

**APPENDIX A**  
**SEDD VERSION 5.1**  
**DATA ELEMENT DICTIONARY (DED)**  
**(August 2005)**

**NOTE:** For those data elements that have the format 'Limited List', the complete list of valid values can be found in Appendix B.

<b>DATA ELEMENT</b>	<b>DESCRIPTION</b>
<hr/>	
<b>AcidReaction</b>	
Format:Limited List	
Category:Description	
Definition:	The reaction of the sample to acid.
Applicable Node(s):	
<b>SamplePlusMethod</b>	The reaction of the sample as received by the laboratory to acid. Example Valid Values: 'Yes', 'No'.
<b>Handling</b>	The reaction of the sample after the handling described by this node to acid. Example Valid Values: 'Yes', 'No'.
<hr/>	
<b>AliquotAmount</b>	
Format:Numeric	
Category:Measurement	
Definition:	The amount (weight or volume) of sample subjected to an analysis. The final results for any given analysis are based on the AliquotAmount used.
Applicable Node(s):	
<b>Analysis</b>	The amount of sample used for this analysis.
<b>PreparationPlusCleanup</b>	If the analytical method requires the prior use of an independent preparative method, then the AliquotAmount is the amount of sample subjected to the preparative method prior to actual analysis of the sample.
<hr/>	
<b>AliquotAmountUnits</b>	
Format:Limited List	
Category:Measurement	
Definition:	Units for AliquotAmount.
Applicable Node(s):	
<b>Analysis</b>	
<b>PreparationPlusCleanup</b>	

---

**AlternateLabAnalysisID**

Format:Identifier

Category:Identification

Definition: Alternate laboratory identifier for an analysis.

Applicable Node(s):

**Analysis**

This value is for information purposes only to facilitate tracking back into the laboratory's systems.

---

**AlternateLabSampleID**

Format:Identifier

Category:Identification

Definition: Alternate laboratory identifier for a sample.

Applicable Node(s):

**SamplePlusMethod**

This value is for information purposes only to facilitate tracking back into the laboratory's systems. It might be used when the laboratory has both a laboratory-wide sample id and a different, department specific one for particular methods.

---

**AmountAdded**

Format:Numeric

Category:Measurement

Definition: The amount (weight or volume) of an analyte that has been spiked into an aliquot at any time during the analysis process.

Applicable Node(s):

**Analyte**

Specifies a known weight or volume of analyte that has been spiked into the aliquot. The StandardConcentration data element must also be used to fully define the amount of analyte added. Used with method QC samples of QCcategory Spike, Blank\_Spike, Spike\_Duplicate and Blank\_Spike\_Duplicate. In addition, AmountAdded can now refer to spikes, surrogates, tracers, standard additions, and calibration standards where known amounts have been added to samples for QC purposes. 'AnalyteType=Spike' should be specified for spiked analytes unless some other AnalyteType is more appropriate or which analytes were spiked is known based on a QCType associated with this data.

---

**AmountAddedUncertainty**

Format:Numeric

Category:Measurement

Definition: The estimated error in the AmountAdded.

Applicable Node(s):

**Analyte**

---

**AmountAddedUncertaintyType**

Format:Limited List

Category:Measurement

Definition: The confidence interval for the AmountAddedUncertainty.

Applicable Node(s):

**Analyte**

Example Valid Values: '1-Sigma', '2-Sigma' or '3-Sigma'.

---

**AmountAddedUncertaintyUnits**

Format:Limited List

Category:Measurement

Definition: Units for AmountAddedUncertainty.

Applicable Node(s):

**Analyte**

---

**AmountAddedUnits**

Format:Limited List

Category:Measurement

Definition: Units for AmountAdded.

Applicable Node(s):

**Analyte**

---

**Analysis**

Format:

Category:

Definition: Parent Element. Contains elements related to analysis.

Applicable Node(s)

**Analysis**

---

**AnalysisBatch**

Format:Identifier

Category:Batch

Definition: A laboratory-defined identifier for a batch of analyses done on one instrument associated with the level of detail at which the instrument is checked to be in control. If multiple analysis batches are used in a continuous sequence, this represents the start of any given analysis batch.

Applicable Node(s):

**Analysis**

Example: Analyses QC'd by the same continuing calibration, continuing calibration verification or similar InstrumentQC.

---

**AnalysisBatchEnd**

Format:Identifier

Category:Batch

Definition: If multiple analysis batches are used in a continuous sequence, this represents the end of any given analysis batch.

Applicable Node(s):

**Analysis**

---

**AnalysisDuration**

Format:Numeric

Category:Measurement

Definition: The length of time of the instrumental analysis.

Applicable Node(s):

**Analysis**

Example: Radiochemical count time, ICP integration time.

**Analyte**

The duration of the instrumental analysis for this analyte.

**Peak**

The duration of the instrumental analysis for this peak.

**PeakReplicate**

The duration of the instrumental analysis for this peak replicate.

---

**AnalysisDurationUnits**

Format:Limited List

Category:Measurement

Definition: Units for AnalysisDuration.

Applicable Node(s):

**Analysis****Analyte****Peak****PeakReplicate**

---

**AnalysisGroup**

Format:

Category:

Definition: Parent Element. Contains elements related to analysis groups.

Applicable Node(s):

**AnalysisGroup**

---

**AnalysisGroupID**

Format:Identifier

Category:Identification

Definition: *Required Conditionally*  
A laboratory-defined identifier that is used to link together multiple analyses on one instrument to generate a single analyte result that is dependent upon each individual analysis.

Applicable Node(s):

**AnalysisGroup**

Example: Analysis groups are used during initial calibration to determine average response factors or other calibration curve characteristics. They would normally be used to report this data for multi-point calibration curves but could also be used to report this data when a single-point calibration is performed. Analysis groups are used when the Method of Standard Additions is used to determine the concentration of a given analyte in a sample. Analysis groups are used when an average result is to be reported for multiple analyses.

**Analysis**

The AnalysisGroup this analysis is part of.

**ReportedResult**

If there is any ambiguity about which analyses underlie this result, the AnalysisGroup that identifies these analyses.

---

**AnalysisRequestID**

Format:Identifier

Category:Tracking

Definition:

A client-defined identifier for the paperwork that authorizes the analyses of specific samples by listed methods.

Applicable Node(s):

**SamplePlusMethod**

Can refer to a 'Request for Analysis' form that is usually different from the Chain-of-Custody form. Sometimes this is identical to the chain of custody identifier.

---

**AnalysisType**

Format:Limited List

Category:Identification

Definition:

*Required*

A client-defined identifier used to define the type of analysis. This identifier is also used to uniquely identify a single analysis from multiple analyses that are used to generate a single result.

Applicable Node(s):

**Analysis**

Example Valid Values:

1. For a regular single analysis, the default Valid Value would be 'Initial'. For a regular single confirmation analysis, the default Valid Value would be 'Confirmation'.
2. During multipoint initial calibrations, this data element would be used to identify the individual analyses performed. Example Valid Value: 'RRF-#', 'CF-#', where '#' can be any number. The numerical part of each term could correspond to the concentration of the analyte in the standard or just simply the standard number.
3. If multiple analyses are averaged or used to produce a single final result, this data element would be used to identify the individual analyses performed. Example Valid Value: 'Initial-#', where '#' can be any integer.
4. During use of the Method of Standard Additions, this data element would be used to identify the individual analyses performed. Example Valid Value: 'MSA-#', where '#' can be any integer.
5. When dilutions, reinjections or reanalyses are performed, this data element would be used to identify the individual analyses performed. Example Valid Values: 'Reanalysis-#', 'Reinjection-#', 'Dilution-#', where '#' can be any integer. A 'Reinjection' involves taking a previously processed aliquot and repeating the analytical method(s) only. This analytical process would normally include repeating the analysis part of the method only with no additional sample preparative method(s) or cleanup method(s) being performed. A 'Reanalysis' involves taking another aliquot of the original sample through the entire analytical process. This analytical process would normally include applying the same preparative method(s), cleanup method(s) and analytical method(s) as were used during the

analysis of the original sample. A 'Dilution' involves taking a previously processed aliquot, performing a dilution and then repeating the analytical method(s) only. This analytical process would normally include repeating the analysis part of the method only with no additional sample preparative method(s) or cleanup method(s) being performed.

**AnalysisGroup**

Client's identifier to define the type of AnalysisGroup. This identifier is only needed if more than one type of AnalysisGroup applies to one SamplePlusMethod or InstrumentQC nodes.

---

**Analyst**

Format:Text

Category:Tracking

Definition: Name or initials for the analyst doing the work.

Applicable Node(s):

**Handling**

**Analysis**

**PreparationPlusCleanup**

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**Analyte**

Format:

Category:

Definition: Parent Element. Contains elements related to analytes.

Applicable Node(s):

**Analyte**

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**AnalyteComparison**

Format:

Category:

Definition: Parent Element. Contains elements related to the comparison of two or more analytes.

Applicable Node(s):

**AnalyteComparison**

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**AnalyteGroup**

Format:

Category:

Definition: Parent Element. Contains elements related to analyte groups.

Applicable Node(s):

**AnalyteGroup**

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**AnalyteGroupID**

Format:Identifier  
Category:Identification  
Definition:

*Required Conditionally*

A laboratory-defined identifier that is used to link together multiple analytes to generate a single analyte result that is dependent upon each individual analyte.

Applicable Node(s):

**AnalyteGroup**

Analyte groups are used to link together analytes that are individually measured to report a different analyte as a final result. For example, an Analyte group would be used to report a Hardness value that was determined by measuring individual Calcium and Magnesium values. The AnalyteGroup this analyte is part of.

**Analyte**

**ReportedResult**

If there is any ambiguity about which analytes underlie this result, the AnalyteGroup that identifies these analytes.

---

**AnalyteName**

Format:Limited List  
Category:Identification  
Definition:

*Required for Portability*

The published reference name for the analyte.

Applicable Node(s):

**ReportedResult**

If no published name is available then the ClientAnalyteName data element should be used.

**Analyte**

**AnalyteComparison**

AnalyteName for the analyte to compare to.

**AnalyteGroup**

AnalyteName for the analyte that belongs to this AnalyteGroup.

**PeakComparison**

AnalyteName for the analyte to compare to.

---

**AnalyteNameContext**

Format:Limited List  
Category:Identification  
Definition:

*Required for Portability*

The published reference source for AnalyteName.

Applicable Node(s):

**ReportedResult**

**Analyte**

**AnalyteComparison**

**AnalyteGroup**

**PeakComparison**

---

**AnalyteType**

Format:Limited List  
Category:Identification  
Definition:  
Applicable Node(s):

*Required*

A client-defined identifier that identifies the type of analyte reported.

**ReportedResult**

Example Valid Values: 'Spike' and 'TIC' (a non-routine analyte that is tentatively identified). For a routine analyte, the default Valid Value is 'Target'.

**Analyte**

Example Valid Values:'Spike', 'TIC' 'Internal\_Standard', 'Surrogate', 'System\_Monitoring\_Compound', and 'Tracer' (Like an internal standard except it is added at the beginning of sample preparation, rather than just before analysis). For a routine analyte, the default Valid Value is 'Target'.

**AnalyteGroup**

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**AnalyzedAmount**

Format: Numeric  
Category: Measurement  
Definition:

The amount (weight or volume) of a prepared extract that is used for an analysis.

Applicable Node(s):

**Analysis**

If the analytical method requires the prior use of preparative or cleanup step(s), then the AnalyzedAmount is the actual amount of this final extract that is used for the analytical method. This would most often be used where a prepared extract is split and used for analysis by two or more techniques.

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**AnalyzedAmountUnits**

Format: Limited List  
Category: Measurement  
Definition:

Units for AnalyzedAmount.

Applicable Node(s):

**Analysis**

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**AnalyzedDate**

Format:Date  
Category:Tracking  
Definition:

The date (and time, if required) of analysis of an aliquot. If analyzed over a range of dates, this is the start date.

Applicable Node(s):

**Analysis**

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**AnalyzedDateTimeZone**

Format:Limited List  
Category:Tracking  
Definition:

Time zone for AnalyzedDate.

Applicable Node(s):

**Analysis**

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**AnalyzedEndDate**

Format:Date

Category:Tracking

Definition: If the aliquot was analyzed over a range of dates (and times, if required), the end of the analysis period.

Applicable Node(s):

**Analysis**

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**AnalyzedEndDateTimeZone**

Format:Limited List

Category:Tracking

Definition: Time zone for AnalyzedEndDate.

Applicable Node(s):

**Analysis**

---

**ApparatusID**

Format:Identifier

Category:Tracking

Definition: The laboratory-defined code for the apparatus used to process the sample or aliquot.

Applicable Node(s):

**Analysis**

Example: An identifier for a Purge-and-trap device.

**Handling**

Example: An identifier for a TCLP device.

**PreparationPlusCleanup**

Example: An identifier for a GPC device.

---

**Artifacts**

Format:Text

Category:Description

Definition: A method-defined concept used to report anomalies in the sample.

Applicable Node(s):

**SamplePlusMethod**

Method-defined concept used to report anomalies in the sample as received by the laboratory.

**Handling**

Method-defined concept used to report anomalies in the sample after the handling described by this node.

---

**Autosampler**

Format:Limited List

Category:Description

Definition: Whether or not an autosampler was used.

Applicable Node(s):

**Analysis**

Example Valid Values: 'Yes', 'No'.

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**BackgroundCorrection**

Format:Limited list

Category:Description

Definition: Whether or not background correction was done.

Applicable Node(s):  
**Analysis** Example Valid Values: 'Yes', 'No'.

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**BackgroundRawData**

Format:Limited List

Category:Description

Definition: Whether or not background raw data was generated when background correction was done.

Applicable Node(s):  
**Analysis** Example Valid Values: 'Yes', 'No'.

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**BackgroundType**

Format:Limited List

Category:Identification

Definition: The type of background correction done during an analysis.

Applicable Node(s):  
**Analysis** Example Valid Values: 'Smith\_Hieftje', 'Deuterium\_Arc', 'Zeeman'.  
**Analyte** Same as Analysis.  
**Peak** Same as Analysis.

---

**BiasErrorRatio**

Format:Numeric

Category:Measurement

Definition: The difference between the Result and ExpectedResult as a fraction of the square root of sum of squares of the ResultUncertainty and ExpectedResultUncertainty.

