

NEW JERSEY LAB ID#:20012 : NEW YORK LAB ID#: 11376

GC/MS SEMI-VOLATILE ANALYSIS CONFORMANCE/NON-CONFORMANCE SUMMARY

CHEMTECH PROJE	CT NUMBER:	bn112524			
SequenceID :	bn112524		NA	NO	YES
1. Chromatograms La	beled/Compounds Ide	entified. (Field samples and Method Blanks)			✓
2. GC/MS Tuning Sp (NOTE THAT THER		Meet Criteria Criteria CRITERIA FOR NY ASP CLP, CLP AND NJ)			_✓
3. GC/MS Tuning Fre series	equency - Performed e	every 24 hours for 600 series and 12 hours for 8000			_✓
analysis and contin		performed within 30 days before sample rmed within 24 hours of sample analysis es			√
5. GC/MS Calibration	n Met:				✓
a. Initial calibration If not met, list those c		ecoveries which fall outside the acceptable range.		✓	
The % RSD is gre Linear Regression		nitial Calibration (8270Sim-BN112524.M) for 4,6-D	Dinitro-2-methylphenol, is pas	sing on	
	bration(CCC) Meet C compounds and their r	riteria ecoveries which fall outside the acceptable range.		<u>✓</u>	
•	· · · · ·	N035293.D) are biased low but not present in param les are found with hit of this compound they will be		•	
6. Blank Contamination	on - If yes, list compo	unds and concentrations in each blank:		✓	
a. B/N Fraction					

d. Acid Fraction

7. Surrogate Recover If not met, list those	ries Meet Criteria compounds and their recoveries which fall outside the acceptable ranges.			✓
a. B/N Fraction				
d. Acid Fraction				
•	rix Spike Duplicate Recoveries Meet Criteria compounds and their recoveries which fall outside the acceptable range.		<u> </u>	
a. B/N Fraction	Recovery of 1.4-Dioxane is marginally biased low and also Recovery and RPD a very few compound P4934-06MS and P4934-07MSD due to matrix interference. No corrective action is required.	d are out of QC	<u>limits in</u>	
d. Acid Fraction				
9. Internal Standard Comments:	Area/Retention Time Shift Meet Criteria		—	<u> </u>
10. Extraction Holdi If not met, list numb	ng Time Met er of days exceeded for each sample:			√
11. Analysis Holding If not met, list numb	g Time Met er of days exceeded for each sample:		<u> </u>	

ADDITIONAL COMMENTS:

Recovery of a very few compound are marginally biased high in PB165198BS/BSD but are not present in parameter list of the associated samples. The data will be used for hardcopies.



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