

| Field Name | Field Title | Data Type | Definition |
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| Age | Age | Number | The age of the organism from which the tissue sample was taken. Default value is "-88" if unknown. A list of possible options is available at the following site (Note: search the first column in the table for "AgeList"): VariableCodesLookUpList |
| AnalysisDate | Analysis Date | Date/Time | The date and time the sample was processed on the analytical instrument. Formatted as dd/mmm/yyyy hh:mm. Default value equals "01/Jan/1950 00:00" if unknown. |
| Analyte | Analyte | Plain Text | Name of the analyte or parameter for which the analysis is conducted and result is reported. A list of possible options is available at this link: AnalyteLookUpList |
| AnalyzingAgency | Analyzing Agency | Plain Text | The agency, organization, or laboratory that performed the analysis on the sample. Default value equals "Not Recorded" if unknown. A list of possible options is available at this link: AgencyLookUpList |
| Anomaly | Anomaly | Plain Text | Describes any anomalies that may be on or in the organism (e.g. Lesion, Parasite, Tumor, etc.). A list of possible options is available at the following site (Note: search the first column in the table for "AnomalyList"): VariableCodesLookUpList |
| BatchVerification | Batch Verification | Plain Text | A unique code given by the SWAMP IQ Data Manager to the lab batch, after the verification of the data has been completed. The code will reflect compliance to SWAMP MQOs (Measurement Quality Objectives), hold times, and overall quality of the data. Default value equals "NR" if unknown. A list of possible options is available at this link: BatchVerificationLookUpList |
| CollectionDevice Name | Collection Device | Plain Text | Name of the device used to collect the sample (e.g. "MPSL- Eboat_(BigE)", "WPCL-DFG Gill Net 1(50m,1.5)", "Individual Collection by bucket sampler", etc.). Default value equals "Not Recorded" if unknown. A list of possible options is available at this link: CollectionDeviceLookUpList |

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| CollectionMethod Name | Collection Method Name | Plain Text | Refers to the general method used to collect the sample, organism, or field observation. Depending on the data types, different types of collection methods will be stated. Some examples are: "Algae_SWAMP", "BMI_CSBP_Transect", "Sed_Core", "Water_Grab", "Autosampler24h", "Habitat_Generic", etc. The default value of "Not Recorded" is utilized if method is unknown. LabQA samples utilize "Not Applicable." A list of possible options is available at this link: CollectionMethodLookupList |
| CollectionReplicate | Collection Replicate | Plain Text | Used to distinguish between replicates created at a single collection in the field. Replicate samples that are collected at the same station and date should either have a value of "2" or "3." Samples collected on different dates, even if they are from the same station, should both have a value of "1." Default value is also "1." |
| CollectionTime | Collection Time | Date/Time | Refers to the time when the first sample of a sampling event at a specific station was collected in the field. Format equals hh:mm in 24 hour time (e.g. 13:30 for 1:30 pm). Default value equals "00:00" if the time sampling started is unknown. *For transplanted bivalves used in tissue analysis, the CollectionTime refers to the time the organisms were retrieved from the field after deployment. |
| CommonName & CompositeCommonName | Common Name | Plain Text | Refers to the common name (i.e. not the scientific name or nomenclature) of the organism collected for the sample. |
| CompAgency | Compositing Agency | Plain Text | The agency that physically created the composite or super composite used in the analysis. A list of possible options is available at this link: AgencyLookupList |
| ComplianceCode | Compliance Code | Plain Text | Unique code referencing the compliance with the associated Quality Assurance Project Plan (QAPP). "Com" is used when all standards are met for the associated QAPP. Default value equals "NR" if unknown. A list of possible options and definitions is available at this link: ComplianceLookupList |
| CompositeComments | Composite Comments | Plain Text | Contains any comments related to the composite or super composite. |