Applicable Node(s):  
**ReportedResult** For method QC of QCCategory Blank\_Spike and Blank\_Spike\_Duplicate, the difference between the Result and ExpectedResult as a fraction of the square root of sum of squares of the ResultUncertainty and ExpectedResultUncertainty. For method QC of QCCategory Spike and Spike\_Duplicate, the spiked Result minus the original Result and the ExpectedResult as a fraction of the square root of sum of squares of the ResultUncertainty of the Results and the ExpectedResultUncertainty.  
**Analyte** Same as in ReportedResult except applied to the results of analyses in an analysis group rather than a QC sample and original pair.  
**Peak** Same as in Analyte when results are measured per peak.

---

**BillingID**

Format:Identifier

Category:Tracking

Definition: A client-defined code to submit with the data for billing purposes.

Applicable Node(s):

**SamplePlusMethod**

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**BiologicalClassName**

Format:Limited List

Category:Description

Definition: A broad classification of a sample organism.

Applicable Node(s):

**SamplePlusMethod**

Not necessarily intended to be the taxonomic class, but that is a possible value. Example Valid Values: 'Animal', 'Commercial\_Animal', 'Fish', or 'Plant'.

---

**BoilingPoint**

Format:Numeric

Category:Measurement

Definition: The boiling point of the sample.

Applicable Node(s):

**SamplePlusMethod****Handling**

The boiling point of the sample after the handling described by this node.

---

**BoilingPointUnits**

Format:Limited List

Category:Measurement

Definition: Units for BoilingPoint.

Applicable Node(s):

**SamplePlusMethod****Handling**

---

**Bottles**

Format:Numeric

Category:Description

Definition: The number of sample bottles received by the laboratory.

Applicable Node(s):

**SamplePlusMethod**

---

**BottleID**

Format:Identifier

Category:Tracking

Definition: An identifier for the bottle containing the sample being analyzed.

Applicable Node(s):

**SamplePlusMethod****Analysis****Handling****PreparationPlusCleanup**

---

**BottleType**

Format:Limited List

Category:Description

Definition:

The size and type of bottle used to contain the sample.

Applicable Node(s):

**SamplePlusMethod**

Example Valid Value: '1-L\_Amber\_Glass'.

---

**CalibrationBasis**

Format:Limited List

Category:Description

Definition:

The node that contains the calibration information for a given analyte.

Applicable Node(s):

**Analyte**

Example Valid Values:

1. When the calibration and subsequent quantitation for a given analyte is based on the use of a single peak when only a single peak is present, the valid value 'Peak' shall be used. All peak and calibration information shall be reported in the Peak node.
2. When the calibration and subsequent quantitation for a given analyte is based on the use of a single peak when multiple peaks are present, the valid value 'Peak' shall be used. All peak and calibration information shall be reported in the Peak node. In order to clearly indicate which peak of the multiple peaks was used for calibration, use the data element PeakID in the Analyte and ReportedResult nodes.
3. When the calibration for a given analyte is based on the use of multiple peaks with a unique calibration curve generated for each peak, the valid value 'Peak' shall be used. All peak and calibration information shall be reported in the Peak node. The method or project shall clearly indicate how each of the individually calculated peak results would be combined together to form the analyte result.
4. When the calibration and subsequent quantitation for a given analyte is based on combining two or more peaks, the valid value 'Analyte' shall be used. All calibration information shall be reported in the Analyte node and all individual peak information shall be reported in the Peak node. The method or project shall clearly indicate how each of the individual peak measurements would be combined to form the response that would be reported and used in the Analyte node to construct the calibration curve.
5. When the calibration and subsequent quantitation for a given analyte is not based on a peak (e.g., pH, conductivity), the valid value 'Analyte' shall be used. All calibration information shall be reported in the Analyte node.

---

**CalibrationFactor**

Format:Numeric

Category:Measurement

Definition: The ratio of the detector response to the amount (mass or concentration) of analyte. It is a factor that is used to convert a detector response to an analyte result.

Applicable Node(s):

**Analyte**

The calibration factor for this analyte.

**Peak**

Same as in Analyte, except applied per peak.

---

**CalibrationFactorUnits**

Format:Text

Category:Measurement

Definition: Units for CalibrationFactor.

Applicable Node(s):

**Analyte****Peak**

---

**CalibrationType**

Format:Limited List

Category:Description

Definition: The calibration model used to define the initial calibration curve for a method.

Applicable Node(s):

**Analyte**

The calibration type for this analyte. Example Valid Values: 'Average\_Response\_Factor', 'Average\_Calibration\_Factor', 'Linear\_Regression', 'Linear\_Regression\_With\_Zero\_Force', 'Quadratic\_Regression', 'Quadratic\_Regression\_With\_Zero\_Force'.

**Peak**

Same as in Analyte, except applied per peak.

---

**CASRegistryNumber**

Format:Identifier

Category:Identification

Definition: The Chemical Abstract Service number for the analyte.

Applicable Node(s):

**ReportedResult**

This number would be represented using dashes between the three sets of numbers (e.g., 75-71-8).

**Analyte****AnalyteComparison**

CASRegistryNumber for the analyte to compare to.

**AnalyteGroup**

CASRegistryNumber for the analyte that belongs to this AnalyteGroup.

**PeakComparison**

CASRegistryNumber for the analyte to compare to.

---

**Checksum**

Format:Numeric

Category:Tracking

Definition: A value based on all other data in a node that can be used to check the integrity of an electronic data deliverable.

Applicable Node(s):

**All**

This field can be used in any node. Its value applies to the node it is in. The required algorithm to compute the data for this field is as follows: For all data in a node, starting with the first data element line, ending before the next node or end of the data stream, and ignoring: 1) The carriage return and linefeed at the end of each line. 2) Any optional leading spaces in data element lines. 3) The entire line with the checksum field. Compute the sum of the ASCII codes of all non-ignored characters. Report this sum as an integer.

---

**Clarity**

Format:Text

Category:Description

Definition: Clarity of the sample or aliquot.

Applicable Node(s):

**SamplePlusMethod  
Handling**

Clarity of the sample as received. Example: 'Clear', 'Cloudy', 'Opaque'.  
Clarity of the sample after the handling described in this node.

**PreparationPlusCleanup**

Clarity of the aliquot after the preparation or cleanup described  
in this node.

---

**CleanedUpDate**

Format:Date

Category:Tracking

Definition: Date (and time, if required) of cleanup of this aliquot. If cleaned up over a range of dates, this is the start date.

Applicable Node(s):

**PreparationPlusCleanup**

---

**CleanedUpDateTimeZone**

Format:Limited List

Category:Tracking

Definition: Time zone for CleanedUpDate.

Applicable Node(s):

**PreparationPlusCleanup**

---

**CleanedUpEndDate**

Format:Date

Category:Tracking

Definition: If the aliquot was cleaned up over a range of dates (and times, if required), the end of the cleanup period.

Applicable Node(s):

**PreparationPlusCleanup**

---

**CleanedUpEndDateTimeZone**

Format:Limited List

Category:Tracking

Definition: Time zone for CleanedUpEndDate.

Applicable Node(s):

**PreparationPlusCleanup**

---

**CleanupBatch**

Format:Identifier

Category:Batch

Definition: A laboratory-defined identifier for a batch of aliquots that are cleaned up together for processing by one method. Together can imply similarity of time, place, and manner of cleanup.

Applicable Node(s):

**PreparationPlusCleanup**

The definition of a cleanup batch depends on the method but might be linked to cleanup specific QC samples such as GPC calibrations.

Example: All analyses associated with one GPC calibration would be in one CleanupBatch of ClientMethodID 3640A. The InstrumentQC in the batch might have QCType GPC\_Calibration.

---

**CleanupID**

Format:Identifier

Category:Identification

Definition: A laboratory-defined identifier for this cleanup event for this aliquot.

Applicable Node(s):

**PreparationPlusCleanup**

---

**CleanupType**

Format:Limited List

Category:Identification

Definition: A client-defined identifier used to define the type of cleanup. This identifier is used to identify the specific cleanup procedure used.

Applicable Node(s):

**PreparationPlusCleanup**

This identifier is used to specify which cleanup method was used when such cleanup method details are part of the analysis (instrumental) method. When client cleanup methods are available, this identifier can be used to identify what method options were used within the cleanup method. Example Valid Values: 'Florisol' or 'Sulfur' cleanup for EPA Method 608, 'Mercury' or 'Copper' option used for a sulfur cleanup for SW846 Method 3660B.

**InstrumentQC**

For Instrument QC with QCLinkage 'CleanupBatch', an identifier that identifies the type of cleanup this QC pertains to. The field's value must match that specified as the CleanupType for cleanups of associated samples.

---

**ClientAnalysisID**

Format:Identifier

Category:Identification

Definition: A client-defined identifier for this analysis.

Applicable Node(s):

**Analysis**

---

**ClientAnalyteID**

Format:Identifier

*Required*

Category:Identification

Definition: A client-defined identifier for an analyte.

Applicable Node(s):

**ReportedResult****Analyte****AnalyteComparison**

ClientAnalyteID for the analyte to compare to.

**AnalyteGroup**

ClientAnalyteID for the analyte that belongs to this AnalyteGroup.

**PeakComparison**

ClientAnalyteID for the analyte to compare to. If not specified, it is assumed to be the same as the analyte for the Peak element this PeakComparison element is in.

---

**ClientAnalyteName**

Format:Text

Category:Identification

Definition: A client-defined common name for an analyte.

Applicable Node(s):

**ReportedResult****Analyte****AnalyteComparison**

ClientAnalyteName for the analyte to compare to.

**AnalyteGroup**

ClientAnalyteName for the analyte that belongs to this AnalyteGroup.

**PeakComparison**

ClientAnalyteName for the analyte to compare to.

---

**ClientDataPackageID**

Format:Identifier

Category:Tracking

Definition: A client-defined identifier for this data deliverable package.

Applicable Node(s):

**Header**

This identifier applies to a single deliverable.

For example, a document number the client assigns to the physical data package or a file name for an electronic deliverable.

---

**ClientDataPackageName**

Format:Text

Category:Tracking

Definition: A client-defined title for this data deliverable package.

Applicable Node(s):

**Header**

---

**ClientDataPackageVersion**

Format:Text

Category:Tracking

Definition: If the laboratory resubmits a data package at the client's request, this field can be used to distinguish the different versions.

Applicable Node(s):

**Header**

---

**ClientDetectionLimit**

Format:Numeric

Category:Description

Definition: A contractually-specified upper limit for the detection limit for the analyte being measured.

Applicable Node(s):

**ReportedResult**

Depending on client and method specific rules, required detection limits might be scaled by factors such as dilution and percent moisture prior to reporting.

**Analyte****Peak**

---

**ClientDetectionLimitUnits**

Format:Limited List

Category:Description

Definition: Units for ClientDetectionLimit.

Applicable Node(s):

**ReportedResult**

If the client specifies that the ClientDetectionLimitUnits must be the same as the ResultUnits, the ClientDetectionLimitUnits need not be specified.

**Analyte**

Same as in ReportedResult.

**Peak**

Same as in ReportedResult.

---

**ClientID**

Format:Identifier

Category:Identification

Definition: An identifier for the person or organization ordering the analysis.

Applicable Node(s):

**SamplePlusMethod**

This identifier is often client-defined. This value is necessary to allow one client to read data reported in a format specified by another. To be fully reliable, ClientID's must be unique across all potential clients.

Examples: EPA Region, AFCID (Air Force Client ID)

**InstrumentQC**

Same as in SamplePlusMethod.

---

**ClientInstrumentQCType**

Format:Limited List

Category:Identification

Definition: A client-defined identifier used to define how a given InstrumentQC sample(s) was implemented. For example, whether one or two mixes were used to perform an initial calibration or a continuing calibration verification.

Applicable Node(s):

**InstrumentQC**

---

**ClientMethodCategory**

Format:Text

Category:Identification

Definition: The client-defined general class or common name for the group of analytes being measured by a given method for this sample.

Applicable Node(s):

**SamplePlusMethod** Examples: VOAs, SVOAs, Metals, PCBs, PESTs.  
**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**ClientMethodCode**

Format:Text

Category:Identification

Definition: A client-defined code for the method used by the laboratory to analyze the sample.

Applicable Node(s):

**SamplePlusMethod**  
**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**ClientMethodID**

Format:Text

*Required*

Category:Identification

Definition: A client-defined method identification number for the method used by the laboratory to analyze the sample.

Applicable Node(s):

**SamplePlusMethod**  
**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**ClientMethodName**

Format:Text

Category:Identification

Definition: A client-defined method name for the method used by the laboratory to analyze the sample.

Applicable Node(s):

**SamplePlusMethod**  
**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**ClientMethodSource**

Format:Text

Category:Identification

Definition: The reference method source for the ClientMethodID and ClientMethodName.

Applicable Node(s):

**SamplePlusMethod**  
**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**ClientMethodType**

Format:Text

Category:Identification

Definition: The method type or technology for the method used by the laboratory to analyze the sample.

Applicable Node(s):

**SamplePlusMethod** The type of technology being used to analyze this sample. Example: GC/MS, GC/MS\_SIM, ICP/AES, IR.

**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**ClientMethodVersion**

Format:Text

Category:Identification

Definition: The version of the method used by the laboratory to analyze the sample.

Applicable Node(s):

**SamplePlusMethod**  
**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**ClientName**

Format:Text

Category:Identification

Definition: Descriptive name for the person or organization ordering the analysis.

Applicable Node(s):

**SamplePlusMethod  
InstrumentQC**

Examples: EPA Region, AFCID (Air Force Client ID).

---

**ClientQuantitationLimit**

Format:Numeric

Category:Description

Definition: A contractually-specified upper limit for the quantitation limit for the analyte being measured.

Applicable Node(s):

**ReportedResult**

Depending on client and method specific rules, required quantitation limits might be scaled by factors such as dilution and percent moisture prior to reporting.

**Analyte****Peak**

---

**ClientQuantitationLimitUnits**

Format:Limited List

Category:Description

Definition: Units for ClientQuantitationLimit.

Applicable Node(s):

**ReportedResult**

If the client specifies that the ClientQuantitationLimitUnits must be the same as the ResultUnits, the ClientQuantitationLimitUnits need not be specified.

**Analyte****Peak**

Same as in ReportedResult.

Same as in ReportedResult.

---

**ClientSampleID**

Format:Identifier

Category:Identification

Definition: *Required*  
A client-defined identifier for a sample.

