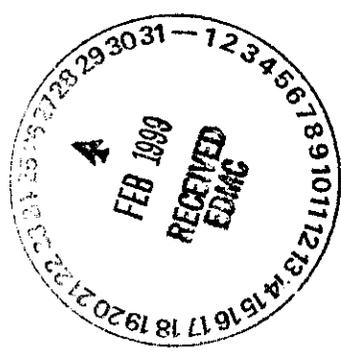


H0171-T/W

NU

0050306



November 12, 1998

Ms. Joan Kessner  
3350 George Washington Way  
Richland, WA 99352  
MSIN: H9-03

Reference: P.O. #TRB-SBB-207925  
Thermo Nutech N804047-7477 SDG H0145, N807068-7485 SDG H0171

Dear Ms. Kessner:

Enclosed are corrected data packages for the above referenced Sample Delivery Groups. In the original SDG H0145 the total uranium results were reported as  $\mu\text{g/L}$ , however the results were actually in units of pCi/L ie. the total uranium result reported for sample BONJN0 was 420  $\mu\text{g/L}$  however the result was actually 420 pCi/L. The corrected report contains total uranium results in  $\mu\text{g/L}$ . In the original SDG H0171 the total uranium results were reported correctly in units of pCi/g, however results were expected in  $\mu\text{g/L}$ . The corrected data package has total uranium reported in  $\mu\text{g/L}$ .

Please call if you have any questions concerning these corrections.

Sincerely,

Larry A. Johnson  
Contract Administrator

LAJ/jv

Enclosure: Corrected Data Packages

TMA/RICHMOND

SAMPLE DELIVERY GROUP H0171

SAMPLE SUMMARY

SDG 7485  
Contact N. Joseph Verville

Client Hanford  
Contract TRB-SBB-207926  
Case no SDG H0171

CLIENT SAMPLE ID	LOCATION	MATRIX	LEVEL	LAB		CHAIN OF CUSTODY	COLLECTED
				SAMPLE ID	SAF NO		
B0PBK9	Hanford Site	WATER		N807068-01	C98-047	C98-047-49	07/16/98 13:31
Method Blank		WATER		N807068-03	C98-047		
Lab Control Sample		WATER		N807068-02	C98-047		
Duplicate (N807068-01)	Hanford Site	WATER		N807068-04	C98-047		07/16/98 13:31

SAMPLE SUMMARY

Page 1

SUMMARY DATA SECTION

Page 3

Lab id TMANC  
Protocol Hanford  
Version Ver 1.2  
Form DVD-CS  
Version 3.06  
Report date 11/12/98

TMA/RICHMOND

SAMPLE DELIVERY GROUP H0171

QC SUMMARY

SDG 7485  
 Contact N. Joseph Verville

Client Hanford  
 Contract TRB-SBB-207925  
 Case no SDG H0171

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
7485	C98-047-49	B0PBK9	WATER				07/17/98	1	N807068-01	7485-001
		Method Blank	WATER						N807068-03	7485-003
		Lab Control Sample	WATER						N807068-02	7485-002
		Duplicate (N807068-01)	WATER				07/17/98	1	N807068-04	7485-004

QC SUMMARY

Page 1

SUMMARY DATA SECTION

Page 4

Lab id TMANC  
 Protocol Hanford  
 Version Ver 1.0  
 Form DVD-QS  
 Version 1.06  
 Report date 11/12/98

TMA/RICHMOND

SAMPLE DELIVERY GROUP H0171

SDG 7485  
Contact N. Joseph Verville

PREP BATCH SUMMARY

Client Hanford  
Contract TRB-SBB-207925  
Case no SDG H0171

TEST	MATRIX	METHOD	PREPARATION ERROR		PLANCHETS ANALYZED				QUALI-	
			BATCH	2σ %	CLIENT	MORE	RE BLANK	LCS		DUP/ORIG MS/ORIG
<b>Beta Counting</b>										
TC	WATER	Technetium 99 in Water	2785-102	10.0	1		1	1	1/1	
<b>Kinetic Phosphorimetry</b>										
U_T	WATER	Uranium, Total in Water	2785-102	9.0	1		1	1	1/1	X

