| | Data | | | | |
|----------------------------|------------|---|----------|-----|--|
| Data Element Name | Туре | Description | Required | SVL | Error Check |
| Client_Sample_ID | Text(35) | Client's identifier for a sample. If a sample is analyzed as a duplicate, matrix spike, or matrix spike duplicate, append suffixes "DUP", "MS", and "MSD" respectively. For Lab QC samples such as blanks and LCS enter the LabSampleID in this field | Yes | No | Not null Length ≤ 35 Correct naming convention for Lab Duplicates, MS, and MSD samples |
| Lab_Analysis_Ref_Method_ID | Text(80) | The laboratory reference method ID. Standard values for methods are specified by Florida DEP and SFWMD. | Yes | Yes | Not null Length ≤ 80 SVL check against project library |
| Lab_Sample_ID | Text(50) | Laboratory tracking number for field samples and laboratory generated QC samples | Yes | No | Not null Length ≤ 50 |
| LabID | Text(7) | Identification of the laboratory performing the analysis. Use DOH certification number if possible | Yes | Yes | Not null Length ≤ 7 SVL check against ADaPT standard value list |
| Client_Analyte_ID | Text(30) | Unique identifier for an analyte name. This is typically the CAS number, NELAC number, or Florida specified ID number | Yes | Yes | Not null Length ≤ 30 SVL check against ClientAnalyteIDs entered in the project library Completeness (in the project target analyte list for the method and matrix or reported as a spike or surrogate for the method and matrix as applicable) |
| Analyte_Name | Text(60) | The chemical name for the analyte. Values for Analyte Names are specified by Florida DEP and SFWMD. | Yes | Yes | Not null Length ≤ 60 SVL check against Analyte Names entered in the project library for a method and matrix Spikes reported in EDD for LCS and MS/MSD match project library for method and matrix For organics, correct surrogates are reported according to the method requirements as established in the project library |
| Result | Number(10) | Reported result for the analyte | Yes | No | Not null Length ≤ 10 Numeric except for microbiologicals, which may be text; and REDOX, which may be negative Result = MDL if Lab_Qualifiers contains "U" |

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|-----------------------------|------------|--|-------------|------|---|
| Data Element Name | Туре | Description | Required | SVL | Error Check |
| Error | Text | The two sigma error for radiochemistry results. Do note enter the "+" or "-" character in this field | Conditional | No | Not null for radiochemistry result, spike, and tracer or carrier records Numeric Length ≤ 10 |
| Result_Units | Text(10) | Units for the result | Yes | Yes | Not null Length ≤ 10 SVL check against the units entered in project library for the method, matrix, and analyte |
| Lab_Qualifiers | Text(7) | A string of single letter result qualifiers assigned by the laboratory. Always use the "U" qualifier for non-detects. Other qualifiers may apply. Order is insignificant. | Conditional | Yes | Not null according to conditions listed at the end of this table Length ≤ 7 SVL check against ADaPT standard values for lab qualifiers Consistency check (see list at end of this table) |
| Detection_Limit | Number(10) | Method detection limit for the measure analyte | Yes | No | Not null for target analytes Length ≤ 10 Numeric Less than or equal to the Reporting Limit Not zero or negative |
| Analyte_Type | Text(7) | Defines the type of result such as surrogate, spike, or target compound. | Yes | Yes | Not null Length ≤ 7 SVL check against the ADaPT standard values for Analyte Type |
| Dilution | Number(10) | Overall dilution of the sample aliquot. A value of one (1) corresponds to nominal method conditions. Insert value of one (1) for method blanks, LCS, and LCSD. | Yes | No | Not null Length ≤ 10 Numeric |
| Percent_Moisture | Number(10) | Percent of sample composed of water. Enter value for soil and sediments sample only. | Conditional | No | Not null if matrix = soil or sediment Length ≤ 10 Numeric |
| Percent_Recovery | Text(5) | Percent recovery value of a spiked or surrogate compound. If sample dilution yields no or very low recovery enter "DIL". If sample matrix interference yields no recovery, enter "INT". If the spike or surrogate was not added to the sample enter "NS" | Conditional | No | Not null if AnalyteType = "SURR", "SPK", or "TRACER" Length ≤ 5 Numeric or "DIL", "INT", or "NS" |
| Relative_Percent_Difference | Number(5) | Relative percent difference between two QC results | Conditional | No | Not null if AnalyteType = "SPK" and QCType = "LCSD" or "MSD"; or Not null if QCType = "DUP Length ≤ 5 Numeric |

