



# EBERLINE

SERVICES

Rev. 1

October 25, 2007

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

Reference: **P.O. #630**  
**Eberline Services R7-07-068-7665, SDG H3544**

Dear Mr. Trent:

Enclosed is a revised report for SDG H3544 that includes the Pa231 analytical results.

Please call if you have any questions concerning this report.

Sincerely,

Melissa C. Mannion  
Senior Program Manager

MCM/njv

Enclosure: Data Package



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2030 Wright Avenue  
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Richmond, California 94804-0040  
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## 1.0 GENERAL

Fluor Hanford Inc. (FH) Sample Delivery Group H3544 was composed of two water samples designated under SAF No. F07-058 with a Project Designation of: 216-A-2 and 216-A-21 Characterization Sampling and Analysis-Groundwater.

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

## 2.0 ANALYSIS NOTES

### 2.1 Tritium Analysis

No problems were encountered during the course of the analyses.

### 2.2 Selenium-79 Analysis

The selenium carrier yields were between 11% and 17%, less than the lower control limit of 20%. No other problems were encountered during the course of the analyses. Eberline Services does not have a stock of Se-79 activity with which to prepare control samples, as a consequence an LCS was not performed.

### 2.3 Iodine-129 Analysis

No problems were encountered during the course of the analyses.

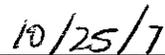
### 2.4 Protactinium-231 Analysis

No 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

  
\_\_\_\_\_  
Date

EBERLINE SERVICES / RICHMOND  
SAMPLE DELIVERY GROUP H3544

SDG 7665  
Contact Melissa C. Mannion

Client Hanford  
Contract No. 630  
Case no SDG\_H3544

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Melissa Mannion  
Prepared by

Melissa Mannion  
Reviewed by

Lab id EBRLNE  
Protocol Hanford  
Version Ver 1.0  
Form DVD-TOC  
Version 3.06  
Report date 10/24/07

00000002

EBERLINE SERVICES / RICHMOND  
SAMPLE DELIVERY GROUP H3544

SDG 7665  
Contact Melissa C. Mannion

REPORT GUIDE

Client Hanford  
Contract No. 630  
Case no SDG H3544

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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EBERLINE SERVICES / RICHMOND  
SAMPLE DELIVERY GROUP H3544

SDG 7665  
Contact Melissa C. Mannion

GUIDE, cont.

Client Hanford  
Contract No. 630  
Case no SDG H3544

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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EBERLINE SERVICES/RICHMOND

SAMPLE DELIVERY GROUP H3544

LAB SAMPLE SUMMARY

SDG 7665  
 Contact Melissa C. Mannion

Client Hanford  
 Contract No. 630  
 Case no SDG H3544

LAB	CLIENT SAMPLE ID	LOCATION	MATRIX	LEVEL	SAF NO	CHAIN OF CUSTODY	COLLECTED
R707068-01	B1NWH4	299-E23-2	WATER		F07-058	F07-058-004	06/25/07 09:46
R707068-02	B1NWH5	299-E23-2 Duplicate	WATER		F07-058	F07-058-005	06/25/07 09:46
R707068-03	Lab Control Sample		WATER		F07-058		
R707068-04	Method Blank		WATER		F07-058		
R707068-05	Duplicate (R707068-02)	299-E23-2 Duplicate	WATER		F07-058		06/25/07 09:46
R707068-06	Spike (R707068-02)	299-E23-2 Duplicate	WATER		F07-058		06/25/07 09:46

LAB SUMMARY

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SUMMARY DATA SECTION

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Lab id EBRLNE  
 Protocol Hanford  
 Version Ver 1.0  
 Form DVD-LS  
 Version 3.06  
 Report date 10/24/07

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**EBERLINE SERVICES/RICHMOND**

SAMPLE DELIVERY GROUP H3544

SDG 7665  
 Contact Melissa C. Mannion

**QC SUMMARY**

Client Hanford  
 Contract No. 630  
 Case no SDG H3544

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
7665	F07-058-004	B1NWH4	WATER		6.125 L		07/12/07 17	R707068-01		7665-001
	F07-058-005	B1NWH5	WATER		6.125 L		07/12/07 17	R707068-02		7665-002
		Method Blank	WATER					R707068-04		7665-004
		Lab Control Sample	WATER					R707068-03		7665-003
		Duplicate (R707068-02)	WATER		6.125 L		07/12/07 17	R707068-05		7665-005
		Spike (R707068-02)	WATER		6.125 L		07/12/07 17	R707068-06		7665-006

