2008-09 NRSA Fish Tissue Data Dictionary for Mercury, Selenium, PBDEs, PCBs, Pesticides, and PFCs
September 2014

The Office of Science and Technology (OST) is providing the fish tissue results from the 2008-09 National Rivers and Streams Assessment (NRSA). The specific analyses include:

- Mercury
- Selenium
- Polybrominated diphenyl ethers (PBDEs)
- Polychlorinated biphenyls (PCBs)
- Pesticides
- 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, Selenium, PBDEs, PCBs, Pesticides, 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.
Site ID	The 9-character identifier assigned by EPA to the site. The first two characters are "FW," for "flowing waters," the next two are the site selection year (08), followed by two characters for the state abbreviation, and a three-digit identifier for sites within the state.
EPA Sample ID	Unique 6-digit number assigned by EPA.
Method	An abbreviation for the analytical technique or method used for the analysis: DMA = Direct mercury analyzer GC/ECD = Gas chromatography/electron capture detection ICP/AES = Inductively coupled plasma/atomic emission spectroscopy HPLC/MS/MS = High performance liquid chromatography/tandem mass spectrometry
% Lipids	Applies only to the PBDE, PCB, and pesticide 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 and PCBs, the abbreviation "BDE" (for brominated diphenyl ether) or "PCB" is followed by the congener number (i.e., "BDE-7" or "PCB-7"). For the pesticide results, the names include any prefixes and Greek letters that indicate isomers or molecular structures. For the PBDEs, PCBs, pesticides, and PFCs there are a number of entries for summed values, including: Summed DDT (5), Summed PBDEs (8), Summed PCBs (21), and Summed PFCs (13), where the number in parentheses indicates the number of individual components in the summed value. This nomenclature was used for those values where fewer than the total number of potential components are determined. 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. For those analytes that that are not unique chemicals, including the summed values for some classes of organics, CAS has not assigned a number and these are listed as "NA," for not applicable.
Amount	Concentration of the analyte, if detected. If this field is blank, the analyte was not detected in the sample. The amounts for mercury and selenium are reported to one decimal place, while the PBDEs, PCBs, pesticides, and PFCs are reported to two decimal places. However, the results have at most three significant figures, regardless of the number of digits displayed (e.g., a mercury value of 353.6 does not imply 4 significant figures).

Data Tabs for Mercury, Selenium, PBDEs, PCBs, Pesticides, and Perfluorinated Compounds	
Field Name	**Description**
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 results, OST used the value of 300 ng/g, which is EPA's tissue-based Water Quality Criterion for methylmercury. • For selenium results, OST used the value of 12,000 ng/g derived from the EPA Guidance for Assessing Chemical Contaminant Data for Use in Fish Advisories, Volume 2 (2000). • For the PBDE results, OST used a screening value of 210 ng/g for Summed PBDEs (8), derived by the California Environmental Protection Agency. • For the PCB results, OST used a screening value of 12 ng/g for Summed PCBs (21), derived from the EPA Guidance for Assessing Chemical Contaminant Data for Use in Fish Advisories, Volume 2 (2000). • For the pesticide results, OST used the screening values for total chlordane (67 ng/g), Summed DDT (69 ng/g), and dieldrin (1.5 ng/g) 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 relative to the HH screening value, as either "Exceeds SV" or "Does not exceed SV".
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 Unit 1 column. The MDLs for mercury and PFCs are reported to 2 decimal places. The MDLs for selenium are reported to no decimal places. The MDLs for the PBDEs, PCBs, and pesticides were determined on both of the GC columns used for each analysis. The higher (maximum) of the two MDLs for each analyte is shown here, reported to two decimal places.
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. The QLs for the PBDEs, PCBs, and pesticides were determined on both of the GC columns used for each analysis. The higher (maximum) of the two QLs for each analyte is shown here.
Unit 1	The weight/weight units (e.g., ng/g).
Unit 2	The "parts per billion" notation ppb, which is equivalent to ng/g.
Lab Qualifier Flag	The data qualifier flag(s) applied by the laboratory.
SCC Code	Qualifiers applied by the Sample Control Center staff at CSC during data validation.
Comments	A text translation of the SCC code combinations applied to each result.
Analyte Type	Applies only to the PBDE, PCB, and pesticide results. Used to differentiate individual "target" analytes from "totals" or summed values.
Class	Applies only to the PBDE, PCB, and pesticide results. A simple code that distinguishes the organochlorine pesticides (OCP) from the polybrominated diphenyl ethers (PBDE) and the polychlorinated biphenyls (PCB). May be useful in sorting results for these classes of analytes.

Data Tabs for Mercury, Selenium, PBDEs, PCBs, Pesticides, and Perfluorinated Compounds	
Field Name	**Description**
Sort Order	Applies to the PBDE, PCB, pesticide, and PFC results. A simple numeric code used to sort the analytes in a consistent order within each analyte class. The PBDEs, PCBs, and pesticides were analyzed together, so the values in this field range from 1 to 58 and cover all three analyte classes. The PBDEs and PCBs are sorted in order by their congener number, with groups of coeluting congeners sorted by the lowest congener number in the group. The pesticides are sorted in alphabetical order by their proper names, where the convention is not to sort based on isomers, Greek letters, etc., but on the parent structure (e.g., cis-Nonachlor and trans-Nonachlor both fall under "N," rather than "c" or "t"). The PFCs are sorted by carbon chain length.