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| CompositeID & CompositeCompositeID | Composite ID | Plain Text | A unique identifier supplied by the Compositing Agency to identify the composited tissue parts. Formats may differ depending on the agency. It can refer to either the original composite or the super composite (when multiple composites are combined). |
| CompositeJunctionRowID | Composite Junction Row ID | Number | Internal database identification for composite samples. Can be disregarded in data analysis. |
| CompositeReplicate | Composite Replicate | Plain Text | Used to distinguish between replicate composites. Default value equals "1." |
| CompositeRowID | Composite Row ID | Number | An internal database identification for composite samples. Can be disregarded in data analysis. |
| CompositeType & CompositeCompositeType | Composite Type | Plain Text | Indicates the type of composite (e.g. "Normal" or "SuperComposite.") A list of possible options is available at the following site (Note: search the first column in the table for "CompositeTypeList"): VariableCodesLookUpList |
| CompositeWeight | Composite Weight | Number | The total weight of the Composite or SuperComposite used in the analysis. Default value is "-88." |
| CompSizeCheck | Comp Size Check | Number | Comparison of organism sizes whose samples make up the composite. |
| DataQuality | Data Quality | Plain Text | <p>Describes the overall quality of the record by taking the QACode, ResultQACode, ComplicanceCode, BatchVerificationCode, and special circumstances into account to assign it to one of the following categories:</p> <ul style="list-style-type: none"> • "Metadata, QC record"- Not a measurement of environmental conditions • "Passed QC"- Data passed all QC checks • "Some review needed"- Data did not pass minor QC checks, some effort needed to review and defend data if used • "Spatial Accuracy Unknown"- Data missing spatial datum information, data should not be used for fine scale spatial analysis • "Extensive review needed"- Data did not pass QC some critical checks, high level of effort needed to defend data if used • "Unknown Data Quality"- Data was not reviewed by the project. Data will need review before use • "Reject Data"- Data was rejected by the project or data did not pass all critical QC checks. Data deemed unusable |

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| | | | The assignments and categories are provisional. A working explanation of the data quality ranking can be found at the following link. This link is open to public comments as well: DataQualityEstimator-DecisionTree . |
| DataQualityIndicator | Data Quality Indicator | Plain Text | <p>Explains the reason for the DataQuality value by indicating which quality assurance check the data did not pass (e.g. BatchVerificationCode, ResultQACode, etc.). If this field contains "Special Rule," this indicates that the data falls into a special circumstance that decreases data quality. This field is left blank for values "Metadata, QC record" and "Passed QC."</p> <p>The assignments and categories are provisional. A working explanation of the data quality ranking can be found at the following link. This link is open to public comments as well: DataQualityEstimator-DecisionTree.</p> |
| Datum | Datum | Plain Text | Represents the associated model of the Earth from which reference points are used to calculate position measurements. GPS devices commonly use datums such as "NAD83" and "WGS84." Default value equals "NR" if unknown. A list of possible options is available at the following site (Note: search the first column in the table for "DatumList"): VariableCodesLookUpList |
| DigestExtractDate | Digest/ Extraction Method Date | Date/Time | The start date and time the digestion or extraction was performed on the sample. Default value equals "01/Jan/1950 00:00" if unknown or if no digestion or extraction method was performed. |
| DigestExtractMethod | Digest/ Extraction Method | Plain Text | References the type of digestion or extraction method performed on the sample prior to analysis. Default value equals "Not Recorded" if unknown or if no digestion or extraction method was performed. A list of possible options is available at this link: DigestExtractLookUpList |
| DilutionFactor | Dilution Factor | Number | Factor by which a sample was diluted and is reported as a whole number. This is equal to the final volume divided by the initial volume of solution (i.e. $DF = V_f \div V_i$). For example, if the DilutionFactor is 100, for every 100 parts of the diluted sample, 1 part is the original sample. The default value is "1," which means no dilution was performed. |
| DWC_AnalyteW Fraction | DWC Analyte W Fraction | Number | A combination of the analyte and fraction. This is an auto concatenated field to assist with data reporting. |
| EarliestDateSampled | Earliest Date Sampled | Date/Time | The date when the first sample of a composite, which contains multiple samples, was collected. |

