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October 9, 2008

Mr. Steve Trent  
Fluor Hanford Inc.  
1200 Jadwin Avenue  
Richland, WA 99352

Reference: **P.O. #33677**  
**Eberline Services R8-09-016-7185, SDG H3847**

Dear Mr. Trent:

Enclosed is a data report for two water samples designated under SAF No. I08-053 received at Eberline Services on September 3, 2008. The samples were analyzed according to the accompanying chain-of-custody documents.

Please call if you have any questions concerning this report.

Sincerely,

*For* Melissa C. Mannion  
Senior Program Manager

NJV

Enclosure: Data Package

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EDMC

**1.0 GENERAL**

Fluor Hanford Inc. (FH) Sample Delivery Group H3847 was composed of two water samples designated under SAF No. 108-053 with a Project Designation of: 2UP1, August 2008.

The samples were received as stated on the Chain-of-Custody document. Any discrepancies are noted on the Eberline Services Sample Receipt Checklist.

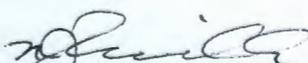
**2.0 ANALYSIS NOTES**

**2.1 Protactinium-231 Analysis**

Sample B1WDN8 and the QC LCS planchet required a rework due to low initial yields. After rework the yields were within the required 20%-105% control limits, however the Pa-231 QC LCS recovery was 125%, greater than the upper control limit of 120% for QC LCS samples. No other problems were encountered during the course of the analyses.

**3.0 Case Narrative Certification Statement**

**"I certify that this data package is in compliance with the SOW, both technically and for completeness, for other than the conditions detailed above. Release of the data obtained in this hard copy data package has been authorized by the Laboratory Manager or a designee, as verified by the following signature."**

  
\_\_\_\_\_  
**Melissa C. Mannion**  
**Senior Program Manager**

10/9/08  
\_\_\_\_\_  
**Date**

EBERLINE SERVICES / RICHMOND  
SAMPLE DELIVERY GROUP H3847

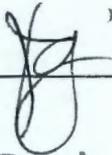
SDG 7185  
Contact Melissa C. Mannion

Client Hanford  
Contract No. 33677  
Case no SDG H3847

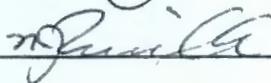
S U M M A R Y   D A T A   S E C T I O N

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Prepared by



Reviewed by



Lab id EBRLNE  
Protocol Fluor  
Version Ver 1.0  
Form DVD-TOC  
Version 3.06  
Report date 10/09/08

EBERLINE SERVICES / RICHMOND

SAMPLE DELIVERY GROUP H3847

SDG 7185  
Contact Melissa C. Mannion

REPORT GUIDE

Client Hanford  
Contract No. 33677  
Case no SDG H3847

ABOUT THE DATA SUMMARY SECTION

The Data Summary Section of a Data Package has all data, in several useful orders, necessary for first level, routine review of the data package for a Sample Delivery Group (SDG). This section follows the Data Package Narrative, which has an overview of the data package and a discussion of special problems. It is followed by the Raw Data Section, which has full details.

The Data Summary Section has several groups of reports:

SAMPLE SUMMARIES

The Sample and QC Summary Reports show all samples, including QC samples, reported in one SDG. These reports cross-reference client and lab sample identifiers.

PREPARATION BATCH SUMMARY

The Preparation Batch Summary Report shows all preparation batches (lab groupings reflecting how work was organized) relevant to the reported SDG with information necessary to check the completeness and consistency of the SDG.

WORK SUMMARY

The Work Summary Report shows all samples and work done on them relevant to the reported SDG.

METHOD BLANKS

The Method Blank Reports, one for each Method Blank relevant to the SDG, show all results and primary supporting information for the blanks.

LAB CONTROL SAMPLES

The Lab Control Sample Reports, one for each Lab Control Sample relevant to the SDG, show all results, recoveries and primary supporting information for these QC samples.

REPORT GUIDES

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SUMMARY DATA SECTION

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Lab id EBRLNE  
Protocol Fluor  
Version Ver 1.0  
Form DVD-RG  
Version 3.06  
Report date 10/09/08  
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EBERLINE SERVICES / RICHMOND

SAMPLE DELIVERY GROUP H3847

SDG 7185  
Contact Melissa C. Mannion

GUIDE, cont.

Client Hanford  
Contract No. 33677  
Case no SDG H3847

ABOUT THE DATA SUMMARY SECTION

DUPLICATES

The Duplicate Reports, one for each Duplicate and Original sample pair relevant to the SDG, show all results, differences and primary supporting information for these QC samples.

MATRIX SPIKES

The Matrix Spike Reports, one for each Spiked and Original sample pair relevant to the SDG, show all results, recoveries and primary supporting information for these QC samples.

