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**LIST OF TABLES**

Table A-1	Data Quality Objectives
Table A-2	Decision Criteria used for Initial Disposal Classification of Sediments under RCRA and TSCA Disposal Rules
Table B-1	Example Sample ID and Horizontal Coordinates
Table B-2	River Section 1 Program Summary
Table B-3	River Section 2 Program Summary
Table B-4	River Section 3 Program Summary
Table B-5	Sample Container and Preservation Requirements
Table B-6a – B-6j	Reference Limit and Evaluation Tables for Analytical Methods
Table B-7a – B-7n	Measurement Performance Criteria Tables for Analytical Methods
Table B-8	Data Collected During Sediment Core Collection
Table B-9	Data Collected During Sample Processing in the Field Lab
Table B-10	Valid Values for PCBs
Table C-1	Summary of Analyses for Initial PE Acceptance Criteria Development
Table C-2	Summary of Analyses for Inter-Laboratory Comparison Study
Table D-1	Format of an Environmental Standards Quality Assurance Review

**APPENDICES**

Appendix 1	SOP for Sediment Core Collection
Appendix 2	SOP for Bathymetric Survey
Appendix 3	SOP for Sub-Bottom Acoustic and Electromagnetic Surveying Equipment
Appendix 4	SOP for Sediment Probing
Appendix 5	SOP for the Analysis of PCBs by SW-846 Method 8082 (GEHR8082)
Appendix 6	SOP for the Extraction and Cleanup of Sediment/Solid Samples for PCB Analysis Using the Pressurized Fluid Extraction by SW-846 Method 3545 (GEHR3545)
Appendix 7	SOP for the Extraction and Cleanup of Sediment/Soil Samples for PCB Analysis Using the Soxhlet Extraction by SW-846 Method 3540C (GEHR3540C)
Appendix 8	SOP for Analysis of PCB Homologs by EPA Method 680 (GEHR680)
Appendix 9	SOP for Data Package Deliverable (DPSOP)
Appendix 10	SOP for Grain Size
Appendix 11	SOP for Atterberg Limit
Appendix 12	SOP for Specific Gravity
Appendix 13	SOP for Bulk Density

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**APPENDICES (Cont.)**

- Appendix 14 *(This appendix is no longer necessary. It has been left for convenience for potential future use).*
- Appendix 15 SOP for Total Organic Carbon
- Appendix 16 SOP for USCS Classification
- Appendix 17 SOP for Side Scan Survey Procedures
- Appendix 18 SOP for Core Processing
- Appendix 19 *(This appendix is no longer necessary. It has been left for convenience for potential future use).*
- Appendix 20 SOP for <sup>137</sup>Cs
- Appendix 21 SOP for TCLP Preparation by 1311
- Appendix 22 SOP for VOAs With TCLP Preparation
- Appendix 23 SOP for SVOAs With TCLP Preparation
- Appendix 24 SOP for Pesticides With TCLP Preparation
- Appendix 25 SOP for Herbicides With TCLP Preparation
- Appendix 26 SOP for Preparation of Metals and Mercury and Analysis of Mercury in Leachate  
(Refer to Appendix 29 for the Analysis of Metals by ICP)
- Appendix 27 SOP for Ignitability
- Appendix 28 SOP for PCDD/PCDF
- Appendix 29 SOP for Preparation and Analyses of Metals and Mercury in Sediment
- Appendix 30 Performance and Reporting of Field Audits
- Appendix 31 Performance and Reporting of Analytical Laboratory Audits
- Appendix 32 SOP for Data Validation of VOA Data (DV8260B)
- Appendix 33 SOP for Data Validation of SVOA Data (DV8270C)
- Appendix 34 SOP for Data Validation of Pesticide Data (DV8081A)
- Appendix 35 SOP for Data Validation of Herbicide Data (DV8151A)
- Appendix 36 SOP for Data Validation of PCBs (DV8082)
- Appendix 37 SOP for Data Validation of PCB (Homolog) Data (by GEHR680)
- Appendix 38 SOP for Data Validation of PCDD and PCDF Data (DV1613B)
- Appendix 39 SOP for Data Validation of ICP Metals Data (DV6010B)
- Appendix 40 SOP for Data Validation of Mercury Data (DV74707471)
- Appendix 41 SOP for Data Validation of TOC Data (DVTOC)
- Appendix 42 EDD Specifications

## **APPENDICES**

## **APPENDIX 42**

**Environmental Standards, Inc.**  
**General Electric Co. Hudson River PCBs Superfund Site**  
**Electronic Data Deliverable Specifications**

## **Introduction**

The purpose of this document is to describe the processing of the analytical data received from the laboratory and includes the required specifications of the electronic data deliverable (EDD) along with the field sample and core data import format.

