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ARIZONA LABORATORY DATA QUALIFIERS

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Arizona Laboratory Data Qualifiers

Revision 1.0
03/20/2002

Developed by the Technical Subcommittee of the Arizona Environmental Laboratory Advisory Committee. This is a revised list with additional qualifiers added to the original list dated 12/11/2000)

Microbiology:

A1 = Too numerous to count.

A2 = Sample incubation period exceeded method requirement.

A3 = Sample incubation period was shorter than method requirement.

A4 = Target organism detected in associated method blank.

A5 = Incubator/water bath temperature was outside method requirements.

A6 = Target organism not detected in associated positive control.

A7 = Micro sample received without adequate headspace.

Method blank:

B1 = Target analyte detected in method blank at or above the method reporting limit.

B2 = Non-target analyte detected in method blank and sample, producing interference.

B3 = Target analyte detected in calibration blank at or above the method reporting limit.

B4 = Target analyte detected in blank at/above method acceptance criteria.

B5 = Target analyte detected in method blank at or above the method reporting limit, but below trigger level or MCL.

B6 = Target analyte detected in calibration blank at or above the method reporting limit, but below trigger level or MCL.

B7 = Target analyte detected in method blank at or above the method reporting limit. Concentration found in the sample was 10 times above the concentration found in the method blank.

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Confirmation:

C1 = Confirmatory analysis not performed as required by the method.

C2 = Confirmatory analysis not performed. Confirmation of analyte presence established by site historical data.

C3 = Qualitative confirmation performed. See case narrative.

C4 = Confirmatory analysis was past holding time.

C5 = Confirmatory analysis was past holding time. Original result not confirmed.

Dilution:

D1 = Sample required dilution due to matrix interference. See case narrative.

D2 = Sample required dilution due to high concentration of target analyte.

D3 = Sample dilution required due to insufficient sample.

D4 = Minimum reporting level (MRL) adjusted to reflect sample amount received and analyzed.

Estimated concentration:

E1 = Concentration estimated. Analyte exceeded calibration range. Reanalysis not possible due to insufficient sample.

E2 = Concentration estimated. Analyte exceeded calibration range. Reanalysis not performed due to sample matrix.

E3 = Concentration estimated. Analyte exceeded calibration range. Reanalysis not performed due to holding time requirements.

E4 = Concentration estimated. Analyte was detected below laboratory minimum reporting level (MRL).

E5 = Concentration estimated. Analyte was detected below laboratory minimum reporting level (MRL), but not confirmed by alternate analysis.

E6 = Concentration estimated. Internal standard recoveries did not meet method acceptance criteria.

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E7 = Concentration estimated. Internal standard recoveries did not meet laboratory acceptance criteria.

Hold time:

H1 = Sample analysis performed past holding time. See case narrative.

H2 = Initial analysis within holding time. Reanalysis for the required dilution was past holding time.

H3 = Sample was received and analyzed past holding time.

H4 = Sample was extracted past required extraction holding time, but analyzed within analysis holding time. See case narrative.

BOD:

K1 = The sample dilutions set-up for the BOD analysis did not meet the oxygen depletion criteria of at least 2 mg/L. Any reported result is an estimated value.

K2 = The sample dilutions set up for the BOD analysis did not meet the criteria of a residual dissolved oxygen of at least 1 mg/L. Any reported result is an estimated value.

K3 = The seed depletion was outside the method acceptance limits.

K4 = The seed depletion was outside the method and laboratory acceptance limits. The reported result is an estimated value.

K5 = The dilution water D.O. depletion was > 0.2 mg/L.

K6 = Glucose/glutamic acid BOD was below method acceptance criteria.

K7 = A discrepancy between the BOD and COD results has been verified by reanalysis of the sample for COD.

K8 = Glucose/glutamic acid BOD was above method acceptance levels.

Laboratory fortified blank/blank spike:

L1 = The associated blank spike recovery was above laboratory acceptance limits. See case narrative.

L2 = The associated blank spike recovery was below laboratory acceptance limits. See case narrative.

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L3 = The associated blank spike recovery was above method acceptance limits. See case narrative.

L4 = The associated blank spike recovery was below method acceptance limits. See case narrative.

Note: The L1, L2, L3 & L4 footnotes need to be added to all corresponding analytes for a sample.

Matrix spike:

M1 = Matrix spike recovery was high, the method control sample recovery was acceptable.

M2 = Matrix spike recovery was low, the method control sample recovery was acceptable.

M3 = The accuracy of the spike recovery value is reduced since the analyte concentration in the sample is disproportionate to spike level. The method control sample recovery was acceptable.

M4 = The analysis of the spiked sample required a dilution such that the spike concentration was diluted below the reporting limit. The method control sample recovery was acceptable.