DATA SHEETS

The Data Sheet Reports, one for each client sample in the SDG, show all results and primary supporting information for these samples.

METHOD SUMMARIES

The Method Summary Reports, one for each test used in the SDG, show all results, QC and method performance data for one analyte on one or two pages. (A test is a short code for the method used to do certain work to the client's specification.)

REPORT GUIDES

The Report Guides, one for each of the above groups of reports, have documentation on how to read the associated reports.

REPORT GUIDES

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SUMMARY DATA SECTION

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Lab id EBRLNE  
Protocol Fluor  
Version Ver 1.0  
Form DVD-RG  
Version 3.06  
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**EBERLINE SERVICES/RICHMOND**

SAMPLE DELIVERY GROUP H3847

**LAB SAMPLE SUMMARY**

SDG 7185  
 Contact Melissa C. Mannion

Client Hanford  
 Contract No. 33677  
 Case no SDG H3847

LAB							CHAIN OF	
SAMPLE ID	CLIENT SAMPLE ID	LOCATION	MATRIX	LEVEL	SAF NO	CUSTODY	COLLECTED	
R809016-01	B1WDN2	HNF-N-506-14	WATER		I08-053	I08-053-20	08/26/08 11:00	
R809016-02	B1WDN8	HNF-N-506-14	WATER		I08-053	I08-053-30	08/29/08 13:04	
R809016-03	Lab Control Sample		WATER		I08-053			
R809016-04	Method Blank		WATER		I08-053			
R809016-05	Duplicate (R809016-02)	HNF-N-506-14	WATER		I08-053		08/29/08 13:04	

Lab id EBRINE  
 Protocol Fluor  
 Version Ver 1.0  
 Form DVD-LS  
 Version 3.06  
 Report date 10/09/08

EBERLINE SERVICES/RICHMOND

SAMPLE DELIVERY GROUP H3847

SDG 7185  
 Contact Melissa C. Mannion

QC SUMMARY

Client Hanford  
 Contract No. 33677  
 Case no SDG H3847

QC BATCH	CHAIN OF CUSTODY	CLIENT SAMPLE ID	MATRIX	% SOLIDS	SAMPLE AMOUNT	BASIS AMOUNT	DAYS SINCE RECEIVED	LAB COLL	LAB SAMPLE ID	DEPARTMENT SAMPLE ID
7185	I08-053-20	B1WDN2	WATER		1.0 L		09/03/08 8	R809016-01		7185-001
	I08-053-30	B1WDN8	WATER		1.0 L		09/03/08 5	R809016-02		7185-002
		Method Blank	WATER					R809016-04		7185-004
		Lab Control Sample	WATER					R809016-03		7185-003
		Duplicate (R809016-02)	WATER		1.0 L		09/03/08 5	R809016-05		7185-005

QC SUMMARY

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SUMMARY DATA SECTION

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Lab id EBRLNE  
 Protocol Fluor  
 Version Ver 1.0  
 Form DVD-QS  
 Version 3.06  
 Report date 10/09/08  
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**EBERLINE SERVICES/RICHMOND**

SAMPLE DELIVERY GROUP H3847

SDG 7185  
 Contact Melissa C. Mannion

**PREP BATCH SUMMARY**

Client Hanford  
 Contract NO. 33677  
 Case no SDG H3847

TEST	MATRIX	METHOD	PREPARATION ERROR		PLANCHETS ANALYZED					QUALI-	
			BATCH	2σ %	CLIENT	MORE	RE	BLANK	LCS		DUP/ORIG
Alpha Spectroscopy											
PA	WATER	Pa-231 in Water	6169-042	14.8	2			1	1	1/1	

Duplicates and Matrix Spikes are those with original (Client) sample in this Sample Delivery Group.  
 Blank and LCS planchets are those in the same preparation batch as some Client, Duplicate or Spike sample.

Lab id EBRLNE  
 Protocol Fluor  
 Version Ver 1.0  
 Form DVD-PBS  
 Version 3.06  
 Report date 10/09/08