## **File Format**

All data from the laboratory must be stored in an ASCII file using a tab-delimited standard format. Maximum length of text fields is indicated in the parentheses under Column Datatype. If the information is less than the maximum length, do not pad the record with spaces.

Each record must be terminated with a carriage return/line feed (i.e., standard DOS text file). The file can be produced using any software with the capability to create ASCII files. Date is reported as MM/DD/YY (month/day/year) and time as HH:MM (hour:minute). Time uses a 24 hour clock, thus 3:30 p.m. will be reported as 15:30.

Six files are required: one each for core data, field samples, laboratory samples, tests, results, and batches. The files must have valid DOS (8.3) filenames. The filename extensions are used to indicate the file type as follows:

- \*.COR for core data rows
- \*.FLD for field sample rows
- \*.SMP for laboratory sample rows
- \*.TST for test rows
- \*.RES for result rows
- \*.BCH for batch rows

The core data file (\*.COR) and field sample file (\*.FLD) are required files that will originate from the field contractor. The filenames for the .COR and .FLD deliverables are defined as the date of the file's creation.

The 8-character portion filenames for the lab generated files must be the same for each group of four files. Filename conventions are defined as the sample delivery group. Although Environmental Standards anticipates that all four files will be prepared and loaded into the database together in one group, this is not necessary. Each file can be loaded separately if desired.

## **Data Integrity Rules**

If a field is to be considered part of the primary key of a table, it is indicated below by the presence of "PK" in the *PK* column. The combination of values in each primary key must be unique within the file. Also, referential integrity must be enforced between tables. That is, the values of `sys_sample_code` present in the Result and Test tables must also be present in the Sample table.

The key fields in the test table may appear complicated, so they are discussed further here. By default, only two fields are defined as part of a unique key: `sys_sample_code` and `lab_anl_method_name`. This means that each combination of sample ID and lab method can be used to uniquely define a lab test event. For this project, we are going to store retests or re-dilutions as separate test events. In order to achieve this, include `analysis_date` and `analysis_time` as part of the unique key of

test. This will allow multiple occurrences of a given combination of sample ID and lab method, provided that analysis date and time is different for each retest. Other common situations are discussed below. The fields that are included as part of the unique key on test are indicated below by the presence of "PK" in the *PK* column. These fields are part of the uniqueness constraint needed by the data management user, so they must be required in the EDD.

- A. The data management users intend to import the full suite of test level information, including column-number and analysis-time. **Environmental Standards, Inc. requires the inclusion of both the column number and analysis time for this project.**
- B. Some metal analyses can be done on unfiltered samples (to obtain total concentrations) or can be done on filtered samples (to get dissolved concentrations). The data management users need to use the same method name value for both of these tests, and therefore require another field to distinguish between these test types. **Environmental Standards, Inc. requires the total or dissolved field to be populated for this project.**

### **Null Format**

Many fields are optional, and the list of valid values may be defined in a project or lab specific manner as determined by the laboratory and project manager. When a field is not listed as required, this means that a null or blank may be appropriate. However, the blank value must still be surrounded by tabs. In other words, the number of fields is always the same, whether or not the fields include data is optional.

### **OPL Naming Convention of Field Samples**

Field Samples being submitted to the data management system follow the standard Organization, Project, Location (OPL) naming structure. As an example, a field sample ID of 'RS1-9594-WS001-' designates:

Organization = RS1  
Project = 9594  
Location = WS001

The field sample ID describes a core collected in River Section 1 (RS1) between river miles 195 and 194 (9594) at a screening location on the western half of the channel (WS) and is core number 1 (001). Additional depth information is added after the location (WS001) to complete the unique field sample ID.

There are to be no dashes used within in the OPL naming convention. For example river miles 195 and 194 should be characterized as 9594 and not 95-94. There is to be no deviation in this regard due to system requirements.

The contractor is responsible to let the lab know the proper Organization, Project, Location (OPL) structure to append to the field sample id on the chain of custody. If the field on the chain of custody is too small for the new sample naming convention, please place the proper OPL codes in the comments field so the lab can append the information to the field sample name. If this information is not present the EDD will fail EDD checks and will be returned to the data generator for corrections.

There are some samples, while having no real sampling location, should also follow the OPL naming convention. They are PE samples and Lab QC samples.

PE samples will use the same organization and project codes as the other samples with which they are sent. The location will be the concatenation of PE and the date in mmddyy format. The sample custodian ID and a sequential number will be used at the end to identify the sample. As an example, a PE sample sent on August 21, 2002 for the project above would look like RS1-9594-PE082102-A01. A second PE sample would have A02 at the end.

Lab QC samples will use the concatenation of LABQC and the SDG for the location code, while maintaining the same organization and project codes. Use the internal laboratory sample ID at the end to identify the sample. For example a method blank QC sample (A3910) for the project mentioned above would look like RS1-9594-LABQC[SDG]-A3910.