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 TMANC  
Protocol Hanford  
Version Ver 1.0  
Form DVD-PBS  
Version 3.06  
Report date 11/12/98

**TMA/RICHMOND**

SAMPLE DELIVERY GROUP H0171

**WORK SUMMARY**

SDG 7485  
 Contact N. Joseph Verville

Client Hanford  
 Contract TRB-SBB-207925  
 Case no SDG H0171

CLIENT SAMPLE ID	LAB SAMPLE ID									
LOCATION	MATRIX	COLLECTED		TEST	SUF-					
CUSTODY	SAF No	RECEIVED	PLANCHET		FIX	ANALYZED	REVIEWED	BY	METHOD	
BOPBK9		N807068-01	7485-001	TC		08/16/98	08/25/98	NJV	Technetium 99 in Water	
Hanford Site	WATER	07/16/98	7485-001	U_T		08/12/98	08/25/98	NJV	Uranium, Total in Water	
C98-047-49	C98-047	07/17/98								
Method Blank		N807068-03	7485-003	TC		08/16/98	08/25/98	NJV	Technetium 99 in Water	
	WATER		7485-003	U_T		08/12/98	08/25/98	NJV	Uranium, Total in Water	
	C98-047									
Lab Control Sample		N807068-02	7485-002	TC		08/20/98	08/25/98	NJV	Technetium 99 in Water	
	WATER		7485-002	U_T		08/12/98	08/25/98	NJV	Uranium, Total in Water	
	C98-047									
Duplicate (N807068-01)		N807068-04	7485-004	TC		08/16/98	08/25/98	NJV	Technetium 99 in Water	
Hanford Site	WATER	07/16/98	7485-004	U_T		08/12/98	08/25/98	NJV	Uranium, Total in Water	
	C98-047	07/17/98								

COUNTS OF TESTS BY SAMPLE TYPE											
TEST	SAF No	METHOD	REFERENCE	CLIENT	MORE	RE	BLANK	LCS	DUP	SPIKE	TOTAL
TC	C98-047	Technetium 99 in Water	TC99TRLSC	1			1	1	1		4
U_T	C98-047	Uranium, Total in Water	UKPA	1			1	1	1		4
<b>TOTALS</b>				<b>2</b>			<b>2</b>	<b>2</b>	<b>2</b>		<b>8</b>

Lab id TMANC  
 Protocol Hanford  
 Version Ver 2.0  
 Form DVD-CWS  
 Version 3.06  
 Report date 11/12/98

TMA / RICHMOND  
SAMPLE DELIVERY GROUP H0171

N807068-03

Method Blank

METHOD BLANK

SDG <u>7485</u>	Client/Case no <u>Hanford</u>	<u>SDG H0171</u>
Contact <u>N. Joseph Verville</u>	Case no <u>TRB-SBB-207925</u>	
Lab sample id <u>N807068-03</u>	Client sample id <u>Method Blank</u>	
Dept sample id <u>7485-003</u>	Material/Matrix <u>WATER</u>	
	SAF No <u>C98-047</u>	

ANALYTE	CAS NO	RESULT pCi/L	2 $\sigma$ ERR (COUNT)	MDA pCi/L	RDL pCi/L	QUALI- FIERS	TEST
Technetium 99	14133-76-7	3.8	6.0	<u>16</u>	15	U	TC
Total Uranium (ug/L)	7440-61-1	0	0.007	0.017	0.10	UX	U_T

QC-BLANK 28723

METHOD BLANKS

Page 1

SUMMARY DATA SECTION

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Lab id <u>TMANC</u>
Protocol <u>Hanford</u>
Version <u>Ver 1.0</u>
Form <u>DVD-DS</u>
Version <u>3.06</u>
Report date <u>11/12/98</u>

