| Field Name | Field Title | Data Type | Definition |
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| **BACollectionComments** | BA Collection Comments | Plain Text | Any notes or comments specifically related to when benthic macro invertebrate (BMI) or algae samples were collected. |
| **BAResult** | BA Result | Number | Represents the number of individuals of a given FinalID and life stage that were identified within a sample. This is for unadjusted (raw) counts and is to be used for cases where Counts is not used. Either BAResult or Counts should be populated (unless a ResQualCode other than "=" is used), but NOT both fields. |
| **BenthicResultRowID** | Benthic Result Row ID | Number | Internal database identification number for every row of benthic data. Can be disregarded in data analysis. |
| **Class** | Class | Plain Text | The taxonomic class of the organism found. |
| **CollectionDepth** | Collection Depth | Number | Records the depth or penetration, from the surface in the water or sediment column, at which the sample was collected. Default value equals "-88" if unknown or not recorded. |
| **CollectionDeviceName** | 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 |
| **CollectionMethodName** | 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. |
| **Comments** | Comments | Plain Text | Comments related to the value in the BAResult column. |

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| **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 |
| **Counts** | Counts | Number | Represents the final numeric result of a given FinalID and stage scaled up to grab size. Counts are adjusted to the area sampled and for biovolumes and it may represent raw counts if the full sample is sorted. Either BAResult or Counts should be populated (unless QACodes and ResQualCodes other than the defaults are used), but NOT both columns. |
| **DataQuality** | Data Quality | Plain Text | 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:<br>• "Metadata, QC record"- Not a measurement of environmental conditions<br>• "Passed QC"- Data passed all QC checks<br>• "Some review needed"- Data did not pass minor QC checks, some effort needed to review and defend data if used<br>• "Spatial Accuracy Unknown"- Data missing spatial datum information, data should not be used for fine scale spatial analysis<br>• "Extensive review needed"- Data did not pass QC some critical checks, high level of effort needed to defend data if used<br>• "Unknown Data Quality"- Data was not reviewed by the project. Data will need review before use<br>• "Reject Data"- Data was rejected by the project or data did not pass all critical QC checks. Data deemed unusable<br><br>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 | 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."<br><br>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. |

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| **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 |
| **DistinctOrganism** | Distinct Organism | Plain Text | Indicates whether or not this record represents a unique taxon in the sample. Distinct taxon equals "1" (or a higher number), and non-distinct equals "0". Default value equals "-88" if unknown. |
| **ExcludedTaxa** | Excluded Taxa | Plain Text | A list of possible options is available at the following site (Note: search the first column in the table for "BMIProgramExcludedTaxaList" or "ProgramExcludedTaxaList"): VariableCodesLookUpList |
| **Family** | Family | Plain Text | The taxonomic family of the organism found. |
| **FinalID** | 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 |
| **Genus** | Genus | Plain Text | The taxonomic genus of the organism found. |
| **GrabSize** | Grab Size | Number | Represents the total area of substrate collected for the sample. This is determined by the sampling device area and, if applicable, the number of transects or grabs sampled. |
| **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 |
| **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. |

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| **Latitude** | Target Latitude | Number | The latitude in decimal degrees of the sample site (should be positive). |
| **LifeStageName** | Life Stage Name | Plain Text | A code that indicates the stage of life of the organism (e.g. adult, juvenile, larvae). Default value equals "NR" for not recorded if unknown. A list of possible options is available at: LifeStageLookUpList |
| **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 (eg. 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: LocationLookUpList |
| **Longitude** | Longitude | Number | The longitude in decimal degrees of the sample site (should be negative). |
| **Orders** | Orders | Plain Text | The taxonomic order of the organism found. |
| **ParentProjectName** | 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: ParentProjectLookUpList |
| **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: PersonnelLookUpList |
| **Phylum** | Phylum | Plain Text | The taxonomic phylum of the organism found. |
| **ProgramName** | Program Name | Plain Text | The name of the program that is associated with the sample. A list of possible options is available at: ProgramLookUpList |
| **ProjectName** | Project Name | Plain Text | The project to which the sample result is associated. A list of possible options is available at: ProjectLookUpList |
| **ProjectCode** | 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: 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 |

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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 |
| **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 |
| **SampleComments** | Sample Comments | Plain Text | Used for any notes or comments specifically related to the sampling event at a particular station and/or the verification of GIS station information. |
| **SampleDate** | 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 Sample Date is the date in which sampling began. |
| **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. |
| **SampleType** | 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 |
| **SieveSize** | Sieve Size | Plain Text | The mesh size that particles in the sieve pass through (e.g. 0.5mm, 1.0mm, none, etc.). A list of possible options is available at the following site (Note: search the first column in the table for "SieveSizeList"): VariableCodesLookUp |
| **SieveSizeUnit** | Sieve Size Unit | Plain Text | The unit measurement for the mesh size (e.g. mm, um, etc.) that particles in the sieve pass through. Default value equals "None" if the unit is recorded in the SieveSize column. A list of possible options is available at this link: UnitLookUp |
| **Species** | Species | Plain Text | The taxonomic species name of the organism found. |

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| **StationCode** | 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** | 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 |
| **TaxonomicQualifier** | Taxonomic Qualifier | Plain Text | These codes are used to indicate reasons why terminal identification was not achieved for a particular taxon. Default value equals "None" if unknown. A list of possible options is available at the following site (Note: search the first column in the table for "TaxonomicQualifierList"): VariableCodesLookUp |
| **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: ListUnitLookUp |
| **UnitCollectionDepth** | Unit Collection Depth | Plain Text | The units used to measure the CollectionDepth. A list of possible options can be found at this link: ListUnitLookUp |
| **UnitGrabSize** | Unit Grab Size | Plain Text | The units used to measure the GrabSize (e.g. m2 or cm2). A list of possible options can be found at this link: ListUnitLookUp |

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