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| FinalID & CompositeFinalID | Final Identification | Plain Text | Refers to the lowest (i.e. most specific) taxon level identified for the organism. A list of possible options is available at this link: OrganismLookUpList |
| ForkLength | Fork Length | Number | The measured length of the organism from the most forward point, with mouth closed, to the center of the fork in the tail. |
| GeometryShape & CompositeGeometryShape | Geometry Shape | Plain Text | The physical shape of the location in which sample was taken; refers to the GIS terms (e.g. "point", "line") that indicates the shape of the location. For example, a "point" would be a location that is one particular spot (1 Lat/Long). "Line" means that the line begins in a single point (1 lat/long) and then ends at a second point; all the locations that connect the 2 points forms a line. A list of possible options is available at the following site (Note: search the first column in the table for "GeometryShapeList"): VariableCodesLookUpList |
| GroupSample | Group Samples | Plain Text | An Identifier used to group samples by the project staff. Not a required field. |
| HomogonizedDate | Homogenized Date | Date/Time | The date that the composite or super composite was homogenized. |
| Hydromod | Hydrological Modification | Plain Text | Indicates if there is any type of alterations in the natural watershed hydrology associated with changes in land cover and use, or notes any observed hydrological modification on the waterbody that was sampled (e.g. "Pipes", "bridges", "ConcreteChannel", etc). Default value is "NR" if unknown. A list of possible options is available at the following site (Note: search the first column in the table for "HydromodList"): VariableCodesLookUpList |
| HydroModLoc | Hydrological Modification Location | Plain Text | Codes that refer to the location of the hydrological modification (HydroMod field). A list of possible options is available at the following site (Note: search the first column in the table for "HydromodLocList"): VariableCodesLookUpList |
| LabBatch | Lab Batch | Plain Text | A unique code, provided by the laboratory, that represents a group of samples processed together. It groups all environmental samples with their supporting QC samples and is used to verify completeness based on the SWAMP QAPrP. It also identifies all samples digested or extracted together in one batch. When a digestion or extraction is not performed as part of the method, the LabBatch represents all samples within a unique analysis |

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| | | | run. Format is "Batch#-AgencyCode" (e.g. "Batch1-SCCWRP"). |
| LabBatchComments | Lab Batch Comments | Plain Text | Records any comments relating to the LabBatch as a whole. Comments should explain any irregularities in sample processing. |
| LabSampleID | Lab Sample ID | Plain Text | An ID assigned by the lab; intended to provide lab-specific identification for an analyzed sample. The format and content is determined by the lab. May have "- Dup," "-MS," or "-MSD" to the end of the ID to help confirm the SampleType and the LabSampleID of the native sample. If the lab does not assign the samples an ID, this column is left blank. |
| LabSubmissionCode | Lab Submission Code | Plain Text | A code assigned by the analyzing laboratory to the LabBatch or ToxBatch (for toxicity tests), that references the quality of the data in the entire batch. If this code is "A" (Acceptable), the laboratory is ensuring that all SWAMP QAQC protocols were met for the lab batch. If anything other than "A" is used, LabBatchComment explains the reason why it was not acceptable. Default value equals "NR" if unknown. A list of possible options is available at this link: LabSubmissionLookUpList |
| LatestDateSampled | Latest Date Sampled | Date/Time | The date when the last sample of a composite, which contains multiple samples, was collected. |
| Latitude & CompositeTargetLatitude | Target Latitude | Number | The latitude in decimal degrees of the sample site (should be positive). |
| LengthSource | Length Source | Plain Text | The physical location where the length measurements were recorded (e.g. field, lab). |
| LocationCode | Location Code | Plain Text | Describes the physical location in the waterbody and the field survey method used where the sample was collected (e.g. "Transect at 177m from start", "First instance where sample was collected in OpenWater", "second instance where a net (e.g. gill, fyke, dip) was used at the thalweg of the waterbody", "Bank, Left", etc.). Default value equals "Not Recorded" if unknown. A list of possible options is available at this link: LocationLookUpList |
| LocationDetailTIComments | Location Detail TI Comments | Plain Text | Comments regarding observations about the location from which samples were taken or where specimens, like bivalves, were deployed. This field could also include other information pertaining to the data. |
| Longitude & CompositeTargetLongitude | Target Longitude | Number | The longitude in decimal degrees of the sample site (should be negative). |