QC SUMMARY

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Lab id EBERLINE  
 Protocol Hanford  
 Version Ver 1.0  
 Form DVD-QS  
 Version 3.06  
 Report date 10/24/07

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EBERLINE SERVICES/RICHMOND

SAMPLE DELIVERY GROUP H3544

SDG 7665  
 Contact Melissa C. Mannion

PREP BATCH SUMMARY

Client Hanford  
 Contract No. 630  
 Case no SDG H3544

TEST	MATRIX	METHOD	PREPARATION ERROR		PLANCHETS ANALYZED				QUALI- FYERS	
			BATCH	2σ %	CLIENT	MORE	RE	BLANK		LCS
Alpha Spectroscopy										
PA	WATER	Pa-231 in Water	6121-048	5.0	2			1	1	1/1
Gamma Spectroscopy										
I	WATER	Iodine 129 in Water	6121-048	5.0	2			1	1	1/1
Liquid Scintillation Counting										
H	WATER	Tritium in Water	6121-048	10.0	2			1	1	1/1 1/1 X
SE_L	WATER	Selenium 79 in Water	6121-048	10.0	2			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.

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**EBERLINE SERVICES/RICHMOND**

SAMPLE DELIVERY GROUP H3544

SDG 7665  
 Contact Melissa C. Mannion

**LAB WORK SUMMARY**

Client Hanford  
 Contract No. 630  
 Case no SDG H3544

LAB SAMPLE	CLIENT SAMPLE ID									
COLLECTED	LOCATION		MATRIX		SUF-					
RECEIVED	CUSTODY	SAF No		PLANCHET	TEST	FIX	ANALYZED	REVIEWED	BY	METHOD
R707068-01	B1NWH4			7665-001	H		08/22/07	08/29/07	BW	Tritium in Water
06/25/07	299-E23-2		WATER	7665-001	I		08/15/07	08/17/07	MWT	Iodine 129 in Water
07/12/07	F07-058-004	F07-058		7665-001	PA		08/22/07	08/28/07	BW	Pa-231 in Water
				7665-001	SE_L		08/22/07	08/29/07	BW	Selenium 79 in Water
R707068-02	B1NWH5			7665-002	H		08/22/07	08/29/07	BW	Tritium in Water
06/25/07	299-E23-2 Duplicate		WATER	7665-002	I		08/16/07	08/17/07	MWT	Iodine 129 in Water
07/12/07	F07-058-005	F07-058		7665-002	PA		08/23/07	08/28/07	BW	Pa-231 in Water
				7665-002	SE_L		08/22/07	08/29/07	BW	Selenium 79 in Water
R707068-03	Lab Control Sample			7665-003	H		08/22/07	08/29/07	BW	Tritium in Water
			WATER	7665-003	I		08/16/07	08/17/07	MWT	Iodine 129 in Water
		F07-058		7665-003	PA		08/22/07	08/28/07	BW	Pa-231 in Water
R707068-04	Method Blank			7665-004	H		08/22/07	08/29/07	BW	Tritium in Water
			WATER	7665-004	I		08/16/07	08/17/07	MWT	Iodine 129 in Water
		F07-058		7665-004	PA		08/22/07	08/28/07	BW	Pa-231 in Water
				7665-004	SE_L		08/22/07	08/29/07	BW	Selenium 79 in Water
R707068-05	Duplicate (R707068-02)			7665-005	H		08/22/07	08/29/07	BW	Tritium in Water
06/25/07	299-E23-2 Duplicate		WATER	7665-005	I		08/16/07	08/17/07	MWT	Iodine 129 in Water
07/12/07		F07-058		7665-005	PA		08/23/07	08/28/07	BW	Pa-231 in Water
				7665-005	SE_L		08/22/07	08/29/07	BW	Selenium 79 in Water
R707068-06	Spike (R707068-02)			7665-006	H		08/22/07	08/29/07	BW	Tritium in Water
06/25/07	299-E23-2 Duplicate		WATER							
07/12/07		F07-058								

WORK SUMMARY

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SUMMARY DATA SECTION

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EBERLINE SERVICES/RICHMOND

SAMPLE DELIVERY GROUP H3544

WORK SUMMARY, cont.

