

Amino Acid Analysis Data Sheet

Sequence: GHKARVLAEAMSQVT
 Lot# A3098-90
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #90
 Mol Wt: 1,597.87
 Amount injected: 45.99 ngs
 Amount Recovered: 34.634 ngs
 Percent Recovery: 75.3%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	20.930	137.14	2.870	20.93	1.0
S	1	19.820	87.08	1.726	19.82	0.9
R	1	22.530	156.19	3.519	22.53	1.0
G	1	24.420	57.05	1.393	24.42	1.1
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	2	45.390	128.13	5.816	22.70	2.1
T	1	22.300	101.11	2.255	22.30	1.0
A	3	63.810	71.08	4.536	21.27	2.9
P	0	0.000	97.12	0.000	0.00	0.0
C	0	0.000	103.14	0.000	0.00	0.0
K	1	22.650	128.18	2.903	22.65	1.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	1	23.410	131.20	3.071	23.41	1.1
V	2	43.280	99.13	4.290	21.64	2.0
I	0	0.000	113.16	0.000	0.00	0.0
L	1	19.920	113.16	2.254	19.92	0.9
F	0	0.000	147.18	0.000	0.00	0.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				34.634		

Performed by: *R. Manicku* 12/05/2019

Verified by: *Moussa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: RVLAEAMSQVTNSAT
 Lot#: A3098-91
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #91
 Mol Wt: 1,577.79
 Amount injected: 23.57 ngs
 Amount Recovered: 20.221 ngs
 Percent Recovery: 85.8%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	2	23.400	87.08	2.038	11.70	1.8
R	1	11.450	156.19	1.788	11.45	0.9
G	0	0.000	57.05	0.000	0.00	0.0
D/N	1	13.320	114.10	1.520	13.32	1.0
E/Q	2	25.750	128.13	3.299	12.88	2.0
T	2	27.910	101.11	2.822	13.96	2.2
A	3	40.050	71.08	2.847	13.35	3.1
P	0	0.000	97.12	0.000	0.00	0.0
C	0	0.000	103.14	0.000	0.00	0.0
K	0	0.000	128.18	0.000	0.00	0.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	1	14.080	131.20	1.847	14.08	1.1
V	2	26.010	99.13	2.578	13.01	2.0
I	0	0.000	113.16	0.000	0.00	0.0
L	1	13.090	113.16	1.481	13.09	1.0
F	0	0.000	147.18	0.000	0.00	0.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				20.221		

Performed by: *R. Mancini* 12/05/2019

Verified by: *Moussa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: EAMSQVTNSATIMMQ
 Lot# A3098-92
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #92
 Mol Wt: 1,641.91
 Amount injected: 25.29 ngs
 Amount Recovered: 23.42 ngs
 Percent Recovery: 92.6%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	2	26.330	87.08	2.293	13.17	1.9
R	0	0.000	156.19	0.000	0.00	0.0
G	0	0.000	57.05	0.000	0.00	0.0
D/N	1	14.150	114.10	1.615	14.15	1.0
E/Q	3	45.140	128.13	5.784	15.05	3.2
T	2	27.740	101.11	2.805	13.87	2.0
A	2	30.340	71.08	2.157	15.17	2.1
P	0	0.000	97.12	0.000	0.00	0.0
C	0	0.000	103.14	0.000	0.00	0.0
K	0	0.000	128.18	0.000	0.00	0.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	3	44.630	131.20	5.855	14.88	3.1
V	1	13.060	99.13	1.295	13.06	0.9
I	1	14.290	113.16	1.617	14.29	1.0
L	0	0.000	113.16	0.000	0.00	0.0
F	0	0.000	147.18	0.000	0.00	0.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				23.420		

Performed by: *R. Manicku* 12/05/2019

Verified by: *Moussa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: QVTNSATIMMQRGNF
 Lot#: A3098-93
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #93
 Mol Wt: 1,697.96
 Amount injected: 44.02 ngs
 Amount Recovered: 38.169 ngs
 Percent Recovery: 86.7%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	1	21.590	87.08	1.880	21.59	0.9
R	1	22.840	156.19	3.567	22.84	1.0
G	1	24.860	57.05	1.418	24.86	1.1
D/N	2	50.170	114.10	5.724	25.09	2.2
E/Q	2	41.160	128.13	5.274	20.58	1.8
T	2	41.460	101.11	4.192	20.73	1.8
A	1	24.820	71.08	1.764	24.82	1.1
P	0	0.000	97.12	0.000	0.00	0.0
C	0	0.000	103.14	0.000	0.00	0.0
K	0	0.000	128.18	0.000	0.00	0.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	2	43.260	131.20	5.676	21.63	1.9
V	1	22.940	99.13	2.274	22.94	1.0
I	1	23.400	113.16	2.648	23.40	1.0
L	0	0.000	113.16	0.000	0.00	0.0
F	1	25.490	147.18	3.752	25.49	1.1
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				38.169		

Performed by: *R. Mancini* 12/05/2019

Verified by: *Maura Barzani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: SATIMMQRGNFRNQR
 Lot# A3098-94
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #94
 Mol Wt: 1,810.10
 Amount injected: 76.64 ngs
 Amount Recovered: 59.472 ngs
 Percent Recovery: 77.6%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	1	28.360	87.08	2.470	28.36	0.9
R	3	98.410	156.19	15.371	32.80	3.0
G	1	32.030	57.05	1.827	32.03	1.0
D/N	2	72.540	114.10	8.277	36.27	2.2
E/Q	2	65.660	128.13	8.413	32.83	2.0
T	1	32.720	101.11	3.308	32.72	1.0
A	1	35.080	71.08	2.493	35.08	1.1
P	0	0.000	97.12	0.000	0.00	0.0
C	0	0.000	103.14	0.000	0.00	0.0
K	0	0.000	128.18	0.000	0.00	0.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	2	70.900	131.20	9.302	35.45	2.2
V	0	0.000	99.13	0.000	0.00	0.0
I	1	30.950	113.16	3.502	30.95	0.9
L	0	0.000	113.16	0.000	0.00	0.0
F	1	30.630	147.18	4.508	30.63	0.9
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				59.472		