**EBERLINE SERVICES/RICHMOND**

SAMPLE DELIVERY GROUP H3847

**LAB WORK SUMMARY**

SDG 7185  
Contact Melissa C. Mannion

Client Hanford  
Contract No. 33677  
Case no SDG H3847

LAB SAMPLE	CLIENT SAMPLE ID	MATRIX	PLANCHET	TEST	SUF-	ANALYZED	REVIEWED	BY	METHOD
COLLECTED	LOCATION				FIX				
RECEIVED	CUSTODY	SAF No							
R809016-01	B1WDN2		7185-001	PA		10/01/08	10/09/08	BW	Pa-231 in Water
08/26/08	HNF-N-506-14								
09/03/08	I08-053-20	I08-053							
R809016-02	B1WDN8		7185-002	PA	R1	10/08/08	10/09/08	BW	Pa-231 in Water
08/29/08	HNF-N-506-14								
09/03/08	I08-053-30	I08-053							
R809016-03	Lab Control Sample		7185-003	PA	R1	10/08/08	10/09/08	BW	Pa-231 in Water
R809016-04	Method Blank		7185-004	PA		10/01/08	10/09/08	BW	Pa-231 in Water
R809016-05	Duplicate (R809016-02)		7185-005	PA		10/01/08	10/09/08	BW	Pa-231 in Water
08/29/08	HNF-N-506-14								
09/03/08		I08-053							

**COUNTS OF TESTS BY SAMPLE TYPE**

TEST	SAF No	METHOD	REFERENCE	CLIENT	MORE	RE	BLANK	LCS	DUP SPIKE	TOTAL
PA	I08-053	Pa-231 in Water	PA231_IE_PLATE_AEA	2			1	1	1	5
<b>TOTALS</b>				2			1	1	1	5

WORK SUMMARY

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SUMMARY DATA SECTION

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Protocol Fluor  
Version Ver 1.0  
Form DVD-LWS  
Version 3.06  
Report date 10/09/08  
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EBERLINE SERVICES / RICHMOND

SAMPLE DELIVERY GROUP H3847

7185-004

Method Blank

METHOD BLANK

SDG <u>7185</u>	Client/Case no <u>Hanford</u>	SDG <u>H3847</u>
Contact <u>Melissa C. Mannion</u>	Contract <u>No. 33677</u>	
Lab sample id <u>R809016-04</u>	Client sample id <u>Method Blank</u>	
Dept sample id <u>7185-004</u>	Material/Matrix <u>WATER</u>	
	SAF No <u>I08-053</u>	

ANALYTE	CAS NO	RESULT pCi/L	2σ ERR (COUNT)	MDA pCi/L	RDL pCi/L	QUALI- FIERS	TEST
Protactinium 231	.14331-85-2	-0.145	0.15	0.696	1.00	U	PA

2UP1, AUGUST 2008

QC-BLANK #67155
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METHOD BLANKS

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SUMMARY DATA SECTION

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Lab id <u>EBRLNE</u>
Protocol <u>Fluor</u>
Version <u>Ver 1.0</u>
Form <u>DVD-DS</u>
Version <u>3.06</u>
Report date <u>10/09/08</u>



**EBERLINE SERVICES/RICHMOND**

SAMPLE DELIVERY GROUP H3847

7185-005

B1WDN8

**DUPLICATE**

SDG <u>7185</u>	Client/Case no <u>Hanford</u>	SDG <u>H3847</u>
Contact <u>Melissa C. Mannion</u>	Contract No. <u>33677</u>	
<b>DUPLICATE</b>	<b>ORIGINAL</b>	
Lab sample id <u>R809016-05</u>	Lab sample id <u>R809016-02</u>	Client sample id <u>B1WDN8</u>
Dept sample id <u>7185-005</u>	Dept sample id <u>7185-002</u>	Location/Matrix <u>HNF-N-506-14</u> <u>WATER</u>
	Received <u>09/03/08</u>	Collected/Volume <u>08/29/08 13:04</u> <u>1.0 L</u>
		Custody/SAF No <u>I08-053-30</u> <u>I08-053</u>

ANALYTE	DUPLICATE	2σ ERR	MDA	RDL	QUALI-	ORIGINAL	2σ ERR	MDA	QUALI-	RPD	3σ	DER
	pCi/L	(COUNT)	pCi/L	pCi/L	FIERS		TEST	pCi/L	(COUNT)	pCi/L	FIERS	‡
Protactinium 231	0.110	0.44	0.841	1.00	U	PA	0	0.13	0.486	U	-	0.5

2UP1, AUGUST 2008

QC-DUP#2 67156

DUPLICATES

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Lab id <u>EBRLNE</u>
Protocol <u>Fluor</u>
Version <u>Ver 1.0</u>
Form <u>DVD-DUP</u>
Version <u>3.06</u>
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**EBERLINE SERVICES / RICHMOND**  
**SAMPLE DELIVERY GROUP H3847**