M5 = Analyte concentration was determined by the method of standard addition (MSA).

M6 = Matrix spike recovery was high. Data reported per ADEQ policy 0154.000.

M7 = Matrix spike recovery was low. Data reported per ADEQ policy 0154.000.

General:

N1 = See case narrative.

N2 = See corrective action report.

Sample quality:

Q1 = Sample integrity was not maintained. See case narrative.

Q2 = Sample received with head space.

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Q3 = Sample received with improper chemical preservation.

Q4 = Sample received and analyzed without chemical preservation.

Q5 = Sample received with inadequate chemical preservation, but preserved by the laboratory.

Q6 = Sample was received above recommended temperature.

Q7 = Sample inadequately dechlorinated.

Q8 = Insufficient sample received to meet method QC requirements. QC requirements satisfy ADEQ policies 0154 and 0155.

Q9 = Insufficient sample received to meet method QC requirements.

Q10= Sample received in inappropriate sample container.

Q11= Sample is heterogeneous. Sample homogeneity could not be readily achieved using routine laboratory practices.

Duplicates:

R1 = RPD exceeded the method control limit. See case narrative.

R2 = RPD exceeded the laboratory control limit. See case narrative.

R3 = Sample RPD between the primary and confirmatory analysis exceeded 40%. Per EPA Method 8000B, the higher value was reported.

R4 = MS/MSD RPD exceeded the method control limit. Recovery met acceptance criteria.

R5 = MS/MSD RPD exceeded the laboratory control limit. Recovery met acceptance criteria.

R6 = LFB/LFBD RPD exceeded the method control limit. Recovery met acceptance criteria.

R7 = LFB/LFBD RPD exceeded the laboratory control limit. Recovery met acceptance criteria.

R8 = Sample RPD exceeded the method control limit.

R9 = Sample RPD exceeded the laboratory control limit.

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Surrogate:

S1 = Surrogate recovery was above laboratory acceptance limits, but within method acceptance limits.

S2 = Surrogate recovery was above laboratory and method acceptance limits.

S3 = Surrogate recovery was above laboratory acceptance limits, but within method acceptance limits. No target analytes were detected in the sample.

S4 = Surrogate recovery was above laboratory and method acceptance limits. No target analytes were detected in the sample.

S5 = Surrogate recovery was below laboratory acceptance limits, but within method acceptance limits.

S6 = Surrogate recovery was below laboratory and method acceptance limits. Reextraction and/or reanalysis confirms low recovery caused by matrix effect.

S7 = Surrogate recovery was below laboratory and method acceptance limits. Unable to confirm matrix effect.

S8 = The analysis of the sample required a dilution such that the surrogate concentration was diluted below the method acceptance criteria. The method control sample recovery was acceptable.

S9 = The analysis of the sample required a dilution such that the surrogate concentration was diluted below the laboratory acceptance criteria. The method control sample recovery was acceptable.

S10 = Surrogate recovery was above laboratory and method acceptance limits. See Case narrative.

S11 = Surrogate recovery was high. Data reported per ADEQ policy 0154.000.

S12 = Surrogate recovery was low. Data reported per ADEQ policy 0154.000.

Method/analyte discrepancies:

T1 = Method promulgated by EPA, but not by ADHS at this time.

T2 = Cited ADHS licensed method does not contain this analyte as part of method compound list.

T3 = Method not promulgated either by EPA or ADHS.

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T4 = Tentatively identified compound. Concentration is estimated and based on the closest internal standard.

Calibration verification:

V1 = CCV recovery was above method acceptance limits. This target analyte was not detected in the sample.

V2 = CCV recovery was above method acceptance limits. This target analyte was detected in the sample. The sample could not be reanalyzed due to insufficient sample.

V3 = CCV recovery was above method acceptance limits. This target analyte was detected in the sample, but the sample was not reanalyzed. See case narrative.

V4 = CCV recovery was below method acceptance limits. The sample could not be reanalyzed due to insufficient sample.

V5 = CCV recovery after a group of samples was above acceptance limits. This target analyte was not detected in the sample. Acceptable per EPA Method 8000B.

V6 = Data reported from one-pont calibration criteria per ADEQ policy 0155.000.

V7 = Calibration verification recovery was above the method control limit for this analyte, however the average % difference or % drift for all the analytes met method criteria.

V8 = Calibration verification recovery was below the method control limit for this analyte, however the average % difference or % drift for all the analytes met method criteria.

Calibration:

W1 = The % RSD for this compound was above 15%. The average % RSD for all compounds in the calibration met the 15% criteria as specified in EPA method 8000B.

EXHIBIT 4.

ELECTRONIC DATA TRANSFER REQUIREMENTS