

**S1a:** Phylogenetic neighbour joining tree obtained by BLAST with 16S rRNA gene sequence

# Basic Local Alignment Search Tool

Job Title: (4) - Nucleotide Sequence (1416 letters)

## Tax BLAST Report

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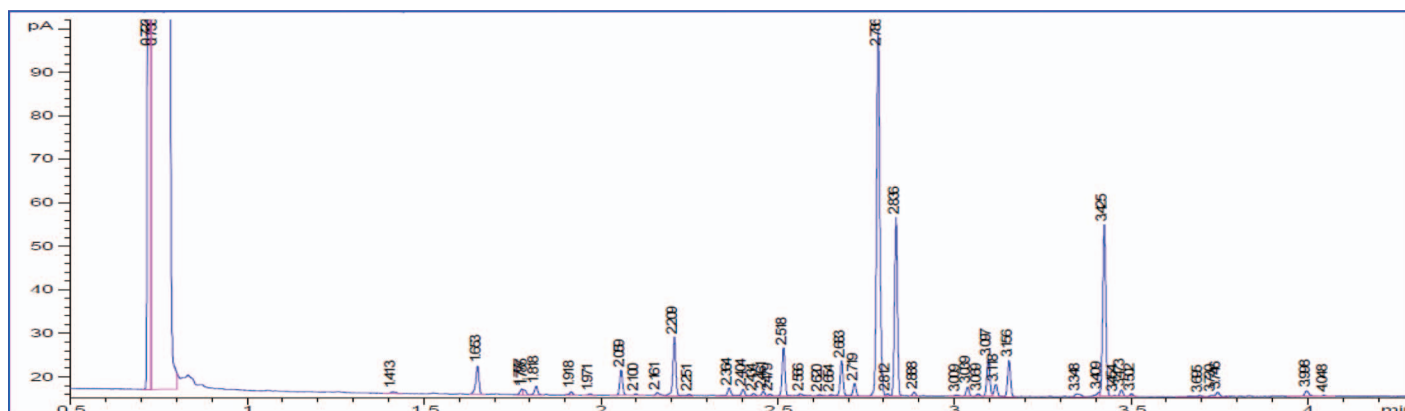
### Lineage Report

Vibrio	[g-proteobacteria]				
. Vibrio harveyi group	[g-proteobacteria]				
. . Vibrio alginolyticus 40B	-----	2464	2 hits	[g-proteobacteria]	<a href="#">Vibrio alginolyticus 40B</a>
. . Vibrio parahaemolyticus Peru-466	.....	2453	3 hits	[g-proteobacteria]	<a href="#">Vibrio parahaemolyticus</a>
. . Vibrio parahaemolyticus AN-5034	.....	2453	5 hits	[g-proteobacteria]	<a href="#">Vibrio parahaemolyticus</a>
. . Vibrio parahaemolyticus RIMD 2210633	.....	2453	22 hits	[g-proteobacteria]	<a href="#">Vibrio parahaemolyticus</a>
. . Vibrio parahaemolyticus K5030	.....	2447	2 hits	[g-proteobacteria]	<a href="#">Vibrio parahaemolyticus</a>
. . Vibrio parahaemolyticus AQ4037	.....	2447	6 hits	[g-proteobacteria]	<a href="#">Vibrio parahaemolyticus</a>
. . Vibrio parahaemolyticus AQ3810	.....	2447	3 hits	[g-proteobacteria]	<a href="#">Vibrio parahaemolyticus</a>
. . Vibrio harveyi HY01	.....	2436	8 hits	[g-proteobacteria]	<a href="#">Vibrio harveyi HY01 1104</a>
. . Vibrio harveyi ATCC BAA-1116	.....	2431	22 hits	[g-proteobacteria]	<a href="#">Vibrio harveyi ATCC BAA-</a>
. . Vibrio harveyi 1DA3	.....	2409	2 hits	[g-proteobacteria]	<a href="#">Vibrio harveyi 1DA3 Cont.</a>
. Vibrio sp. Ex25	-----	2453	26 hits	[g-proteobacteria]	<a href="#">Vibrio sp. Ex25 scf 1101</a>
. Vibrio coralliilyticus ATCC BAA-450	....	2309	2 hits	[g-proteobacteria]	<a href="#">Vibrio coralliilyticus A</a>
. Vibrio vulnificus CMCP6	.....	2300	18 hits	[g-proteobacteria]	<a href="#">Vibrio vulnificus CMCP6</a>
. Vibrio vulnificus YJ016	.....	2294	18 hits	[g-proteobacteria]	<a href="#">Vibrio vulnificus YJ016</a>
. Vibrio orientalis CIP 102891	.....	2276	8 hits	[g-proteobacteria]	<a href="#">Vibrio orientalis CIP 10</a>
. Vibrio furnissii CIP 102972	.....	2259	3 hits	[g-proteobacteria]	<a href="#">Vibrio furnissii CIP 102</a>