### Examples

Below are examples of sample types to be used in the project, showing when fields need to be populated and when it is not necessary to populate fields.

*QC fields in a normal field sample (i.e., Sample\_type\_code = FS, TB, etc.)*

The following table shows a subset of the fields in the result file for a normal field sample. Notice that all QC fields are blank.

cas_rn	result value	qc original conc	qc spike added	qc spike measured	qc spike recovery	qc dup original conc	qc dup spike added	qc dup spike measured	qc dup spike recovery
93-76-5	1.56								
94-75-7	3.17								
94-82-6	2.31								

*QC fields in a normal field sample with surrogates (i.e., Sample\_type\_code = FS, TB, etc.)*

The following table shows a subset of the fields in the result file for a normal field sample. Notice that QC fields are blank except on surrogate rows.

Cas_rn	Result value	result unit	result type code	qc original conc	qc spike added	qc spike measured	qc spike recovery
93-76-5	1.56	mg/l	TRG				
94-75-7	3.17	mg/l	TRG				
PHEN2F		mg/l	SUR		12.5	12.9	103

*QC fields in a matrix spike (i.e., Sample\_type\_code = MS)*

The following table shows some of the fields in the result file for a matrix spike sample. Notice that all "dup" QC fields are blank, and that the result\_value field is not needed. Also, the qc\_rpd field would be blank for these rows.

Cas_rn	Result value	qc original conc	qc spike added	qc spike measured	qc spike recovery	qc dup original conc	qc dup spike added	qc dup spike measured	qc dup spike recovery
93-76-5		1.56	4.18	5.36	90.9				
94-75-7		3.17	4.18	7.15	95.2				
94-82-6		2.31	4.22	5.66	79.3				

*QC fields in a matrix spike duplicate (i.e., Sample\_type\_code = SD)*

The following table shows a subset of the fields in the result file for a matrix spike duplicate sample. Notice that all "dup" QC fields are completed, and that the result\_value field is not needed. **Also, the qc\_rpd field would be completed for these rows.**

cas_rn	result value	qc original conc	qc spike added	qc spike measured	qc spike recovery	qc dup original conc	qc dup spike added	qc dup spike measured	qc dup spike recovery
93-76-5						1.56	4.23	5.70	97.8
94-75-7						3.17	4.23	7.62	105
94-82-6						2.31	4.13	5.33	73.1

*QC fields in an LCS (i.e., laboratory control sample, blank spike, Sample\_type\_code = LCS)*

The following table shows a subset of the fields in the result file for an LCS sample. **The qc\_rpd field would be blank for these rows.**

Cas_rn	Result value	qc original conc	qc spike added	qc spike measured	qc spike recovery	qc dup original conc	qc dup spike added	qc dup spike measured	qc dup spike recovery
93-76-5			5.00	5.26	105				
94-75-7			1.00	1.02	102				
94-82-6			12.5	12.9	103				

*Retests*

The following table shows how to report retests in an example where a sample was retested at dilution. The end user would see the first two constituents (75-25-2, and 67-66-3) in the initial test, and constituent 95-95-4 in the diluted retest. The other results would be "turned off" by setting the reportable\_result field to "No".

Test_type	cas_rn	result_value	reportable_result
initial	75-25-2	1.2	Yes
initial	67-66-3	3.4	Yes
initial	95-95-4	100	No
retest	75-25-2	0	No
retest	67-66-3	0	No
retest	95-95-4	78.3	Yes

### *Second Columns*

The following table shows how to report first and second column confirmation results. The end user would see the first and third constituents (75-25-2, and 95-95-4) as "primary" in the first column, and constituent 67-66-3 as "primary" in the second column. The other results would be "turned off" by setting the reportable\_result field to "No".

column_number	cas_rn	result_value	reportable_result
1C	75-25-2	1.2	Yes
1C	67-66-3	3.4	No
1C	95-95-4	5.6	Yes
2C	75-25-2	1.3	No
2C	67-66-3	3.7	Yes
2C	95-95-4	5.4	No

### *Units*

Units are to be reported consistently for the duration of the project. The result\_unit field is required to be reported as specified in the reference values. Associated measurements (i.e., reporting detection limit, method detection limit) should be reported consistently with the result units.

