

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

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

CHEMTECH PROJE	CT NUMBER:	bm082024			
SequenceID :	bm082024		NA	NO	YES
1. Chromatograms La	beled/Compounds Ide	ntified. (Field samples and Method Blanks)			✓
2. GC/MS Tuning Specifications. DFTPP Meet Criteria Criteria (NOTE THAT THERE ARE DIFFERENT CRITERIA FOR NY ASP CLP, CLP AND NJ)					<b>_</b>
3. GC/MS Tuning Fre series	equency - Performed e	very 24 hours for 600 series and 12 hours for 8000			<u> </u>
analysis and contin	•	erformed within 30 days before sample med within 24 hours of sample analysis s			✓
5. GC/MS Calibration	n Met:				✓
a. Initial calibration If not met, list those c		coveries which fall outside the acceptable range.			<b>√</b>
b. Continuous Calibration(CCC) Meet Criteria If not met, list those compounds and their recoveries which fall outside the acceptable range.				<u>✓</u>	
Compound #77 is compound #79 is t	e	DCCC(BM047263.D) but not present in parameter l	list of the associated samples	s. And	
6. Blank Contamination		<u>✓</u>			
a. B/N Fraction					

d. Acid Fraction

7. Surrogate Recoveries Meet Criteria If not met, list those compounds and their recoveries which fall outside the acceptable ranges.		<u>√</u>	
a. B/N Fraction			
d. Acid Fraction			
8. Matrix Spike/Matrix Spike Duplicate Recoveries Meet Criteria If not met, list those compounds and their recoveries which fall outside the acceptable range.		<u> </u>	
a. B/N Fraction The Recovery and RPD failed for some compound in P3643-02MS, P3643-03MSD, P3637-02MS/MS interference.	D, P3652-011	MSD due to matri	<u>x</u>
d. Acid Fraction			
9. Internal Standard Area/Retention Time Shift Meet Criteria Comments:			<u> </u>
10. Extraction Holding Time Met If not met, list number of days exceeded for each sample:			<u>✓</u>
11. Analysis Holding Time Met If not met, list number of days exceeded for each sample:		<u>√</u>	

### ADDITIONAL COMMENTS:

Recovery of some compound fail in PB162861BS which are not present in parameter list of the associated samples. Terphenyl-d14 is slightly biased high and recovery of a very few compounds are marginally biased in the PB162798BS. The data will be used for hardcopies.

Tailing of Benzidine is biased high (0.44) in the DFTPP (BM047262.D) this tune is used to load the sequence with the consent of the lab manager.



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