Performed by: *R. Manicku* 12/05/2019

Verified by: *Mousa Bazarani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: MMQRGNFRNQRKTVK
 Lot# A3098-95
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #95
 Mol Wt: 1,894.27
 Amount injected: 40.62 ngs
 Amount Recovered: 28.719 ngs
 Percent Recovery: 70.7%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	0	0.000	87.08	0.000	0.00	0.0
R	3	46.900	156.19	7.325	15.63	3.0
G	1	16.960	57.05	0.968	16.96	1.1
D/N	2	29.910	114.10	3.413	14.96	1.9
E/Q	2	28.100	128.13	3.600	14.05	1.8
T	1	15.050	101.11	1.522	15.05	1.0
A	0	0.000	71.08	0.000	0.00	0.0
P	0	0.000	97.12	0.000	0.00	0.0
C	0	0.000	103.14	0.000	0.00	0.0
K	2	30.360	128.18	3.892	15.18	2.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	2	31.770	131.20	4.168	15.89	2.1
V	1	14.880	99.13	1.475	14.88	1.0
I	0	0.000	113.16	0.000	0.00	0.0
L	0	0.000	113.16	0.000	0.00	0.0
F	1	16.010	147.18	2.356	16.01	1.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				28.719		

Performed by: *R. Manicku* 12/05/2019

Verified by: *Moussa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: GNFRNQRKTVKCFNC
 Lot# A3098-96
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #96
 Mol Wt: 1,815.12
 Amount injected: 14.99 ngs
 Amount Recovered: 11.019 ngs
 Percent Recovery: 73.5%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	0	0.000	87.08	0.000	0.00	0.0
R	2	13.690	156.19	2.138	6.85	2.0
G	1	7.230	57.05	0.412	7.23	1.1
D/N	3	22.070	114.10	2.518	7.36	3.2
E/Q	1	7.300	128.13	0.935	7.30	1.1
T	1	6.610	101.11	0.668	6.61	1.0
A	0	0.000	71.08	0.000	0.00	0.0
P	0	0.000	97.12	0.000	0.00	0.0
C	2	0.000	103.14	0.000	0.00	0.0
K	2	13.580	128.18	1.741	6.79	2.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	1	6.120	99.13	0.607	6.12	0.9
I	0	0.000	113.16	0.000	0.00	0.0
L	0	0.000	113.16	0.000	0.00	0.0
F	2	13.580	147.18	1.999	6.79	2.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				11.019		

Performed by: *R. Marchini* 12/05/2019

Verified by: *Moussa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: NQRKTVKCFNCGKEG
 Lot#: A3098-97
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #97
 Mol Wt: 1,711.99
 Amount injected: 79.82 ngs
 Amount Recovered: 57.707 ngs
 Percent Recovery: 72.3%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	0	0.000	87.08	0.000	0.00	0.0
R	1	37.840	156.19	5.910	37.84	1.0
G	2	80.960	57.05	4.619	40.48	2.1
D/N	2	81.590	114.10	9.309	40.80	2.1
E/Q	2	76.540	128.13	9.807	38.27	2.0
T	1	38.520	101.11	3.895	38.52	1.0
A	0	0.000	71.08	0.000	0.00	0.0
P	0	0.000	97.12	0.000	0.00	0.0
C	2	0.000	103.14	0.000	0.00	0.0
K	3	115.950	128.18	14.862	38.65	3.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	1	35.180	99.13	3.487	35.18	0.9
I	0	0.000	113.16	0.000	0.00	0.0
L	0	0.000	113.16	0.000	0.00	0.0
F	1	39.520	147.18	5.817	39.52	1.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				57.707		

Performed by: *R. Manicki* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: TVKCFNCGKEGHIAK
 Lot#: A3098-98
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #98
 Mol Wt: 1,634.95
 Amount injected: 52.37 ngs
 Amount Recovered: 37.392 ngs
 Percent Recovery: 71.4%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	29.070	137.14	3.987	29.07	1.1
S	0	0.000	87.08	0.000	0.00	0.0
R	0	0.000	156.19	0.000	0.00	0.0
G	2	57.310	57.05	3.270	28.66	2.2
D/N	1	28.260	114.10	3.224	28.26	1.1
E/Q	1	26.370	128.13	3.379	26.37	1.0
T	1	24.110	101.11	2.438	24.11	0.9
A	1	23.500	71.08	1.670	23.50	0.9
P	0	0.000	97.12	0.000	0.00	0.0
C	2	0.000	103.14	0.000	0.00	0.0
K	3	76.840	128.18	9.849	25.61	2.9
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	1	23.290	99.13	2.309	23.29	0.9
I	1	25.790	113.16	2.918	25.79	1.0
L	0	0.000	113.16	0.000	0.00	0.0
F	1	29.540	147.18	4.348	29.54	1.1
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				37.392		

Performed by: *R. Manicku* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: FNCGKEGHIAKNCRA
 Lot# A3098-99
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #99
 Mol Wt: 1,647.91
 Amount injected: 57.65 ngs
 Amount Recovered: 41.279 ngs
 Percent Recovery: 71.6%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	29.420	137.14	4.035	29.42	1.0
S	0	0.000	87.08	0.000	0.00	0.0
R	1	29.150	156.19	4.553	29.15	1.0
G	2	61.430	57.05	3.505	30.72	2.1
D/N	2	56.960	114.10	6.499	28.48	2.0
E/Q	1	27.630	128.13	3.540	27.63	0.9
T	0	0.000	101.11	0.000	0.00	0.0
A	2	53.970	71.08	3.836	26.99	1.9
P	0	0.000	97.12	0.000	0.00	0.0
C	2	0.000	103.14	0.000	0.00	0.0
K	2	56.690	128.18	7.267	28.35	1.9
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	1	30.150	113.16	3.412	30.15	1.0
L	0	0.000	113.16	0.000	0.00	0.0
F	1	31.480	147.18	4.633	31.48	1.1
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				41.279		

Performed by: *R. Manickavelu* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: KEGHIAKNCRAPRKK
 Lot# A3098-100
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #100
 Mol Wt: 1,736.09
 Amount injected: 117.64 ngs
 Amount Recovered: 73.287 ngs
 Percent Recovery: 62.3%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	42.210	137.14	5.789	42.21	0.9
S	0	0.000	87.08	0.000	0.00	0.0
R	2	92.070	156.19	14.380	46.04	2.0
G	1	45.700	57.05	2.607	45.70	1.0
D/N	1	44.480	114.10	5.075	44.48	1.0
E/Q	1	43.420	128.13	5.563	43.42	1.0
T	0	0.000	101.11	0.000	0.00	0.0
A	2	86.200	71.08	6.127	43.10	1.9
P	1	48.370	97.12	4.698	48.37	1.1
C	1	0.000	103.14	0.000	0.00	0.0
K	4	186.240	128.18	23.872	46.56	4.1
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	1	45.730	113.16	5.175	45.73	1.0
L	0	0.000	113.16	0.000	0.00	0.0
F	0	0.000	147.18	0.000	0.00	0.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				73.287		