7185-001

B1WDN2

**D A T A   S H E E T**

SDG <u>7185</u>	Client/Case no <u>Hanford</u>	SDG <u>H3847</u>
Contact <u>Melissa C. Mannion</u>	Contract No. <u>33677</u>	
Lab sample id <u>R809016-01</u>	Client sample id <u>B1WDN2</u>	
Dept sample id <u>7185-001</u>	Location/Matrix <u>HNF-N-506-14</u>	<u>WATER</u>
Received <u>09/03/08</u>	Collected/Volume <u>08/26/08 11:00</u>	<u>1.0 L</u>
	Custody/SAF No <u>I08-053-20</u>	<u>I08-053</u>

ANALYTE	CAS NO	RESULT pCi/L	2σ ERR (COUNT)	MDA pCi/L	RDL pCi/L	QUALI- FIERS	TEST
Protactinium 231	14331-85-2	0.052	0.21	0.400	1.00	U	PA

2UP1, AUGUST 2008

Lab id <u>EBRLNE</u>
Protocol <u>Fluor</u>
Version <u>Ver 1.0</u>
Form <u>DVD-DS</u>
Version <u>3.06</u>
Report date <u>10/09/08</u>

**EBERLINE SERVICES / RICHMOND**  
**SAMPLE DELIVERY GROUP H3847**

7185-002

B1WDN8

**D A T A   S H E E T**

SDG <u>7185</u>	Client/Case no <u>Hanford</u>	SDG <u>H3847</u>
Contact <u>Melissa C. Mannion</u>	Contract <u>No. 33677</u>	
Lab sample id <u>R809016-02</u>	Client sample id <u>B1WDN8</u>	
Dept sample id <u>7185-002</u>	Location/Matrix <u>HNF-N-506-14</u>	<u>WATER</u>
Received <u>09/03/08</u>	Collected/Volume <u>08/29/08 13:04</u>	<u>1.0 L</u>
	Custody/SAF No <u>I08-053-30</u>	<u>I08-053</u>

ANALYTE	CAS NO	RESULT pCi/L	2σ ERR (COUNT)	MDA pCi/L	RDL pCi/L	QUALI- FIERS	TEST
Protactinium 231	14331-85-2	0	0.13	0.486	1.00	U	PA

2UP1, AUGUST 2008

**DATA SHEETS**

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**SUMMARY DATA SECTION**

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Lab id <u>EBRLNE</u>
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Form <u>DVD-DS</u>
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Report date <u>10/09/08</u>

**EBERLINE SERVICES/RICHMOND**

SAMPLE DELIVERY GROUP H3847

Test PA Matrix WATER  
 SDG 7185  
 Contact Melissa C. Mannion

**LAB METHOD SUMMARY**

PA-231 IN WATER  
 ALPHA SPECTROSCOPY

Client Hanford  
 Contract No. 33677  
 Contract SDG H3847

**RESULTS**

LAB	RAW	SUF-	Protactinium	
SAMPLE ID	TEST FIX	PLANCHET	CLIENT SAMPLE ID	231
Preparation batch 6169-042				
R809016-01		7185-001	B1WDN2	U
R809016-02	R1	7185-002	B1WDN8	U
R809016-03	R1	7185-003	Lab Control Sample	<u>HIGH</u>
R809016-04		7185-004	Method Blank	U
R809016-05		7185-005	Duplicate (R809016-02)	- U

Nominal values and limits from method RDLs (pCi/L) 1.00  
 2UP1, AUGUST 2008

**METHOD PERFORMANCE**

LAB	RAW	SUF-	MDA	ALIQ	PREP	DILU-	YIELD	EFF	COUNT	FWHM	DRIFT	DAYS	ANAL-		
SAMPLE ID	TEST FIX	CLIENT SAMPLE ID	pCi/L	L	FAC	TION	%	%	min	keV	KeV	HELD	PREPARED	YZED	DETECTOR
Preparation batch 6169-042 2σ prep error 14.8 % Reference Lab Notebook #6169, pg. 42															
R809016-01		B1WDN2	0.400	0.150			40		400			36	09/30/08	10/01	SS-027
R809016-02	R1	B1WDN8	0.486	0.150			32		408			40	10/07/08	10/08	SS-057
R809016-03	R1	Lab Control Sample	0.359	0.150			43		409				10/07/08	10/08	SS-058
R809016-04		Method Blank	0.696	0.150			31		401				09/30/08	10/01	SS-040
R809016-05		Duplicate (R809016-02)	0.841	0.150			24		402				09/30/08	10/01	SS-042

Nominal values and limits from method 1.00 0.150 20-105 200 180

PROCEDURES REFERENCE PA231\_IE\_PLATE\_AEA  
 SPP-007 Aqueous Sample Receipt by Chemistry Laboratory, rev 0  
 SPP-062 Sample Aliquoting, rev 0  
 CP-910 Protactinium-231 in Soil, (0 to 0.25 g) Aliquot, rev 2

AVERAGES ± 2 SD MDA 0.556 ± 0.411  
 FOR 5 SAMPLES YIELD 34 ± 15

METHOD SUMMARIES

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SUMMARY DATA SECTION

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EBERLINE SERVICES / RICHMOND

SAMPLE DELIVERY GROUP H3847

SDG 7185  
Contact Melissa C. Mannion

REPORT GUIDE

Client Hanford  
Contract No. 33677  
Case no SDG H3847

SAMPLE SUMMARY

The Sample and QC Summary Reports show all samples, including QC samples, reported in one Sample Delivery Group (SDG).