TMA/RICHMOND

SAMPLE DELIVERY GROUP H0171

N807068-02

Lab Control Sample

LAB CONTROL SAMPLE

SDG <u>7485</u>	Client/Case no <u>Hanford</u>	SDG <u>H0171</u>
Contact <u>N. Joseph Verville</u>	Case no <u>TRB-SBB-207925</u>	
Lab sample id <u>N807068-02</u>	Client sample id <u>Lab Control Sample</u>	
Dept sample id <u>7485-002</u>	Material/Matrix <u>WATER</u>	
	SAP No <u>C98-047</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
Technetium 99	250	14	15	15		TC	262	10	95	82-118	80-120
Total Uranium (ug/L)	78	10	<u>0.17</u>	0.10	X	U_T	74.2	3.0	105	75-125	80-120

QC-LCS 28722

Lab id <u>TMANC</u>
Protocol <u>Hanford</u>
Version <u>Ver 1.0</u>
Form <u>DVD-LCS</u>
Version <u>3.06</u>
Report date <u>11/12/98</u>

TMA/RICHMOND

SAMPLE DELIVERY GROUP H0171

N807068-04

B0PBK9

DUPLICATE

SDG <u>7485</u>	Client/Case no <u>Hanford</u>	<u>SDG H0171</u>
Contact <u>N. Joseph Verville</u>	Case no <u>TRB-SBB-207925</u>	
<b>DUPLICATE</b>	<b>ORIGINAL</b>	
Lab sample id <u>N807068-04</u>	Lab sample id <u>N807068-01</u>	Client sample id <u>B0PBK9</u>
Dept sample id <u>7485-004</u>	Dept sample id <u>7485-001</u>	Location/Matrix <u>Hanford Site</u> <u>WATER</u>
	Received <u>07/17/98</u>	Collected <u>07/16/98 13:31</u>
		Custody/SAF No <u>C98-047-49</u> <u>C98-047</u>

ANALYTE	DUPLICATE pCi/L	2σ ERR (COUNT)	MDA pCi/L	RDL pCi/L	QUALI- FIERS	TEST	ORIGINAL pCi/L	2σ ERR (COUNT)	MDA pCi/L	QUALI- FIERS	RPD %	3σ TOT	PROT LIMIT
Technetium 99	5000	150	<u>55</u>	15		TC	5000	160	<u>33</u>		0	22	
Total Uranium (ug/L)	320	43	<u>1.7</u>	0.10	X	U_T	380	51	<u>1.7</u>	X	17	14	

QC-DUP#1 28724

Lab id TMANC  
 Protocol Hanford  
 Version Ver 1.0  
 Form DVD-DUP  
 Version 3.06  
 Report date 11/12 98

**TMA / RICHMOND**  
**SAMPLE DELIVERY GROUP H0171**

N807068-01

B0PBK9

**DATA SHEET**

SDG <u>7485</u>	Client/Case no <u>Hanford</u>	SDG <u>H0171</u>
Contact <u>N. Joseph Verville</u>	Case no <u>TRB-SBB-207925</u>	
Lab sample id <u>N807068-01</u>	Client sample id <u>B0PBK9</u>	
Dept sample id <u>7485-001</u>	Location/Matrix <u>Hanford Site</u>	<u>WATER</u>
Received <u>07/17/98</u>	Collected <u>07/16/98 13:31</u>	
	Custody/SAF No <u>C98-047-49</u>	<u>C98-047</u>

ANALYTE	CAS NO	RESULT pCi/L	2 $\sigma$ ERR (COUNT)	MDA pCi/L	RDL pCi/L	QUALI- FIERS	TEST
Technetium 99	14133-76-7	5000	160	<u>33</u>	15		TC
Total Uranium (ug/L)	7440-61-1	380	51	<u>1.7</u>	0.10	X	U_T

Lab id <u>TMANC</u>
Protocol <u>Hanford</u>
Version <u>Ver 1.0</u>
Form <u>DVD-DS</u>
Version <u>3.06</u>
Report date <u>11/12/98</u>