### Taxonomy Report

Vibrio	150 hits	16 orgs	[root; cellular organisms; E
. Vibrio harveyi group	75 hits	10 orgs	
. . Vibrio alginolyticus 40B	2 hits	1 orgs	[Vibrio alginolyticus]
. . Vibrio parahaemolyticus	41 hits	6 orgs	
. . . Vibrio parahaemolyticus Peru-466	3 hits	1 orgs	
. . . Vibrio parahaemolyticus AN-5034	5 hits	1 orgs	
. . . Vibrio parahaemolyticus RIMD 2210633	22 hits	1 orgs	
. . . Vibrio parahaemolyticus K5030	2 hits	1 orgs	
. . . Vibrio parahaemolyticus AQ4037	6 hits	1 orgs	
. . . Vibrio parahaemolyticus AQ3810	3 hits	1 orgs	
. . Vibrio harveyi	32 hits	3 orgs	
. . . Vibrio harveyi HY01	8 hits	1 orgs	
. . . Vibrio harveyi ATCC BAA-1116	22 hits	1 orgs	
. . . Vibrio harveyi 1DA3	2 hits	1 orgs	
. Vibrio sp. Ex25	26 hits	1 orgs	
. Vibrio coralliilyticus ATCC BAA-450	2 hits	1 orgs	[Vibrio coralliilyticus]
. Vibrio vulnificus	36 hits	2 orgs	
. . Vibrio vulnificus CMCP6	18 hits	1 orgs	
. . Vibrio vulnificus YJ016	18 hits	1 orgs	
. Vibrio orientalis CIP 102891	8 hits	1 orgs	[Vibrio orientalis]
. Vibrio furnissii CIP 102972	3 hits	1 orgs	[Vibrio furnissii]