## Core Data Import Format

#	Attribute Name	Column Datatype	PK	Required	Attribute Definition
1	core_ID	Text(14)	PK	required	Unique core ID
2	core_date	Date		required	Date core was collected (in MM/DD/YY format).
3	core_time	Time		required	Time core was collected (in 24-hr (military) HH:MM format).
4	sampling_technique	Text(4)		required if applicable	Indicates how sample was collected. Valid values are CORE or GRAB
5	weight	Text(4)		required if applicable	The weight of the full core or grab sample
6	weight_unit	Text(4)		required if applicable	Unit of measurement for the weight of the full core or grab sample
7	northing	Text(20)		required	Northing coordinate (NY state plane east NAD83)
8	easting	Text(20)		required	Easting coordinate (NY state plane east NAD83)
9	coordinate_unit	Text(15)			Unit of measurement for the northing and easting coordinates
10	water_depth	Text(5)		required	Water depth at core collection location
11	water_depth_unit	Text(15)			Unit of measurement for the core collection location water depths
12	core_recovered	Yes/No		required	Indicates if core collection was possible at target coordinates. If "No", target coordinates are entered in Northing and Easting fields.
13	pen_depth	Text(4)			Total penetration depth of sediment core tube
14	field_rec_depth	Text(5)			Total length of sediment core recovered
15	lab_rec_depth	Text(5)			Recovery depth measured at the field lab
16	probe_depth	Text(5)		required	Depth of penetration of sediment probe
17	prp_depth_unit	Text(15)			Units of measurement for the penetration depths of the core tube and sediment probe, and the recovery depths.
18	probe_sed_type	Text(20)		required	General sediment texture description based on probing – 'FINE', 'COARSE', 'ROCK'
19	probe_desc	Text(255)			Additional information from sediment probing results.
20	core_tube	Text(10)			Type of core tube used to collect sediment sample – 'LEXAN', 'ALUMINUM'
21	sampler	Text(30)			Name or initials of sampler.
22	sampling_company_code	Text(10)			Contractor code. For valid value list consult the reference values for the project.

## Field Sample Import Format

#	Attribute Name	Column Datatype	PK	Required	Ref. Value?	Attribute Definition
1	sys_sample_code	Text(20)	PK	required		Unique sample identifier. Each sample must have a unique value, including blanks and duplicates. This field must be populated as follows: COC#, which is "COC" followed by a number, then a dash (-), then the Item#, which is a sequential three digit number that is typed on the Chain-of-Custody to the left of each sample (ex: the first sample on the chain would be COC042602-001, second sample would be COC042602-002, etc.). This file should only contain field samples, including field blanks, equipment blanks, and field duplicates. This table should not include laboratory samples. <b>Required</b>
2	sample_name	Text(30)		required		Unique field sample ID. Each sample must have a unique value. <b>The Organization, Project, Location naming convention, as described on page 2, must be followed.</b>
3	sample_matrix_code	Text(10)		required	Yes	Code which distinguishes between different types of sample matrix. For example, soil samples must be distinguished from ground water samples. The matrix of the sample as analyzed may be different from the matrix of the sample as retrieved (e.g. TCLP leachates), so this field is required at the sample level. For valid value list, consult the reference values supplied for this project.
4	sample_type_code	Text(10)		required	Yes	Code which distinguishes between different types of samples. For valid value list, consult the reference values supplied for this project.

5	sample_source	Text(10)		required	Yes	This field identifies where the sample came from, either <b>Field</b> or <b>Lab</b> . In this import, this should always be <b>Field</b> .
6	parent_sample_code	Text(20)		required if applicable		Must be blank for normal field samples. The value of "sys_sample_code" that uniquely identifies the sample that was the source of this sample.
7	sample_date	Date		required		Date sample was collected (in MM/DD/YY format).
8	sample_time	Time		required		Time of sample collection in 24-hr (military) HH:MM format.
9	start_depth	Text(5)		required		Beginning depth (top) of soil sample.
10	end_depth	Text(5)		required		Ending depth (bottom) of soil sample.
11	depth_unit	Text(15)		required		Unit of measurement for the sample begin and end depths.
12	test_requested	Text(35)	PK	required	Yes	Laboratory analytical method name or description. For valid value list, consult the reference values supplied for this project.
13	preservative_chemical	Text(50)		required if applicable		If sample is preserved, enter type of preservative in this field (use chemical symbol). If sample is unpreserved, this field must be null.
14	preservative_temperature	Text(5)		required if applicable		Temperature to which sample is cooled in the format of number and unit without the degree symbol (i.e. if temp. is 4 degrees Celcius it should be reported as "4C" not "4°C").
15	chain_of_custody	Text(15)		required		Chain of custody identifier. A single sample may be assigned to only one chain of custody.
16	sent_to_lab_date	Date				Date sample was sent to lab (in MM/DD/YY format for EDD). Not included in the laboratory EDD.
17	custodian_initials	Text(5)				Initials of sample processing custodian
18	texture_desc	Text(11)			Yes	Uniform codes indicating sediment type or composition (primary/some/little/trace). Example: CS/--/--/OR (sample is primarily coarse sand with

						trace organics). For valid value list, consult the reference values supplied for the project.
19	num_containers	Integer		required		Number of sample containers
20	general_desc	Text(255)				General visual description information for sediment core section.
21	cultural_obs	Text(255)				Description of cultural artifacts (if any) found in the sample.
22	sample_archived	Yes/No				Indicates if a split sample was archived.
23	cooler_id	Text(30)		required		Sample container identifier.
24	epa_split	Yes/No				Indicates if the sample was chosen as a split by the EPA.
25	tat_expected	Double		required		Expected turn-around-time in number of business days for laboratory results.
26	matrix_spike_yn	Yes/No		required	Yes	"Y" if the sample was chosen for matrix spike analysis, "N" if not chosen.
27	matrix_spike_dup_yn	Yes/No		required	Yes	"Y" if the sample was chosen for matrix spike duplicate analysis, "N" if not chosen.
28	jar_lot_number	Text(30)		required		ID of the sample jar, assigned by the supplier.