TMA/RICHMOND

SAMPLE DELIVERY GROUP H0171

Test TC Matrix WATER
SDG 7485
Contact N. Joseph Verville

METHOD SUMMARY

TECHNETIUM 99 IN WATER
BETA COUNTING

Client Hanford
Contract TRB-SBB-207925
Case no SDG H0171

RESULTS

CLIENT SAMPLE ID LAB RAW SUP- Technetium
SAMPLE ID TEST FIX PLANCHET 99

Preparation batch 2785-102

Table with 4 columns: Sample ID, Lab ID, Test Fix, and Technetium. Rows include B0PBK9, BLK (QC ID=28723), LCS (QC ID=28722), and Duplicate (N807068-01).

Nominal values and limits from method RDLs (pCi/L) 15

METHOD PERFORMANCE

CLIENT SAMPLE ID LAB RAW SUP- MDA ALIQ PREP DILU- YIELD EFF COUNT FWHM DRIFT DAYS ANAL-
SAMPLE ID TEST FIX pCi/L L PAC TION % % min keV KeV HELD PREPARED YZED DETECTOR

Preparation batch 2785-102 2 sigma prep error 10.0 % Reference Lab Notebook #2785 pg. 102

Table with 12 columns: Sample ID, Lab ID, Test Fix, MDA, Aliq, Prep, Dilution, Yield, Efficiency, Count, FWHM, Drift Days, and Analysis. Rows include B0PBK9, BLK (QC ID=28723), LCS (QC ID=28722), and Duplicate (N807068-01).

Nominal values and limits from method 15 0.200 20-105 50 180

PROCEDURES REFERENCE TC99TRLSC
EP-020 Sample Leach For Technetium-99, rev 0
EP-540 Technetium-99 Purification, rev 0

AVERAGES +/- 2 SD MDA 30 = 38
FOR 4 SAMPLES YIELD 14 = 12

METHOD SUMMARIES

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SUMMARY DATA SECTION

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Lab id TMANC
Protocol Hanford
Version Ver 1.0
Form DVD-CMS
Version 3.06
Report date 11/12/98

**TMA/RICHMOND**

SAMPLE DELIVERY GROUP H0171

**METHOD SUMMARY**

URANIUM, TOTAL IN WATER  
KINETIC PHOSPHORIMETRY

Test U T Matrix WATER  
SDG 7485  
Contact N. Joseph Verville

Client Hanford  
Contract TRB-SBB-207925  
Case no SDG H0171

**RESULTS**

CLIENT SAMPLE ID	LAB SAMPLE ID	RAW SUP- TEST FIX	PLANCHET	Total Uranium
Preparation batch 2785-102				
B0PBK9	N807068-01		7485-001	380 X
BLK (QC ID=28723)	N807068-03		7485-003	U X
LCS (QC ID=28722)	N807068-02		7485-002	ok X
Duplicate (N807068-01)	N807068-04		7485-004	ok X
Nominal values and limits from method		RDLs (ug/L)	0.10	

**METHOD PERFORMANCE**

CLIENT SAMPLE ID	LAB SAMPLE ID	RAW SUP- TEST FIX	MDA ug/L	ALIQ L	PREP FAC	DILU- TION	YIELD %	EFF %	COUNT min	FWHM keV	DRIFT KeV	DAYS HELD	ANAL- YZED	DETECTOR
Preparation batch 2785-102 2σ prep error 9.0 % Reference Lab Notebook #2785 pg. 102														
B0PBK9	N807068-01		<u>1.7</u>	0.0200								27	08/12/98	08/12 KPA-001
BLK (QC ID=28723)	N807068-03		0.017	0.0200									08/12/98	08/12 KPA-001
LCS (QC ID=28722)	N807068-02		<u>0.17</u>	0.0200									08/12/98	08/12 KPA-001
Duplicate (N807068-01) (QC ID=28724)	N807068-04		<u>1.7</u>	0.0200								27	08/12/98	08/12 KPA-001
Nominal values and limits from method			0.10	0.0200	180									