Performed by: *R. Manicku* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: IAKNCRAPRKKGCWK
 Lot# A3098-101
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #101
 Mol Wt: 1,759.18
 Amount injected: 34.97 ngs
 Amount Recovered: 22.976 ngs
 Percent Recovery: 65.7%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	0	0.000	87.08	0.000	0.00	0.0
R	2	34.420	156.19	5.376	17.21	2.0
G	1	18.810	57.05	1.073	18.81	1.1
D/N	1	16.070	114.10	1.834	16.07	0.9
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	0	0.000	101.11	0.000	0.00	0.0
A	2	32.960	71.08	2.343	16.48	1.9
P	1	16.070	97.12	1.561	16.07	0.9
C	2	0.000	103.14	0.000	0.00	0.0
K	4	66.730	128.18	8.553	16.68	3.9
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	1	19.760	113.16	2.236	19.76	1.1
L	0	0.000	113.16	0.000	0.00	0.0
F	0	0.000	147.18	0.000	0.00	0.0
W	1	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				22.976		

Performed by: *R. Mancini* 12/05/2019

Verified by: *Moussa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: CRAPRKKGCWKCGKE
 Lot# A3098-102
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #102
 Mol Wt: 1,750.15
 Amount injected: 41.32 ngs
 Amount Recovered: 27.108 ngs
 Percent Recovery: 65.6%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	0	0.000	87.08	0.000	0.00	0.0
R	2	44.070	156.19	6.883	22.04	2.0
G	2	46.620	57.05	2.660	23.31	2.1
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	1	21.510	128.13	2.756	21.51	1.0
T	0	0.000	101.11	0.000	0.00	0.0
A	1	21.960	71.08	1.561	21.96	1.0
P	1	22.770	97.12	2.211	22.77	1.0
C	3	0.000	103.14	0.000	0.00	0.0
K	4	86.100	128.18	11.036	21.53	3.9
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	0	0.000	113.16	0.000	0.00	0.0
F	0	0.000	147.18	0.000	0.00	0.0
W	1	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				27.108		

Performed by: *R. Manicki* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: RKKGCWKCCKEGHQM
 Lot# A3098-103
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #103
 Mol Wt: 1,776.15
 Amount injected: 25.5 ngs
 Amount Recovered: 16.829 ngs
 Percent Recovery: 66.0%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	12.270	137.14	1.683	12.27	1.0
S	0	0.000	87.08	0.000	0.00	0.0
R	1	11.950	156.19	1.866	11.95	1.0
G	3	36.990	57.05	2.110	12.33	3.0
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	2	24.120	128.13	3.090	12.06	2.0
T	0	0.000	101.11	0.000	0.00	0.0
A	0	0.000	71.08	0.000	0.00	0.0
P	0	0.000	97.12	0.000	0.00	0.0
C	2	0.000	103.14	0.000	0.00	0.0
K	4	50.430	128.18	6.464	12.61	4.1
Y	0	0.000	163.18	0.000	0.00	0.0
M	1	12.310	131.20	1.615	12.31	1.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	0	0.000	113.16	0.000	0.00	0.0
F	0	0.000	147.18	0.000	0.00	0.0
W	1	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				16.829		

Performed by: *R. Manicki* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: CWKCGKEGHQMKDCT
 Lot# A3098-104
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #104
 Mol Wt: 1,754.07
 Amount injected: 42.72 ngs
 Amount Recovered: 31.099 ngs
 Percent Recovery: 72.8%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	24.970	137.14	3.424	24.97	1.0
S	0	0.000	87.08	0.000	0.00	0.0
R	0	0.000	156.19	0.000	0.00	0.0
G	2	50.330	57.05	2.871	25.17	2.0
D/N	1	26.740	114.10	3.051	26.74	1.1
E/Q	2	48.580	128.13	6.225	24.29	2.0
T	1	22.070	101.11	2.231	22.07	0.9
A	0	0.000	71.08	0.000	0.00	0.0
P	0	0.000	97.12	0.000	0.00	0.0
C	3	0.000	103.14	0.000	0.00	0.0
K	3	78.140	128.18	10.016	26.05	3.1
Y	0	0.000	163.18	0.000	0.00	0.0
M	1	25.000	131.20	3.280	25.00	1.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	0	0.000	113.16	0.000	0.00	0.0
F	0	0.000	147.18	0.000	0.00	0.0
W	1	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				31.099		

Performed by: *R. Marcedini* 12/05/2019

Verified by: *Moussa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: GKEGHQMKDCTERQA
 Lot# A3098-105
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #105
 Mol Wt: 1,717.91
 Amount injected: 51.15 ngs
 Amount Recovered: 37.03 ngs
 Percent Recovery: 72.4%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	22.980	137.14	3.151	22.98	1.0
S	0	0.000	87.08	0.000	0.00	0.0
R	1	22.840	156.19	3.567	22.84	1.0
G	2	45.280	57.05	2.583	22.64	2.0
D/N	1	23.430	114.10	2.673	23.43	1.0
E/Q	4	92.440	128.13	11.844	23.11	4.0
T	1	19.600	101.11	1.982	19.60	0.8
A	1	24.800	71.08	1.763	24.80	1.1
P	0	0.000	97.12	0.000	0.00	0.0
C	1	0.000	103.14	0.000	0.00	0.0
K	2	49.630	128.18	6.362	24.82	2.1
Y	0	0.000	163.18	0.000	0.00	0.0
M	1	23.660	131.20	3.104	23.66	1.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	0	0.000	113.16	0.000	0.00	0.0
F	0	0.000	147.18	0.000	0.00	0.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				37.030		

Performed by: *R. Manickavelu* 12/05/2019

Verified by: *Mousa Barzani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: HMKDCTERQANFLG
 Lot# A3098-106
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #106
 Mol Wt: 1,778.01
 Amount injected: 39.21 ngs
 Amount Recovered: 30.267 ngs
 Percent Recovery: 77.2%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	18.240	137.14	2.501	18.24	1.0
S	0	0.000	87.08	0.000	0.00	0.0
R	1	18.550	156.19	2.897	18.55	1.0
G	1	18.920	57.05	1.079	18.92	1.0
D/N	2	38.130	114.10	4.351	19.07	2.1
E/Q	3	54.740	128.13	7.014	18.25	3.0
T	1	16.630	101.11	1.681	16.63	0.9
A	1	18.120	71.08	1.288	18.12	1.0
P	0	0.000	97.12	0.000	0.00	0.0
C	1	0.000	103.14	0.000	0.00	0.0
K	1	18.950	128.18	2.429	18.95	1.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	1	17.990	131.20	2.360	17.99	1.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	1	17.770	113.16	2.011	17.77	1.0
F	1	18.040	147.18	2.655	18.04	1.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				30.267		