Applicable Node(s):

**SamplePlusMethod**

This should be the basis on which the client identifies the sample. However, not all clients define values for laboratory-generated QC samples.

---

**Coeffa0**

Format:Numeric

Category:Measurement

Definition:

Value for the zeroth order coefficient in a polynomial or regression equation. This term is sometimes referred to as the 'b' value or 'y-intercept' for a linear regression.

Applicable Node(s):

**Analyte**  
**Peak**

---

**Coeffa1**

Format:Numeric

Category:Measurement

Definition:

Value for the first order coefficient in a polynomial or regression equation. This term is sometimes referred to as the 'slope' for a linear regression.

Applicable Node(s):

**Analyte**  
**Peak**

---

**Coeffa2**

Format:Numeric

Category:Measurement

Definition:

Value for the second order coefficient in a polynomial equation.

Applicable Node(s):

**Analyte**  
**Peak**

---

**Coeffa3**

Format:Numeric

Category:Measurement

Definition:

Value for the third order coefficient in a polynomial equation.

Applicable Node(s):

**Analyte**  
**Peak**

---

**CoeffOfDetermination**

Format:Numeric

Category:Measurement

Definition:  
equation.

Coefficient of Determination. The goodness of fit for a polynomial.

Applicable Node(s):

**Analyte**  
**Peak**

Used for an analyte in AnalysisGroup.  
Same as in Analyte, except applied per peak.

---

**CoeffOfDeterminationLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the CoeffOfDetermination.

Applicable Node(s):

**Analyte**  
**Peak**

---

**CoeffOfDeterminationLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the CoeffOfDetermination limits.

Applicable Node(s):

**Analyte** Example Valid Values: 'Method', 'Client', 'Laboratory'.  
**Peak**

---

**CollectedDate**

Format:Date

Category:Tracking

Definition: Date (and time, if required) the sample was collected. If collected over a range of dates, this is the start date.

Applicable Node(s):

**SamplePlusMethod**

---

**CollectedDateTimeZone**

Format:Limited List

Category:Tracking

Definition: Time zone for CollectedDate.

Applicable Node(s):

**SamplePlusMethod**

---

**CollectedEndDate**

Format:Date

Category:Tracking

Definition: If the sample was collected over a range of dates (and times, if required), the end of the collection period.

Applicable Node(s):

**SamplePlusMethod**

---

**CollectedEndDateTimeZone**

Format:Limited List

Category:Tracking

Definition: Time zone for CollectedEndDate.

Applicable Node(s):

**SamplePlusMethod**

---

**Color**

Format:Text

Category:Description

Definition: Color of the sample or aliquot.

Applicable Node(s):

**SamplePlusMethod** Color of the sample as received.**Handling** Color of the sample after the handling described by this node.**PreparationPlusCleanup** Color of the aliquot after the preparation or cleanup described by this node.

---

**Column**

Format:Text

Category:Description

Definition: Name of the column or cartridge used by this method.

Applicable Node(s):

**Analysis****PreparationPlusCleanup**

---

**ColumnInternalDiameter**

Format:Numeric

Category:Description

Definition: Internal diameter of the column or cartridge.

Applicable Node(s):

**Analysis****PreparationPlusCleanup**

---

**ColumnInternalDiameterUnits**

Format:Limited List

Category:Description

Definition: Units for ColumnInternalDiameter.

Applicable Node(s):

**Analysis****PreparationPlusCleanup**

---

**ColumnLength**

Format:Numeric

Category:Description

Definition: Length of the column or cartridge used by this method.

Applicable Node(s):

**Analysis****PreparationPlusCleanup**

---

**ColumnLengthUnits**

Format:Limited List

Category:Description

Definition: Units for ColumnLength.

Applicable Node(s):

**Analysis****PreparationPlusCleanup**

---

**Comment**

Format:Text

Category:Description

Definition: A free-form comment that can occur in any parent data element.

Applicable Node(s):

**All**Its value applies to the data in the node it is in. Readers are not required to take any action based on these comments, but they may choose to record them as text comments in their database.

---

**Composite**

Format:Limited List

Category:Description

Definition: Whether or not the sample as received by the laboratory is a composite.

Applicable Node(s):

**SamplePlusMethod**Example Valid Values: 'Yes', 'No'.

---

**Conductance**

Format:Numeric

Category:Measurement

Definition: The conductance of the sample.

Applicable Node(s):

**SamplePlusMethod**

---

**ConductanceUnits**

Format:Limited List

Category:Measurement

Definition: Units for Conductance.

Applicable Node(s):

**SamplePlusMethod**

---

**ConfirmationAnalysisID**

Format:Identifier

Category:Identification

Definition: A laboratory-defined identifier for an analysis that confirms the results of this analysis. Based on client rules, final results can be reported for a method from either the primary or confirmation analysis.

Applicable Node(s):

**Analysis****AnalysisGroup**

The LabAnalysisID for the confirmation analysis.

Same as Analysis except confirming results from this AnalysisGroup.

---

---

**Consolidation**

Format:Limited List

Category:Description

Definition: Degree of consolidation of the sample.

Applicable Node(s):  
**SamplePlusMethod** Example Valid Values: 'Weak', 'Moderate'.

---

**CoolerID**

Format:Identifier

Category:Tracking

Definition: A client-defined code for the cooler or other shipping container used to transport the sample to the laboratory.

Applicable Node(s):  
**SamplePlusMethod**

---

**CorrectionFactor**

Format:Numeric

Category:Measurement

Definition: The correction factor for this peak, based on interanalyte effects from the analyte named in this node.

Applicable Node(s):  
**AnalyteComparison**

---

**CorrelationCoeff**

Format:Numeric

Category:Measurement

Definition: The correlation coefficient (r) resulting from linear regression of data.

Applicable Node(s):  
**Analyte** Used for an analyte in AnalysisGroup.  
Example: The method of standard additions or initial calibrations.  
**Peak** Same as in Analyte, except applied per peak.

---

**CorrelationCoeffLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the CorrelationCoeff.

Applicable Node(s):  
**Analyte**  
**Peak**

---

**CorrelationCoeffLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the CorrelationCoeff limits.

Applicable Node(s):  
**Analyte** Example Valid Values: 'Method', 'Client', 'Laboratory'.  
**Peak**

---

**CountingError**

Format:Numeric

Category:Measurement

Definition:

For methods based on counting discrete events, such as are common in radiochemistry, the error in the net count rate, usually scaled to the same units as the result.

Applicable Node(s):

**ReportedResult****Analyte**

Extended to anything considered to be the result of any analysis. Within an AnalysisGroup node, applies to a mean or other value computed from several analyses.

**Peak**

Same as in an Analyte node when results are measured per peak.

---

**CountingErrorType**

Format:Limited List

Category:Measurement

Definition:

The confidence interval for the CountingError.

Applicable Node(s):

**ReportedResult****Analyte****Peak**

Example Valid Values: '1-Sigma', '2-Sigma', '3-Sigma'.

---

**CountingErrorUnits**

Format:Limited List

Category:Measurement

Definition:

Units for CountingError.

Applicable Node(s):

**ReportedResult****Analyte****Peak**

---

**CreatedDate**

Format:Date

Category:Tracking

Definition:

The date (and time, if required) a QC sample was generated or derived in the laboratory.

Applicable Node(s):

**SamplePlusMethod**

---

**CreatedDateTimeZone**

Format:Limited List

Category:Tracking

Definition:

Time zone for CreatedDate.

Applicable Node(s):

**SamplePlusMethod**

---

**CustodyID**

Format:Identifier

Category:Tracking

Definition: A client-defined code for the chain of custody document associated with receipt of this sample in the laboratory.

Applicable Node(s):

**SamplePlusMethod**

---

**DateFormat**

Format:Limited List

Category:Identification

Definition: A value that specifies the format of all date/time values in an electronic data deliverable.

Applicable Node(s):

**Header**

A value that specifies the format of all date/time values that follow this Header node. Allowed values for this field are listed with the description of allowed date formats for field values. A required DateFormat value may be specified by the client or implementation.

---

**Density**

Format:Numeric

Category:Measurement

Definition: The density of the sample.

Applicable Node(s):

**SamplePlusMethod  
Handling**

The density of the sample after the handling described by this node.

---

**DensityUnits**

Format:Limited List

Category:Measurement

Definition: Units for Density.

Applicable Node(s):

**SamplePlusMethod  
Handling**

---

**DetectionLimit**

Format:Numeric

Category:Measurement

Definition: Detection limit for the analyte being measured. Detection limits are defined in terms of the presence or absence of the analyte.

Applicable Node(s):

**ReportedResult  
Analyte**

Within AnalysisGroup, applies to a detection limit value computed from several analyses.

**Peak**

Same as in Analyte when results are measured per peak.

---

**DetectionLimitType**

Format:Limited List

Category:Measurement

Definition: One of a list of client-defined acronyms that specify the type of detection limit.

Applicable Node(s):

**ReportedResult****Analyte****Peak**

Example Valid Values: 'CRDL', 'MDL', 'IDL'.

---

**DetectionLimitUnits**

Format:Limited List

Category:Measurement

Definition: Units for DetectionLimit.

Applicable Node(s):

**ReportedResult****Analyte****Peak**

---

**DetectorID**

Format:Identifier

Category:Tracking

Definition: A laboratory-defined code for a detector.

Applicable Node(s):

**Analysis**

---

**DetectorType**

Format:Limited List

Category:Identification

Definition: The type of detector used in the instrumental analysis.

Applicable Node(s):

**Analysis**

Example Valid Values: 'FID', 'MS'.

---

**DifferenceErrorRatio**

Format:Numeric

Category:Measurement

Definition: The absolute value of the difference of two values as a fraction of the square root of sum of squares of their ResultUncertainties.

Applicable Node(s):

**ReportedResult****Analyte****Peak**

Used with method QC of QCcategory Duplicate, Serial\_Dilution, Spike\_Duplicate, and Blank\_Spike\_Duplicate.

Same as in ReportedResult except applied to the results of analyses in an analysis group rather than a QC sample and original pair.

Same as in Analyte when results are measured per peak.

---

**DilutionFactor**

Format:Numeric

Category:Measurement

Definition:

The overall dilution of the aliquot subjected to this analysis. A value of one corresponds to nominal conditions for the method. Values greater than one correspond to dilutions. Values less than one correspond to concentrations.

Applicable Node(s):

**Analysis**

Exactly which factors are included in the DilutionFactor may depend on the method. The most common useage involves dilution of a prepared extract immediately prior to analysis. Under these conditions the initial sample weight or volume would not normally be taken into account unless the sample were to be directly introduced into the instrument.

---

**Drift**

Format:Numeric

Category:Measurement

Definition:

The difference between the actual location of a peak and its predicted position.

Applicable Node(s):

**Analysis**

Example: For alpha spectroscopy, Drift is computed using the tracer peak.

**Analyte**

Same except applied to a specific analyte.

**Peak**

Same except applied to a specific peak.

---

**DriftUnits**

Format:Limited List

Category:Measurement

Definition:

Units for Drift.

Applicable Node(s):

**Analysis****Analyte****Peak**

---

**EDDID**

Format:Limited List

Category:Identification

Definition:

*Required*

Applicable Node(s):

**Header**

A value that specifies the format of an electronic data deliverable.

Must have the value SEDD. It can be checked by readers to determine that following data are in a SEDD compatible format. Since this field need not be the first line in Header, readers need to be prepared to read all the Header lines before making this check.

---

**EDDImplementationID**

Format:Limited List

*Required*

Category:Identification

Definition:

A value that identifies the specific implementation (DTD or Schema) of an electronic data deliverable.

Applicable Node(s):

**Header**

A value specified in a SEDD implementation document (DTD or Schema) as the identifier of the implementation. This value should be checked by readers to determine that following data are in a processible format. For example, an implementation might specify what data elements are required in the EDD, including any implementation defined fields. Since this field need not be the first line in Header, readers need to be prepared to read all the fields in Header before checking this value.

---

**EDDImplementationVersion**

Format:Limited List

*Required*

Category:Identification

Definition:

A value that identifies the version of the specific implementation (DTD or Schema) of an electronic data deliverable.

Applicable Node(s):

**Header**

A value specified in each revision of a SEDD implementation document (DTD or Schema). The value in an EDD indicates the version of the implementation that following data is compatible with. Reader programs may have to adapt their behavior based on this value. In particular, the list of implementation defined fields may change with version number. Implementors should assign version numbers so that later versions have later alphanumeric version numbers.

---

**EDDVersion**

Format:Limited List

*Required*

Category:Identification

Definition:

A value that specifies the version of the format of an electronic data deliverable.

Applicable Node(s):

**Header**

Specified in each revision of the SEDD Specification. Specified by the writer of an EDD to indicate the version of SEDD that following data is compatible with. Reader programs may have to adapt their behavior based on this value. In particular, the list of SEDD defined fields may change with version number.

---

**Efficiency**

Format:Numeric

Category:Measurement

Definition: Efficiency of the instrument as a percent. Usually used in radiochemistry to mean the counts detected as a percentage of the decays actually occurring.

Applicable Node(s):

**Analysis****Analyte****Peak**

Efficiency as applied to a specific analyte.

Efficiency as applied to a specific analyte and peak.

---

**Energy**

Format:Numeric

Category:Description

Definition: The energy of an emission.

Applicable Node(s):

**Peak****PeakComparison**

For example, decay energy as used in radiochemistry.

---

**EnergyUnits**

Format:Limited List

Category:Description

Definition: Units for Energy.

Applicable Node(s):

**Peak****PeakComparison**

---

**EquipmentBatch**

Format:Identifier

Category:Batch

Definition: An identifier for a batch of samples collected using the same equipment in a defined period of time. Operationally, this batch associates a field equipment blank with a group of samples.

Applicable Node(s):

**SamplePlusMethod**

This value is currently often not known to the laboratory. It might be merged with laboratory data by a validator.

---

**ExpectedResult**

Format:Numeric

Category:Measurement

Definition:

The expected final result of an analyte that has been spiked into an aliquot at any time during the analysis process or the true value of an analyte in the sample analyzed.