SDG 7665  
 Contact Melissa C. Mannion

Client Hanford  
 Contract No. 630  
 Case no SDG H3544

COUNTS OF TESTS BY SAMPLE TYPE											
TEST	SAF No	METHOD	REFERENCE	CLIENT	MORE	RE	BLANK	LCS	DUP	SPIKE	TOTAL
H	F07-058	Tritium in Water	906.0_H3_LSC	2			1	1	1	1	6
I	F07-058	Iodine 129 in Water	I129_SEP_LEPS_GS	2			1	1	1		5
PA	F07-058	Pa-231 in Water	PA231_IE_PLATE_AEA	2			1	1	1		5
SE_L	F07-058	Selenium 79 in Water	SE79_SEP_DIS_LSC	2			1		1		4
TOTALS				8			4	3	4	1	20

WORK SUMMARY

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EBERLINE SERVICES / RICHMOND  
 SAMPLE DELIVERY GROUP H3544

7665-004

Method Blank

METHOD BLANK

SDG <u>7665</u>	Client/Case no <u>Hanford</u>	SDG <u>H3544</u>
Contact <u>Melissa C. Mannion</u>	Contract No. <u>630</u>	
Lab sample id <u>R707068-04</u>	Client sample id <u>Method Blank</u>	
Dept sample id <u>7665-004</u>	Material/Matrix <u>WATER</u>	
	SAF No <u>F07-058</u>	

ANALYTE	CAS NO	RESULT pCi/L	2σ ERR (COUNT)	MDA pCi/L	RDL pCi/L	QUALI- FIERS	TEST
Tritium	10028-17-8	690	1000	<u>1700</u>	400	U	H
Protactinium 231	14331-85-2	0.033	0.065	0.25	1.0	U	PA
Iodine 129	15046-84-1	0.269	0.91	2.1	5.0	U	I
Selenium 79	15758-45-9	-0.004	0.096	0.16	50	U	SE_L

216A2/216A21 CharactrztnSamp&Ana-GW

QC-BLANK 62362
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Lab id <u>EBRLNE</u>
Protocol <u>Hanford</u>
Version <u>Ver 1.0</u>
Form <u>DVD-DS</u>
Version <u>3.06</u>
Report date <u>10/24/07</u>

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EBERLINE SERVICES/RICHMOND

SAMPLE DELIVERY GROUP H3544

7665-003

Lab Control Sample

LAB CONTROL SAMPLE

SDG <u>7665</u>	Client/Case no <u>Hanford</u>	SDG <u>H3544</u>
Contact <u>Melissa C. Mannion</u>	Contract No. <u>630</u>	
Lab sample id <u>R707068-03</u>	Client sample id <u>Lab Control Sample</u>	
Dept sample id <u>7665-003</u>	Material/Matrix <u>WATER</u>	
	SAF No <u>F07-058</u>	

ANALYTE	RESULT pCi/L	2σ ERR (COUNT)	MDA pCi/L	RDL pCi/L	QUALI- FIERS TEST	ADDED pCi/L	2σ ERR pCi/L	REC %	3σ LMTS (TOTAL)	PROTOCOL LIMITS
Tritium	21000	1500	<u>1800</u>	400	H	20500	820	102	80-120	80-120
Protactinium 231	5.69	0.50	0.080	1.0	PA	6.05	0.24	94	85-115	80-120
Iodine 129	249	2.9	2.9	5.0	I	232	9.3	107	90-110	80-120

216A2/216A21 CharacterztnSamp&Ana-GW

QC-LCS 62361
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Lab id <u>EBERLINE</u>
Protocol <u>Hanford</u>
Version <u>Ver 1.0</u>
Form <u>DVD-LCS</u>
Version <u>3.06</u>
Report date <u>10/24/07</u>

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**EBERLINE SERVICES/RICHMOND**