## Sample Import Format

#	Attribute Name	Column Datatype	PK	Required	Ref. Value?	Attribute Definition
1	sys_sample_code	Text(20)	PK	required		<p>Unique sample identifier. Each sample must have a unique value, including spikes and duplicates. Laboratory QC samples must also have unique identifiers. For matrix spike, matrix spike duplicate, and laboratory replicate samples, this field must be populated as follows: COC#, which is "COC" followed by a number, then a dash (-), then the Item#, which is a sequential three digit number that is typed on the Chain-of-Custody to the left of each sample (ex: COC042602-001), followed by "MS" for matrix spike, "SD" for matrix spike duplicate, or "LR" for laboratory replicate. This table should <b>only</b> contain laboratory-generated samples, including lab blanks, blank spikes, matrix spikes, matrix spike duplicates, and laboratory replicates. This table should not include field samples.</p> <p><b>Required</b></p>
2	lab_sample_id	Text(60)		required		<p>Laboratory sample identifier. <b>The Organization, Project, Location naming convention, as described on page 2, must be followed. Required</b></p>
3	sample_type_code	Text(10)		required	Yes	<p>Code which distinguishes between different types of sample. For valid value list, consult the reference values supplied for the project.</p>
4	sample_matrix_code	Text(10)		required	Yes	<p>Code which distinguishes between different types of sample matrix. For example, soil samples must be distinguished from ground water samples. The matrix</p>

						of the sample as analyzed may be different from the matrix of the sample as retrieved (e.g. TCLP leachates), so this field is required at the sample level. For valid value list, consult the reference values supplied for the project.
5	sample_source	Text(10)		required	Yes	Must be "Lab" for internally generated laboratory QC samples. For example, a matrix spike duplicate sample would be a "Lab" sample.
6	parent_sample_code	Text(20)		required where applicable		The value of "sys_sample_code" that uniquely identifies the sample that was the source of this sample. For example, the value of this field for a laboratory replicate sample would identify the normal sample of which this sample is a replicate (same sys_sample_code as replicate without the "LR" designation). Required in the laboratory EDD for all laboratory "clone" samples (e.g., spikes and duplicates). Must be blank for samples that have no parent (e.g., lab blanks and lab control samples). This field must be filled out for those samples which have "parents."
7	Comment	Text(255)				Sample comments as necessary (optional).
8	sample_date	Date/Time				Must be blank for laboratory generated samples. Date of sample collection in MM/DD/YY format. <b>Will be a blank field for this project.</b>
9	sample_time	Text(5)				Must be blank for laboratory generated samples. Time of sample collection in 24-hr (military) HH:MM format. <b>Will be a blank field for this project.</b>

10	standard_solution_source	Text(20)				Relevant only for laboratory-generated samples. Textual description of the source of standard solutions as needed for certain laboratory samples (e.g., LCS).
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## Test Import Format

#	Attribute Name	Column Datatype	PK	Required	Ref. Value?	Attribute Definition
1	sys_sample_code	Text(20)	PK	required		Unique sample identifier. Each sample must have a unique value, including spikes and duplicates. Laboratory QC samples must also have unique identifiers. For matrix spike, matrix spike duplicate, and laboratory replicate samples, this field must be populated as follows: COC#, which is "COC" followed by a number, then a dash (-), then the Item#, which is a sequential three digit number that is typed on the Chain-of-Custody to the left of each sample (ex: COC042602-001), followed by "MS" for matrix spike, "SD" for matrix spike duplicate, or "LR" for laboratory replicate. <b>Required</b>
2	lab_anl_method_name	Text(35)	PK	required	Yes	Laboratory analytical method name or description. For valid value list, consult the reference values supplied for this project.
3	analysis_date	Date/Time	PK	required		Date of sample analysis in MM/DD/YY format. Must refer to the beginning of the analysis for this project.
4	analysis_time	Text(5)	PK	required		Time of sample analysis in 24-hr (military) HH:MM format. Must refer to the beginning of the analysis for this project. Note that this field, combined with the "analysis_date" field is used to distinguish between retests and reruns. Please ensure that retests have "analysis_date" and/or "analysis_time" different from the original test event (and fill out the test_type field as needed).
5	total_or_dissolved	Text(1)	PK	required	Yes	It must be either "T" for total [metal] concentration, "D" for dissolved or filtered [metal] concentration, or "N" for organic (or other) constituents for which neither "total" nor "dissolved" is applicable.