PROCEDURES	REFERENCE	UKPA
EP-040		Environmental Water Dissolution, rev 1
EP-044		Preparation of Total Uranium by Kinetic Phosphorimetry, rev 1
EP-928		Total Uranium by Kinetic Phosphorimetry, rev 0

AVERAGES ± 2 SD	MDA	<u>0.90</u>	±	<u>1.9</u>
FOR 4 SAMPLES	YIELD	_____	±	_____

**TMA / RICHMOND**  
**SAMPLE DELIVERY GROUP H0171**

SDG 7485  
Contact N. Joseph Verville

**REPORT GUIDE**

Client Hanford  
Contract TRB-SBB-207925  
Case no SDG H0171

**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.

**REPORT GUIDES**

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**SUMMARY DATA SECTION**

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Lab id TMANC  
Protocol Hanford  
Version Ver 1.0  
Form DVD-RG  
Version 3.06  
Report date 11/12/98

TMA / RICHMOND  
SAMPLE DELIVERY GROUP H0171

SDG 7485  
Contact N. Joseph Verville

REPORT GUIDE

Client Hanford  
Contract TRB-SBB-207925  
Case no SDG H0171

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.

Lab id TMANC  
Protocol Hanford  
Version Ver 1.0  
Form DVD-RG  
Version 3.06  
Report date 11/12/98

TMA / RICHMOND  
SAMPLE DELIVERY GROUP H0171

SDG 7485  
Contact N. Joseph Verville

REPORT GUIDE

Client Hanford  
Contract TRB-SBB-207925  
Case no SDG H0171

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.

REPORT GUIDES

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SUMMARY DATA SECTION

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Lab id TMANC  
Protocol Hanford  
Version Ver 1.0  
Form DVD-RG  
Version 3.06  
Report date 11/12/98

TMA/RICHMOND  
SAMPLE DELIVERY GROUP H0171

SDG 7485  
Contact N. Joseph Verville

REPORT GUIDE

Client Hanford  
Contract TRB-SBB-207925  
Case no SDG H0171

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).

REPORT GUIDES

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SUMMARY DATA SECTION

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Lab id TMANC  
Protocol Hanford  
Version Ver 1.0  
Form DVD-RG  
Version 3.06  
Report date 11/12/98

TMA/RICHMOND  
SAMPLE DELIVERY GROUP H0171

SDG 7485  
Contact N. Joseph Verville

GUIDE, cont.

Client Hanford  
Contract TRB-SBE-207925  
Case no SDG H0171

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.

REPORT GUIDES

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SUMMARY DATA SECTION

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Lab id TMANC  
Protocol Hanford  
Version Ver 1.0  
Form DVD-RG  
Version 3.06  
Report date 11/12/98

TMA / RICHMOND  
SAMPLE DELIVERY GROUP H0171

SDG 7485  
Contact N. Joseph Verville

GUIDE, cont.

Client Hanford  
Contract TRB-SBB-207925  
Case no SDG H0171

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.

REPORT GUIDES

Page 6

SUMMARY DATA SECTION

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Lab id TMANC  
Protocol Hanford  
Version Ver 1.0  
Form DVD-RG  
Version 3.06  
Report date 11/12/98

TMA / RICHMOND  
SAMPLE DELIVERY GROUP H0171

SDG 7485  
Contact N. Joseph Verville

REPORT GUIDE

Client Hanford  
Contract TRB-SBB-207925  
Case no SDG H0171

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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Form DVD-RG  
Version 3.06  
Report date 11/12/98

TMA / RICHMOND  
SAMPLE DELIVERY GROUP H0171

SDG 7485  
Contact N. Joseph Verville

REPORT GUIDE

Client Hanford  
Contract TRB-SBB-207925  
Case no SDG H0171

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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**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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**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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