SAMPLE DELIVERY GROUP H3544

7665-005

B1NWH5

**DUPLICATE**

SDG <u>7665</u>	Client/Case no <u>Hanford</u>	SDG <u>H3544</u>
Contact <u>Melissa C. Mannion</u>	Contract No. <u>630</u>	
<b>DUPLICATE</b>	<b>ORIGINAL</b>	
Lab sample id <u>R707068-05</u>	Lab sample id <u>R707068-02</u>	Client sample id <u>B1NWH5</u>
Dept sample id <u>7665-005</u>	Dept sample id <u>7665-002</u>	Location/Matrix <u>299-E23-2 Duplicate</u> <u>WATER</u>
	Received <u>07/12/07</u>	Collected/Volume <u>06/25/07 09:46</u> <u>6.125 L</u>
		Custody/SAP No <u>F07-058-005</u> <u>F07-058</u>

ANALYTE	DUPLICATE		MDA		RDL		QUALI-		ORIGINAL		MDA		QUALI-		RPD		3σ		DER	
	pCi/L	2σ ERR (COUNT)	pCi/L		pCi/L		FIERS	TEST	pCi/L	2σ ERR (COUNT)	pCi/L		FIERS	%	TOT		σ			
Tritium	1080	130	170		400		H		1110	120	170			3	32	0.3				
Protactinium 231	0	6.9	<u>26</u>		1.0		U	PA	0.038	0.23	0.42		U	-	-	0				
Iodine 129	-0.727	0.87	2.0		5.0		U	I	-0.073	1.3	3.0		U	-	-	0.8				
Selenium 79	0.045	0.10	0.17		50		U	SE_L	0.013	0.12	0.20		U	-	-	0.4				

216A2/216A21 CharactrztnSamp&Ana-GW

QC-DUP#2 62363

DUPLICATES

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Report date <u>10/24/07</u>

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EBERLINE SERVICES/RICHMOND

SAMPLE DELIVERY GROUP H3544

7665-006

B1NWH5

MATRIX SPIKE

SDG <u>7665</u>	Client/Case no <u>Hanford</u>	SDG <u>H3544</u>
Contact <u>Melissa C. Mannion</u>	Contract No. <u>630</u>	
MATRIX SPIKE	ORIGINAL	
Lab sample id <u>R707068-06</u>	Lab sample id <u>R707068-02</u>	Client sample id <u>B1NWH5</u>
Dept sample id <u>7665-006</u>	Dept sample id <u>7665-002</u>	Location/Matrix <u>299-E23-2 Duplicate</u> <u>WATER</u>
	Received <u>07/12/07</u>	Collected/Volume <u>06/25/07 09:46</u> <u>6.125 L</u>
		Custody/SAF No <u>F07-058-005</u> <u>F07-058</u>

ANALYTE	SPIKE pCi/L	2σ ERR (COUNT)	MDA pCi/L	RDL pCi/L	QUALI- FIERS TEST	ADDED pCi/L	2σ ERR pCi/L	ORIGINAL pCi/L	2σ ERR (COUNT)	REC 3σ % (TOTAL)	LMTS (LIMITS)	PROTOCOL LIMITS
Tritium	28600	400	180	400	X H	27600	1100	1110	120	100	83-117	60-140

216A2/216A21 CharactrztnSamp&Ana-GW

QC-MS#2 62364

MATRIX SPIKES

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Lab id <u>EBRLNE</u>
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**EBERLINE SERVICES / RICHMOND**  
**SAMPLE DELIVERY GROUP H3544**

7665-001

B1NWH4

**DATA SHEET**

SDG <u>7665</u>	Client/Case no <u>Hanford</u>	SDG <u>H3544</u>
Contact <u>Melissa C. Mannion</u>	Contract No. <u>630</u>	
Lab sample id <u>R707068-01</u>	Client sample id <u>B1NWH4</u>	
Dept sample id <u>7665-001</u>	Location/Matrix <u>299-E23-2</u>	<u>WATER</u>
Received <u>07/12/07</u>	Collected/Volume <u>06/25/07 09:46</u>	<u>6.125 L</u>
	Custody/SAF No <u>F07-058-004</u>	<u>F07-058</u>

ANALYTE	CAS NO	RESULT pCi/L	2σ ERR (COUNT)	MDA pCi/L	RDL pCi/L	QUALI- FIERS	TEST
Tritium	10028-17-8	1040	130	170	400		H
Protactinium 231	14331-85-2	0.084	0.11	0.22	1.0	U	PA
Iodine 129	15046-84-1	-0.257	1.3	3.0	5.0	U	I
Selenium 79	15758-45-9	-0.024	0.15	0.26	50	U	SE_L

