units shown in the Units columns.</p> <p>For mercury, MDLs are reported to 2 decimal places. For PCBs, MDLs are reported to 5 decimal places. For PFAS, MDLs are reported to 3 decimal places.</p>
QL (Column L)	<p>The nominal quantitation limit (QL) or “Minimum Level” for the chemical, based on the lowest calibration standard analyzed, not adjusted for sample size, in the units shown in the Units columns.</p>
Unit 1 (Column M)	<p>The weight/weight units of nanograms per gram or ng/g (see Unit 2 description below for equivalent unit).</p>
Unit 2 (Column N)	<p>The “parts per billion” notation ppb, which is equivalent to ng/g.</p>
Lab Qualifier Flag (Column O)	<p>The data qualifier flag(s) applied by the laboratory. <i>For mercury, no lab qualifier flags were required.</i></p> <p>For the other chemicals, the following flags were used, either singly or in combination:            U = Not detected            B = Chemical also present in the method blank            C = Chemical 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            H = Estimated concentration (for reason not covered by “J”)            J = Estimated value (between the MDL and QL values)            K = Ion abundance ratio is outside of the acceptance limits, but the chemical meets all the other identification criteria            NQ = Not quantified because the associated labeled compound was not detected</p>
SCC Code (Column P)	<p>Qualifiers applied by the Sample Control Center staff at CSRA (EPA analytical support contractor) during data validation. <i>For mercury, no SCC codes were required.</i></p> <p>The individual SCC codes applied to the other results (PCBs and PFAS) are identified and defined in the table of SCC codes below.</p>
Comments (Column Q)	<p>A text translation of the SCC code combinations applied to each result. <i>For mercury, no SCC codes were required, so no comments were needed.</i></p>
Sort Order (Column R)	<p>Applies only to PCBs and PFAS. A field used to sort the chemical names in a consistent order within each chemical group.</p> <p>For PCBs, the values in this field range from 1 to 160. For PFAS, the values in this field range from 1 to 33.</p>

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<b>Sample Information Tab for All Chemicals</b>	
<b>Field Name</b>	<b>Description</b>
EPA Region (Column A)	The EPA Region in which the fish composite sample was collected.
State (Column B)	U.S. Postal Service 2-letter abbreviation for the state in which the fish composite sample was collected.
Site ID (Column C)	The identifier assigned by EPA to each river sampling site.
River Name (Column D)	The name of the river from which the fish composite sample was collected.
Latitude (Column E)	Latitude, in decimal format, to 5 decimal places.
Longitude (Column F)	Longitude, in decimal format, to 5 decimal places.
Site Type (Column G)	Urban, Non-urban designation (based on Census Bureau GIS data).
Stream Order (Column H)	A measure of stream position within a drainage network system. Streams that have no tributaries flowing into them are called first-order streams. Stream orders in this study range from fifth-order (5) to greater than eighth-order (8+), which are defined as rivers for this study.
Sample Collection Date (Column I)	Sample collection date, in MM/DD/YYYY format.
EPA Sample ID (Column J)	Unique 6-digit number assigned by EPA to each fish composite sample.
Specimen ID (Column K)	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 (Column L)	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).
Family (Column M)	Latin name of the Family based on Nelson <i>et al.</i> (2004). (see full citation directly below)
Species - Scientific Name (Column N)	Latin name (Genus and species) based on Nelson <i>et al.</i> (2004), <i>Common and Scientific Names of Fishes from the United States, Canada, and Mexico</i> , Sixth Edition.
Species - Common Name (Column O)	Generally accepted common name based on Nelson <i>et al.</i> (2004).
Total Length (mm) (Column P)	Length of each individual fish specimen in millimeters (mm).
Included in composite? (Column Q)	This field indicates if the fish specimen was included in the fillet tissue sample for analysis or not. The options are either “Yes” or “No” and the rationale is explained in the “Fillet Sample Preparation Instructions” field to the far right.
Predator or Bottom Dweller (Column R)	Classification of the fish species as either: P = Predator species, or BD = Bottom-dweller species
Composite Classification (Column S)	Routine vs. Non-routine composite, based on the fish composite sample criteria specified in the human health fish sampling procedures and identified online in the 2018-19 NRSA Fish Tissue Study web page.
Deviation (Column T)	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 (Column U)	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.

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<b>Individual SCC Codes Applied to the 2018-19 NRSA Fish Tissue Study Results</b>		
<b>SCC Code</b>	<b>Comments</b>	<b>Implication</b>
B, RMAX	Blank Contamination, Result is a Maximum Value	Blank contamination was observed, and the target chemical 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 chemical 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 chemical 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 chemical 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 chemical 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 chemical 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 chemical 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 chemical 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 chemical 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 chemical 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 chemical.
HLCS, RNAF	High Lab Control Sample Recovery, Result is Not Affected	The recovery in the LCS was high, but the chemical was not detected in the associated fillet tissue sample, so there was no high bias concern 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 a chemical, all the detected results for that chemical 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 chemical, the non-detected results for that chemical were not affected, and the RNAF flag was applied.

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HVER, J	High CALVER, Estimated	The results for the calibration verification associated with the chemical were above the acceptance limit, suggesting a possible high bias. Detected chemicals also are considered estimated values.
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 chemical 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 chemical was recovered below acceptance criteria, suggesting the possible presence of matrix interferences or incomplete recovery of both the labeled compound and target chemical during the extract cleanup processes used in the analytical procedure. The use of isotope dilution quantitation automatically corrects the results for the target chemical, even when the labeled compound recovery is below expectations. This flag is applied when the chemical associated with the labeled analog is not detected in the sample.
LLBL, J	Low Labeled Compound Recovery, Estimated	The labeled analog of the target chemical was recovered below acceptance criteria, suggesting the possible presence of matrix interferences or incomplete recovery of both the labeled compound and target chemical during the extract cleanup processes used in the analytical procedure. The use of isotope dilution quantitation automatically corrects the results for the target chemical, even when the labeled compound recovery is below expectations. When the chemical associated with the labeled analog is detected in the sample, the result is also flagged as an estimated value.
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 chemical. When low LCS recovery was observed for a chemical, the results for that chemical were qualified in all of the samples in the batch with the LCS.
LMI, J	Lock mass interference, Estimated	There was an interference with the lock mass monitored by the high-resolution mass spectrometer to ensure accurate mass identification. That interference may affect the quantification of the chemical and the result is flagged as an estimated value.
LMI, RNAF	Lock mass interference, Result is Not Affected	There was an interference with the lock mass monitored by the high-resolution mass spectrometer to ensure accurate mass identification. That interference may affect the quantification of the chemical, but when the chemical was not detected, the result is not affected.
LND, NQ	Labeled compound Not Detected, Not Quantified	The labeled compound associated with this chemical could not be detected due to interferences or other causes. Therefore, the chemical could not be quantified by isotope dilution and was reported as a non-detect at the MDL.
NPD, RNON	No definitive peak shoulder for coeluter, Result Reported as Non-detect	Coeluting PCB congeners cannot be completely separated by the gas chromatograph and one or more of the coeluting congeners will appear as a "shoulder" on the peak for the other congeners. If such a shoulder is not present, the chemical has not been identified and the result is reported as not detected.
RRT, J	RRT outside of window, Estimated	The relative retention time of the chemical shifted outside of its expected window and as a result, the quantification of the chemical may be affected, and the result is considered an estimated value.

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RTI, RMAX	Retention Time Interference; Result is a Maximum Value	There was an interference apparent at the retention time of the chemical. Although it did not prevent the identification of the chemical, it likely affected the quantitative result, and the result is considered a maximum 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).