

QA/QC SUMMARY

PROJECT:	ANIMIDA 2014		
PARAMETER:	Methyl mercury		
LABORATORY:	Battelle Sequim		
MATRIX:	Tissue		
SAMPLE CUSTODY:	A total of 20 tissue samples were received as outlined in the table below. The samples were freeze-dried upon receipt and then stored at room temperature until analysis. The samples were assigned a central file number (3471) and entered into Battelle's sample log-in system. Some corrections were made to the COC as per the attached e-mail to correct discrepancies found during log-in. All samples were received at a temperature within the optimal temperature range for unpreserved tissue samples (4±2°C).		
Sample Receipt Date	Number of Samples	Cooler Temperature	Comments
9/24/14	20 (crab, cod, clam and amphipod)	2.1°C	

QA/QC DATA QUALITY OBJECTIVES:

	Reference Method	Range of Recovery	SRM/OPR Accuracy	Relative Precision	Achieved Detection Limit (dry wt)
Methyl Hg	EPA 1630 M	65-135%	≤35%	≤35%	0.00145 µg/g

METHOD: All samples were freeze-dried and ball-milled upon receipt. The samples were collected between 7/31/14 and 8/7/14. The samples were analyzed on 11/18/14, which is within the EPA holding time of 1 year. All samples were analyzed on a dry weight basis and are reported on both a dry weight basis and a wet weight basis calculated from the % moisture values determined for the samples.

BLANKS: Three method blanks were analyzed with each analytical batch of samples. Methyl Hg was not detected in any of the blanks. None of the data were blank corrected.

BLANK SPIKES (OPR/LCS): Two ongoing precision and recovery (OPR) samples were analyzed with each analytical batch of 20 or fewer samples. All recoveries were within the criteria limits specified in the table above.

MATRIX SPIKES: Two matrix spike - matrix spike duplicate pairs were analyzed for Methyl Hg with the batch of 20 samples. All recoveries were within the criteria limits specified above. The RPDs on the MS/MSD pairs were within the method acceptance criteria for precision.

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REPLICATES: One sample was analyzed in duplicate for Methyl Hg with the batch of 20 samples. Precision is reported by calculating the relative percent difference (RPD) of replicate results. The RPD was within the method acceptance criteria limits listed above.

SRM: One sample of the certified reference material DORM-3 (dogfish protein) was analyzed with the batch of 20 samples for Methyl Hg. The recovery was within the criteria limits listed above.

Data Release:

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