6	column_number	Text(2)	PK	required	Yes	Required, it must be either "1C" for first column analyses, "2C" for second column analyses, or "NA" for analyses for which neither "1C" nor "2C" is applicable. If any "2C" tests are reported, then there must be corresponding "1C" tests present also. Also, laboratories will be reporting which of the two columns is to be considered "primary". This distinction is handled by the "reportable_result" field in the result table.
7	test_type	Text(10)	PK	required	Yes	Type of test. Valid values include "initial", "reextract", and "reanalysis".
8	lab_matrix_code	Text(10)		required	Yes	Code which distinguishes between different types of lab sample matrix. The matrix of the sample as analyzed may be different from the matrix of the sample as retrieved (e.g. TCLP leachates). Valid values include "W" and "S".
9	analysis_location	Text(2)		required	Yes	Must be either "FI" for field instrument or probe, "FL" for mobile field laboratory analysis, or "LB" for fixed-based laboratory analysis.
10	basis	Text(10)		required	Yes	It must be either "Wet" for wet-weight basis reporting, "Dry" for dry-weight basis reporting, or "NA" for tests for which this distinction is not applicable.
11	dilution_factor	Text(4)		required		Effective test dilution factor.
12	prep_method	Text(35)		required if applicable	Yes	Laboratory sample preparation method name or description. For valid values consult the reference list supplied for the project.
13	prep_date	Date/Time		required if applicable		Date of sample preparation in MM/DD/YY format. Must refer to the end of the prep for this project.
14	prep_time	Text(5)		required if applicable		Time of sample preparation in 24-hr (military) HH:MM format. Must refer to the end of the prep for this project.
15	leachate_method	Text(15)		required if		Laboratory leachate generation

				applicable		method name or description. A list of valid method names is not required for the laboratory EDD unless otherwise specified by the project manager.
16	leachate_date	Date/Time		required if applicable		Date of leachate preparation in MM/DD/YY format. Must refer to the end of the leachate for this project.
17	leachate_time	Text(5)		required if applicable		Time of leachate preparation in 24-hr (military) HH:MM format. Must refer to the end of the leachate for this project.
18	lab_name_code	Text(10)		required		Unique identifier of the laboratory. Must be consistent throughout the project.
19	data_package_level	Text(10)		required	Yes	Data package level. Values are "A", "B", or "AB".
20	lab_sample_id	Text(20)		required		Laboratory sample identifier.
21	percent_moisture	Text(5)		required		Percent moisture of the sample portion used in this test; this value may vary from test to test for any sample. Numeric format is "NN.MM", i.e., 70.1% could be reported as "70.1" but not as "70.1%".
22	subsample_amount	Text(14)		required		Amount of original sample used in sample preparation.
23	subsample_amount_unit	Text(15)		required		Unit of measurement for subsample amount.
24	analyst_name	Text(30)				Name or initials of laboratory analyst. This is an optional field for the laboratory EDD unless otherwise specified by the project manager.
25	instrument_id	Text(50)				Instrument identifier. This is an optional field for the laboratory EDD unless otherwise specified by the project manager.
26	sample_receipt_date	Date/Time		required		Must be blank for laboratory generated samples. Date of sample collection in MM/DD/YY format.
27	sample_receipt_time	Text(5)		required		Must be blank for laboratory generated samples. Time of sample collection in 24-hr (military) HH:MM format.
28	sample_delivery_group	Text(10)		required		Sample delivery group.
29	Comment	Text(255)				Comments about the test as necessary.

30	final_volume	Text(15)		required if applicable		The final amount/volume of the sample, extract, or digestate after sample preparation.
31	final_volume_unit	Text(15)		required if applicable		The unit of measure that corresponds to the final volume.

## Result Import Format

#	Attribute Name	Type	PK	Required	Ref. Value?	Attribute Definition
1	sys_sample_code	Text(20)	PK	required		<p>Unique sample identifier. Each sample must have a unique value, including spikes and duplicates. Laboratory QC samples must also have unique identifiers. For matrix spike, matrix spike duplicate, and laboratory replicate samples, this field must be populated as follows: COC#, which is "COC" followed by a number, then a dash (-), then the Item#, which is a sequential three digit number that is typed on the Chain-of-Custody to the left of each sample (ex: COC042602-001), followed by "MS" for matrix spike, "SD" for matrix spike duplicate, or "LR" for laboratory replicate.</p> <p><b>Required</b></p>
2	lab_anl_method_name	Text(35)	PK	required	Yes	<p>Laboratory analytical method name or description. For valid value list, consult the reference values supplied for the project.</p>
3	analysis_date	Date/Time	PK	required		<p>Date of sample analysis in MM/DD/YY format. Must refer to the beginning of the analysis for this project.</p>
4	analysis_time	Text(5)	PK	required		<p>Time of sample analysis in 24-hr (military) HH:MM format. Must refer to the beginning of the analysis for this project. Note that this field, combined with the "analysis_date" field is used to distinguish between retests and reruns. Please ensure that retests have "analysis_date" and/or "analysis_time" different from the original test event (and fill out the test_type field as needed).</p>