The Sample Summary Report fully identifies client samples and gives the corresponding lab sample identification. The QC Summary Report shows at the sample level how the lab organized the samples into batches and generated QC samples. The Preparation Batch and Method Summary Reports show this at the analysis level.

The following notes apply to these reports:

- \* LAB SAMPLE ID is the lab's primary identification for a sample.
- \* DEPARTMENT SAMPLE ID is an alternate lab id, for example one assigned by a radiochemistry department in a lab.
- \* CLIENT SAMPLE ID is the client's primary identification for a sample. It includes any sample preparation done by the client that is necessary to identify the sample.
- \* QC BATCH is a lab assigned code that groups samples to be processed and QCed together. These samples should have similar matrices.

QC BATCH is not necessarily the same as SDG, which reflects samples received and reported together.

- \* All Lab Control Samples, Method Blanks, Duplicates and Matrix Spikes are shown that QC any of the samples. Due to possible reanalyses, not all results for all these QC samples may be relevant to the SDG. The Lab Control Sample, Method Blank, Duplicate, Matrix Spike and Method Summary Reports detail these relationships.

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SAMPLE DELIVERY GROUP H3847

SDG 7185  
Contact Melissa C. Mannion

REPORT GUIDE

Client Hanford  
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PREPARATION BATCH SUMMARY

The Preparation Batch Summary Report shows all preparation batches in one Sample Delivery Group (SDG) with information necessary to check the completeness and consistency of the SDG.

The following notes apply to this report:

- \* The preparation batches are shown in the same order as the Method Summary Reports are printed.
- \* Only analyses of planchets relevant to the SDG are included.
- \* Each preparation batch should have at least one Method Blank and LCS in it to validate client sample results.
- \* The QUALIFIERS shown are all qualifiers other than U, J, B, L and H that occur on any analysis in the preparation batch. The Method Summary Report has these qualifiers on a per sample basis.

These qualifiers should be reviewed as follows:

- X Some data has been manually entered or modified. Transcription errors are possible.
- P One or more results are 'preliminary'. The data is not ready for final reporting.
- 2 There were two or more results for one analyte on one planchet imported at one time. The results in DVD may not be the same as on the raw data sheets.

Other lab defined qualifiers may occur. In general, these should be addressed in the SDG narrative.

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SAMPLE DELIVERY GROUP H3847

SDG 7185

Contact Melissa C. Mannion

Client Hanford

Contract No. 33677

Case no SDG H3847

REPORT GUIDE

WORK SUMMARY

The Work Summary Report shows all samples, including QC samples, and all relevant analyses in one Sample Delivery Group (SDG). This report is often useful as supporting documentation for an invoice.

The following notes apply to this report:

- \* TEST is a code for the method used to measure associated analytes. Results and related information for each analyte are on the Data Sheet Report. In special cases, a test code used in the summary data section is not the same as in associated raw data. In this case, both codes are shown on the Work Summary.
- \* SUFFIX is the lab's code to distinguish multiple analyses (recounts, reworks, reanalyses) of a fraction of the sample. The suffix indicates which result is being reported. An empty suffix normally identifies the first attempt to analyze the sample.
- \* The LAB SAMPLE ID, TEST and SUFFIX uniquely identify all supporting data for a result. The Method Summary Report for each TEST has method performance data, such as yield, for each lab sample id and suffix and procedures used in the method.
- \* PLANCHET is an alternate lab identifier for work done for one test. It, combined with the TEST and SUFFIX, may be the best link to raw data.
- \* For QC samples, only analyses that directly QC some regular sample are shown. The Lab Control Sample, Method Blank, Duplicate, Matrix Spike and Method Summary Reports detail these relationships.
- \* The SAS (Special Analytical Services) Number is a client or lab assigned code that reflects special processing for samples, such as rapid turn around. Counts of tests done are lists by SAS number since it is likely to affect prices.

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SUMMARY DATA SECTION

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Lab id EBRLNE

Protocol Fluor

Version Ver 1.0

Form DVD-RG

Version 3.06

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SAMPLE DELIVERY GROUP H3847

SDG 7185  
 Contact Melissa C. Mannion

REPORT GUIDE

Client Hanford  
 Contract No. 33677  
 Case no SDG\_H3847

DATA SHEET

The Data Sheet Report shows all results and primary supporting information for one client sample or Method Blank. This report corresponds to both the CLP Inorganics and Organics Data Sheet.