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|--------------------|------------|---|-------------|-----|---|
| Data Element Name | Туре | Description | Required | SVL | Error Check |
| Reporting_Limit | Text(10) | Practical quantitation limit for the measured analyte. Also used as the reporting limit | Conditional | No | Not null if AnalyteType = "TRG" or "SPK" Length ≤ 10 Numeric Not zero or negative |
| Project_Number | Text(30) | Number assigned by the client to associate a sample to a project, purchase order, or requisition | Yes | Yes | Length ≤ 30 SVL check against ADaPT standard values for Project Number if entered |
| Project_Name | Text(90) | Project name assigned by the client | Yes | Yes | Length ≤ 90 Check against ADaPT standard values for Project Name if entered |
| End_Date_Collected | Date/Time | The date and time of sample collection. Format as: MM/DD/YYYY hh:mm where MM = two digit month, DD = two digit date, YYYY = four digit year, hh = two digit hour, and mm = two digit minutes | Conditional | No | Not null if QCType = "N", "DUP", "MS", or "MSD" Valid date/time value Correctly formatted as MM/DD/YYYY hh:mm Logical (does not supersede sample preparation and/or sample analysis date/time value) |
| Matrix_ID | Text(20) | The sample matrix for the reported analyte. The standard values for Matrix_ID are specified by the State of Florida | Yes | Yes | Not null Length ≤ 20 SVL check against ADaPT standard values for MatrixID |
| QC_Type | Text(7) | Identifies the type of sample (i.e.: method blank, LCS, LCSD, laboratory duplicate, MS, MSD, or normal field sample. For normal field samples enter "N" | Yes | Yes | Not null Length ≤ 7 SVL check against ADaPT standard values for QC_Type |
| Shipping_Batch_ID | Text(25) | Unique identifier assigned to a cooler or shipping container or, group of coolers or shipping containers that links samples together. The Shipping_Batch_ID is provided by the client on the chain of custody. | Conditional | No | Required if QC_Type = N, DUP, MS, or MSD Length ≤ 25 |
| Temperature | Number(10) | Temperature in degrees C of the sample as received by the lab | No | No | Numeric, if reported Length ≤ 10 if reported |
| Preparation_Type | Text(25) | The method used to prepare the sample. For methods that do not have a preparation method as part of the analysis enter "No Prep" | Yes | Yes | Not null Length ≤ 25 SVL check against ADaPT standard values for Preparation_Type |
| Analysis_Type | Text(10) | Indicates the type of analysis (i.e. dilutions, re-analyses or re-extracts). This field provides distinction among records when multiple analyses are submitted for the same sample and method. Enter RES for the initial analysis. | Yes | Yes | Not null Length ≤10 SVL check against ADaPT standard values for Analysis_Type |

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| Data Element Name | Type | Description | Required | SVL | Error Check |
| Reportable_Result | Text(3) | indication of whether of not the laboratory chooses and individual analyte result as reportable. Enter "YES" if the result is reportable. Enter "NO" if the result not. | Conditional | Yes | Not null if Analyte lype = "IRG" Length ≤ 3 if reported Value = "YES" or "NO" Duplicate "YES" for a given ClientSampleID, Method, Matrix, ClientAnalyteID, and TotalOrDissolved value |
| Date_Prepared | Date/Time | The date and time of sample preparation or extraction. Format as: MM/DD/YYYY hh:mm where MM = two digit month, DD = two digit date, YYYY = four digit year, hh = two digit hour, and mm = two digit minutes | Yes | No | Not null Valid date/time value Correctly formatted as MM/DD/YYYY hh:mm Logical (Date_Prepared does not precede Date_Collected and supersede Date_Analyzed |
| Date_Analyzed | Date/Time | The date and time of sample analysis. Format as: MM/DD/YYYY hh:mm where MM = two digit month, DD = two digit date, YYYY = four digit year, hh = two digit hour, and mm = two digit minutes | Yes | No | Not null Valid date/time value Correctly formatted as MM/DD/YYYY hh:mm Logical (Date_Analyzed does not precede Date_Collected and Date_Analyzed) |
| Total_Or_Dissolved | Text(3) | Indicates if the result is reported on a total or dissolved sample fraction. Report only for aqueous results | Yes | Yes | Not null Reported as "TOT" or "DIS" for water matrices and "N/A" for non-water matrices Length ≤ 3 |
| Prep_Batch_ID | Text(13) | Unique laboratory identifier for a batch of samples of similar matrix prepared together for analysis by one method and treated as a group for method blank, LCS, and LCSD association. The Prep_Batch-ID links method blanks and laboratory control samples (LCS/LCSD) to associated samples. | Yes | No | Not null Length ≤13 Each distinct Prep_Batch_ID for a method and matrix has records for the same method and matrix where QCType = MB and LCS Each distinct Prep_Batch_ID for a method and matrix for each MB and LCS contains one or more sample records with the same method, matrix, and Prep_Batch_ID. |

| | Data | | | | |
|------------------------|-----------|--|-------------|-----|--|
| Data Element Name | Туре | Description | Required | SVL | Error Check |
| Method_Batch_ID | Text(13) | Unique laboratory identifier for a batch of samples of similar matrix analyzed by one method and treated as a group for laboratory duplicate, matrix spike, and matrix spike duplicate association. The Method_Batch_ID links laboratory duplicates, matrix spikes, and matrix spike duplicates to associated samples. | Yes | No | Not null Length ≤ 13 For non-metal inorganic methods, each distinct Method_Batch_ID for a method and matrix has records reported where QCType = MS and DUP For metals each distinct Method_Batch_ID for a method and matrix has records reported where QCType = MS and DUP For organic methods each distinct Method_Batch_ID for a method_Batch_ID for a method and matrix has records where QCType = MS and MSD or QCType Each Method_Batch_ID for a method and matrix has records where QCType = MS and MSD Each Method_Batch_ID for a method and matrix has sample records with the same method, matrix and Method_Batch_ |
| Preservation_Intact | Text(3) | Indicates if the sample was preserved properly based on measurement at the time of sample receipt at the laboratory. This applies to each bottle collected | Yes | Yes | Not null Length ≤ 3 Reported as "Yes" or "No" Preservation_Intact = "No" if Lab_Qualifiers contains "Y" |
| QC_Spike_Added | Number(5) | Value of spike or surrogate compound entered as a numeric character | Conditional | No | Length ≤ 5 if reported Required for SFWMD |
| Result_Comments | Text(255) | Free-form text where data provider relates information they consider relevant to the sample that is not included in the above fields. | Conditional | No | Not null for certain constraints Length ≤ 255 |
| Lab_Reporting_Batch_ID | Text(13) | Laboratory identifier for a group of samples and laboratory QC all reported within one EDD or batch. The Lab_Reporting_Batch_ID is equivalent to the sample delivery group, lab work number, login ID, etc. | Yes | No | Not null Length ≤ 13 The same value is reported in all records within the EDD |