Performed by: *R. Manicki* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: DCTERQANFLGKIWP
 Lot# A3098-107
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #107
 Mol Wt: 1,778.03
 Amount injected: 19.56 ngs
 Amount Recovered: 16.021 ngs
 Percent Recovery: 81.9%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	0	0.000	87.08	0.000	0.00	0.0
R	1	11.120	156.19	1.737	11.12	1.0
G	1	11.470	57.05	0.654	11.47	1.0
D/N	2	23.920	114.10	2.729	11.96	2.2
E/Q	2	20.480	128.13	2.624	10.24	1.9
T	1	10.110	101.11	1.022	10.11	0.9
A	1	11.310	71.08	0.804	11.31	1.0
P	1	11.540	97.12	1.121	11.54	1.1
C	1	0.000	103.14	0.000	0.00	0.0
K	1	10.850	128.18	1.391	10.85	1.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	1	11.100	113.16	1.256	11.10	1.0
L	1	10.360	113.16	1.172	10.36	0.9
F	1	10.260	147.18	1.510	10.26	0.9
W	1	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				16.021		

Performed by: *R. Manickam* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: RQANFLGKIWPSHKG
 Lot# A3098-108
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #108
 Mol Wt: 1,739.02
 Amount injected: 38.14 ngs
 Amount Recovered: 27.688 ngs
 Percent Recovery: 72.6%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	18.150	137.14	2.489	18.15	1.0
S	1	15.500	87.08	1.350	15.50	0.9
R	1	18.580	156.19	2.902	18.58	1.0
G	2	38.450	57.05	2.194	19.23	2.1
D/N	1	20.310	114.10	2.317	20.31	1.1
E/Q	1	17.290	128.13	2.215	17.29	1.0
T	0	0.000	101.11	0.000	0.00	0.0
A	1	18.750	71.08	1.333	18.75	1.0
P	1	19.430	97.12	1.887	19.43	1.1
C	0	0.000	103.14	0.000	0.00	0.0
K	2	33.630	128.18	4.311	16.82	1.9
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	1	18.490	113.16	2.092	18.49	1.0
L	1	17.650	113.16	1.997	17.65	1.0
F	1	17.670	147.18	2.601	17.67	1.0
W	1	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				27.688		

Performed by: *R. Manicki* 12/05/2019

Verified by: *Mousa Bazarji* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: FLGKIWPSHKGRPGN
 Lot#: A3098-109
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #109
 Mol Wt: 1,693.98
 Amount injected: 71.94 ngs
 Amount Recovered: 51.867 ngs
 Percent Recovery: 72.1%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	36.960	137.14	5.069	36.96	1.1
S	1	29.280	87.08	2.550	29.28	0.8
R	1	37.770	156.19	5.899	37.77	1.1
G	3	108.220	57.05	6.174	36.07	3.1
D/N	1	35.880	114.10	4.094	35.88	1.0
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	0	0.000	101.11	0.000	0.00	0.0
A	0	0.000	71.08	0.000	0.00	0.0
P	2	71.310	97.12	6.926	35.66	2.1
C	0	0.000	103.14	0.000	0.00	0.0
K	2	66.090	128.18	8.471	33.05	1.9
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	1	35.960	113.16	4.069	35.96	1.0
L	1	32.260	113.16	3.651	32.26	0.9
F	1	33.730	147.18	4.964	33.73	1.0
W	1	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				51.867		

Performed by: *R. Manicku* 12/05/2019

Verified by: *Moussa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: IWPSHKGRPGNFLQS
 Lot#: A3098-110
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #110
 Mol Wt: 1,723.96
 Amount injected: 35.47 ngs
 Amount Recovered: 27.204 ngs
 Percent Recovery: 76.7%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	16.710	137.14	2.292	16.71	0.9
S	2	32.920	87.08	2.867	16.46	1.8
R	1	18.040	156.19	2.818	18.04	1.0
G	2	35.450	57.05	2.022	17.73	2.0
D/N	1	20.250	114.10	2.311	20.25	1.1
E/Q	1	17.990	128.13	2.305	17.99	1.0
T	0	0.000	101.11	0.000	0.00	0.0
A	0	0.000	71.08	0.000	0.00	0.0
P	2	36.680	97.12	3.562	18.34	2.0
C	0	0.000	103.14	0.000	0.00	0.0
K	1	19.750	128.18	2.532	19.75	1.1
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	1	18.160	113.16	2.055	18.16	1.0
L	1	17.420	113.16	1.971	17.42	1.0
F	1	16.780	147.18	2.470	16.78	0.9
W	1	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				27.204		

Performed by: *R. Manicku* 12/05/2019

Verified by: *Moussa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: HKGRPGNFLQSRPEP
 Lot#: A3098-111
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #111
 Mol Wt: 1,719.93
 Amount injected: 85.45 ngs
 Amount Recovered: 61.868 ngs
 Percent Recovery: 72.4%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	35.620	137.14	4.885	35.62	1.0
S	1	36.350	87.08	3.165	36.35	1.0
R	2	74.040	156.19	11.564	37.02	2.0
G	2	73.530	57.05	4.195	36.77	2.0
D/N	1	36.890	114.10	4.209	36.89	1.0
E/Q	2	69.300	128.13	8.879	34.65	1.9
T	0	0.000	101.11	0.000	0.00	0.0
A	0	0.000	71.08	0.000	0.00	0.0
P	3	111.290	97.12	10.808	37.10	3.1
C	0	0.000	103.14	0.000	0.00	0.0
K	1	36.070	128.18	4.623	36.07	1.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	1	36.590	113.16	4.141	36.59	1.0
F	1	36.670	147.18	5.397	36.67	1.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				61.868		