**S1b: BLAST report of 16S rRNA gene sequence**

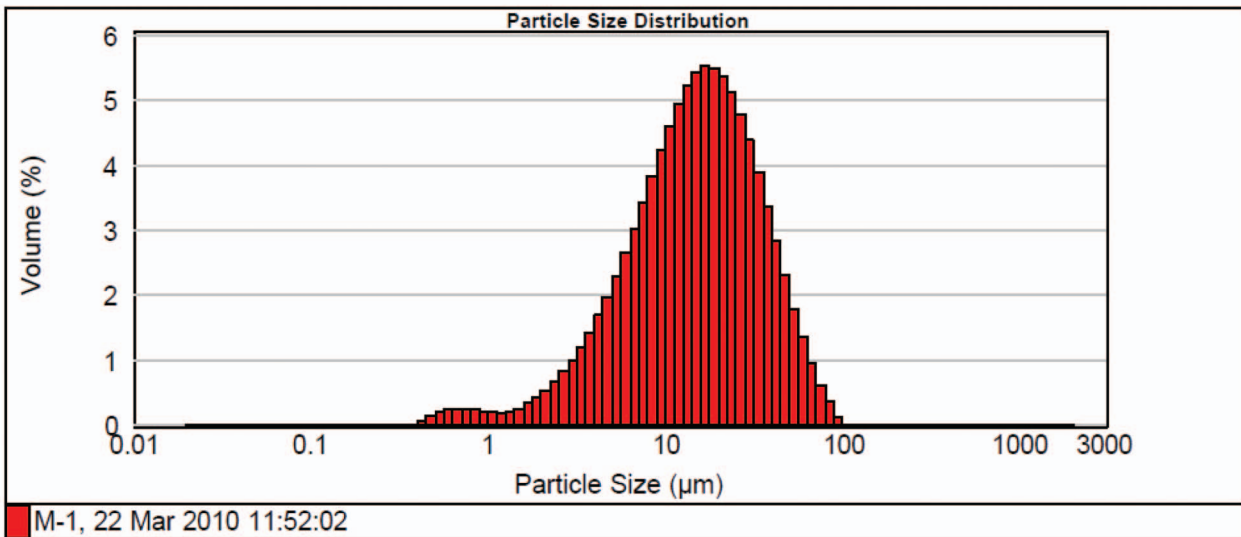


RT	Response	Ar/Hr	RFact	ECL	Peak Name	Percent	Comment1	Comment2
0.7228	616651	0.007	----	6.5656		----	< min rt	
0.7384	2.97E+8	0.027	----	6.6701	SOLVENT PEAK	----	< min rt	
1.4125	816	0.012	1.146	10.9457	Sum In Feature 2	0.34	ECL deviates -0.007	unknown 10.9525
1.6528	8465	0.010	1.062	11.9988	12:0	3.23	ECL deviates -0.001	Reference 0.001
1.7772	1483	0.008	1.032	12.4690	11:0 3OH	0.55	ECL deviates 0.004	
1.7851	1210	0.008	----	12.4989	unknown 12.502	----	ECL deviates -0.003	
1.8182	2376	0.009	1.023	12.6240	13:0 iso	0.87	ECL deviates 0.001	Reference 0.003
1.9177	1051	0.009	1.003	13.0001	13:0	0.38	ECL deviates 0.000	Reference 0.002
1.9709	542	0.010	----	13.1825		----		
2.0591	6841	0.009	0.981	13.4851	12:0 3OH	2.41	ECL deviates 0.002	
2.1005	572	0.009	0.975	13.6271	14:0 iso	0.20	ECL deviates -0.001	Reference 0.000
2.1611	1139	0.011	----	13.8353		----		
2.2095	15477	0.009	0.962	14.0010	14:0	5.35	ECL deviates 0.001	Reference 0.001
2.2511	453	0.008	0.957	14.1358	13:0 iso 3OH	0.16	ECL deviates 0.004	
2.3644	2456	0.010	0.946	14.5033	Sum In Feature 1	0.84	ECL deviates 0.000	13:0 3OH/15:1 iso H
2.4037	1936	0.009	0.943	14.6306	15:0 iso	0.66	ECL deviates -0.001	Reference -0.002
2.4338	714	0.009	0.940	14.7280	15:0 anteiso	0.24	ECL deviates 0.003	Reference 0.002
2.4611	1264	0.009	0.938	14.8167	15:1 w8c	0.43	ECL deviates 0.003	
2.4792	591	0.009	0.937	14.8754	15:1 w6c	0.20	ECL deviates 0.000	
2.5181	12731	0.009	----	15.0014	15:0	----	ECL deviates 0.001	
2.5661	1118	0.013	0.931	15.1520	14:0 iso 3OH	0.37	ECL deviates 0.005	
2.6202	690	0.012	----	15.3218		----		
2.6536	551	0.010	0.926	15.4269	16:1 w7c alcohol	0.18	ECL deviates 0.013	
2.6826	9704	0.009	0.924	15.5180	Sum In Feature 2	3.22	ECL deviates 0.003	14:0 3OH/16:1 iso I
2.7194	3591	0.009	0.922	15.6334	16:0 iso	1.19	ECL deviates 0.000	Reference -0.003