The following notes apply to this report:

- \* TEST is a code for the method used to measure an analyte. If the TEST is empty, no data is available; the analyte was not analyzed for.
- \* The LAB SAMPLE ID and TEST uniquely identify work within the Summary Data Section of a Data Package. The Work Summary and Method Summary Reports further identify raw data that underlies this work.

The Method Summary Report for each TEST has method performance data, such as yield, for each Lab Sample ID and a list of procedures used in the method.

- \* ERRORS can be labeled TOTAL or COUNT. TOTAL implies a preparation (non-counting method) error has been added, as square root of sum of squares, to the counting error denoted by COUNT. The preparation errors, which may vary by preparation batch, are shown on the Method Summary Report.
- \* A RESULT can be 'N.R.' (Not Reported). This means the lab did this work but chooses not to report it now, possibly because it was reported at another time.
- \* When reporting a Method Blank, a RESULT can be 'N.A.' (Not Applicable). This means there is no reported client sample work in the same preparation batch as the Blank's result. This is likely to occur when the Method Blank is associated with reanalyses of selected work for a few samples in the SDG.

The following qualifiers are defined by the DVD system:

- U The RESULT is less than the MDA (Minimum Detectable Activity).

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DATA SHEET

If the MDA is blank, the ERROR is used as the limit.

- J The RESULT is less than the RDL (Required Detection Limit) and no U qualifier is assigned.
  - B A Method Blank associated with this sample had a result without a U flag and, after correcting for possibly different aliquots, that result is greater than or equal to the MDA for this sample.
- Normally, B is not assigned if U is. When method blank subtraction is shown on this report, B flags are assigned based on the unsubtracted values while U's are assigned based on the subtracted ones. Both flags can be assigned in this case.
- For each sample result, all Method Blank results in the same preparation batch are compared. The Method Summary Report documents this and other QC relationships.
- L Some Lab Control Sample that QC's this sample had a low recovery. The lab can disable assignment of this qualifier.
  - H Similar to 'L' except the recovery was high.
  - P The RESULT is 'preliminary'.
  - X Some data necessary to compute the RESULT, ERROR or MDA was manually entered or modified.
  - 2 There were two or more results available for this analyte. The reported result may not be the same as in the raw data.

Other qualifiers are lab defined. Definitions should be in the SDG narrative.

The following values are underlined to indicate possible problems:

- \* An MDA is underlined if it is bigger than its RDL.

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- \* An ERROR is underlined if the 1.645 sigma counting error is bigger than both the MDA and the RESULT, implying that the MDA may not be a good estimate of the 'real' minimum detectable activity.
- \* A negative RESULT is underlined if it is less than the negative of its 2 sigma counting ERROR.
- \* When reporting a Method Blank, a RESULT is underlined if greater than its MDA. If the MDA is blank, the 2 sigma counting error is used in the comparison.

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LAB CONTROL SAMPLE

The Lab Control Sample Report shows all results, recoveries and primary supporting information for one Lab Control Sample.

The following notes apply to this report:

- \* All fields in common with the Data Sheet Report have similar usage. Refer to its Report Guide for details.
- \* An amount ADDED is the lab's value for the actual amount spiked into this sample with its ERROR an estimate of the error of this amount.

An amount added is underlined if its ratio to the corresponding RDL is outside protocol specified limits.

- \* REC (Recovery) is RESULT divided by ADDED expressed as a percent.
- \* The first, computed limits for the recovery reflect:
  1. The error of RESULT, including that introduced by rounding the result prior to printing.

If the limits are labeled (TOTAL), they include preparation error in the result. If labeled (COUNT), they do not.
  2. The error of ADDED.
  3. A lab specified, per analyte bias. The bias changes the center of the computed limits.
- \* The second limits are protocol defined upper and lower QC limits for the recovery.
- \* The recovery is underlined if it is outside either of these ranges.

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DUPLICATE

The Duplicate Report shows all results, differences and primary supporting information for one Duplicate and associated Original sample.

The following notes apply to this report:

- \* All fields in common with the Data Sheet Report have similar usage. This applies both to the Duplicate and Original sample data. Refer to the Data Sheet Report Guide for details.

If the Duplicate has data for a TEST and the lab did not do this test to the Original, the Original's RESULTS are underlined.

- \* The RPD (Relative Percent Difference) is the absolute value of the difference of the RESULTS divided by their average expressed as a percent.