Performed by: *R. Mancini* 12/05/2019

Verified by: *Maura Barzani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: PGNFLQSRPEPTAPP
 Lot# A3098-112
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #112
 Mol Wt: 1,607.80
 Amount injected: 52.55 ngs
 Amount Recovered: 45.191 ngs
 Percent Recovery: 86.0%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	1	22.530	87.08	1.962	22.53	0.8
R	1	29.290	156.19	4.575	29.29	1.0
G	1	28.720	57.05	1.638	28.72	1.0
D/N	1	30.660	114.10	3.498	30.66	1.1
E/Q	2	55.400	128.13	7.098	27.70	2.0
T	1	26.770	101.11	2.707	26.77	1.0
A	1	28.610	71.08	2.034	28.61	1.0
P	5	145.370	97.12	14.118	29.07	5.2
C	0	0.000	103.14	0.000	0.00	0.0
K	0	0.000	128.18	0.000	0.00	0.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	1	28.980	113.16	3.279	28.98	1.0
F	1	29.090	147.18	4.281	29.09	1.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				45.191		

Performed by: *R. Manicki* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: LQSRPEPTAPPEESF
 Lot# A3098-113
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #113
 Mol Wt: 1,684.83
 Amount injected: 45.32 ngs
 Amount Recovered: 39.203 ngs
 Percent Recovery: 86.5%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	2	42.730	87.08	3.721	21.37	1.8
R	1	23.800	156.19	3.717	23.80	1.0
G	0	0.000	57.05	0.000	0.00	0.0
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	4	93.330	128.13	11.958	23.33	4.0
T	1	20.990	101.11	2.122	20.99	0.9
A	1	25.220	71.08	1.793	25.22	1.1
P	4	97.420	97.12	9.461	24.36	4.1
C	0	0.000	103.14	0.000	0.00	0.0
K	0	0.000	128.18	0.000	0.00	0.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	1	24.700	113.16	2.795	24.70	1.0
F	1	24.700	147.18	3.635	24.70	1.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				39.203		

Performed by: *R. Manicku* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: PEPTAPPEESFRFGE
 Lot#: A3098-114
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #114
 Mol Wt: 1,689.81
 Amount injected: 50.33 ngs
 Amount Recovered: 43.586 ngs
 Percent Recovery: 86.6%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	1	19.560	87.08	1.703	19.56	0.8
R	1	27.680	156.19	4.323	27.68	1.1
G	1	27.890	57.05	1.591	27.89	1.1
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	4	103.520	128.13	13.264	25.88	4.0
T	1	24.110	101.11	2.438	24.11	0.9
A	1	26.650	71.08	1.894	26.65	1.0
P	4	106.370	97.12	10.331	26.59	4.1
C	0	0.000	103.14	0.000	0.00	0.0
K	0	0.000	128.18	0.000	0.00	0.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	0	0.000	113.16	0.000	0.00	0.0
F	2	54.640	147.18	8.042	27.32	2.1
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				43.586		

Performed by: *R. Manicku* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: APPEESFRFGEEETT
 Lot# A3098-115
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #115
 Mol Wt: 1,697.78
 Amount injected: 14.7 ngs
 Amount Recovered: 12.747 ngs
 Percent Recovery: 86.7%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	1	6.620	87.08	0.576	6.62	0.9
R	1	7.561	156.19	1.181	7.56	1.0
G	1	7.930	57.05	0.452	7.93	1.1
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	4	31.500	128.13	4.036	7.88	4.2
T	3	21.690	101.11	2.193	7.23	2.9
A	1	7.650	71.08	0.544	7.65	1.0
P	2	15.160	97.12	1.472	7.58	2.0
C	0	0.000	103.14	0.000	0.00	0.0
K	0	0.000	128.18	0.000	0.00	0.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	0	0.000	113.16	0.000	0.00	0.0
F	2	15.570	147.18	2.292	7.79	2.1
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				12.747		

Performed by: *R. Manicki* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: ESFRFG EETTTPSQK
 Lot#: A3098-116
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #116
 Mol Wt: 1,743.86
 Amount injected: 27.06 ngs
 Amount Recovered: 22.079 ngs
 Percent Recovery: 81.6%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	2	26.230	87.08	2.284	13.12	2.0
R	1	13.340	156.19	2.084	13.34	1.0
G	1	13.220	57.05	0.754	13.22	1.0
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	4	48.700	128.13	6.240	12.18	3.7
T	3	36.650	101.11	3.706	12.22	2.8
A	0	0.000	71.08	0.000	0.00	0.0
P	1	13.390	97.12	1.300	13.39	1.0
C	0	0.000	103.14	0.000	0.00	0.0
K	1	13.680	128.18	1.754	13.68	1.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	0	0.000	113.16	0.000	0.00	0.0
F	2	26.890	147.18	3.958	13.45	2.1
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				22.079		

Performed by: *R. Manekhi* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: FGEEITTPSQKQEPI
 Lot# A3098-117
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #117
 Mol Wt: 1,691.82
 Amount injected: 32.57 ngs
 Amount Recovered: 28.209 ngs
 Percent Recovery: 86.6%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	1	16.370	87.08	1.425	16.37	0.9
R	0	0.000	156.19	0.000	0.00	0.0
G	1	17.870	57.05	1.019	17.87	1.0
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	5	81.720	128.13	10.471	16.34	4.7
T	3	48.240	101.11	4.878	16.08	2.8
A	0	0.000	71.08	0.000	0.00	0.0
P	2	35.340	97.12	3.432	17.67	2.0
C	0	0.000	103.14	0.000	0.00	0.0
K	1	17.700	128.18	2.269	17.70	1.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	1	17.640	113.16	1.996	17.64	1.0
L	0	0.000	113.16	0.000	0.00	0.0
F	1	18.470	147.18	2.718	18.47	1.1
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				28.209		

Performed by: *R. Mancini* 12/05/2019

Verified by: *Moussa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: TTTPSQKQEPIDKEL
 Lot# A3098-118
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #118
 Mol Wt: 1,714.90
 Amount injected: 62.71 ngs
 Amount Recovered: 51.049 ngs
 Percent Recovery: 81.4%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	1	28.610	87.08	2.491	28.61	0.9
R	0	0.000	156.19	0.000	0.00	0.0
G	0	0.000	57.05	0.000	0.00	0.0
D/N	1	31.440	114.10	3.587	31.44	1.0
E/Q	4	117.320	128.13	15.032	29.33	3.9
T	3	84.540	101.11	8.548	28.18	2.8
A	0	0.000	71.08	0.000	0.00	0.0
P	2	62.190	97.12	6.040	31.10	2.0
C	0	0.000	103.14	0.000	0.00	0.0
K	2	64.360	128.18	8.250	32.18	2.1
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	1	31.010	113.16	3.509	31.01	1.0
L	1	31.740	113.16	3.592	31.74	1.0
F	0	0.000	147.18	0.000	0.00	0.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				51.049		