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.
Site ID	The 9-character identifier assigned by EPA to the site. The first two characters are "FW," for "flowing waters," the next two are the site selection year (08), followed by two characters for the state abbreviation, and a three-digit identifier for sites within the state.
River Name	The name of the river from which the sample was collected.
Latitude	Latitude, in decimal format, to 5 decimal places.
Longitude	Longitude, in decimal format, to 5 decimal places.
EPA Sample ID	Unique 6-digit number assigned by EPA .
Site Type	Urban, Non-urban designation (based on Census Bureau GIS data).
Stream Order	A measure of stream position within a drainage network system. Streams that have no tributaries flowing into them are called first-order streams. Streams in this study range from fifth-order (5) to greater than eighth-order (8+).
Sample Date	Actual sampling date, in MM/DD/YYYY format.
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 NRSA, 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 B = 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.
Processing Issues	Any issues that arose during processing of the specimens to form the composite fillet tissue sample.

2008-09 NRSA Fish Tissue Data Qualifier Codes for Mercury, Selenium, PBDEs, PCBs, Pesticides, and Perfluorinated Compounds – September 2014

Individual SCC Codes Applied to the 2008-09 NRSA 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.
CPDX	RPD Between Results on Two GC Columns Exceeded Acceptance Criterion	The precision of the results from the two GC columns, measured as the RPD, exceeded the acceptance limits. This may have been due to a positive interference in one of the two analyses.
CPDX, RNAF	RPD Between Results on Two GC Columns Exceeded Acceptance Criterion, Result is Not Affected	The precision of the results from the two GC columns, measured as the RPD, exceeded the acceptance limits. This may have been due to a positive interference in one of the two analyses. When the results for both columns were below the detection limit, the RNAF flag was applied.
HICAL, RNAF	High Initial Calibration RSD, Result is Not Affected	The results for the linearity check of the initial calibration associated with the analyte were above the acceptance limit, suggesting a possible high bias. The non-detected results for that analyte were not affected, and the RNAF flag was applied.
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.
HSRM	High Standard Reference Material Result	High result for the standard reference material (SRM) indicated a positive interference or a high bias. When high SRM result was observed for an analyte, the results for that analyte were qualified in all of the samples in the batch with the SRM.
HSRM, RNAF	High Standard Reference Material Result, Result is Not Affected	High result for the standard reference material (SRM) indicated a positive interference or a 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.
HSSR	High Surrogate Spike Recovery	High surrogate recovery indicated a positive interference or a high bias. When high surrogate recovery was observed, the results for all analytes in that sample were qualified.
HSSR, RNAF	High Surrogate Spike Recovery, Result is Not Affected	High surrogate recovery indicated a positive interference or a 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.
HVER	High CALVER	The results for the calibration verification associated with the analyte were above the acceptance limit, suggesting a possible high bias.

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Individual SCC Codes Applied to the 2008-09 NRSA Results		
SCC Code	**Comments**	**Implication**
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.
INSL	Insufficient Spike Level	The amount of analyte added to the matrix spike sample was much lower than the amount in the unspiked sample. As a result, the calculated recovery for the matrix spike is not indicative of method performance in the matrix.
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.
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.
LSRM	Low Standard Reference Material Result	Low result for the standard reference material (SRM) indicated a negative interference or a low bias. When low SRM result was observed for an analyte, the results for that analyte were qualified in all of the samples in the batch with the SRM.
LSSR	Low Surrogate Spike Recovery	Low surrogate recovery indicated a negative interference or a low bias. When low surrogate recovery was observed, the results for all analytes in that sample were qualified.
NCNF	Result Not Confirmed on Second Column	The result for the analyte was not or could not be confirmed on the second GC column, due to interferences or coelution with another analyte. As a result, the identification of the analyte is less certain than in instances where the analyte was confirmed.
NCNF, RNAF	Result Not Confirmed on Second Column, Result is Not Affected	The result for the analyte was not or could not be confirmed on the second GC column, due to interferences or coelution with another analyte, but the analyte was reported as not detected, so there was no concern with the identification and the RNAF flag is applied.
RPDX	RPD Between Lab Duplicates or MS/MSD Exceeded Acceptance Criterion	When applied to results for mercury, selenium, or PFCs, the precision of the results from the original sample and the laboratory duplicate, measured as the relative percent difference (RPD), exceeded the acceptance limits. This may have been due to inhomogeneity of the sample aliquots, or a positive interference in one of the two analyses. When applied to results for PBDEs, PCBs, or pesticides, the precision of the recoveries in the matrix spike (MS) and matrix spike duplicate (MSD) analyses, measured as the RPD, exceeded the acceptance limits. This may have been due to inhomogeneity of the sample aliquots, or a positive interference in one of the two analyses.
RPDX, RNAF	RPD Between Lab Duplicates Exceeded Acceptance Criterion, Result is Not Affected	When applied to results for mercury, selenium, or PFCs, the precision of the results from the original sample and the laboratory duplicate, measured as the RPD, exceeded the acceptance limits, but the results for both aliquots were below the detection limit, so the RNAF flag was applied.

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).