5	total_or_dissolved	Text(1)	PK	required	Yes	It must be either "T" for total [metal] concentration, "D" for dissolved or filtered [metal] concentration, or "N" for organic (or other) constituents for which neither "total" nor "dissolved" is applicable.
6	column_number	Text(2)	PK	required	Yes	Required, it must be either "1C" for first column analyses, "2C" for second column analyses, or "NA" for analyses for which neither "1C" nor "2C" is applicable. If any "2C" tests are reported, then there must be corresponding "1C" tests present. Also, laboratories are reporting which of the two columns is to be considered "primary". This distinction is handled by the "reportable_result" field in the result table.
7	test_type	Text(10)	PK	required	Yes	Type of test. Valid values include "initial", "reextract", and "reanalysis".
8	cas_rn	Text(15)	PK	required	Yes	Chemical Abstracts Registry Number for the parameter if available. Otherwise consult the reference values supplied for this project.
9	chemical_name	Text(60)		required	Yes	Chemical name is used only in review of EDD. For valid value list, consult the reference values supplied for the project. <b>Required</b>
10	result_value	Text(20)		required where applicable		Analytical result reported at the project specified number of significant digits. Must be blank for non-detects.
11	result_error_delta	Text(20)				Error range applicable to the result value; typically used only for radiochemistry results.
12	result_type_code	Text(10)		required	Yes	Must be either "TRG" for a target or regular result, and "SUR" for surrogates.

13	reportable_result	Text(10)		required	Yes	Must be either "Yes" for results which are considered to be reportable, or "No" for other results. This field has many purposes. For example, it can be used to distinguish between multiple results where a sample is retested after dilution. It can also be used to indicate which of the first or second column result should be considered primary. The proper value of this field in both of these two examples should be provided by the laboratory (only one result should be flagged as reportable).
14	detect_flag	Text(2)			Yes	Must be either "Y" for detected analytes or "N" for non-detects.
15	lab_qualifiers	Text(7)		required	Yes	Qualifier flags assigned by the laboratory. For valid value list, consult the reference values supplied for the project
16	organic_yn	Yes/No		required	Yes	Must be either "Y" for organic constituents or "N" for inorganic constituents.
17	method_detection_limit	Text(20)		required		Method detection limit. Required for all results for which such a limit is appropriate.
18	reporting_detection_limit	Text(20)		required		Detection limit that reflects conditions such as dilution factors and moisture content. Required for all results for which such a limit is appropriate.
19	quantitation_limit	Text(20)		required		Concentration level above which results can be quantified with confidence. It must reflect conditions such as dilution factors and moisture content. Required for all results for which such a limit is appropriate.
20	result_unit	Text(15)		required if applicable	Yes	Units of measurement for the result. For valid value list, consult the reference values supplied for the project.

21	detection_limit_unit	Text(15)		required		Units of measurement for the detection limit(s).
22	tic_retention_time	Text(8)				Retention time in seconds for tentatively identified compounds. TICs will not be used on this project.
23	result_comment	Text(255)				Result specific comments.
24	qc_original_conc	Text(14)		required where applicable		The concentration of the analyte in the original (unspiked) sample. This field is required for matrix spikes and not necessary for surrogate compounds or LCS samples (where the original concentration is assumed to be zero). If original (unspiked) sample is a non-detect, then populate this field with a "0" as opposed to the detection limit. For matrix spikes, if using an original sample result that is less than the reporting limit for background correction, then populate this field with the below reporting limit original sample result, as opposed to "0".
25	qc_spike_added	Text(14)		required where applicable		The concentration of the analyte added to the original sample. Required for matrix spikes, surrogate compounds, and LCSs.
26	qc_spike_measured	Text(14)		required where applicable		The measured concentration of the analyte. Use zero for spiked compounds that were not detected in the sample. Required for matrix spikes, surrogate compounds, and LCSs.
27	qc_spike_recovery	Text(14)		required where applicable		The percent recovery calculated. Always required for spikes, surrogate compounds, and LCSs. Report as percentage multiplied by 100 (e.g., report "120%" as "120").