216A2/216A21 CharactrztnSamp&Ana-GW

Lab id <u>EBRLINE</u>
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EBERLINE SERVICES / RICHMOND  
SAMPLE DELIVERY GROUP H3544

7665-002

BLNWH5

DATA SHEET

SDG <u>7665</u>	Client/Case no <u>Hanford</u>	SDG <u>H3544</u>
Contact <u>Melissa C. Mannion</u>	Contract No. <u>630</u>	
Lab sample id <u>R707068-02</u>	Client sample id <u>BLNWH5</u>	
Dept sample id <u>7665-002</u>	Location/Matrix <u>299-E23-2 Duplicate</u>	<u>WATER</u>
Received <u>07/12/07</u>	Collected/Volume <u>06/25/07 09:46</u>	<u>6.125 L</u>
	Custody/SAF No <u>F07-058-005</u>	<u>F07-058</u>

ANALYTE	CAS NO	RESULT pCi/L	2σ ERR (COUNT)	MDA pCi/L	RDL pCi/L	QUALI- FIERS	TEST
Tritium	10028-17-8	1110	120	170	400		H
Protactinium 231	14331-85-2	0.038	0.23	0.42	1.0	U	PA
Iodine 129	15046-84-1	-0.073	1.3	3.0	5.0	U	I
Selenium 79	15758-45-9	0.013	0.12	0.20	50	U	SE L

216A2/216A21 CharactrztnSamp&Ana-GW

DATA SHEETS

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**EBERLINE SERVICES/RICHMOND**

SAMPLE DELIVERY GROUP H3544

**LAB METHOD SUMMARY**

PA-231 IN WATER  
ALPHA SPECTROSCOPY

Test PA Matrix WATER  
SDG 7665  
Contact Melissa C. Mannion

Client Hanford  
Contract No. 630  
Contract SDG H3544

**RESULTS**

LAB	RAW	SUF-	Protactinium	
SAMPLE ID	TEST FIX	PLANCHET	CLIENT SAMPLE ID	231
Preparation batch 6121-048				
R707068-01		7665-001	B1NWH4	U
R707068-02		7665-002	B1NWH5	U
R707068-03		7665-003	Lab Control Sample	ok
R707068-04		7665-004	Method Blank	U
R707068-05		7665-005	Duplicate (R707068-02)	- U
Nominal values and limits from method RDLs (pCi/L) 1.0				
216A2/216A21 CharactrxztnSamp&Ana-GW				

**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 6121-048 2σ prep error 5.0 % Reference Lab Notebook #6121, pg. 26															
R707068-01		B1NWH4	0.22	0.150			31		939			58	08/22/07	08/22	SS-055
R707068-02		B1NWH5	0.42	0.150			26		938			59	08/22/07	08/23	SS-028
R707068-03		Lab Control Sample	0.080	0.150			87		939				08/22/07	08/22	SS-057
R707068-04		Method Blank	0.25	0.150			27		939				08/22/07	08/22	SS-058
R707068-05		Duplicate (R707068-02)	26	0.150			37		9			59	08/22/07	08/23	SS-063
Nominal values and limits from method 1.0 0.150 20-105 200 180															

PROCEDURES REFERENCE PA231\_IE\_PLATE\_AEA  
CP-910 Protactinium-231 in Soil, (0 to 0.25 g) Aliquot, rev 2  
CP-008 Heavy Element Electroplating, rev 9

AVERAGES ± 2 SD MDA 5.4 ± 23  
FOR 5 SAMPLES YIELD 42 ± 51

Lab id EBRLE  
Protocol Hanford  
Version Ver 1.0  
Form DVD-LMS  
Version 3.06  
Report date 10/24/07

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**EBERLINE SERVICES/RICHMOND**

SAMPLE DELIVERY GROUP H3544

**LAB METHOD SUMMARY**

IODINE 129 IN WATER  
GAMMA SPECTROSCOPY

Test I Matrix WATER  
SDG 7665  
Contact Melissa C. Mannion

Client Hanford  
Contract No. 630  
Contract SDG H3544

**RESULTS**

LAB	RAW	SUF-		
SAMPLE ID	TEST FIX	PLANCHET	CLIENT SAMPLE ID	Iodine 129
Preparation batch 6121-048				
R707068-01		7665-001	B1NWH4	U
R707068-02		7665-002	B1NWH5	U
R707068-03		7665-003	Lab Control Sample	ok
R707068-04		7665-004	Method Blank	U
R707068-05		7665-005	Duplicate (R707068-02)	- U