2.7855	108651	0.010	0.919	15.8410	Sum In Feature 3	35.89	ECL deviates 0.001	16:1 w7c/16:1 w6c
2.8122	717	0.009	0.918	15.9249	16:1 w5c	0.24	ECL deviates -0.003	
2.8362	46087	0.009	0.917	16.0001	16:0	15.19	ECL deviates 0.000	Reference -0.004
2.8877	1251	0.009	0.915	16.1615	15:0 iso 3OH	0.41	ECL deviates 0.000	
3.0085	865	0.017	----	16.5402		----		
3.0390	2602	0.009	0.910	16.6359	17:0 iso	0.85	ECL deviates -0.001	Reference -0.007
3.0686	802	0.009	0.909	16.7285	17:0 anteiso	0.26	ECL deviates -0.004	Reference -0.011
3.0971	10552	0.009	0.909	16.8180	17:1 w8c	3.45	ECL deviates 0.003	
3.1180	3715	0.010	0.908	16.8835	17:1 w6c	1.21	ECL deviates 0.003	
3.1557	9771	0.009	0.907	17.0018	17:0	3.19	ECL deviates 0.002	Reference -0.005
3.3477	1393	0.013	0.904	17.6059	18:3 w6c (6,9,12)	0.45	ECL deviates 0.006	
3.4088	1260	0.009	0.903	17.7983	18:1 w9c	0.41	ECL deviates 0.004	
3.4250	49201	0.010	0.903	17.8494	Sum In Feature 8	15.96	ECL deviates 0.002	18:1 w7c
3.4538	342	0.007	0.902	17.9399	18:1 w5c	0.11	ECL deviates 0.003	
3.4734	1902	0.009	0.902	18.0016	18:0	0.62	ECL deviates 0.002	Reference -0.009
3.5023	817	0.008	----	18.0944		----		
3.6952	859	0.016	----	18.7151		----		
3.7302	572	0.011	0.898	18.8274	Sum In Feature 7	0.18	ECL deviates -0.010	19:1w7c/19:1 w6c
3.7459	1580	0.011	0.898	18.8780	Sum In Feature 7	0.51	ECL deviates -0.009	19:0 cyclo w10c/19w6
3.9981	2779	0.013	----	19.6986		----		
4.0476	747	0.016	0.892	19.8607	20:1 w7c	0.24	ECL deviates 0.011	
----	2456	----	----	----	Summed Feature 1	0.84	15:1 iso H/13:0 3OH	13:0 3OH/15:1 iso H
----	10519	----	----	----	Summed Feature 2	3.56	12:0 aldehyde ?	unknown 10.9525
----	----	----	----	----	----	----	16:1 iso I/14:0 3OH	14:0 3OH/16:1 iso I
----	108651	----	----	----	Summed Feature 3	35.89	16:1 w7c/16:1 w6c	16:1 w6c/16:1 w7c
----	2153	----	----	----	Summed Feature 7	0.69	19:1w7c/19:1 w6c	19:1 w6c/w7c/19cy
----	----	----	----	----	----	----	19:0 cyclo w10c/19w6	
----	49201	----	----	----	Summed Feature 8	15.96	18:1 w7c	18:1 w6c