Applicable Node(s):

**ReportedResult**

Specifies the expected final result of analyte that has been spiked into the aliquot. For these spiked samples, the expected final result would be determined only from the amount of analyte spiked and would not include any native analyte concentrations that might have been present in the original sample. Used with method QC samples of QC Category Blank\_Spike, Spike, Spike\_Duplicate and Blank\_Spike\_Duplicate. Spike analytes should have AnalyteType=Spike. Can also specify the actual true value of an analyte in a sample, such as would be the case for a Standard Reference Material (SRM).

**Analyte**

Same as in the ReportedResult node extended so ExpectedResult can now refer to spikes, surrogates, internal standards, tracers, standard additions, and calibration standards where known amounts have been added to samples for QC purposes. AnalyteType=Spike should be specified for spiked analytes unless some other AnalyteType is more appropriate or which analytes were spiked is known based on a QCType associated with this data.

---

**ExpectedResultUncertainty**

Format:Numeric

Category:Measurement

Definition:

The estimated error in the ExpectedResult.

Applicable Node(s):

**ReportedResult****Analyte**

---

**ExpectedResultUncertaintyType**

Format:Limited List

Category:Measurement

Definition:

The confidence interval for the ExpectedResultUncertainty.

Applicable Node(s):

**ReportedResult****Analyte**

Example Valid Values: '1-Sigma', '2-Sigma', '3-Sigma'.

---

**ExpectedResultUncertaintyUnits**

Format:Limited List

Category:Measurement

Definition:

Units for ExpectedResultUncertainty.

Applicable Node(s):

**ReportedResult****Analyte**

---

**ExpectedResultUnits**

Format:Limited List

Category:Measurement

Definition: Units for ExpectedResult.

Applicable Node(s):

**ReportedResult  
Analyte**

---

**FieldSampleID**

Format:Identifier

Category:Identification

Definition: An identifier assigned to a sample by the sampler, not the client.

Applicable Node(s):

**SamplePlusMethod** This value is currently often not known to the laboratory. It could be useful as a link into the sampling records system.

---

**Filtered**

Format:Limited List

Category:Description

Definition: Whether or not the sample as received by the laboratory was field filtered.

Applicable Node(s):

**SamplePlusMethod** Example Valid Values: 'Yes', 'No'.

---

**FilterSize**

Format:Numeric

Category:Description

Definition: Filter pore size for samples, aliquots or extracts that are filtered.

Applicable Node(s):

**SamplePlusMethod  
Handling  
Analysis  
PreparationPlusCleanup**

---

**FilterSizeUnits**

Format:LimitedList

Category:Description

Definition: Units for FilterSize.

Applicable Node(s):

**SamplePlusMethod  
Handling  
Analysis  
PreparationPlusCleanup**

---

**FinalAmount**

Format:Numeric

Category:Measurement

Definition: The amount (weight or volume) of material (i.e., digestate, extract, distillate, etc.) generated as the outcome of processing the sample through the sample preparation and/or cleanup steps.

Applicable Node(s):

**Analysis****PreparationPlusCleanup**

---

**FinalAmountUnits**

Format:Limited List

Category:Measurement

Definition: Units for FinalAmount.

Applicable Node(s):

**Analysis****PreparationPlusCleanup**

---

**FlowRate**

Format:Numeric

Category:Description

Definition: Rate of flow of a gas or liquid mobile phase as often used in chromatography.

Applicable Node(s):

**Analysis**

---

**FlowRateUnits**

Format:Limited List

Category:Description

Definition: Units for FlowRate.

Applicable Node(s):

**Analysis**

---

**Frequency**

Format:Numeric

Category:Description

Definition: The frequency of an emission or absorption.

Applicable Node(s):

**Peak****PeakComparison**

---

**FrequencyUnits**

Format:Limited List

Category:Description

Definition: Units for Frequency.

Applicable Node(s):

**Peak****PeakComparison**

---

---

**GeneratingSystemID**

Format:Identifier

Category:Tracking

Definition: A laboratory-defined value that identifies the software system used to generate an electronic data deliverable.

Applicable Node(s):

**Header**

This value may be built into commercial software. The reader may use this value to adapt to known quirks of the generating system.

---

**GeneratingSystemVersion**

Format:Text

Category:Tracking

Definition: A laboratory-defined version number for the software system used to generate an electronic data deliverable.

Applicable Node(s):

**Header**

---

**Gradient**

Format:Numeric

Category:Description

Definition: Temperature gradient for GC or mobile phase gradient for HPLC.

Applicable Node(s):

**Analysis**

---

**GradientUnits**

Format:Limited List

Category:Description

Definition: Units for Gradient.

Applicable Node(s):

**Analysis**

---

**HandledDate**

Format:Date

Category:Tracking

Definition: Date (and time, if required) of Handling of this sample. If handled over a range of dates, this is the start date.

Applicable Node(s):

**Handling**

---

**HandledDateTimeZone**

Format:Limited List

Category:Tracking

Definition: Time zone for HandledDate.

Applicable Node(s):

**Handling**

---

**HandledEndDate**

Format:Date

Category:Tracking

Definition: If the sample was handled over a range of dates (and times, if required), the end of the handled period.

Applicable Node(s):

**Handling**

---

**HandledEndDateTimeZone**

Format:Limited List

Category:Tracking

Definition: Time zone for HandledEndDate.

Applicable Node(s):

**Handling**

---

**Handling**

Format:

Category:

Definition: Parent Element. Contains elements related to sample handling.

Applicable Node(s)

**Handling**

---

**HandlingBatch**

Format:Identifier

Category:Batch

Definition: A laboratory-defined identifier for a batch of samples that are handled together. Together can imply similarity of time, place, and manner of handling.

Applicable Node(s):

**Handling**

The definition of a handling batch depends on the method but might be linked to handling specific QC samples.  
Example: All samples associated with one TCLP apparatus blank would be in one HandlingBatch of ClientMethodID 1311. The method QC sample in the batch might have QCType TCLP\_Blank.

---

**HandlingDuration**

Format:Numeric

Category:Measurement

Definition: The duration of the handling.

Applicable Node(s):

**Handling**Example: TCLP leaching time.

---

**HandlingDurationUnits**

Format:Limited List

Category:Measurement

Definition: Units for HandlingDuration.

Applicable Node(s):

**Handling**

---

---

**HandlingFactor**

Format:Numeric

Category:Measurement

Definition: A factor that reflects processing done early in sample handling.

Applicable Node(s):

**Handling**

For example, used in radiochemistry with a hot laboratory that does preliminary processing prior to more routine activities.

---

**HandlingFactorUnits**

Format:Limited List

Category:Measurement

Definition: Units for HandlingFactor.

Applicable Node(s):

**Handling**

---

**HandlingID**

Format:Identifier

Category:Identification

Definition: A laboratory-defined identifier for this handling event for this sample.

Applicable Node(s):

**Handling**

---

**HandlingType**

Format:Limited List

Category:Identification

Definition: A client-defined code used to define the type of preliminary processing done to a sample prior to aliquotting. This code is used to identify the specific handling procedure used.

Applicable Node(s):

**Handling**

This code is used to specify which handling method was used when such handling method details are part of the analysis (instrumental) method. When client cleanup method codes are available, this code is used to identify what method options were used within the handling method. Example Valid Values: 'Ashed', 'Dried', 'Filtered', 'Decanted'.

**SamplePlusMethod**

For a method QC sample with QCLinkage 'HandlingBatch', a code that identifies the type of handling this QC pertains to. The field's value must match that specified as the HandlingType for handlings of associated samples.

---

**Header**

Format:

Category:

Definition: Parent Element. Contains elements relating to submitted data file.

Applicable Node(s):

**Header**

---

**HeatedPurge**

Format:Limited List

Category:Description

Definition: Whether or not volatiles analysis used a heated purge.

Applicable Node(s):  
**Analysis** Example Valid Values: 'Yes', 'No'.

---

**InitialAmount**

Format:Numeric

Category:Measurement

Definition: The amount (weight or volume) of material used for processing the sample through any handling and/or cleanup steps.

Applicable Node(s):  
**Handling** The amount of material used for this handling method.**PreparationPlusCleanup** The amount of material used for this cleanup method.

---

**InitialAmountUnits**

Format:Limited List

Category:Measurement

Definition: Units for InitialAmount.

Applicable Node(s):  
**Handling**  
**PreparationPlusCleanup**

---

**InjectionVolume**

Format:Numeric

Category:Measurement

Definition: The volume of sample injected/purged into the instrument or onto a specific column when an injection is split between two or more columns.

Applicable Node(s):  
**Analysis**

---

**InjectionVolumeUnits**

Format:Limited List

Category:Measurement

Definition: Units for InjectionVolume.

Applicable Node(s):  
**Analysis**

---

**InstrumentID**

Format:Identifier

Category:Tracking

Definition: A laboratory-defined code for an instrument.

Applicable Node(s):  
**Analysis**

---

**InstrumentQC**

Format:

Category:

Definition: Parent Element. Contains elements related to instrument QC.

Applicable Node(s):  
**InstrumentQC**

---

**InstrumentSerialNumber**

Format:Text

Category:Tracking

Definition: The serial number of the instrument used for this analysis.

Applicable Node(s):  
**Analysis**

---

**InterelementCorrection**

Format:Limited List

Category:Description

Definition: Whether or not ICP interelement or interanalyte correction factors were applied.

Applicable Node(s):  
**Analysis** Example Valid Values: 'Yes', 'No'.

---

**IntermediateResult**

Format:Numeric

Category:Measurement

Definition: This value represents the results of this analysis, not for a method, and would normally not include sample aliquot, dilution or other sample information.

Applicable Node(s):  
**Analyte** The result for this analyte for an analysis, not a method. This value is normally the result obtained directly from a calibration curve.  
**Peak** Same as in Analyte when results are measured per peak.  
**PeakReplicate**

---

**IntermediateResultLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the IntermediateResult.

Applicable Node(s):  
**Analyte** This would typically represent the upper limit of the calibrated or linear range for this analyte.  
**Peak** Same as in Analyte when results are measured per peak.  
**PeakReplicate**

---

**IntermediateResultLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the IntermediateResult.

Applicable Node(s):

**Analyte**

This would typically represent the lower limit of the calibrated or linear range for this analyte.

**Peak**

Same as in Analyte when results are measured per peak.

**PeakReplicate**

---

**IntermediateResultLimitType**

Format:Limited List

Category:Measurement

Definition: The term used to define the specific type of IntermediateResultLimit for the method being performed.

Applicable Node(s):

**Analyte**

Example Valid Values: 'Linear\_Range'.

**Peak**

Same as in Analyte when results are measured per peak.

**PeakReplicate**

---

**IntermediateResultUncertainty**

Format:Numeric

Category:Measurement

Definition: The estimated error in the IntermediateResult.

Applicable Node(s):

**Analyte****Peak****PeakReplicate**

---

**IntermediateResultUncertaintyType**

Format:Limited List

Category:Measurement

Definition: The confidence interval for the IntermediateResultUncertainty.

Applicable Node(s):

**Analyte**

Example Valid Values: '1-Sigma', '2-Sigma', '3-Sigma'.

**Peak****PeakReplicate**

---

**IntermediateResultUncertaintyUnits**

Format:Limited List

Category:Measurement

Definition: Units for IntermediateResultUncertainty.

Applicable Node(s):

**Analyte****Peak****PeakReplicate**

---

**IntermediateResultUnits**

Format:Limited List

Category:Measurement

Definition: Units for IntermediateResult.

Applicable Node(s):

**Analyte****Peak****PeakReplicate**

---

**LabAddress1**

Format:Text

Category:Description

Definition: Primary address of the laboratory performing this analysis.

Applicable Node(s):

**SamplePlusMethod**

---

**LabAddress2**

Format:Text

Category:Description

Definition: Secondary address of the laboratory performing this analysis.

Applicable Node(s):

**SamplePlusMethod**

---

**LabAnalysisID**

Format:Identifier

*Required*

Category:Identification

Definition: A laboratory-defined identifier for an analysis that uniquely identifies a single run for a single aliquot.

Applicable Node(s):

**Analysis**

This value shall be unique at least for all analyses in one laboratory reporting batch in the context of one method.

Example: A LIMS-assigned value or a value manually assigned by laboratory personnel. It could reference a run number or a page number from a laboratory notebook.

**ReportedResult**

If there is any ambiguity about which analysis underlies this result, the LabAnalysisID of this analysis.

Example: To identify from which of several dilutions the reported result is chosen.

---

**LabAnalyteID**

Format:Identifier

*Required For Traceability*

Category:Identification

Definition:

A laboratory-defined identifier for the analyte.

Applicable Node(s):

**ReportedResult**

This identifier gives traceability into the laboratory's systems.

**Analyte****AnalyteGroup****PeakComparison**

LabAnalyteID for the analyte to compare to. If not specified, it is assumed to be the same as the analyte for Peak this PeakComparison is in.

**AnalyteComparison**

LabAnalyteID for the analyte to compare to.

---

**LabCity**

Format:Text

Category:Description

Definition:

Primary address (City) of the laboratory performing this analysis.

Applicable Node(s):

**SamplePlusMethod**

---

**LabContact**

Format:Text

Category:Description

Definition:

The person at the laboratory to contact with questions about this data.

Applicable Node(s):

**SamplePlusMethod**

---

**LabContract**

Format:Text

Category:Tracking

Definition:

A client-defined contract number under which the laboratory analyzes the samples.

Applicable Node(s):

**SamplePlusMethod**

---

**LabDataPackageID**

Format:Identifier

Category:Tracking

Definition:

A laboratory-defined identifier for this data deliverable package.

Applicable Node(s):

**Header**

This identifier applies to a single deliverable.

For example, a document number the laboratory assigns to the physical data package or a file name for an electronic deliverable. Use LabReportingBatch for the logical notion of a group of samples reported as a unit.

---

**LabDataPackageName**

Format:Text

Category:Tracking

Definition: A laboratory-defined title for this data deliverable package.

Applicable Node(s):

**Header**

---

**LabDataPackageVersion**

Format:Text

Category:Tracking

Definition: If the laboratory resubmits a data package, this field can be used to distinguish the different versions.

Applicable Node(s):

**Header**

---

**LabFileID**

Format:Identifier

Category:Identification

Definition: The path and file name where the raw data from the analysis is stored.

Applicable Node(s):

**Analysis**

---

**LabID**

Format:Identifier

*Required*

Category:Identification

Definition: Identifier for the laboratory performing this analysis.