Nominal values and limits from method      RDLs (pCi/L)      5.0  
216A2/216A21 CharactrztnSamp&Ana-GW

**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 6121-048      2σ prep error 5.0 %      Reference Lab Notebook #6121, pg. 26															
R707068-01		B1NWH4	3.0	0.500			68		766			51	08/14/07	08/15	XSPEC-002
R707068-02		B1NWH5	3.0	0.500			71		611			52	08/14/07	08/16	XSPEC-002
R707068-03		Lab Control Sample	2.9	0.500			82		651				08/14/07	08/16	XSPEC-004
R707068-04		Method Blank	2.1	0.500			85		1002				08/14/07	08/16	XSPEC-002
R707068-05		Duplicate (R707068-02)	2.0	0.500			74		949			52	08/14/07	08/16	XSPEC-004

Nominal values and limits from method      5.0      0.500      20-105      300      100      180

PROCEDURES    REFERENCE    I129\_SEP\_LEPS\_GS  
SPP-062      Sample Aliquoting, rev 0  
CP-530      Iodine-129 Purification, rev 1

AVERAGES ± 2 SD      MDA 2.6 ± 1.0  
FOR 5 SAMPLES      YIELD 76 ± 14

Lab id EBRLNE  
Protocol Hanford  
Version Ver 1.0  
Form EVD-LMS  
Version 3.06  
Report date 10/24/07

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**EBERLINE SERVICES/RICHMOND**

SAMPLE DELIVERY GROUP H3544

**LAB METHOD SUMMARY**

TRITIUM IN WATER

LIQUID SCINTILLATION COUNTING

Test H Matrix WATER  
 SDG 7665  
 Contact Melissa C. Mannion

Client Hanford  
 Contract No. 630  
 Contract SDG H3544

**RESULTS**

LAB	RAW	SUF-			
SAMPLE ID	TEST FIX	PLANCHET	CLIENT SAMPLE ID	Tritium	
Preparation batch 6121-048					
R707068-01		7665-001	BLNWH4	1040	
R707068-02		7665-002	BLNWH5	1110	
R707068-03		7665-003	Lab Control Sample	ok	
R707068-04		7665-004	Method Blank	<u>690</u>	U
R707068-05		7665-005	Duplicate (R707068-02)	ok	
R707068-06		7665-006	Spike (R707068-02)	ok	X

Nominal values and limits from method RDLs (pCi/L) 400  
 216A2/216A21 CharactrzttnSamp&Ana-GW

**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	PAC	TION	%	%	min	keV	KeV	HELD PREPARED	YZED DETECTOR
Preparation batch 6121-048 2σ prep error 10.0 % Reference Lab Notebook #6121, pg. 26													
R707068-01		BLNWH4	170	0.0100			100	200	58	08/22/07	08/22	LSC-004	
R707068-02		BLNWH5	170	0.0100			100	200	58	08/22/07	08/22	LSC-004	
R707068-03		Lab Control Sample	<u>1800</u>	0.0100			10	200		08/22/07	08/22	LSC-004	
R707068-04		Method Blank	<u>1700</u>	0.0100			10	200		08/22/07	08/22	LSC-004	
R707068-05		Duplicate (R707068-02)	170	0.0100			100	200	58	08/22/07	08/22	LSC-004	
R707068-06		Spike (R707068-02)	180	0.0300			33	200	58	08/22/07	08/22	LSC-004	

Nominal values and limits from method 400 0.0100 25 180

PROCEDURES REFERENCE 906.0\_H3\_LSC  
 CP-210 Tritium in Water Samples by Distillation, rev 8

AVERAGES ± 2 SD MDA 700 ± 1600  
 FOR 6 SAMPLES YIELD 59 ± 92

Lab id EBRLNE  
 Protocol Hanford  
 Version Ver 1.0  
 Form DVD-IMS  
 Version 3.06  
 Report date 10/24/07

