

SDG NARRATIVE

USEPA
SDG # MYD5W7
CASE # 51495
CONTRACT # 68HERH20D0011
SOW# SFAM01.1
LAB NAME: Alliance Technical Group, LLC
LAB CODE: ACE
LAB ORDER ID #P2797
MODIFIED ANALYSIS#3221.2

A. Number of Samples and Date of Receipt

15 Soil & 05 Water sample were delivered to the laboratory intact on 06/08/2024, 06/10/2024.

B. Parameters

Test requested for Metals CLP MS Full = Antimony, Arsenic, Barium, Beryllium, Cadmium, Chromium, Cobalt, Copper, Lead, Nickel, Selenium, Silver, Thallium, Vanadium & Zinc.

Test requested for Metals CLP MS = Antimony, Arsenic, Barium, Beryllium, Cadmium, Chromium, Cobalt, Copper, Lead, Nickel, Selenium, Silver, Thallium, Vanadium & Zinc.

C. Cooler Temp

Indicator Bottle: Presence/Absence

Cooler: 2.1°C, 22.9°C

D. Detail Documentation (related to Sample Handling Shipping, Analytical Problem, Temp of Cooler etc):

Issue 1: A "P" or "M" prefix was listed at the beginning of a CLP sample ID.

Issue 2: The laboratory received samples without ice. The coolers had temperatures 24.2 degrees C, 23.2 degrees C, 23.8 degrees C, 24.1 degrees C, and 26.1 degrees C upon arrival. The laboratory would like to know how to proceed.



284 Sheffield Street Mountainside, NJ 07092

E. Corrective Action taken for above:

Resolution 1: To maintain COC integrity, ASB requests no changes to the Sample IDs. The laboratory will note the issue in the SDG Narrative and proceed with the analysis of the samples.

Resolution 2: Per Region 9, Case 51495 is for metals. There are no rinsates in those cooler so they don't require ice. The laboratory should note the issue in the SDG narrative and proceed with the analysis of the samples.

F. Analytical Techniques:

All analyses were based on CLP Methodology by method SFAM01.1.

G. Calculation:

Calculation for ICP-MS Soil Sample:

Conversion of Results from µg /L or ppb to mg/kg:

Concentration (mg/kg) =
$$C \times \frac{Vf}{W \times S} \times DF / 1000$$

Where,

C = Instrument value in ppb (The average of all replicate integrations)

Vf = Final digestion volume (mL)

W = Initial aliquot amount (g) (Fraction of Sample amount taken in prep)

S = % Solids / 100 (Fraction of Percent Solids)

DF = Dilution Factor

Example Calculation For Sample MYD4P4 For Antimony:

If
$$C = 1.83 \text{ ppb}$$

 $Vf = 500 \text{ ml}$
 $W = 1.23 \text{ g}$
 $S = 0.986(98.6/100)$
 $DF = 1$

Concentration (mg/kg) =
$$1.83 \text{ x} \frac{500}{1.23 \text{ x} 0.986} \text{ x } 1 / 1000$$

= 0.7544 mg/kg

= 0.75 mg/kg (Reported Result with Signification)



284 Sheffield Street Mountainside, NJ 07092

Calculation for ICP-MS Water Sample:

Concentration or Result (
$$\mu$$
g/L) = C x Vf x DF

Vi

Where,

C = Instrument value in ppb (The average of all replicate integrations)

Vf = Final digestion volume (mL)

Vi = Initial aliquot amount (mL) (Sample amount taken in prep)

DF = Dilution Factor

Example Calculation For Sample MYD599 For Zinc:

If C = 1.43 ppb

$$Vf = 50 \text{ ml}$$

 $Vi = 50 \text{ ml}$
 $DF = 1$
Concentration or Result (μ g/L) = 1.43 x $\frac{50}{50}$ x 1
= 1.43 μ g/L

= 1.4 µg/L (Reported Result with Signification)

H. QA/QC

Calibrations met requirements. Interference check met requirements. Blank analyses did not indicate any presence of contamination. Laboratory Control sample was within control limits. Spike sample (MYD4P9S) did meet requirements except for Vanadium. Duplicate sample did meet requirements. Serial Dilution did meet requirements.

Collision cell is being used to remove potential interferences. The analytes Na, Mg, Al, K, V, Cr, Mn, Fe, Co, Ni, Cu, Zn, As are being analyzed with collision cell and analytes Be, B, Ca, Ti, Se, Sr, Zr, Mo, Ag, Cd, Sn, Sb, Ba, Tl, Pb, U are being analyzed with Non-Collision Cell. Helium gas is used for the Collision Cell analysis.