Applicable Node(s):

**SamplePlusMethod**

This identifier is often client-defined. This is generally the laboratory that has done all of the work or, if part of the work is subcontracted, the laboratory responsible for the reporting of the data. To be fully reliable, LabIDs must be unique across all potential laboratories.

**InstrumentQC****Handling****PreparationPlusCleanup****Analysis**

---

**LabInstrumentQCID**

Format:Identifier

*Required Conditionally*

Category:Identification

Definition: A laboratory-defined identifier that uniquely identifies a single InstrumentQC analysis (i.e., Instrument\_Performance\_Check, Continuing\_Calibration\_Verification, etc.) or group of analyses (i.e., Initial\_Calibration, etc.).

Applicable Node(s):

**InstrumentQC**

---

**LabManager**

Format:Text

Category:Description

Definition: The person at the laboratory who takes final responsibility for this data.

Applicable Node(s):  
**SamplePlusMethod**

---

**LabManagerTitle**

Format:Text

Category:Description

Definition: The corporate title of the LabManager.

Applicable Node(s):  
**SamplePlusMethod**

---

**LabMethodID**

Format:Identifier

*Required For Traceability*

Category:Identification

Definition: A laboratory-defined code for the method used by the laboratory to analyze the sample.

Applicable Node(s):  
**SamplePlusMethod**  
**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**LabMethodName**

Format:Text

Category:Identification

Definition: The laboratory-defined descriptive name for this method.

Applicable Node(s):  
**SamplePlusMethod**  
**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**LabName**

Format:Text

Category:Identification

Definition: Descriptive name for the laboratory performing this analysis.

Applicable Node(s):  
**SamplePlusMethod**  
**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**LabNarrativeID**

Format:Identifier

Category:Tracking

Definition: A laboratory-defined code for any narrative document associated with this data.

Applicable Node(s):

**SamplePlusMethod**

---

**LabQualifiers**

Format:Text

Category:Description

Definition: A laboratory-assigned string of result qualifiers (usually a single character for each qualifier), based on client or laboratory-defined rules and values.

Applicable Node(s):

**ReportedResult****Analyte****AnalyteGroup****Peak****AnalyteComparison****PeakComparison**

---

**LabQualifiersDefinition**

Format:Text

Category:Description

Definition: Definition for the qualifier(s) as reported in LabQualifiers.

Applicable Node(s):

**Header**

The following format should be used - Qualifier:Definition. When reporting more than one definition, each definition should be separated by a ';'.

---

**LabReceiptDate**

Format:Date

Category:Tracking

Definition: Date (and time, if required) the sample was received in the laboratory.

Applicable Node(s):

**SamplePlusMethod**

---

**LabReceiptDateTimeZone**

Format:Limited List

Category:Tracking

Definition: Time zone for LabReceiptDate.

Applicable Node(s):

**SamplePlusMethod**

---

**LabReportedDate**

Format:Date

Category:Tracking

Definition: Date (and time, if required) this data package was reported by the laboratory to the client.

Applicable Node(s):

**Header**

---

**LabReportedDateTimeZone**

Format:Limited List

Category:Tracking

Definition: Time zone for LabReportedDate.

Applicable Node(s):

**Header**

---

**LabReportingBatch**

Format:Identifier

Category:Batch

Definition: A laboratory-defined identifier for a batch of samples reported as a group by the laboratory. In addition, this batch can be used to link certain QC samples to regular ones.

Applicable Node(s):

**SamplePlusMethod**

---

**LabResultStatus**

Format:Limited List

Category:Tracking

Definition: Laboratory-assigned status for results for this sample and method.

Applicable Node(s):

**SamplePlusMethod  
ReportedResult** Example Valid Values: 'Preliminary', 'Final'.

---

**LabSampleID**

Format:Identifier

Category:Identification

Definition: *Required For Traceability*  
A laboratory-defined identifier for a sample that uniquely identifies a single sample that is subjected to an analysis.

Applicable Node(s):

**SamplePlusMethod** This code is the primary link into the laboratory's record keeping system. It is not necessarily one-to-one with the ClientSampleID.

---

**LabState**

Format:Text

Category:Description

Definition: Primary address (State) of the laboratory performing this analysis.

Applicable Node(s):

**SamplePlusMethod**

---

---

**LabType**

Format:Limited List

Category:Description

Definition: The term used to describe the type of laboratory analyzing this sample.

Applicable Node(s):

**SamplePlusMethod**

Example Valid Values: 'Field', 'Fixed', 'Mobile'.

---

**LabZipcode**

Format:Text

Category:Description

Definition: Primary address (Zipcode) of the laboratory performing this analysis.

Applicable Node(s):

**SamplePlusMethod**

---

**LocationID**

Format:Identifier

Category:Tracking

Definition: Identifier for the sampling location at a site.

Applicable Node(s):

**SamplePlusMethod**

Often client-defined.

Examples: Operable\_Unit, Well, Tank, Station, Facility (building), Installation, Aggregate\_Area.

---

**LocationName**

Format:Text

Category:Tracking

Definition: Descriptive name for the sampling location at a site.

Applicable Node(s):

**SamplePlusMethod**

May be laboratory-defined.

Examples: Operable\_Unit, Well, Tank, Station, Facility (building), Installation, Aggregate\_Area.

---

**LotNumber**

Format:Text

Category:Description

Definition: A manufacturer-assigned batch number for something used in this analysis.

Applicable Node(s):

**Analyte**

Example: The vendor/manufacturer-assigned lot number for a purchased standard.

**PreparationPlusCleanup**

Example: Florisil cartridge lot number.

---

**ManualIntegration**

Format:Limited List

Category:Description

Definition: Whether or not manual integration was used.

Applicable Node(s):

**Analyte****Peak**

Example Valid Values: 'Yes', 'No'.

---

**Mass**

Format:Numeric

Category:Measurement

Definition: The measured mass of this analyte or peak.

Applicable Node(s):

**Analyte****Peak****PeakComparison**

---

**MassChargeRatio**

Format:Numeric

Category:Description

Definition: The mass/charge relationship recorded in MS detection.

Applicable Node(s):

**Peak****PeakComparison**

---

**MassLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the Mass.

Applicable Node(s):

**Analyte****Peak****PeakComparison**

---

**MassLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the Mass.

Applicable Node(s):

**Analyte****Peak****PeakComparison**

---

**MassLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the Mass limits.

Applicable Node(s):

**Analyte**  
**Peak**  
**PeakComparison**

---

**MassUnits**

Format:Limited List

Category:Measurement

Definition: Units for Mass.

Applicable Node(s):

**Analyte**  
**Peak**  
**PeakComparison**

---

**MatrixID**

Format:Limited List

*Required*

Category:Identification

Definition: A more specific description of the sample matrix or media.

Applicable Node(s):

**SamplePlusMethod** For example, the general matrixID 'Aqueous' could be further broken down and given the MatrixName 'Water', 'Surface\_Water', 'Ground\_Water', or 'Drinking\_Water'.  
**Handling** MatrixID of the sample after the handling described by this node.  
**PreparationPlusCleanup** MatrixID of the aliquot after the preparation or cleanup described by this node.

---

**MatrixMedium**

Format:Limited List

*Required for Portability*

Category:Identification

Definition: An identifier for the general sample matrix or media.

Applicable Node(s):

**SamplePlusMethod** Example Valid Values: 'Aqueous', 'Solid', 'Air', 'Non\_Aqueous', 'Biological\_Tissue'.  
**Handling** MatrixMedium of the sample after the handling described by this node.  
**PreparationPlusCleanup** MatrixMedium of the aliquot after the preparation or cleanup described by this node.

---

**MeanCalibrationFactor**

Format:Numeric

Category:Measurement

Definition: The average or mean Calibration Factor.

Applicable Node(s):

**Analyte** The mean calibration factor for this analyte.  
**Peak** Same as in Analyte, except applied per peak.

---

**MeanCalibrationFactorUnits**

Format:Text

Category:Measurement

Definition: Units for MeanCalibrationFactor.

Applicable Node(s):

**Analyte**

**Peak**

---

**MeanRelativeResponse**

Format:Numeric

Category:Measurement

Definition: The average or mean Relative Response.

Applicable Node(s):

**Analyte**

The mean relative response for this analyte.

---

**MeanRelativeResponseLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the MeanRelativeResponse.

Applicable Node(s):

**Analyte**

---

**MeanRelativeResponseLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the MeanRelativeResponse.

Applicable Node(s):

**Analyte**

---

**MeanRelativeResponseLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the MeanRelativeResponse limits.

Applicable Node(s):

**Analyte**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

---

**MeanRetentionTime**

Format:Numeric

Category:Measurement

Definition: The average or mean Retention Time.

Applicable Node(s):

**Analyte**

The mean retention time for this analyte.

**Peak**

Same as in Analyte, except applied per peak.

---

---

**MeanRetentionTimeLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the mean Retention Time.

Applicable Node(s):

**Analyte****Peak**

---

**MeanRetentionTimeLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the mean Retention Time.

Applicable Node(s):

**Analyte****Peak**

---

**MeanRetentionTimeLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the MeanRetentionTime limits

Applicable Node(s):

**Analyte****Peak**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

---

**MeanRetentionTimeUnits**

Format: Limited List

Category: Measurement

Definition: Units for MeanRetentionTime

Applicable Node(s):

**Analyte****Peak**

---

**MeanRRF**

Format:Numeric

Category:Measurement

Definition: The average or mean Relative Response Factor.

Applicable Node(s):

**Analyte****Peak****PeakComparison**

The mean relative response factor for this analyte.

Same as in Analyte, except applied per peak.

---

**MeanRRFLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the MeanRRF.

Applicable Node(s):

**Analyte**  
**Peak**  
**PeakComparison**

---

**MeanRRFLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the MeanRRF limits.

Applicable Node(s):

**Analyte** Example Valid Values: 'Method', 'Client', 'Laboratory'.  
**Peak**  
**PeakComparison**

---

**MeltingPoint**

Format:Numeric

Category:Measurement

Definition: The temperature at which the sample melts.

Applicable Node(s):

**SamplePlusMethod**

---

**MeltingPointUnits**

Format:Limited List

Category:Measurement

Definition: Units for MeltingPoint.

Applicable Node(s):

**SamplePlusMethod**

---

**MethodBatch**

Format:Identifier

Category:Batch

Definition: A laboratory-defined identifier for a batch of samples analyzed by one method and treated as a group for QC purposes. A method batch should group samples with similar matrices and potential interferences.

Applicable Node(s):

**SamplePlusMethod** This is a broader grouping than a preparation batch. In particular, a reanalysis of a sample stays in the same method batch, while it is likely to be in a different preparation batch. Operationally, this batch associates sample dependent QC such as duplicates and matrix spikes with a group of samples that may or may not be prepared at the same time.

---

**MethodCategory**

Format:Limited List

Category:Identification

Definition: The general class or common name for the group of analytes being measured by a given method for this sample.

Applicable Node(s):

**SamplePlusMethod** Example Valid Values: 'VOAs', 'SVOAs', 'Metals', 'PCBs', 'PESTs'.  
**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**MethodCode**

Format:Limited List

Category:Identification

Definition: The published reference code for the method used by the laboratory to analyze the sample.

Applicable Node(s):

**SamplePlusMethod**  
**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**MethodID**

Format:Limited List

Category:Identification

Definition: *Required for Portability*  
The published reference method identification number for the method used by the laboratory to analyze the sample.

Applicable Node(s):

**SamplePlusMethod** Example Valid Value: '8260B'. If no published reference method identification number is available then the ClientMethodID data element must be used.  
**InstrumentQC**  
**Handling**  
**PreparationPlusCleanup**  
**Analysis**

---

**MethodLevel**

Format:Limited List

Category:Description

Definition: Approximate level of analytes in the sample, usually specified in client-defined concentration ranges and determined via a screening procedure.

Applicable Node(s):

**SamplePlusMethod** Example Valid Values: 'Low', 'Medium', 'High'.

---

**MethodName**

Format:Limited List

Category:Identification

Definition: The published reference method name for the method used by the laboratory to analyze the sample.

Applicable Node(s):

**SamplePlusMethod**

Example Valid Value: 'Volatile Organic Compounds by Gas Chromatography/Mass Spectrometry (GC/MS)'. If no published reference method name is available then the ClientMethodName data element should be used.

**InstrumentQC****Handling****PreparationPlusCleanup****Analysis**

---

**MethodSource**

Format:Limited List

Category:Identification

Definition: The published reference method source for the MethodID and MethodName.

MethodName.

Applicable Node(s):

**SamplePlusMethod**

Example Valid Value: 'USEPA\_OSW'. If no published reference method source is available then the ClientMethodSource data element must be used.

**InstrumentQC****Handling****PreparationPlusCleanup****Analysis**

---

**MethodType**

Format:Limited List

Category:Identification

Definition: The method type or technology for the method as used by the laboratory to analyze the sample.

Applicable Node(s):

**SamplePlusMethod**

Example Valid Values: 'GC/MS', 'GC/MS\_SIM', 'ICP/AES', 'ICP/MS', 'IR'.

**InstrumentQC****Handling****PreparationPlusCleanup****Analysis**

---

**MethodVersion**

Format:Limited List

*Required for Portability*

Category:Identification

Definition:

The version of the method used by the laboratory to analyze the sample.

Applicable Node(s):

**SamplePlusMethod****InstrumentQC****Handling****PreparationPlusCleanup****Analysis**

---

**MobilePhase**

Format:Text

Category:Description

Definition:

The mobile phase composition used for HPLC, or other similar procedures.

Applicable Node(s):

**Analysis**

---

**NumberDilutions**

Format:Numeric

Category:Description

Definition:

Number of dilutions done to this aliquot.

Applicable Node(s):

**Analysis**

---

**NumberPhases**

Format:Numeric

Category:Description

Definition:

The number of phases observed for the sample.

Applicable Node(s):

**SamplePlusMethod**

---

**OrganismLength**

Format:Numeric

Category:Measurement

Definition:

Length of an Organism.

Applicable Node(s):

**SamplePlusMethod**

---

**OrganismLengthUnits**

Format:Limited List

Category:Measurement

Definition:

Units for OrganismLength.

Applicable Node(s):

**SamplePlusMethod**

---

---

**OrganismPortion**

Format:Limited List

Category:Description

Definition: Portion of an organism used for analysis.

Applicable Node(s):  
**SamplePlusMethod**

---

**OrganismSex**

Format:Limited List

Category:Description

Definition: Sex of an organism.