If both RESULTS are less than their MDAs, no RPD is computed and a '-' is printed.

For an analyte, if the lab did work for both samples but has data for only one, the MDA from the sample with data is used as the other's result in the RPD.

- \* The first, computed limit is the sum, as square root of sum of squares, of the errors of the results divided by the average result as a percent, hence the relative error of the difference rather than the error of the relative difference. The errors include those introduced by rounding the RESULTS prior to printing.

If this limit is labeled TOT, it includes the preparation error in the RESULTS. If labeled CNT, it does not.

This value reported for this limit is at most 999.

- \* The second limit for the RPD is the larger of:

1. A fixed percentage specified in the protocol.

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2. A protocol factor (typically 2) times the average MDA as a percent of the average result. This limit applies when the results are close to the MDAs.

- \* The RPD is underlined if it is greater than either limit.
- \* If specified by the lab, the second limit column is replaced by the Difference Error Ratio (DER), which is the absolute value of the difference of the results divided by the quadratic sum of their one sigma errors, the same errors as used in the first limit.

Except for differences due to rounding, the DER is the same as the RPD divided by the first RPD limit with the limit scaled to 1 sigma.

- \* The DER is underlined if it is greater than the sigma factor, typically 2 or 3, shown in the header for the first RPD limit.

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MATRIX SPIKE

The Matrix Spike Report shows all results, recoveries and primary supporting information for one Matrix Spike and associated Original sample.

The following notes apply to this report:

- \* All fields in common with the Data Sheet Report have similar usage. This applies both to the Spiked and Original sample data. Refer to the Data Sheet Report Guide for details.

If the Spike has data for a TEST and the lab did not do this test to the Original, the Original's RESULTS are underlined.

- \* An amount ADDED is the lab's value for the actual amount spiked into the Spike sample with its ERROR an estimate of the error of this amount.

An amount is underlined if its ratio to the corresponding RDL is outside protocol specified limits.

- \* REC (Recovery) is the Spike RESULT minus the Original RESULT divided by ADDED expressed as a percent.

- \* The first, computed limits for the recovery reflect:

1. The errors of the two RESULTS, including those introduced by rounding them prior to printing.

If the limits are labeled (TOTAL), they include preparation error in the result. If labeled (COUNT), they do not.

2. The error of ADDED.

3. A lab specified, per analyte bias. The bias changes the center of the computed limits.

- \* The second limits are protocol defined upper and lower QC limits

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for the recovery.

These limits are left blank if the Original RESULT is more than a protocol defined factor (typically 4) times ADDED. This is a way of accounting for that when the spike is small compared to the amount in the original sample, the recovery is unreliable.

- \* The recovery is underlined (out of spec) if it is outside either of these ranges.

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METHOD SUMMARY

The Method Summary Report has two tables. One shows up to five results measured using one method. The other has performance data for the method. There is one report for each TEST, as used on the Data Sheet Report.

The following notes apply to this report:

- \* Each table is subdivided into sections, one for each preparation batch. A preparation batch is a group of aliquots prepared at roughly the same time in one work area of the lab using the same method.

There should be Lab Control Sample and Method Blank results in each preparation batch since this close correspondence makes the QC meaningful. Depending on lab policy, Duplicates need not occur in each batch since they QC sample dependencies such as matrix effects.

- \* The RAW TEST column shows the test code used in the raw data to identify a particular analysis if it is different than the test code in the header of the report. This occurs in special cases due to method specific details about how the lab labels work.

The Lab Sample or Planchet ID combined with the (Raw) Test Code and Suffix uniquely identify the raw data for each analysis.

- \* If a result is less than both its MDA and RDL, it is replaced by just 'U' on this report. If it is greater than or equal to the RDL but less than the MDA, the result is shown with a 'U' flag.

The J and X flags are as on the data sheet.

- \* Non-U results for Method Blanks are underlined to indicate possible contamination of other samples in the preparation batch. The Method Blank Report has supporting data.
- \* Lab Control Sample and Matrix Spike results are shown as: ok, No data, LOW or HIGH, with the last two underlined. 'No data'

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means no amount ADDED was specified. 'LOW' and 'HIGH' correspond to when the recovery is underlined on the Lab Control Sample or Matrix Spike Report. See these reports for supporting data.

- \* Duplicate sample results are shown as: ok, No data, or OUT, with the last two underlined. 'No data' means there was no original sample data found for this duplicate. 'OUT' corresponds to when the RPD is underlined on the Duplicate Report. See this report for supporting data.
- \* If the MDA column is labeled 'MAX MDA', there was more than one result measured by the reported method and the MDA shown is the largest MDA. If not all these results have the same RDL, the MAX MDA reflects only those results with RDL equal to the smallest one.