28	qc_dup_original_conc	Text(14)		required where applicable		The concentration of the analyte in the original sample. Is required for matrix spike duplicates and lab replicates only. If original sample is a non-detect, then populate this field with a "0" as opposed to the detection limit. For matrix spike duplicates, if using an original sample result that is less than the reporting limit for background correction, then populate this field with the below reporting limit original sample result, as opposed to "0".
29	qc_dup_spike_added	Text(14)		required where applicable		The concentration of the analyte added to the original sample. Required for matrix spike duplicates.
30	qc_dup_spike_measured	Text(14)		required where applicable		The measured concentration of the analyte in the duplicate (for background corrected matrix spike duplicates). Use zero for spiked compounds that were not detected in the sample. Required for matrix spike duplicates and lab replicates.
31	qc_dup_spike_recovery	Text(14)		required where applicable		The duplicate percent recovery calculated. Always required for spike or LCS duplicates, surrogate compounds, and any other spiked and duplicated sample. Also complete the qc_spike_recovery field. Report as percentage multiplied by 100 (e.g., report "120%" as "120").
32	qc_rpd	Text(8)		required where applicable		The relative percent difference calculated. Required for duplicate samples as appropriate. Report as percentage multiplied by 100 (e.g., report "120%" as "120").

33	qc_spike_lcl	Text(8)		required where applicable		Lower control limit for spike recovery. Required for spikes, spike duplicates, surrogate compounds, LCS and any spiked sample. Report as percentage multiplied by 100 (e.g., report "120%" as "120").
34	qc_spike_ucl	Text(8)		required where applicable		Upper control limit for spike recovery. Required for spikes, spike duplicates, surrogate compounds, LCS and any spiked sample. Report as percentage multiplied by 100 (e.g., report "120%" as "120").
35	qc_rpd_cl	Text(8)		required where applicable		Relative percent difference control limit. Required for any duplicated sample. Report as percentage multiplied by 100 (e.g., report "120%" as "120").
36	qc_spike_status	Text(10)		required where applicable		Used to indicate whether the spike recovery was within control limits. Use the "*" character to indicate failure, otherwise leave blank. Required for matrix spikes, surrogate compounds, and LCSs.
37	qc_dup_spike_status	Text(10)		required where applicable		Used to indicate whether the duplicate spike recovery was within control limits. Use the "*" character to indicate failure, otherwise leave blank. Required for any spiked and duplicated sample.
38	qc_rpd_status	Text(10)		required where applicable		Used to indicate whether the relative percent difference was within control limits. Use the "*" character to indicate failure, otherwise leave blank. Required for any duplicated sample.

## Batch Import Format

#	Attribute Name	Column Datatype	PK	Required	Ref. Value?	Attribute Definition
1	sys_sample_code	Text(20)	PK	required		Unique sample identifier. Each sample must have a unique value, including spikes and duplicates. Laboratory QC samples must also have unique identifiers. For matrix spike, matrix spike duplicate, and laboratory replicate samples, this field must be populated as follows: COC#, which is "COC" followed by a number, then a dash (-), then the Item#, which is a three digit number that is typed on the Chain-of-Custody to the left of each sample, followed by "MS" for matrix spike, "SD" for matrix spike duplicate, or "LR" for laboratory replicate. <b>Required</b>
2	lab_anl_method_name	Text(35)	PK	required	Yes	Laboratory analytical method name or description. For valid value list, consult the reference values supplied for this project.
3	analysis_date	Date/Time	PK	required		Date of sample analysis in MM/DD/YY format. May refer to either beginning or end of the analysis long as it is consistent throughout the project.
4	analysis_time	Text(5)	PK	required		Time of sample analysis in 24-hr (military) HH:MM format. May refer to either beginning or end as long as it is consistent throughout the project. Note that this field, combined with the "analysis_date" field is used to distinguish between retests and reruns. Please ensure that retests have "analysis_date" and/or "analysis_time" different from the original test event (and fill out the test_type field as needed).
5	total_or_dissolved	Text(1)	PK	required	Yes	It must be either "T" for total [metal] concentration, "D" for dissolved or filtered [metal] concentration, or "N" for organic (or other) constituents for which neither "total" nor "dissolved" is applicable.
6	column_number	Text(2)	PK	required	Yes	If required, then it must be either "1C" for first column analyses, "2C" for second column analyses, or "NA" for analyses for which neither "1C" nor "2C" is applicable. If any

						"2C" tests are reported, then there must be corresponding "1C" tests present. Also, laboratories will be reporting which of the two columns is to be considered "primary". This distinction is handled by the "reportable_result" field in the result table.
7	test_type	Text(10)	PK	required	Yes	Type of test. Valid values include "initial", "reextract", and "reanalysis".
8	test_batch_type	Text(10)	PK	required	Yes	Lab batch type. Valid values include "Prep", "Analysis", and "Leach". Additional valid values may optionally be provided by the project manager. This is a required field for all batches.
9	test_batch_id	Text(20)		required		Unique identifier for all lab batches. Must be unique within a database. For example, the same identifier can not be used for a prep batch and an analysis batch.