Applicable Node(s):  
**SamplePlusMethod** Example Valid Values: 'Male' or 'Female'.

---

**OriginalClientSampleID**

Format:Identifier

Category:Identification

Definition: *Required Conditionally*  
The client sample ID number of the original regular sample from which the QC sample was derived.Applicable Node(s):  
**SamplePlusMethod** For a method QC sample of QCcategory Duplicate, Serial\_Dilution, Spike, or Spike\_Duplicate there must be an associated regular sample the QC sample is derived from. This sample is called the original. The value of OriginalClientSampleID matches that of the ClientSampleID for this original sample.

---

**OriginalLabAnalysisID**

Format:Identifier

Category:Identification

Definition: *Required Conditionally*  
The LabAnalysisID of a previous or original analysis this analysis is based on.Applicable Node(s):  
**Analysis** This data element would only be used for AnalysisType equal to 'Dilution-##' or 'Reinjection-##', where ## can be any integer starting at '01' and incrementing up to '99'.

---

**OriginalLabSampleID**

Format:Identifier

*Required Conditionally*

Category:Identification

Definition:

The laboratory sample ID number of the original regular sample from which the QC sample was derived.

Applicable Node(s):

**SamplePlusMethod**

For a method QC sample with QCcategory Duplicate, Serial\_Dilution, Spike or Spike\_Duplicate there must be an associated regular sample the QC sample is derived from. This sample is called the original. The value of OriginalLabSampleID matches that of the LabSampleID for this original sample. For a method QC sample with QCcategory Blank\_Spike\_Duplicate, the value of OriginalLabSampleID matches that of the LabSampleID for the associated Blank\_Spike.

---

**Peak**

Format:

Category:

Definition:

Parent Element. Contains elements related to analyte peaks.

Applicable Node(s):

**Peak**

---

**PeakComparison**

Format:

Category:

Definition:

Parent element. Contains elements relating to the comparison of multiple peaks.

Applicable Node(s):

**PeakComparison**

---

**PeakID**

Format:Identifier

*Required Conditionally*

Category:Identification

Definition:

A laboratory-specified value, possibly based on client-specified rules, that identifies a peak associated with an analyte. Its value should be unique among all peaks for one analyte within a run sequence, but not necessarily have physical meaning.

Applicable Node(s):

**Peak**

Examples: Nominal mass for GCMS peaks, integer wavelength for ICP peaks, sequence number (1, 2, ...) for multicomponent GC peaks. PeakID is conceptually similar to ClientAnalyteID, except it identifies a peak rather than an analyte.

**ReportedResult**

If there is any ambiguity about which peak underlies this result, the PeakID of that peak.

**Analyte**

If there is any ambiguity about which peak underlies this analyte's result, the PeakID of that peak.

**PeakComparison**

Peak identifier for the peak to compare to. It is combined with the LabAnalyteID (or ClientAnalyteID) in the same PeakComparison node to fully specify the peak to compare to.

---

**PeakRatio**

Format:Numeric

Category:Measurement

Definition: The ratio of the response of two peaks.

Applicable Node(s):

**Peak****PeakComparison**

The response of the peak this PeakComparison node is in as a ratio of the response of the peak identified by the PeakID and LabAnalyteID (or ClientAnalyteID) in this node.

---

**PeakRatioLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the PeakRatio.

Applicable Node(s):

**Peak****PeakComparison**

---

**PeakRatioLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the PeakRatio.

Applicable Node(s):

**Peak****PeakComparison**

---

**PeakRatioLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the PeakRatio limits.

Applicable Node(s):

**Peak****PeakComparison**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

---

**PeakReplicate**

Format:

Category:

Definition: Parent Element. Contains elements related to multiple peak measurements.

Applicable Node(s):

**PeakReplicate**

---

**PeakReplicateID**

Format:Identifier

*Required Conditionally*

Category:Identification

Definition:

A laboratory-specified value, possibly based on client-specified rules, that identifies a single peak measurement from a series of replicate measurements.

Applicable Node(s):

**PeakReplicateID**

---

**PercentBreakdown**

Format:Numeric

Category:Measurement

Definition:

The percent breakdown of an analyte.

Applicable Node(s):

**Analyte**

Example: DDT breakdown as reported for pesticide methods.

**Peak**

The percent breakdown of an analyte when results are measured per peak.

---

**PercentBreakdownLimitHigh**

Format:Numeric

Category:Measurement

Definition:

The upper limit for the PercentBreakdown.

Applicable Node(s):

**Analyte****Peak**

---

**PercentBreakdownLimitType**

Format:Limited List

Category:Measurement

Definition:

The source for the PercentBreakdown limits.

Applicable Node(s):

**Analyte**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

**Peak**

---

**PercentDifference**

Format:Numeric

Category:Measurement

Definition:

The difference between two measured values as a percentage of one of them. The denominator value is usually the more certain one, although details can be method specific.

Applicable Node(s):

**ReportedResult****Analyte**

Can be applied to the results of analyses in an analysis group rather than a QC sample and original pair.

**Peak**

Can be used when results are measured per peak.

**PeakComparison**

Can be used to compare values in two PeakComparison elements.

---

**PercentDifferenceLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the PercentDifference.

Applicable Node(s):

**ReportedResult**

**Analyte**

**Peak**

**PeakComparison**

---

**PercentDifferenceLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the PercentDifference.

Applicable Node(s):

**ReportedResult**

**Analyte**

**Peak**

**PeakComparison**

---

**PercentDifferenceLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the PercentDifference limits.

Applicable Node(s):

**ReportedResult**

**Analyte**

**Peak**

**PeakComparison**

---

**PercentLipid**

Format:Numeric

Category:Measurement

Definition: Percent of the sample composed of lipid material.

Applicable Node(s):

**SamplePlusMethod**

---

**PercentMatch**

Format:Numeric

Category:Measurement

Definition: Percent match of an analyte as compared with a library mass spectrum.

Applicable Node(s):

**Analyte**

---

**PercentMoisture**

Format:Numeric

Category:Measurement

Definition: Percent of the sample composed of water.

Applicable Node(s):

**SamplePlusMethod  
Handling**

Percent of sample composed of water after the handling described by this node.

---

**PercentPhase**

Format:Numeric

Category:Measurement

Definition: Percent of sample in analyzed phase.

Applicable Node(s):

**SamplePlusMethod  
Handling**This element may generalize ones like PercentSolids.  
Percent of sample in analyzed phase after the handling described by this node.

---

**PercentPreparationUncertainty**

Format:Numeric

Category:Measurement

Definition: The uncertainty introduced into the final result by all laboratory activities other than instrumental analysis expressed as a percentage of the result value.

Applicable Node(s):

**ReportedResult  
Analysis  
Analyte**

Same except applies to all results from this analysis.

---

**PercentRatio**

Format:Numeric

Category:Measurement

Definition: The ratio, expressed as a percentage, of the response of two peaks.

Applicable Node(s):

**Peak  
PeakComparison**

The response of the peak this PeakComparison node is in as a percentage of the response of the peak identified by the PeakID and ClientAnalyteID in this node. Example: Used with mass spectral peaks in System Monitoring Compounds.

---

**PercentRatioLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the PercentRatio.

Applicable Node(s):

**Peak  
PeakComparison**

---

**PercentRatioLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the PercentRatio.

Applicable Node(s):

**Peak**  
**PeakComparison**

---

**PercentRatioLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the PercentRatio limits.

Applicable Node(s):

**Peak** Example Valid Values: 'Method', 'Client', 'Laboratory'.  
**PeakComparison**

---

**PercentRecovery**

Format:Numeric

Category:Measurement

Definition: The recovery of an analyte expressed as a percentage of the amount added. If a numeric result cannot be calculated then the PercentRecoveryType data element should be used.

Applicable Node(s):

**ReportedResult** For method QC of QCcategory Blank\_Spike and Blank\_Spike\_Duplicate, the result as a percentage of the amount added. For method QC of QCcategory Spike and Spike\_Duplicate, the spiked result minus the original result as a percentage of the ExpectedResult.  
**Analyte** Same as in ReportedResult except applied to the results from an analysis such as a surrogate or analyses in an analysis group rather than a QC sample and original pair.  
**Peak** Same as in Analyte when results are measured per peak.

---

**PercentRecoveryLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the PercentRecovery. Units are the same as for PercentRecovery.

Applicable Node(s):

**ReportedResult**  
**Analyte**  
**Peak**

---

**PercentRecoveryLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the PercentRecovery. Units are the same as for PercentRecovery.

Applicable Node(s):

**ReportedResult****Analyte****Peak**

---

**PercentRecoveryLimitType**

Format:Limited List

Category:Measurement

Definition: The source of the PercentRecovery limits.

Applicable Node(s):

**ReportedResult****Analyte****Peak**Example Valid Values: 'Method', 'Client', 'Laboratory'.

---

**PercentRecoveryType**

Format:Limited List

Category:Measurement

Definition: Would be used to report non-numeric PercentRecovery results when the Percent Recovery was calculated but a numerical value could not be determined.

Applicable Node(s):

**ReportedResult****Analyte****Peak**Example Valid Value: 'Not\_Calculable'.

---

**PercentRSD**

Format:Numeric

Category:Measurement

Definition: The standard deviation as a percentage of the mean (percent relative standard deviation).

Applicable Node(s):

**Analyte****Peak****PeakComparison**

Used for an analyte in AnalysisGroup.

Used for an analyte, except applied per peak.

Same as in Peak except applied to PeakComparison values.

---

**PercentRSDLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the PercentRSD.

Applicable Node(s):

**Analyte****Peak****PeakComparison**

---

**PercentRSDLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the PercentRSD.

Applicable Node(s):

**Analyte**  
**Peak**  
**PeakComparison**

---

**PercentRSDLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the PercentRSD limits.

Applicable Node(s):

**Analyte** Example Valid Values: 'Method', 'Client', 'Laboratory'.  
**Peak**  
**PeakComparison**

---

**PercentSolids**

Format:Numeric

Category:Measurement

Definition: Percent of the sample composed of solid material.

Applicable Node(s):

**SamplePlusMethod**  
**Handling** Percent of the sample composed of solid material after the handling described by this node.

---

**PercentValley**

Format:Numeric

Category:Measurement

Definition: The valley between this analyte and another one, as a percentage of the shorter one. The second analyte is assumed to be known based on the method.

Applicable Node(s):

**Analyte**  
**Peak**  
**PeakComparison** The valley between the peak this PeakComparison node is in and the peak identified by the PeakID and LabAnalyteID in this node as a percentage of the height of the shorter one.

---

**PercentValleyLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the PercentValley.

Applicable Node(s):

**Analyte**  
**Peak**  
**PeakComparison**

---

**PercentValleyLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the PercentValley limits.

Applicable Node(s):

**Analyte**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

**Peak****PeakComparison**

---

**pH**

Format:Numeric

Category:Measurement

Definition: The negative of the logarithm of the hydrogen ion potential.

Applicable Node(s):

**SamplePlusMethod****Handling**The negative of the logarithm of the hydrogen ion potential after the handling described by this node.

---

**PhaseAnalyzed**

Format:Limited List

Category:Description

Definition: That portion or fraction of a multiphase sample actually analyzed.

Applicable Node(s):

**SamplePlusMethod**Example Valid Values: 'Upper', 'Middle', 'Lower'.

---

**PreparationBatch**

Format:Identifier

Category:Batch

Definition: A laboratory-defined identifier for a batch of aliquots that are prepared together for analysis by one method. Together can imply similarity of time, place, and manner of preparation.

Applicable Node(s):

**Analysis****PreparationPlusCleanup**

---

**PreparationID**

Format:Identifier

Category:Identification

Definition: A laboratory-defined identifier for this preparation event for this aliquot.

Applicable Node(s):

**PreparationPlusCleanup**

---

**PreparationPlusCleanup**

Format:

Category:

Definition: Parent element. Contains elements related to preparations and cleanups.

Applicable Node(s):

**PreparationPlusCleanup**

---

---

**PreparationPlusCleanupType**

Format:Limited List

Category:Identification

Definition: Whether or not the data in this node is related to a preparation or cleanup activity.

Applicable Node(s):

**PreparationPlusCleanup**

Example Valid Values: 'Preparation', 'Cleanup'.

---

**PreparationType**

Format:Limited List

Category:Identification

Definition: A client-defined identifier used to define the type of preparation. This identifier is used to identify the specific preparation procedure used.

Applicable Node(s):

**Analysis**

This identifier is used to specify which preparation method was used when such preparation method details are part of the analysis (instrumental) method. When client preparation methods are available, this identifier is used to identify what method options were used within the preparation method.

Example Valid Values: 'Separatory\_Funnel' or 'Continuous\_Extraction' for EPA Method 625. For Method SW846 3520C, whether the extraction performed was 'Acid\_Base', 'Acid only', or 'Base only'.

**PreparationPlusCleanup**

---

**PreparedDate**

Format:Date

Category:Tracking

Definition: Date (and time, if required) of preparation of this aliquot. Preparation is used generally to include method specific techniques such as extraction, digestion, and separation. If prepared over a range of dates, this is the start date.

Applicable Node(s):

**Analysis****PreparationPlusCleanup**

---

**PreparedDateTimeZone**

Format:Limited List

Category:Tracking

Definition: Time zone for PreparedDate.

Applicable Node(s):

**Analysis****PreparationPlusCleanup**

---

**PreparedEndDate**

Format:Date

Category:Tracking

Definition: If the aliquot was prepared over a range of dates (and times, if required), the end of the preparation period.

Applicable Node(s):

**Analysis****PreparationPlusCleanup**

---

**PreparedEndDateTimeZone**

Format:Limited List

Category:Tracking

Definition: Time zone for PreparedEndDate.

Applicable Node(s):

**Analysis****PreparationPlusCleanup**

---

**Preservative**

Format:Text

Category:Description

Definition: Preservative added to the sample.

Applicable Node(s):

**SamplePlusMethod**

---

**PreservedBy**

Format:Text

Category:Description

Definition: Organization that added preservative to the sample.

Applicable Node(s):

**SamplePlusMethod**

---

**PriorityID**

Format:Limited List

Category:Tracking

Definition: A client-defined term that identifies the priority assigned to this data. The priority may affect the desired turn around time and the cost of the analysis.

Applicable Node(s):

**SamplePlusMethod**Example Valid Values: 'Rush', 'Normal'.

---

---

**ProcedureID**

Format:Identifier

Category:Identification

Definition: A laboratory-defined identifier for the laboratory's Standard Operating Procedure (SOP) for this method.