Internal Standard Association for ICP-MS analysis.

Target Analyte	Associated Internal Standard
Antimony	159Tb
Arsenic	89Y



284 Sheffield Street Mountainside, NJ 07092

Barium	159Tb	
Beryllium	6Li	
Cadmium	159Tb	
Chromium	45Sc	
Cobalt	45Sc	
Copper	45Sc	
Lead	209Bi	
Nickel	45Sc	
Selenium	89Y	
Silver	159Tb	
Thallium	209Bi	
Vanadium	45Sc	
Zinc	45Sc	

I certify that the data package is in compliance with the terms and conditions of the contract both technically and for completeness, for other than the conditions detailed above. Release of the data contained in this hard copy data package has been authorized by the Laboratory Director or his designee, as verified by the following signature.

Signature	Name: Nimisha Pandya	
Date	Title: Document Control Officer	

Date: 09/04/2024	MA: 3221.1	Title: ICP-MS Re-Digestion and Re-Analysis of
		Soils with Additional Laboratory QC
Method Source: SFAM01.1	Method: ICP-MS	
Matrix: Cail/Cadimont		

Matrix: Soil/Sediment

Summary of Modification

The purpose of this modified analysis is to re-prepare samples by EPA Draft Method 3050C (see below) with additional modified LCS and Matrix Spikes and analyze for the scheduled target analytes by ICP-MS. Unless specifically modified by this modification, all analyses, Quality Control (QC), and reporting requirements specified in the SOW listed in your current EPA agreement remain unchanged and in full force and effect.

I. Analyte Modifications

Not applicable

Not applicable

e 🔀

II. Calibration and QC Requirements

The Laboratory shall:

- Use the Method Detection Limits (MDLs) determined for routine soil analyses (i.e., Method 200.8) to report the results for these analyses. The Laboratory is NOT required to perform an MDL study for Draft Method 3050C.
- Prepare and analyze an additional Laboratory Control Sample (LCS) spiked at the CRQL. Percent Recovery limits do NOT apply to this LCS and no corrective actions are required.
- Prepare a Matrix Spike spiked at three times the levels specified in the SOW.
- Prepare and analyze an additional Matrix Spike sample spiked at five times the levels specified for this Modified Analysis (i.e., 15x the levels specified in the SOW).
- Post-Digestion Spike requirements apply to to the 5x Matrix Spike only.
- Post-Digestion Spike corrective actions apply to Sb.

III. Preparation and Method Modifications

Not applicable

The Laboratory shall:

- Prepare and analyze the sample by EPA Draft Method 3050C as follows:
 - Mix sample thoroughly and transfer 1.00 1.50 g to a digestion vessel.
 - \circ Add 10 mL 1:1 HNO₃ and 5 mL 1:1 HCl, heat the sample at 95°C (±3°C) and reflux 10 -15 minutes.
 - Add 5 mL concentrated HNO₃ and reflux for 30 minutes at 95°C (±3°C), repeat until digestion complete.
 - o Concentrate sample to 5 mL or reflux without boiling for 2 hours at 95°C (±3°C).
 - \circ Cool sample, add 2mL water and 3 mL 30% H₂O₂. Heat at 95°C (±3°C) and add additional 1 mL aliquots of 30% H₂O₂ until effervescence is minimal.
 - Dilute to 100 mL with water, centrifuge or filter as necessary prior to analysis.
- The same sample extracts can be used for ICP-AES analysis. Separate Matrix Spikes and LCS will need to be prepared for both ICP-AES and ICP-MS analyses.
- Analyze the samples starting at an initial 5x dilution. Subsequently, dilute samples as necessary to bring the analyte concentrations within the calibration range of the instrument per the SOW.
- Method Blanks, both LCSs, and all instrument QC are to be analyzed undiluted.

IV. Special Reporting Requirements

Not applicable

The Laboratory shall:

- Ensure the SDG Narrative is updated as stated in the SOW, including any technical and
 administrative problems encountered and the resolution or corrective actions taken. These
 problems may include interference problems encountered during analysis, dilutions, re-analyses
 and/or re-preparations performed, and problems with the analysis of samples. Also include a
 discussion of any SOW Modified Analyses, including a copy of the approved modification form
 with the SDG Narrative.
- The Initial analysis data are reported with a dilution factor of 1.0 and a final volume of 500 mL, per the SOW.
- Report the additional LCS as "LCSD" in the raw data and in the EDD with QCType "Laboratory_Control_Sample_Duplicate".
- Report the additional Matrix Spike with an "SRE" suffix in the raw data and EDD.
- Report any Post-Digestion Spike of the additional 5x Matrix Spike with an "ARE" suffix.