MDAs are underlined if greater than the printed RDL.

- \* Aliquots are underlined if less than the nominal value specified for the method.
- \* Preparation factors are underlined if greater than the nominal value specified for the method.
- \* Dilution factors are underlined if greater than the nominal value specified for the method.
- \* Residues are underlined if outside the range specified for the method. Residues are not printed if yields are.
- \* Yields, which may be gravimetric, radiometric or some type of recovery depending on the method, are underlined if outside the range specified for the method.
- \* Efficiencies are underlined if outside the range specified for the method. Efficiencies are detector and geometry dependent so this test is only approximate.

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- \* Count times are underlined if less than the nominal value specified for the method.
- \* Resolutions (as FWHM; Full Width at Half Max) are underlined if greater than the method specified limit.
- \* Tracer drifts are underlined if their absolute values are greater than the method specified limit. Tracer drifts are not printed if percent moistures are.
- \* Days Held are underlined if greater than the holding time specified in the protocol.
- \* Analysis dates are underlined if before their planchet's preparation date or, if a limit is specified, too far after it.

For some methods, ratios as percentages and error estimates for them are computed for pairs of results. A ratio column header like '1+3' means the ratio of the first result column and the third result column.

Ratios are not computed for Lab Control Sample, Method Blank or Matrix Spike results since their matrices are not necessarily similar to client samples'.

The error estimate for a ratio of results from one planchet reflects only counting errors since other errors should be correlated. For a ratio involving different planchets, if QC limits are computed based on total errors, the error for the ratio allows for the preparation errors for the planchets.

The ratio is underlined (out of spec) if the absolute value of its difference from the nominal value is greater than its error estimate. If no nominal value is specified, this test is not done.

For Gross Alpha or Gross Beta results, there may be a column showing the sum of other Alpha or Beta emitters. This sum includes all relevant

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results in the DVD database, whether reported or not. Results in the sum are weighted by a particles/decay value specified by the lab for each relevant analyte. Results less than their MDA are not included. No sums are computed for Lab Control, Method Blank or Matrix Spike samples since their various planchets may not be physically related.

If a ratio of total isotopic to Gross Alpha or Beta is shown, the error for the ratio reflects both the error in the Gross result and the sum, as square root of sum of squares, of the errors in the isotopic results.

For total elemental uranium or thorium results, there may be a column showing the total weight computed from associated isotopic results. Ignoring results less than their MDAs, this is a weighted sum of the isotopic results. The weights depend on the molecular weight and half-life of each isotope so as to convert activities (decays) to weight (atoms).

If a ratio of total computed to measured elemental uranium or thorium is shown, the error for the ratio reflects the errors in all the measurements.

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*9/13/08*

Client: F. HAWFORD City PICETLAND State WA  
 Date/Time received 09/03/08 09:30 CoC No. 108-053-2030  
 Container I.D. No. GRP-08-015 Requested TAT (Days) 30 P.D. Received Yes [ ] No [ ]

INSPECTION

- 1 Custody seals on shipping container intact? Yes  No [ ] N/A [ ]
- 2 Custody seals on shipping container dated & signed? Yes  No [ ] N/A [ ]
- 3 Custody seals on sample containers intact? Yes  No [ ] N/A [ ]
- 4 Custody seals on sample containers dated & signed? Yes  No [ ] N/A [ ]
- 5 Packing material is: Wet [ ] Dry
- 6 Number of samples in shipping container 2 Sample Matrix W
- 7 Number of containers per sample 1 (Or see CoC \_\_\_\_\_)
- 8 Samples are in correct container Yes  No [ ]
- 9 Paperwork agrees with samples? Yes  No [ ]
- 10 Samples have Tape [ ] Hazard labels [ ] Rad labels [ ] Appropriate sample labels
- 11 Samples are In good condition  Leaking [ ] Broken Container [ ] Missing
- 12 Samples are Preserved  Not preserved  pH 1/7 Preservative HNO3
- 13 Describe any anomalies

14 Was P.M. notified of any anomalies? Yes [ ] No [ ] Date \_\_\_\_\_  
 15 Inspected by MFW Date 09/03/08 Time 11:15

Customer Sample No	Beta/Gamma cpm	Ion Chamber mR/hr	Wipe	Customer Sample No	Beta/Gamma cpm	Ion Chamber mR/hr	wipe
<u>All staples</u>	<u>&lt;60</u>						

Ion Chamber Ser. No \_\_\_\_\_ Calibration date \_\_\_\_\_  
 Alpha Meter Ser. No \_\_\_\_\_ Calibration date \_\_\_\_\_  
 Beta/Gamma Meter Ser. No 100482 Calibration date 10JUL08