Applicable Node(s):

**Analysis**  
**Handling**  
**PreparationPlusCleanup**

---

**ProcedureName**

Format:Text

Category:Identification

Definition: Description of the laboratory's Standard Operating Procedure (SOP) for this method.

Applicable Node(s):

**Analysis**  
**Handling**  
**PreparationPlusCleanup**

---

**ProjectID**

Format:Identifier

Category:Tracking

Definition: A client-defined identifier for the project this sample is part of. Typically, a project consists of samples from one site collected over some defined period of time.

Applicable Node(s):

**SamplePlusMethod** Example: Case No., Episode, Sampling Round.

---

**ProjectName**

Format:Text

Category:Tracking

Definition: Descriptive name for the project this sample is a part of.

Applicable Node(s):

**SamplePlusMethod** Examples: Case No., Episode, Sampling Round.

---

**QCCategory**

Format:Limited List

Category:Identification

Definition: A generic identifier that specifies the basic properties or category of a method QC sample.

Applicable Node(s):

**SamplePlusMethod** Example Valid Values:

1. 'Blank' -- A QC sample with 'nothing' in it. Examples: Field, equipment, method (reagent), sulfur and storage blanks.
2. 'Blank\_Spike' -- A QC sample with a known amount added to a Blank. Examples: laboratory control samples, QC check samples, and interference check samples.

3. 'Duplicate' -- A reanalysis of a regular sample done for QC purposes. Examples: duplicates and splits.
4. 'Blank\_Spike\_Duplicate' -- A reanalysis of a BlankSpike.
5. 'Serial\_Dilution' -- A dilution and reanalysis of a regular sample done for QC purposes.
6. 'Spike' -- A reanalysis of a regular sample with a known amount added and done for QC purposes. Examples: matrix spikes, post digestion spikes, and analytical spikes.
7. 'Spike\_Duplicate' -- A second reanalysis of a regular sample with a known amount added and done for QC purposes. There must be another sample with QCcategory 'Spike' with the same original sample.

---

### **QCLinkage**

Format:Limited List

Category:Identification

Definition:

*Required For Portability*

For a QC sample, specifies which batch is the basis for the association between the QC sample and the regular samples.

Applicable Node(s):

#### **SamplePlusMethod**

Allowed Valid Values include the following fields that define batches: 'SamplingBatch', 'EquipmentBatch', 'ShippingBatch', 'LabReportingBatch', 'MethodBatch', 'HandlingBatch', 'PreparationBatch', 'AnalysisBatch', 'CleanupBatch', 'StorageBatch'. If QCLinkage is 'HandlingBatch', there should be a HandlingType element in the SamplePlusMethod node whose value clarifies which type of handling batch is intended.

Example: In SamplePlusMethod, if the QCType is Duplicate, the QCcategory is Duplicate and the QCLinkage is MethodBatch, a reader knows that this data is for a client-defined type of QC called a Duplicate, that it is processed with rules typical for Duplicates and that it is to be associated with other SamplePlusMethod elements with the same value for the MethodBatch field. QCLinkage is most useful if the batch it names is a required element, based on implementation rules. The correct linkage for a field QC sample may not be known to the laboratory, so must be merged with laboratory data at a later time.

#### **InstrumentQC**

Same as in SamplePlusMethod except allowed Valid Values for instrument QC are 'CleanupBatch', 'PreparationBatch', 'AnalysisBatch', and 'RunBatch'. If QCLinkage is 'CleanupBatch', there should be a CleanupType element in InstrumentQC whose value clarifies which type of cleanup batch is intended.

---

**QCType**

Format:Limited List  
Category:Identification  
Definition:

*Required*

The client-defined term used to define the specific type of sample being analyzed.

Applicable Node(s):

**SamplePlusMethod**

In the context of the ClientMethodID and MatrixID, this term determines all special processing rules for the sample. The default Valid Value is 'Field\_Sample' for a regular sample. The presence of any other term in this field defines the sample as a method, client or performance QC sample. A laboratory may not know that certain samples are QC. In this case the laboratory reports them as regular samples ('Field\_Sample') and their type is changed later, possibly by the validator.

**InstrumentQC**

For instrument QC, a client-defined term that specifies what type of instrument QC data follows. In the context of the ClientMethodID, the value must imply enough detail for the reader to understand the method specific details of the following AnalysisGroup, Analysis, PrepPlusCleanup, Analyte, Peak, PeakComparison, and AnalyteComparison elements.

---

**QuantitationBasis**

Format:Limited List  
Category:Description  
Definition:

The basis on which sample quantitation is performed (e.g., using internal standards).

Applicable Node(s):

**Analysis**

**Analyte**

Example valid values: 'Internal\_Standard' or 'External\_Standard'.

---

**QuantitationLimit**

Format:Numeric  
Category:Measurement  
Definition:

Quantitation limit for the analyte being measured. Quantitation limits are defined in terms of a specified degree of uncertainty for results at this level.

Applicable Node(s):

**ReportedResult**

**Analyte**

**Peak**

Within AnalysisGroup, applies to a quantitation limit value computed from several analyses.

Same as in Analyte when results are measured per peak.

---

**QuantitationLimitType**

Format:Limited List

Category:Measurement

Definition: One of a list of client-defined acronyms that specify the type of quantitation limit.

Applicable Node(s):

**ReportedResult****Analyte****Peak**

Example Valid Values: 'CRQL', 'PQL'.

---

**QuantitationLimitUnits**

Format:Limited List

Category:Measurement

Definition: Units for QuantitationLimit.

Applicable Node(s):

**ReportedResult****Analyte****Peak**

If the client specifies that the QuantitationLimitUnits must be the same as the ResultUnits, the QuantitationLimitUnits need not be specified.

Same as in ReportedResult.

Same as in ReportedResult.

---

**Quarantine**

Format:Limited List

Category:Description

Definition: Whether or not the sample as received by the laboratory is to be quarantined.

Applicable Node(s):

**SamplePlusMethod**

Example Valid Values: 'Yes', 'No'.

---

**Quench**

Format:Numeric

Category:Measurement

Definition: Result of quench calculation for scintillation counters.

Applicable Node(s):

**Analysis**

---

**RefractiveIndex**

Format:Numeric

Category:Measurement

Definition: Refractive index of the sample.

Applicable Node(s):

**SamplePlusMethod**

---

**RelativeResponse**

Format:Numeric

Category:Measurement

Definition: The ratio of the response of one analyte to another.

Applicable Node(s):

**Analyte**

The relative response for this analyte, based on the assumption that the method specifies the analyte to compare to and which peaks to use.

---

**RelativeResponseLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the RelativeResponse.

Applicable Node(s):

**Analyte**

---

**RelativeResponseLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the RelativeResponse.

Applicable Node(s):

**Analyte**

---

**RelativeResponseLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the RelativeResponse limits.

Applicable Node(s):

**Analyte**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

---

**RelativeRetentionTime**

Format:Numeric

Category:Measurement

Definition: The ratio of two retention times. A relative retention time is the ratio of the retention time of a compound to another.

Applicable Node(s):

**Analyte**

The relative retention time for this analyte, based on the assumption that the method specifies the analyte to compare to and which peaks to use.

**Peak**

The relative retention time for this peak, based on the assumption that the method specifies the peak to compare to.

**PeakComparison**

The relative retention time of the peak this PeakComparison node is in compared to the peak identified by the PeakID and LabAnalyteID (or ClientAnalyteID) in this node.

---

**RelativeRetentionTimeLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the RelativeRetentionTime.

Applicable Node(s):

**Analyte**

**Peak**

**PeakComparison**

---

**RelativeRetentionTimeLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the RelativeRetentionTime.

Applicable Node(s):

**Analyte**

**Peak**

**PeakComparison**

---

**RelativeRetentionTimeLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the RelativeRetentionTime limits.

Applicable Node(s):

**Analyte**

**Peak**

**PeakComparison**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

---

**ReportedResult**

Format:

Category:

Definition: Parent element. Contains elements related to final reportable results.

Applicable Node(s):

**ReportedResult**

---

**ReportingLimit**

Format:Numeric

Category:Measurement

Definition: Reporting limit for the analyte being measured. Reporting limits are defined in terms of a number below which data is reported as not detected.

Applicable Node(s):

**ReportedResult**

**Analyte**

**Peak**

Within AnalysisGroup, applies to a reporting limit value computed from several analyses.

Same as in Analyte when results are measured per peak.

---

**ReportingLimitType**

Format:Limited List

Category:Measurement

Definition: One of a list of client-defined acronyms that specify the type of reporting limit.

Applicable Node(s):

**ReportedResult**  
**Analyte**  
**Peak**

Example Valid Values: 'MDL', 'PQL'.

---

**ReportingLimitUnits**

Format:Limited List

Category:Measurement

Definition: Units for ReportingLimit.

Applicable Node(s):

**ReportedResult**

If the client specifies that the ReportingLimitUnits must be the same as the ResultUnits, the ReportingLimitUnits need not be specified.

**Analyte**

Same as in ReportedResult.

**Peak**

Same as in ReportedResult.

---

**RequestorID**

Format:Identifier

Category:Tracking

Definition: An identifier for the organization that requested that this sample be analyzed.

Applicable Node(s):

**SamplePlusMethod**

May not be the same as the client, which specifies the SOW to follow.

---

**RequesterName**

Format:Text

Category:Tracking

Definition: A name for the organization that requested that this sample be analyzed.

Applicable Node(s):

**SamplePlusMethod**

---

**Residue**

Format:Numeric

Category:Measurement

Definition: Solid material remaining after preparation of an aliquot.

Applicable Node(s):

**Analysis**

---

**ResidueUnits**

Format:Limited List

Category:Measurement

Definition: Units for Residue.

Applicable Node(s):

**Analysis**

---

**Resolution**

Format:Numeric

Category:Measurement

Definition: A sample and method dependent estimate of the resolution of the instrument used in the analysis.

Applicable Node(s):

**Analysis****Analyte****Peak****PeakReplicate**

For example, in isotopic alpha spectroscopy, the width of the tracer peak.

A possibly sample and method dependent estimate of the resolution of the instrument that applies to the analysis and analyte.

Resolution for this peak. Details of how resolution is computed depend on the method.

---

**ResolutionLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the Resolution. Units are the same as for Resolution.

Applicable Node(s):

**Analysis****Analyte****Peak****PeakReplicate**

---

**ResolutionLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the Resolution. Units are the same as for Resolution.

Applicable Node(s):

**Analysis****Analyte****Peak****PeakReplicate**

---

**ResolutionLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the Resolution limits.

Applicable Node(s):

**Analysis****Analyte****Peak****PeakReplicate**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

---

**ResolutionType**

Format:Limited List

Category:Measurement

Definition: The basis for the determination of the estimated resolution.

Applicable Node(s):

**Analysis****Analyte****Peak****PeakReplicate**

Example Valid Values: 'Peak Width at 10% Peak Height'.

---

**ResolutionUnits**

Format:Limited List

Category:Measurement

Definition: Units for Resolution.

Applicable Node(s):

**Analysis****Analyte****Peak****PeakReplicate**

---

**Response**

Format:Numeric

Category:Measurement

Definition: Response from a detector.

Applicable Node(s):

**Analyte****Peak****PeakComparison****PeakReplicate**

---

**ResponseLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the Response. Units are the same as for Response.

Applicable Node(s):

**Analyte****Peak****PeakComparison****PeakReplicate**

---

**ResponseLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the Response. Units are the same as for Response.

Applicable Node(s):

**Analyte****Peak****PeakComparison****PeakReplicate**

---

**ResponseLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the Response limits.

Applicable Node(s):

**Analyte****Peak****PeakComparison****PeakReplicate**Example Valid Values: 'Method', 'Client', 'Laboratory'.

---

**ResponseType**

Format:Limited List

Category:Measurement

Definition: Specifies whether the response has been adjusted or corrected (i.e., for background) or not.

Applicable Node(s):

**Analyte****Peak****PeakComparison****PeakReplicate**Example Valid Values: 'Corrected'.

---

**ResponseUnits**

Format:Limited List

Category:Measurement

Definition: Units for Response.

Applicable Node(s):

**Analyte****Peak****PeakComparison****PeakReplicate**

---

**Result**

Format:Numeric

Category:Measurement

Definition:

Reportable final result for the analyte.

Applicable Node(s):

**ReportedResult**

The final result for a method accounting for all aliquot amounts, dilutions, moisture determinations, etc.

**Analyte**

Same as in ReportedResult when results are measured based on a single analysis. Within AnalysisGroup, applies to the mean or other value computed from several analyses.

**AnalyteGroup**

Same as in ReportedResult when results are reported based on two or more measured analytes.

**Peak****PeakReplicate**

Same as in Analyte when results are measured per peak.

---

**ResultBasis**

Format:Limited List

Category:Measurement

Definition:

The basis upon which the final results were calculated.

Applicable Node(s):

**Analysis**

Example Valid Values: 'Dry', 'Wet', 'Total', 'Dissolved'.

**ReportedResult**

---

**ResultLimitHigh**

Format:Numeric

Category:Measurement

Definition:

The upper limit for a result. Units are the same as for Result.

Applicable Node(s):

**ReportedResult****Analyte****Peak****PeakReplicate**

---

**ResultLimitLow**

Format:Numeric

Category:Measurement

Definition:

The lower limit for a result. Units are the same as for Result.

Applicable Node(s):

**ReportedResult****Analyte****Peak****PeakReplicate**

---

**ResultLimitType**

Format:Limited List

Category:Measurement

Definition:

The source for the Result limits.

Applicable Node(s):

**ReportedResult**  
**Analyte**  
**Peak**  
**PeakReplicate**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

---

**ResultType**

Format:Limited List

Category:Measurement

Definition:

Specifies whether this analyte was detected or not detected. For positive detections, specifies whether the result is equal to ('='), greater than ('&gt;'), or less than ('&lt;') the value reported. For non-detects, the valid value 'Not\_Detected' would be used. Can also be used to report method non-numeric results.

Applicable Node(s):

**ReportedResult**  
  
**Analyte**  
**AnalyteGroup**  
**Peak**  
**PeakReplicate**

Example valid values: For detections - '=', '&gt;', '&lt;'; For non-detects - 'Not\_Detected'; For non-numeric results - 'Pass' or 'Fail', 'Positive' or 'Negative', 'Present' or 'Absent'.

