2020 GLHHFTS Fish Tissue Data Dictionary for Fatty Acids November 2023

The Office of Science and Technology (OST) is providing the fish tissue results from the 2020 Great Lakes Human Health Fish Fillet Tissue Study (GLHHFFTS) from the analysis of 38 omega-3 and omega-6 fatty acids.

This document represent represents the "data dictionary" for the fatty acid results. The field names and descriptions for the analytical results are specific to the fatty acid results. 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.

Data Tab for Fatty Acids				
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 of the Great Lake from which the sample was collected.			
	The identifier assigned by EPA to the site. The first three characters are "NGL," the next two are the site selection year (20), followed by the State abbreviation and the 4-digit site location.			
Site ID	<i>Note:</i> The sample from NGL20_IN-10001 did not yield enough homogenized tissue to support the fatty acid analysis, so no records for that sample have been included in the file.			
EPA Sample ID	Unique 6-digit number assigned by EPA.			
Tissue Type	An indication of the tissue used for the analysis. For the 2020 GLHHFFTS, all of the samples were prepared from composited fillet tissue.			
Analyte	Common name or abbreviation for the analyte.			
Lipid Number	Lipid numbers take the form C:DnX, where C is the number of carbon atoms in the fatty acid and D is the number of double bonds. Where applicable, the fatty acid double bond location is identified by nX, where X is the carbon number of the first double bond relative to the terminal alkyl end of the fatty acid.			
CAS Number	Chemical Abstracts Service Registry Number assigned by CAS to the analyte.			
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 the fatty acids, 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 Stearic acid value of 245.58 does not imply 5 significant figures).			
Units	The weight/weight units of µg/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 fatty acids, MDLs are reported to 2 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.			
Lab Flag	The data qualifier flag(s) applied by the laboratory. For fatty acids, no lab qualifier flags were required.			
SCC Code	Qualifiers applied by the Sample Control Center staff at GDIT during data validation. The individual SCC codes are identified and defined in the table of SCC codes below.			
Comments	A text translation of the SCC code combinations applied to each result.			
Sort Order	A field used to sort the analyte names in a consistent order. For fatty acids, the values range from 1 to 38			

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Sample Information Tab				
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.			
Sita ID	The identifier assigned by EPA to the site. The first three characters are "NGL," the next two are the site selection year (20), followed by the State abbreviation and the 4-digit site location.			
	<i>Note:</i> The sample from NGL20_IN-10001 did not yield enough homogenized tissue to support the fatty acid analysis, so no records for that sample have been included in the file.			
Lake	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.			
EPA Sample ID	Unique 6-digit number assigned by EPA.			
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	Latin name (Genus and species) based on Nelson et al. (2004), Common and Scientific			
Name	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 GLHHFFTS, all of the samples were prepared from fillet tissue.			
Total Length (mm)	Length of each individual specimen in millimeters (mm).			
Included in Fillet 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).			
Fillet Sample Preparation 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 Fatty Acid Results					
SCC Code	Comments	Implication			
HRPD, J	High RPD between the original analysis and its duplicate, result is 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 between the original analysis and its duplicate, 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.			

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Individual SCC Codes Applied to the Fatty Acid Results					
SCC Code	Comments	Implication			
HSRM, J	High SRM recovery, result is estimated	Results for the standard reference material (SRM) analyzed with the batch of samples were high, indicating a potential high bias. As a result, the results for detected chemicals are considered estimated values.			
HSRM, RNAF	High SRM recovery, result is not affected	Results for the standard reference material (SRM) analyzed with the batch of samples were high, indicating a potential high bias. However, the results for nondetected chemicals are not affected.			
HSSR, J	High surrogate spike recovery, result is estimated	Surrogate (non-target) compounds are added to every sample before extraction and are used to assess the overall analytical process. When surrogate recoveries are high, there may be a high bias for the target analytes and the results for detected chemicals are considered estimated values.			
LSRM	Low SRM recovery. Nondetects may have a greater risk of false negative results.	Results for the standard reference material (SRM) analyzed with the batch of samples were low, indicating a potential low bias. As a result, the reported nondetects may have a greater risk of being false negatives.			
LSRM, J	Low SRM recovery, result is estimated	Results for the standard reference material (SRM) analyzed with the batch of samples were low, indicating a potential low bias. As a result, the results for detected chemicals are considered estimated values.			

Note: Commas are used to separate related parts of a single code (e.g., "HSSR, J" is considered one code), while semicolons are used to separate different codes (e.g., "HSSR, J; LSRM, J" is the combination of two codes).