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| Matrix | Matrix Name | Plain Text | Refers to the sample matrix; the substance in which the analyte is evaluated in or the components of a sample other than the analyte of interest (e.g. "samplewater", "tissue"). Default value equals "Not Recorded" if unknown. A list of possible options is available at: MatrixLookUpList |
| MDL | Method Detection Limit | Number | The Method Detection Limit (MDL) is the detection limit associated with the method used to measure the analyte in the sample. This is the lowest possible calculated level, or the minimum concentration of an analyte that can be reported with a stated level of confidence that the analyte concentration is greater than zero. If an MDL is unknown, then the default value is "- 88" with a QACode of "NMDL." |
| Method | Method Name | Plain Text | Refers to the method used by the laboratory to analyze the sample. Default value equals "Not Recorded" if unknown. A list of possible options is available at this link: MethodLookUpList |
| NumberFishperComp | Number of Fish per Composite | Number | The number of fish from which samples were taken to create the analyzed composite. Default value is "-99" if unknown or not applicable. |
| OrganismGroup | Organism Group | Plain Text | The taxonomic group that the organism of the sample belongs to (e.g. Fish, Bivalves, Crustacean, Mammal, Bird or Amphibian). The value of "Not Applicable" is used for lab QA samples. A list of possible options is available at the following site (Note: search the first column in the table for "OrganismGroupList"): VariableCodesLookUpList |
| OrganismID | Organism ID | Plain Text | A unique identification code assigned to the organism by the field crew or the agency that has the first possession of the fish and the field data sheets associated with it. Formats vary depending on the agency or field crew. For samples that are field duplicates, "-Dup" is added to the end of the ID to help confirm that the collection is a field duplicate of the native sample. |
| OrganismWeight | Organism Weight | Number | The weight of the whole organism used for the tissue sample. |
| ParentProjectName & CompositeParentProject Name | Parent Project Name | Plain Text | A larger or on-going project in which the specific project that the samples were collected for is associated with. A list of possible options can be found at this link: ParentProjectLookUpList |

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| PartsComments | Parts Comments | Plain Text | Records any comments relating to the tissue parts. |
| PersonnelCode | Personnel Code | Plain Text | Name of the personnel that either collected the sample in the field, or analyzed the sample in the laboratory. A list of possible options is available at this link: PersonnelLookUpList |
| PrepPreservationDate | Preparation Preservation Date | Date/Time | Date and time the preparation or preservation was started. Format is "dd/mmm/yyyy hh:mm." Default value is "01/Jan/1950 00:00" if the date and time the process started isn't known or if no process was performed. |
| PrepPreservationName | Preparation Preservation Name | Plain Text | References the preparation or preservation method performed on the samples prior to analysis. Default value equals "Not Recorded" if unknown. A list of possible options is available at this link: PrepPreservationLookUpList |
| ProcessedOrganisms ExpandedComments | Processed Organisms Expanded Comments | Plain Text | Further comments on the processed organism used in the analysis. |
| ProgramName & CompositeProgramName | Program Name | Plain Text | The name of the program that is associated with the sample. A list of possible options is available at this link: ProgramLookUpList |
| ProjectCode & CompositeProjectCode | Project Code | Plain Text | A code that references the project that is associated with the sample. In some cases, there may not be a specific project but only a program, in which the ProjectCode would be just the program. A list of possible options is available at this link: ProjectLookUpList |
| ProjectName & CompositeProjectName | Project Name | Plain Text | The project to which the sample result is associated. A list of possible options is available at this link: ProjectLookUpList |
| ProtocolCode | Protocol | Plain Text | Represents the sampling protocol used, which includes the set of methods, methodology and/or specifications, such as "MPSL-DFG_Field_v1.0." Default value is "Not Recorded." LabQA samples will have "Not Applicable." A list of possible options is available at this link: ProtocolLookUpList |
| QACode | Quality Assurance Code | Plain Text | Codes that indicate data quality by describing any special conditions, situations or outliers that occurred during or prior to the analysis to achieve the result. The default code, indicating no special conditions, is "None." A list of possible options is available at this link: QALookUpList |