---

**ResultUncertainty**

Format:Numeric

Category:Measurement

Definition:

The estimated error in the result due to all effects related to analysis by the laboratory.

Applicable Node(s):

**ReportedResult**  
**Analyte**  
  
**Peak**  
**PeakReplicate**

Extended to anything considered to be the result of any analysis. Within AnalysisGroup, applies to a mean or other value computed from several analyses.

Same as in Analyte when results are measured per peak.

---

**ResultUncertaintyType**

Format:Limited List

Category:Measurement

Definition:

The confidence interval for the ResultUncertainty.

Applicable Node(s):

**ReportedResult**

Example Valid Values: '1-Sigma', '2-Sigma', '3-Sigma'.

**Analyte****Peak****PeakReplicate**

---

**ResultUncertaintyUnits**

Format:Limited List

Category:Measurement

Definition:

Units for ResultUncertainty.

Applicable Node(s):

**ReportedResult**

If the client specifies that the ResultUncertaintyUnits must be the same as the ResultUnits, the ResultUncertaintyUnits need not be specified.

**Analyte**

Same as in ReportedResult.

**Peak**

Same as in ReportedResult.

**PeakReplicate**

---

**ResultUnits**

Format:Limited List

Category:Measurement

Definition:

Units for Result.

Applicable Node(s):

**ReportedResult****Analyte****AnalyteGroup****Peak****PeakReplicate**

---

**RetentionTime**

Format:Numeric

Category:Measurement

Definition:

The time between injection and detection for a target analyte using chromatography or other techniques.

Applicable Node(s):

**ReportedResult**

In Results, this is the retention time from the analysis underlying this result.

**Analyte**

Same as in ReportedResult. Used when there is a well defined retention time for the analyte, not just for a peak measurement for the analyte. For example, this applies to GCMS analyses.

**Peak**

Same as in ReportedResult except for a single peak. Used with techniques like GC where there can be multiple peaks with different retention times for one analyte.

---

**RetentionTimeLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for a retention time window. Units are the same as for RetentionTime.

Applicable Node(s):

**Analyte****Peak**

---

**RetentionTimeLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for a retention time window. Units are the same as for RetentionTime.

Applicable Node(s):

**Analyte****Peak**

---

**RetentionTimeLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the RetentionTime limits.

Applicable Node(s):

**Analyte****Peak**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

---

**RetentionTimeUnits**

Format:Limited List

Category:Measurement

Definition: Units for RetentionTime.

Applicable Node(s):

**ReportedResult****Analyte****Peak**

---

**RPD**

Format:Numeric

Category:Measurement

Definition: The relative percent difference. The absolute value of the difference of two values as a percentage of their average. If a numeric result cannot be calculated then the RPDType data element should be used.

Applicable Node(s):

**ReportedResult**

Used with method QC of QCcategory Duplicate, Spike\_Duplicate, and Blank\_Spike\_Duplicate.

**Analyte**

Same as in ReportedResult except applied to the results of analyses in an analysis group rather than a QC sample and original pair.

**Peak**

Same as in Analyte when results are measured per peak.

**PeakComparison**

Same as in ReportedResult except used to compare values in two PeakComparison elements.

---

**RPDLimitHigh**

Format:Numeric

Category:Measurement

Definition: The upper limit for the RPD.

Applicable Node(s):

**Analyte****ReportedResult****Peak****PeakComparison**

---

**RPDLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the RPD.

Applicable Node(s):

**Analyte****ReportedResult****Peak****PeakComparison**

---

**RPDLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the RPD limits.

Applicable Node(s):

**Analyte**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

**ReportedResult****Peak****PeakComparison**

---

**RPDType**

Format:Limited List

Category:Measurement

Definition:

Would be used to report non-numeric RPD results when the RPD was calculated but a numerical value could not be determined as is possible when one of the two values is not detected.

Applicable Node(s):

**ReportedResult**  
**Analyte**  
**Peak**

Example Valid Value: 'Not\_Calculable'.

---

**RRF**

Format:Numeric

Category:Measurement

Definition:

The relative response factor. The ratio of two response factors. A response factor is the ratio of a response to an amount added.

Applicable Node(s):

**Analyte**  
  
**Peak**  
  
**PeakComparison**

The relative response factor for this analyte, based on the assumption that the method specifies the analyte to compare to and which peaks to use.  
The relative response factor for this peak, based on the assumption that the method specifies the peak to compare to.  
The relative response factor of the peak this PeakComparison node is in compared to the peak identified by the PeakID and LabAnalyteID (or ClientAnalyteID) in this node.

---

**RRFLimitHigh**

Format:Numeric

Category:Measurement

Definition:

The upper limit for the RRF.

Applicable Node(s):

**Analyte**  
**Peak**  
**PeakComparison**

---

**RRFLimitLow**

Format:Numeric

Category:Measurement

Definition:

The lower limit for the RRF.

Applicable Node(s):

**Analyte**  
**Peak**  
**PeakComparison**

---

**RRFLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the RRF limits.

Applicable Node(s):

**Analyte****Peak****PeakComparison**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

---

**RunBatch**

Format:Identifier

Category:Batch

Definition: A laboratory-defined identifier for a batch of analyses done on one instrument that make up a sequence of analyses during which the instrument is continuously in control.

Applicable Node(s):

**Analysis**

Example: A batch of samples analyzed on one instrument under the control of one initial calibration or similar InstrumentQC.

---

**SampleAmount**

Format:Numeric

Category:Measurement

Definition: The amount (weight or volume) of material as received by a laboratory or as produced by a handling process that will be aliquotted and processed as a sample for analysis.

Applicable Node(s):

**SamplePlusMethod**

Weight or volume of sample as received by the laboratory. The SampleAmount would not be directly used in the computation of a final result.

Example: When the TCLP method is used, the SampleAmount represents the final leachate volume generated by the TCLP method. In this case, it is the leachate itself that is treated as the sample, not the original material as received by the laboratory. The final results as reported by the laboratory would reflect the concentrations of analytes in the leachate, not in the original material.

**Handling**

Weight or volume of sample after the handling described by this node.

---

**SampleAmountUnits**

Format:Limited List

Category:Measurement

Definition: Units for SampleAmount.

Applicable Node(s):

**SamplePlusMethod****Handling**

---

**SamplePlusMethod**

Format:

Category:

Definition: Parent element. Contains elements related to field sample and analysis method.

Applicable Node(s):

**SamplePlusMethod**

---

**SamplingBatch**

Format:Identifier

Category:Batch

Definition: An identifier for a batch of samples collected together. Operationally, this batch associates a field blank with a group of samples.

Applicable Node(s):

**SamplePlusMethod**This value is currently often not known to the laboratory. It might be merged with laboratory data by a validator.

---

**ScreenValue**

Format:Numeric

Category:Measurement

Definition: Result from a screening analysis of the sample.

Applicable Node(s):

**SamplePlusMethod**Example: As in an alpha particle screen.

---

**ScreenValueUnits**

Format:Limited List

Category:Measurement

Definition: Units for ScreenValue.

Applicable Node(s):

**SamplePlusMethod**

---

**ServicesID**

Format:Identifier

Category:Tracking

Definition: A client-defined identifier for optional services performed for this data. This includes nonstandard work, such as modified detection limits, or changed QC requirements.

Applicable Node(s):

**SamplePlusMethod**

---

**ShippingBatch**

Format:Identifier

Category:Batch

Definition: An identifier for a batch of samples shipped together, such as in the same crate, cooler, or ice chest.

Applicable Node(s):

**SamplePlusMethod**

Operationally, this batch associates a trip blank with a group of samples. This value, as defined by the shippers, is currently often not known to the laboratory. It might be merged with laboratory data by a validator.

---

**SignalToNoiseRatio**

Format:Numeric

Category:Measurement

Definition: The ratio of the analyte signal to the background signal.

Applicable Node(s):

**Analyte**

The method will often define how the analyte and background signals are to be measured.

**Peak**

---

**SignalToNoiseRatioLimitLow**

Format:Numeric

Category:Measurement

Definition: The lower limit for the SignalToNoiseRatio.

Applicable Node(s):

**Analyte****Peak**

---

**SignalToNoiseRatioLimitType**

Format:Limited List

Category:Measurement

Definition: The source for the SignalToNoiseRatio limits.

Applicable Node(s):

**Analyte**

Example Valid Values: 'Method', 'Client', 'Laboratory'.

**Peak**

---

**SiteID**

Format:Identifier

Category:Tracking

Definition: A client-defined identifier for the broadly defined site where the sample was collected.

Applicable Node(s):

**SamplePlusMethod**

---

**SiteName**

Format:Text

Category:Tracking

Definition: Descriptive name for the broadly defined site where the sample was collected.

Applicable Node(s):

**SamplePlusMethod**

---

**Solvent**

Format:Text

Category:Description

Definition: The solvent(s) used during the extraction of the sample.

Applicable Node(s):

**PreparationPlusCleanup**

---

**StandardConcentration**

Format:Numeric

Category:Description

Definition: The actual concentration of the standard used.

Applicable Node(s):

**Analyte**

When spiking an aliquot, this represents the actual concentration of the spiking solution used. This does not represent the concentration of the standard in the aliquot processed unless the standard solution itself represents the sample that will be directly processed as could be the case during calibration.

---

**StandardConcentrationUnits**

Format:Limited List

Category:Description

Definition: Units for StandardConcentration.

Applicable Node(s):

**Analyte**

---

**StandardDeviation**

Format:Numeric

Category:Measurement

Definition: The standard deviation of several measurements of one analyte.

Applicable Node(s):

**Analyte**

The standard deviation for this analyte.

**Peak**

Same as in Analyte, except applied per peak.

**PeakComparison**

---

**StandardDeviationUnits**

Format:Limited List

Category:Measurement

Definition: Units for StandardDeviation.

Applicable Node(s):

**Analyte**

If the client specifies that the StandardDeviationUnits must be the same as the ResultUnits, the StandardDeviationUnits need not be specified.

**Peak**

Same as in Analyte when results are measured per peak.

**PeakComparison**

Same as in Analyte except as applied to PeakComparison values.

---

**StandardID**

Format:Identifier

Category:Tracking

Definition: A laboratory-defined identifier for a standard, such as a spiking material or SRM, used in this analysis.

Applicable Node(s):

**Analyte****Analysis**

---

**StandardSource**

Format:Text

Category:Tracking

Definition: The source for a standard used in this analysis.

Applicable Node(s):

**Analyte****Analysis**

---

**StorageBatch**

Format:Identifier

Category:Batch

Definition: An identifier for a batch of samples that are stored together in a defined period of time (e.g., samples stored in the same refrigerator or freezer).

Applicable Node(s):

**SamplePlusMethod**

Operationally, this batch can associate a VOC refrigerator storage blank with a group of VOC samples.

---

**SuspendedSolids**

Format:Numeric

Category:Measurement

Definition: Solids remaining on the filter paper after filtration of a water or other liquid sample.

Applicable Node(s):

**SamplePlusMethod****Handling**

Solids remaining on the filter paper after filtration of a water or other liquid sample after the handling described by this node.

---

**SuspendedSolidsUnits**

Format:Limited List

Category:Measurement

Definition: Units for SuspendedSolids.

Applicable Node(s):

**SamplePlusMethod  
Handling**

---

**TailingFactor**

Format:Numeric

Category:Measurement

Definition: The unitless factor describing the amount of tailing observed in a chromatographic or other peak.

Applicable Node(s):

**Analyte**

The exact equation or formula used may be method specific. The TailingFactor is normally calculated by dividing the peak tail distance by the peak front distance measured at a given peak height (usually at 10% of the peak height).

**Peak**

---

**TailingFactorLimitHigh**

Format: Numeric

Category: Measurement

Definition: The upper limit for the TailingFactor.

Applicable Node(s):

**Analyte****Peak**

---

**TailingFactorLimitType**

Format: Limited List

Category: Measurement

Definition: The source for the TailingFactor limit.

Applicable Node(s):

**Analyte****Peak**

---

**Temperature**

Format:Numeric

Category:Measurement

Definition: The temperature of the sample as received or the method as performed.

Applicable Node(s):

**SamplePlusMethod****Handling****Analysis****PreparationPlusCleanup**

The temperature of the sample as received.

The temperature of the Handling process.

The temperature of the Analysis process.

The temperature of the PreparationPlusCleanup process.

---

**TemperatureUnits**

Format:Limited List

Category:Measurement

Definition: Units for Temperature.

Applicable Node(s):

**SamplePlusMethod****Handling****Analysis****PreparationPlusCleanup**

---

**Texture**

Format:Text

Category:Description

Definition: Descriptive information about a solid sample.

Applicable Node(s):

**SamplePlusMethod** Descriptive information about a solid sample as received. Example: 'Fine', 'Medium', 'Coarse'; or 'Boulder', 'Pebble', 'Sand'.**Handling** Descriptive information about a solid sample after the handling described by this node.

---

**Turbidity**

Format:Numeric

Category:Measurement

Definition: The turbidity of the sample.

Applicable Node(s):

**SamplePlusMethod**

---

**TurbidityUnits**

Format:Limited List

Category:Measurement

Definition: Units for Turbidity.

Applicable Node(s):

**SamplePlusMethod**

---

**Wavelength**

Format:Numeric

Category:Description

Definition: The wavelength used for an analytical measurement.

Applicable Node(s):

**Analysis** e.g., for UV/VIS, GFAA, ICP.**Analyte****Peak****PeakComparison**

---

---

**WavelengthUnits**

Format:Limited List

Category:Description

Definition: Units for Wavelength.

Applicable Node(s):

**Analysis****Analyte****Peak****PeakComparison**

---

**WeightingFactor**

Format:Limited List

Category:Description

Definition: The factor used to define how the regression analysis was applied to an initial calibration curve for a method.

Applicable Node(s):

**Analyte**

The weighting factor for this analyte. Example Valid Values: 'Inverse\_Of\_Concentration', 'Inverse\_Square\_Of\_Concentration'.

**Peak**Same as in Analyte, except applied per peak.

---

**Yield**

Format:Numeric

Category:Measurement

Definition: A measure of the success of the preparation part of the method as a percent.

Applicable Node(s):

**Analysis**For radiochemistry, the number of atoms of interest making it through sample preparation as a percentage of the number in the aliquot.

---