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EBERLINE SERVICES/RICHMOND

SAMPLE DELIVERY GROUP H3544

LAB METHOD SUMMARY

SELENIUM 79 IN WATER

LIQUID SCINTILLATION COUNTING

Test SE L Matrix WATER  
 SDG 7665  
 Contact Melissa C. Mannion

Client Hanford  
 Contract No. 630  
 Contract SDG H3544

RESULTS

LAB RAW SUP-  
 SAMPLE ID TEST FIX PLANCHET CLIENT SAMPLE ID Selenium 79

Preparation batch 6121-048

R707068-01	7665-001	BLNWH4	U
R707068-02	7665-002	BLNWH5	U
R707068-04	7665-004	Method Blank	U
R707068-05	7665-005	Duplicate (R707068-02)	- U

Nominal values and limits from method RDLs (pCi/L) 50  
 216A2/216A21 CharactrzttnSamp&Ana-GW

METHOD PERFORMANCE

LAB RAW SUP- 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 6121-048 20 prep error 10.0 % Reference Lab Notebook #6121, pg. 26

R707068-01	BLNWH4	0.26	0.500	<u>11</u>	50	58	08/21/07	08/22	LSC-004
R707068-02	BLNWH5	0.20	0.500	<u>14</u>	50	58	08/21/07	08/22	LSC-004
R707068-04	Method Blank	0.16	0.500	<u>17</u>	50		08/21/07	08/22	LSC-004
R707068-05	Duplicate (R707068-02)	0.17	0.500	<u>16</u>	50	58	08/21/07	08/22	LSC-004

Nominal values and limits from method 50 0.500 20-105 25 180

PROCEDURES REFERENCE SE79\_SEP\_DIS\_LSC  
 RP-340 Selenium-79 in Solids and Water, rev 0

AVERAGES ± 2 SD MDA 0.20 ± 0.090  
 FOR 4 SAMPLES YIELD 14 ± 5

Lab id EBRLNE  
 Protocol Hanford  
 Version Ver 1.0  
 Form DVD-LMS  
 Version 3.06  
 Report date 10/24/07

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SAMPLE DELIVERY GROUP H3544

SDG 7665  
Contact Melissa C. Mannion

REPORT GUIDE

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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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SDG 7665  
Contact Melissa C. Mannion

REPORT GUIDE

Client Hanford  
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Case no SDG\_H3544

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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SDG 7665  
Contact Melissa C. Mannion

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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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Version Ver 1.0  
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SDG 7665  
 Contact Melissa C. Mannion

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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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DATA SHEET

- \* 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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Version Ver 1.0  
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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.

Lab id EBRLNE  
 Protocol Hanford  
 Version Ver 1.0  
 Form DVD-RG  
 Version 3.06  
 Report date 10/24/07

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SDG 7665  
Contact Melissa C. Mannion

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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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DUPLICATE

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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Protocol Hanford  
Version Ver 1.0  
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SAMPLE DELIVERY GROUP H3544

SDG 7665  
 Contact Melissa C. Mannion

REPORT GUIDE

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 Case no SDG\_H3544

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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 Protocol Hanford  
 Version Ver 1.0  
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SDG 7665  
Contact Melissa C. Mannion

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MATRIX SPIKE

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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Lab id EBRLNE  
Protocol Hanford  
Version Ver 1.0  
Form DVD-RG  
Version 3.06  
Report date 10/24/07

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SAMPLE DELIVERY GROUP H3544

SDG 7665  
Contact Melissa C. Mannion

REPORT GUIDE

Client Hanford  
Contract No. 630  
Case no SDG\_H3544

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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Protocol Hanford  
Version Ver 1.0  
Form DVD-RG  
Version 3.06  
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SDG 7665  
 Contact Melissa C. Mannion

GUIDE, cont.

Client Hanford  
 Contract No. 630  
 Case no SDG H3544

METHOD SUMMARY

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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EBERLINE SERVICES / RICHMOND

SAMPLE DELIVERY GROUP H3544

SDG 7665  
 Contact Melissa C. Mannion

GUIDE, cont.

Client Hanford  
 Contract No. 630  
 Case no SDG\_H3544

METHOD SUMMARY

- \* 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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METHOD SUMMARY

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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SUMMARY DATA SECTION

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