## S2: Fatty Acid profile done by GC coupled with MIDI

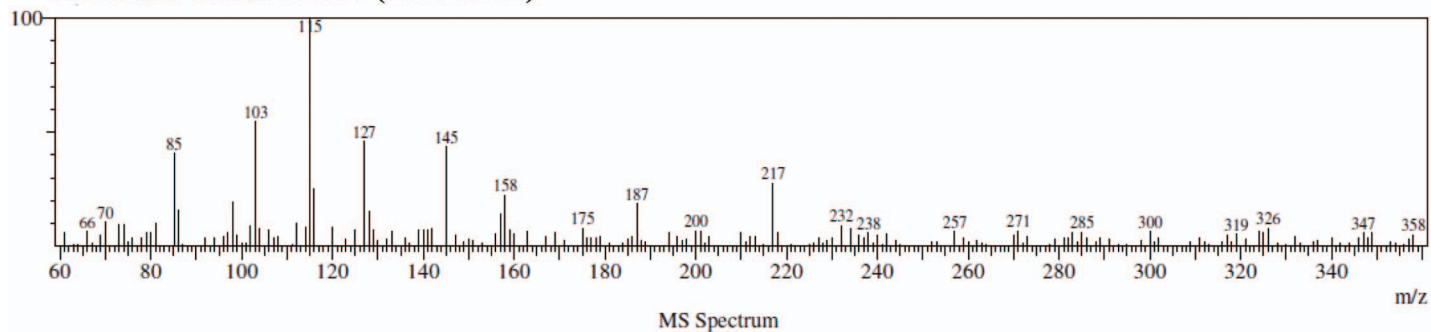
**Particle Name:** Polysaccharide      **Accessory Name:** Hydro 2000S (A)      **Obscuration:** 4.33 %  
**Particle RI:** 1.530    **Absorption:** 0.1    **Analysis model:** General purpose  
**Dispersant Name:** Water      **Size range:** 0.020 to 2000.000 um    **Weighted Residual:** 1.663 %  
**Dispersant RI:** 1.330