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| ResQualCode | Result Qualifier Code | Plain Text | A code that indicates specific details about the analytical result of the sample, such as if the analyte was detected but not quantifiable or if the result was a field estimation. Default value is "=", which means that the recorded result is the actual result. A list of possible options is available at this link: ResQualLookUpList |
| Result | Result | Number | Final numeric result of a given analyte, stored as text to retain trailing zeros. The result should be reported with the appropriate number of significant figures. Result may be left blank as long as an appropriate ResQualCode is provided. |
| ResultComments | Result Comments | Plain Text | Any comments related to the results or analysis of the sample. |
| ResultReplicate | Result Replicate | Number | Used to distinguish between replicates created at a single collection in the field. Replicate samples are collected at the same station and date. Therefore, samples collected on different dates but from the same station should have a value of "1." Default value is also "1." This field is utilized for pre-composite replicates. |
| RL | Reporting Limit | Number | Stands for "Reporting Limits" of the sample analyzed is the minimum value below which data are documented as non-quantifiable, as determined by the laboratory. The default value of "-88" is utilized for surrogates, grain size samples, or if no RL was used. |
| SampleComments | Sample Comments | Plain Text | Used for any notes or comments specifically related to the sampling event at a particular station and/or the GIS station information verification. |
| SampleDate & CompositeSampleDate | Sample Date | Date/Time | Refers to the date the sample was collected in the field. Default value equals "01/01/1950" for unknown or null values. For samples with collection times that last longer than one day, like auto samplers, the SampleDate is the date in which sampling began. *For transplanted bivalves, the SampleDate is the date the transplanted organisms were collected, removed, or retrieved from the field. |
| SampleDateRange (Days) | Sample Date Range (Days) | Number | The number of days in which samples were taken from the environment. |
| SampleID | Sample ID | Plain Text | A unique identifier supplied by the sampling agency, and is used to track the sample throughout the sampling and analysis processes. This field can be used to tie a result to the sample. |

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| SampleTypeCode & CompositeSampleTypeCode | Sampling Type | Plain Text | Refers to the type or purpose of the sample that is collected or analyzed (i.e. indicates if the sample was used as a control, for calibration purposes, is a combination of multiple samples, used for algae bioassessment, etc.) Default value equals "Not Recorded" if unknown. A list of possible options is at this link: SampleTypeLookupList |
| SamplingAgency | Sampling Agency | Plain Text | Refers to the organization or agency that collected the sample. Default value equals "Not Recorded" if unknown. A list of possible options is available at this link: AgencyLookupList |
| Sex | Sex | Plain Text | The sex of the organism (e.g. Male, Female, Unknown). A list of possible options is available at the following site (Note: search the first column in the table for "SexList"): VariableCodesLookupList |
| SexSummary | Sex Summary | Plain Text | States the sex of the organisms from which samples were taken to make up the composite. A list of possible options is available at the following site (Note: search the first column in the table for "SexList"): VariableCodesLookupList |
| SizeDescr | Size Description | Plain Text | A description of the size of organisms (e.g. small, large, 100- 150cm). The size is determined by the discretion of the project as a grouping characteristic, and used only when sizes are estimated. Individual fish measurements are recorded in TotalLength or ForkLength, not this field. |
| StationCode & CompositeStationCode | Station Code | Plain Text | An alphanumeric code that represents the sampling site at which the sample was collected. The format is ###ABC123, where ### is the Hydrologic Unit number and ABC123 is an alphanumeric description of the station. An example is "111EELBRN", which is Hydrologic Unit 111 and an abbreviated code to indicate "Eel River - South Fork near Branscomb." Some stations may have a code that deviates from this format because the program or organization collecting the sample has their own code system. A complete list of stations and station information is available at this link: StationLookupList |
| StationName & CompositeStationName | Station Name | Plain Text | The name of the station at which the sample was collected. A complete list of stations and station information is available at this link: StationLookupList |
| SubmittingAgency | Submitting Agency | Plain Text | The organization or agency that is responsible for submission of the data to the database. A list of possible options is available at this link: AgencyLookupList |
| TagNumber | Tag Number | Number | References the individual tag number assigned to and placed on the organism (usually only fish). |