**Concentration:** 0.0052 %Vol    **Vol. Weighted Mean D[4,3]:** 19.402 um      **Specific Surface Area:** 0.728143 m<sup>2</sup>/g  
**Span (10% - 90%):** 2.347      **Uniformity:** 0.729458      **Surface Weighted Mean D[3,2]:** 8.240 um  
**Result units:** Volume      **Percentage below 10.00 µm :** 31.57%      **Percentage below 4.50 µm :** 10.37%  
d(0.1): 4.394 um      d(0.5): 15.278 um      d(0.9): 40.248 um

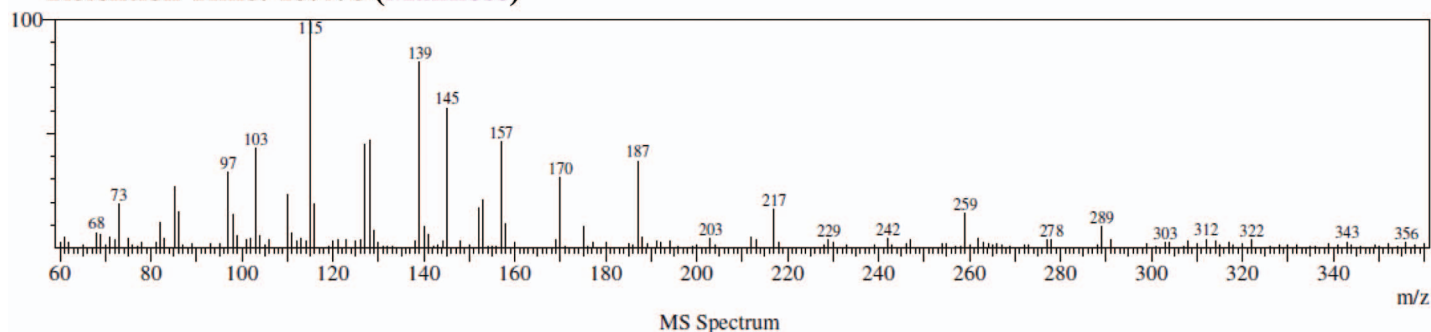


### S3: Particle Size Analysis

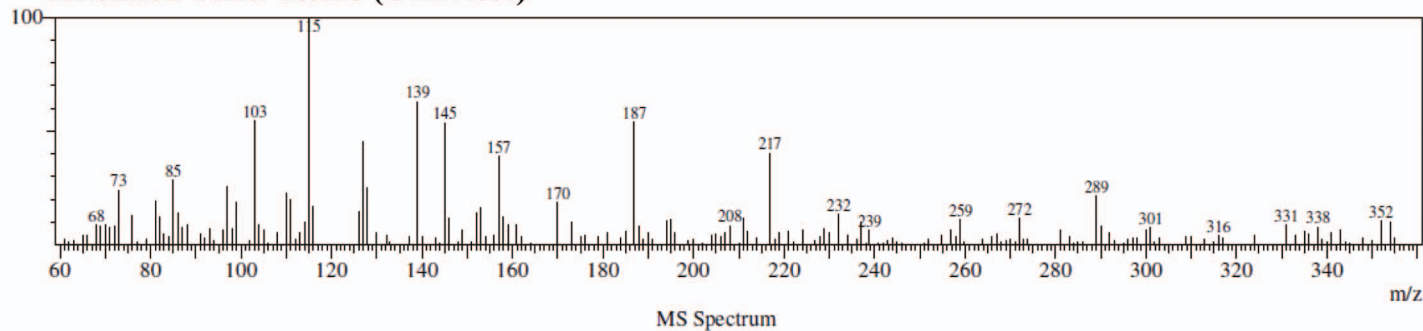
**Retention Time: 11.137 (Arabinose)**



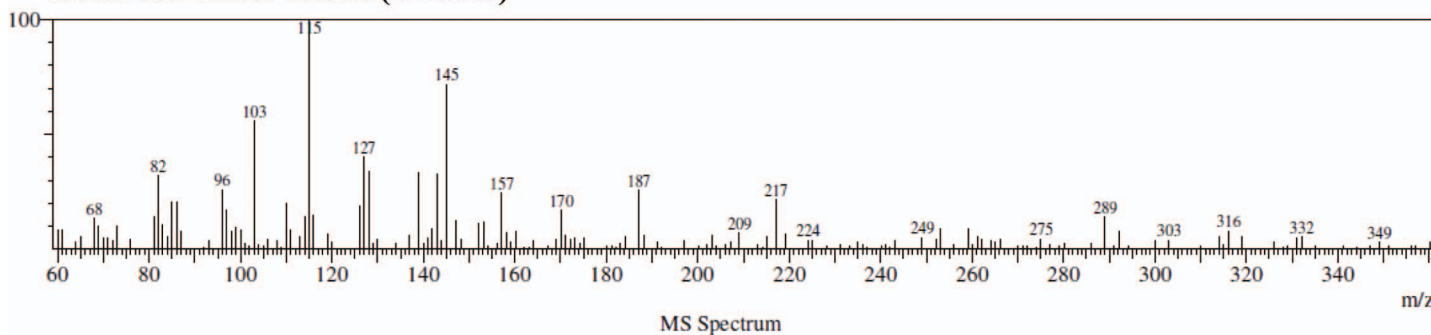
**Retention Time: 15.476 (Mannose)**



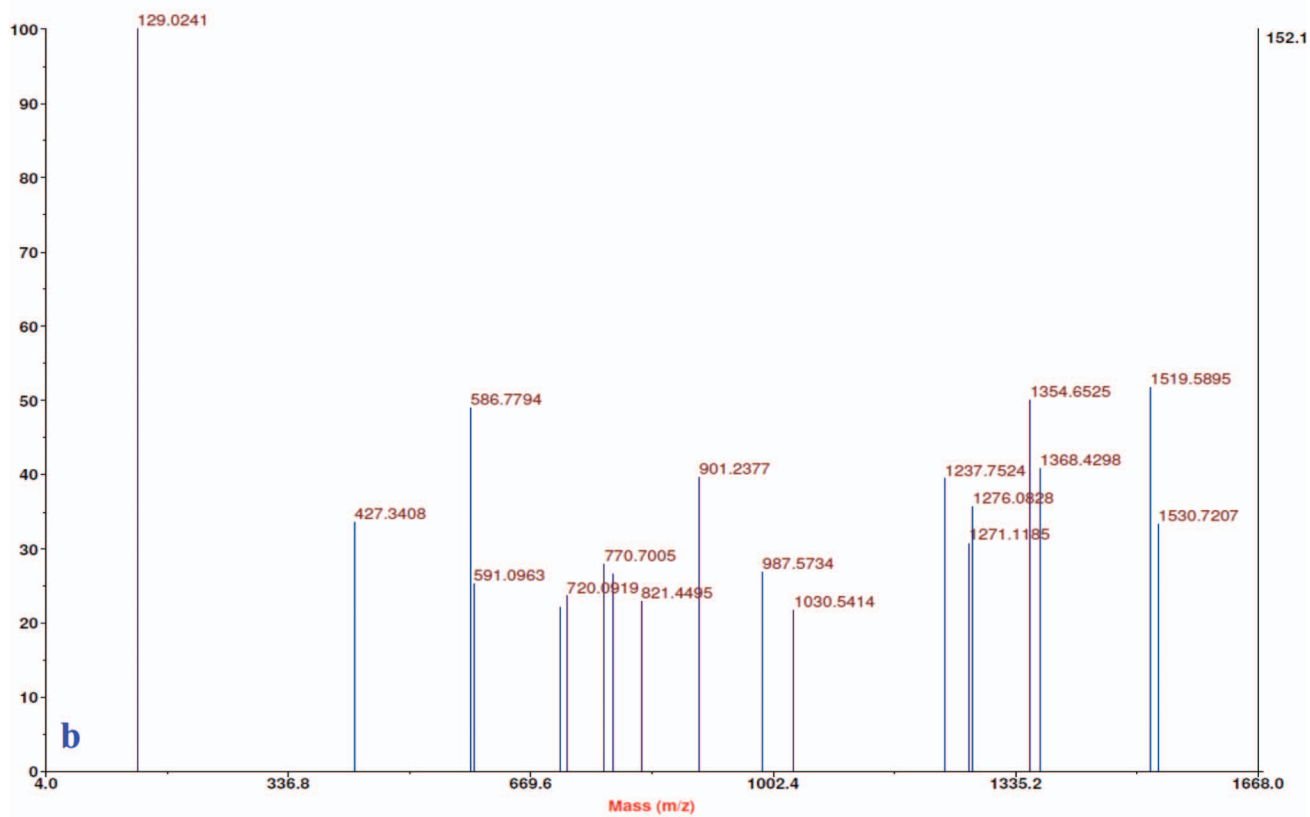
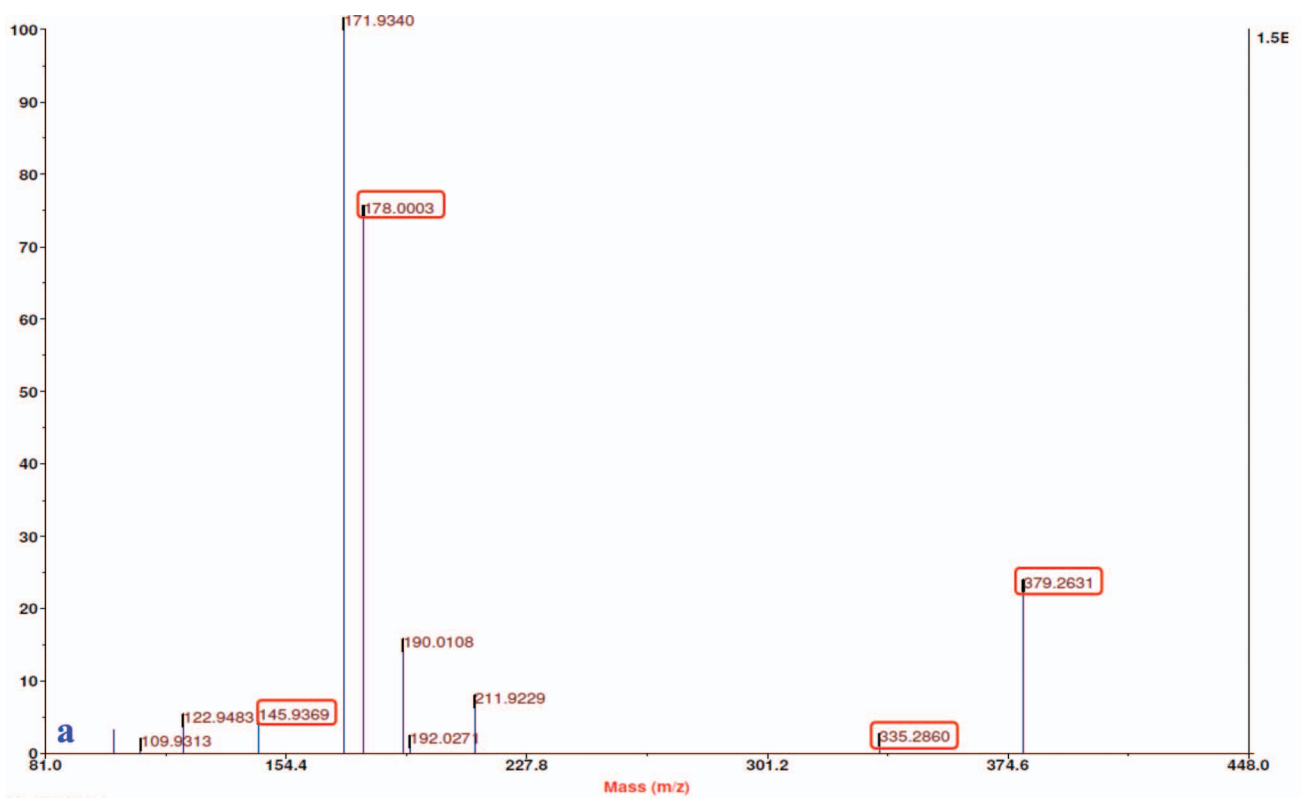
**Retention Time: 16.116 (Galactose)**



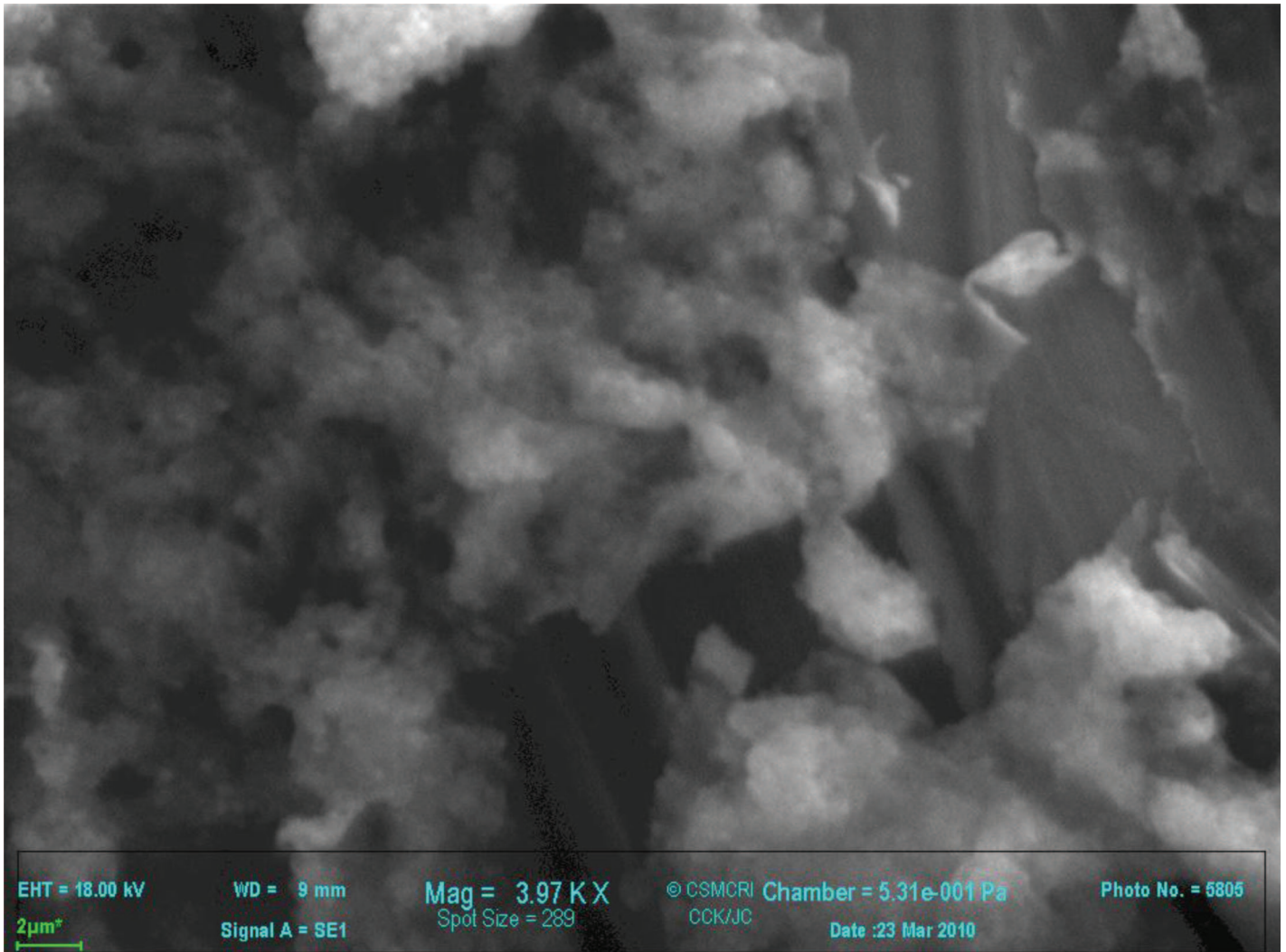
**Retention Time: 16.716 (Glucose)**



**S4: MS Spectra (Intensity [Y axis] Vs m/z [X axis]) coupled with GC of EPS**



**S 5: MALDI TOF–TOF spectra in positive ion (a) linear mode-low range and (b) reflector mode- high precursor; processed, centroid and de-isotoped**



**S6: Scanning Electron Microscopy of EPS**