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| TissueCollectionComments | Tissue Collection Comments | Plain Text | Records any comments relating to the collection of the tissue sample for laboratory analysis. |
| TissueID | Tissue ID | Plain Text | A unique identifier that is assigned to the tissue part and is used to differentiate between different parts of the same fish or composited fish, versus an individual fish. |
| TissueName & CompositeTissueName | Tissue Name | Plain Text | The name of the tissue part used in the composite and analysis. A list of possible options is available at this link: TissueLookUpList |
| TissuePrep & CompositeTissuePrep | Tissue Prep | Plain Text | References the preparation or preservation method performed on the tissue part in order to create the composite. A list of possible options is available at this link: PrepPreservationLookUpList |
| TissueResultRowID | Tissue Result Row ID | Plain Text | Internal database identification code. Can be disregarded for analysis. |
| TissueWeight | Tissue Weight | Number | The measured weight of the tissue part included in the composite. |
| TLAvgLength(mm) | Total Average Length (mm) | Number | The average total length of fish used, in millimeters, from which samples were taken and added to the composite sample. |
| TLMax(mm) | Total Maximum Length (mm) | Number | The length of the longest fish used, in millimeters, from which a sample was taken and added to the composite. |
| TLMin(mm) | Total Minimum Length (mm) | Number | The length of the shortest fish used, in millimeters, from which a sample was taken and added to the composite. |
| TotalCount | Total Count | Number | The total number of alive organisms in the tissue sample associated with the same OrganismID. For example, if a bag has 45 mussels but 10 are dead, the TotalCount would be 35 and a comment regarding the 10 dead mussels would be recorded in the ProcessedOrganismsExpandedComments. |

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| TotalLength | Total Length | Number | The measured length of the organism from the most forward point of the head, with mouth closed, to the farthest tip of the tail. |
| Unit | Unit | Plain Text | Indicates the units used in the measurement of the analyte. Chemistry results are indicated by weight of analyte/volume of sample (e.g. "ng/L"). Results from sediment and tissue samples are indicated by weight/weight and includes whether the sample result is reported as wet weight (ww) or dry weight (dw) (e.g. "ng/g ww"). Surrogate recovery results use a unit of "%". Toxicity test results are recorded as percent that survived ("%"), weight of surviving individuals ("mg/ind"), cells per volume ("cells/ml"), reproduction rate ("neonates/adults"), etc. Taxonomic units are indicated by "count" or volume/area (e.g. "um3/cm2"). A list of possible options is available at this link: UnitLookupList |
| UnitCompositeWeight | Unit Composite Weight | Plain Text | The units used in measuring the weight of the Composite or SuperComposite. A list of possible options can be found at this link: UnitLookupList |
| UnitLengthFish | Unit Length Fish | Plain Text | The units used in measuring the length of the fish. A list of possible options can be found at this link: UnitLookupList |
| UnitTissueWeight | Unit Tissue Weight | Plain Text | The units used in measuring the weight of the tissue that was analyzed. A list of possible options can be found at this link: UnitLookupList |
| UnitWeightFish | Unit Weight Fish | Plain Text | The units used in measuring the weight of the fish. A list of possible options can be found at this link: UnitLookupList |
| WeightAvg(g) | Average Weight (g) | Number | Average weight, in grams, of the organisms whose samples make up the composite. |
| WeightSource | Weight Source | Plain Text | The physical location where the weight measurements were recorded (e.g. field, lab). |

For questions, comments, or concerns regarding these field names and definitions, please send an email with the subject line, "Tissue Data Dictionary," to: OIMA-Helpdesk@waterboards.ca.gov