Performed by: *R. Manicki* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: SQKQEPIDKELYPLA
 Lot# A3098-119
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #119
 Mol Wt: 1,758.99
 Amount injected: 43.65 ngs
 Amount Recovered: 35.704 ngs
 Percent Recovery: 81.8%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	1	17.110	87.08	1.490	17.11	0.8
R	0	0.000	156.19	0.000	0.00	0.0
G	0	0.000	57.05	0.000	0.00	0.0
D/N	1	21.540	114.10	2.458	21.54	1.1
E/Q	4	80.560	128.13	10.322	20.14	3.9
T	0	0.000	101.11	0.000	0.00	0.0
A	1	21.510	71.08	1.529	21.51	1.1
P	2	41.950	97.12	4.074	20.98	2.0
C	0	0.000	103.14	0.000	0.00	0.0
K	2	42.750	128.18	5.480	21.38	2.1
Y	1	20.120	163.18	3.283	20.12	1.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	1	20.680	113.16	2.340	20.68	1.0
L	2	41.780	113.16	4.728	20.89	2.0
F	0	0.000	147.18	0.000	0.00	0.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				35.704		

Performed by: *R. Mancini* 12/05/2019

Verified by: *Moussa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: EPIDKELYPLASLRS
 Lot# A3098-120
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #120
 Mol Wt: 1,730.98
 Amount injected: 71.29 ngs
 Amount Recovered: 58.098 ngs
 Percent Recovery: 81.5%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	2	61.220	87.08	5.331	30.61	1.8
R	1	35.670	156.19	5.571	35.67	1.0
G	0	0.000	57.05	0.000	0.00	0.0
D/N	1	35.030	114.10	3.997	35.03	1.0
E/Q	2	62.110	128.13	7.958	31.06	1.8
T	0	0.000	101.11	0.000	0.00	0.0
A	1	33.960	71.08	2.414	33.96	1.0
P	2	69.960	97.12	6.795	34.98	2.1
C	0	0.000	103.14	0.000	0.00	0.0
K	1	34.980	128.18	4.484	34.98	1.0
Y	1	35.220	163.18	5.747	35.22	1.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	1	34.580	113.16	3.913	34.58	1.0
L	3	105.060	113.16	11.889	35.02	3.1
F	0	0.000	147.18	0.000	0.00	0.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				58.098		0.0

Performed by: *R. Manicki* 12/05/2019

Verified by: *Moussa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: KELYPLASLRSLFGN
 Lot#: A3098-121
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #121
 Mol Wt: 1,707.99
 Amount injected: 40.57 ngs
 Amount Recovered: 32.982 ngs
 Percent Recovery: 81.3%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	2	35.070	87.08	3.054	17.54	1.8
R	1	19.330	156.19	3.019	19.33	1.0
G	1	19.250	57.05	1.098	19.25	1.0
D/N	1	21.600	114.10	2.465	21.60	1.1
E/Q	1	19.720	128.13	2.527	19.72	1.0
T	0	0.000	101.11	0.000	0.00	0.0
A	1	19.920	71.08	1.416	19.92	1.0
P	1	19.780	97.12	1.921	19.78	1.0
C	0	0.000	103.14	0.000	0.00	0.0
K	1	21.600	128.18	2.769	21.60	1.1
Y	1	18.240	163.18	2.976	18.24	0.9
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	4	78.820	113.16	8.919	19.71	4.0
F	1	19.150	147.18	2.818	19.15	1.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				32.982		0.0

Performed by: *R. Manickam* 12/05/2019

Verified by: *Nousha Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: PLASLRSLFGNDPSS
 Lot# A3098-122
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #122
 Mol Wt: 1,560.74
 Amount injected: 47.02 ngs
 Amount Recovered: 40.247 ngs
 Percent Recovery: 85.6%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	4	98.460	87.08	8.574	24.62	3.8
R	1	25.360	156.19	3.961	25.36	1.0
G	1	25.250	57.05	1.441	25.25	1.0
D/N	2	54.030	114.10	6.165	27.02	2.1
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	0	0.000	101.11	0.000	0.00	0.0
A	1	27.200	71.08	1.933	27.20	1.0
P	2	52.370	97.12	5.086	26.19	2.0
C	0	0.000	103.14	0.000	0.00	0.0
K	0	0.000	128.18	0.000	0.00	0.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	3	81.640	113.16	9.238	27.21	3.1
F	1	26.150	147.18	3.849	26.15	1.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				40.247		

Performed by: *R. Manicku* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Amino Acid Analysis Data Sheet

Sequence: LRSFLGNDPSSQ
 Lot# A3098-123
 ID#:
 Project #: Cat# 12425 HIV-1 Consensus B Gag Peptide Pool #123
 Mol Wt: 1,320.43
 Amount injected: 40.46 ngs
 Amount Recovered: 33.786 ngs
 Percent Recovery: 83.5%
 Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis

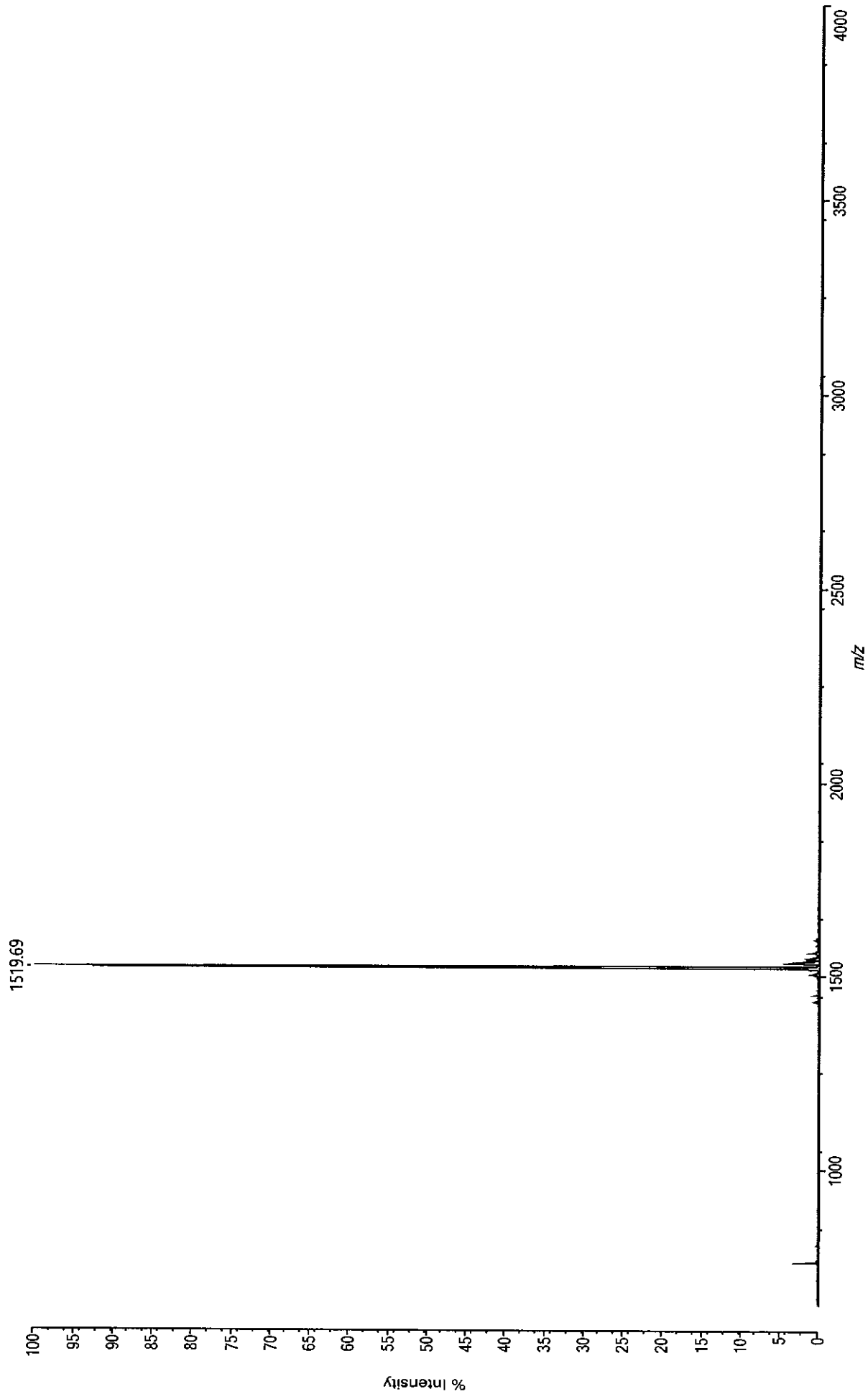
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	3	75.080	87.08	6.538	25.03	2.9
R	1	25.980	156.19	4.058	25.98	1.0
G	1	25.730	57.05	1.468	25.73	1.0
D/N	2	52.560	114.10	5.997	26.28	2.0
E/Q	1	25.620	128.13	3.283	25.62	1.0
T	0	0.000	101.11	0.000	0.00	0.0
A	0	0.000	71.08	0.000	0.00	0.0
P	1	26.110	97.12	2.536	26.11	1.0
C	0	0.000	103.14	0.000	0.00	0.0
K	0	0.000	128.18	0.000	0.00	0.0
Y	0	0.000	163.18	0.000	0.00	0.0
M	0	0.000	131.20	0.000	0.00	0.0
V	0	0.000	99.13	0.000	0.00	0.0
I	0	0.000	113.16	0.000	0.00	0.0
L	2	52.340	113.16	5.923	26.17	2.0
F	1	27.070	147.18	3.984	27.07	1.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				33.786		

Performed by: *R. Manicku* 12/05/2019

Verified by: *Mousa Bazani* 12/05/2019

Data: A3098-1 [MW=1518.72] CB_0001:A2 Thursday, November 14, 2019 2:24:54 PM Cal:Named Calibration "TOFMIX_8/27/2019" by MALDI Solutions Admin on Tuesday, August 27, 2019 4:32:14 PM (Original)
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

Processed data (averaged) : 319.8 mV [sum=2022.9 mV], Smoothed = 10, profiles # 1 - 50

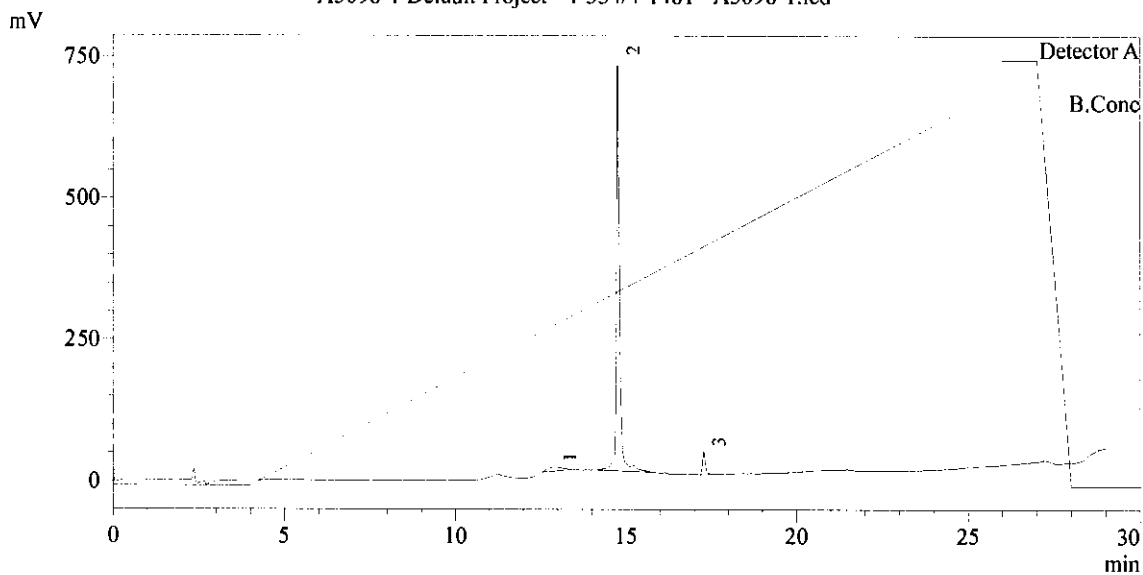


Sample Information

Acquired by : System Administrator
 Sample Name : A3098-1
 Sample ID : A3098-1
 Data Filename : A3098-1.lcd
 Method Filename : ANAPEP_29.lcm
 Date Acquired : 11/14/2019 2:58:17 PM
 Data Processed : 11/14/2019 3:27:24 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram

A3098-1 Default Project - 4-334/4-1481 - A3098-1.lcd



1 Detector A / 220nm

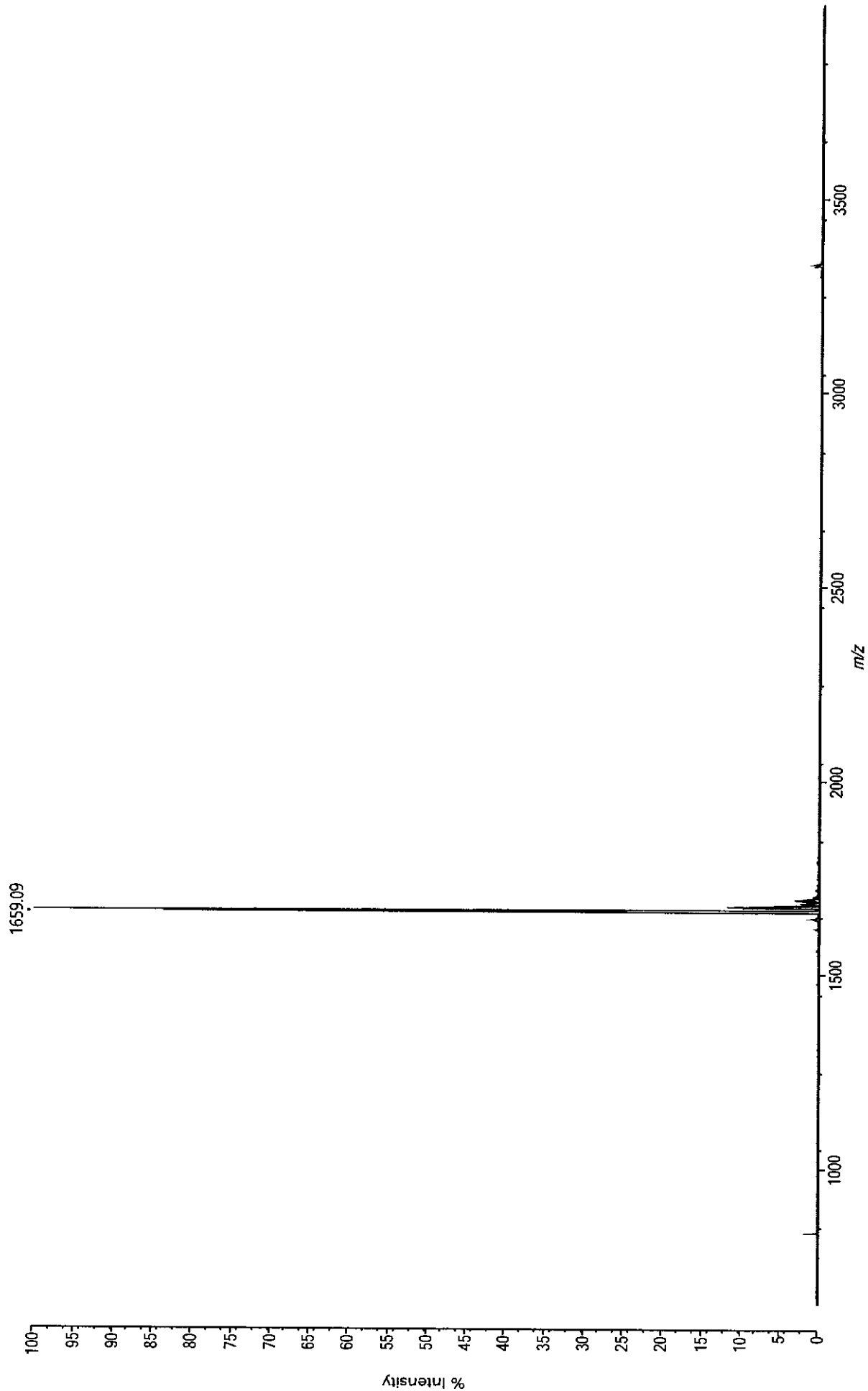
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	12.899	216522	7219	0.932	4.230
2	14.758	4665655	726365	93.743	91.156
3	17.275	236124	41267	5.326	4.613
Total				100.000	100.000

Data: A3098-2 [MW=1659.87] CB_0001:B2 Thursday, November 14, 2019 2:25:55 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 2:26:30 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

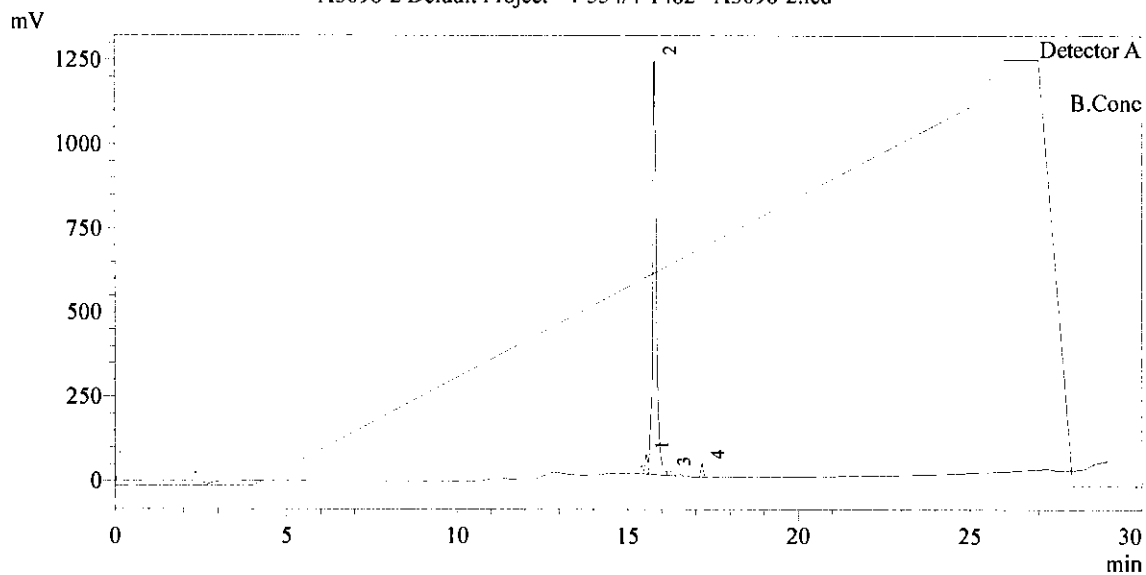
Processed data (averaged) : 197.6 mV [sum=1249.7 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A3098-2
 Sample ID : A3098-2
 Data Filename : A3098-2.lcd
 Method Filename : ANAPEP_29.lcm
 Date Acquired : 11/14/2019 3:32:30 PM
 Data Processed : 11/14/2019 4:01:38 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 A3098-2 Default Project - 4-334/4-1482 - A3098-2.lcd



1 Detector A / 220nm

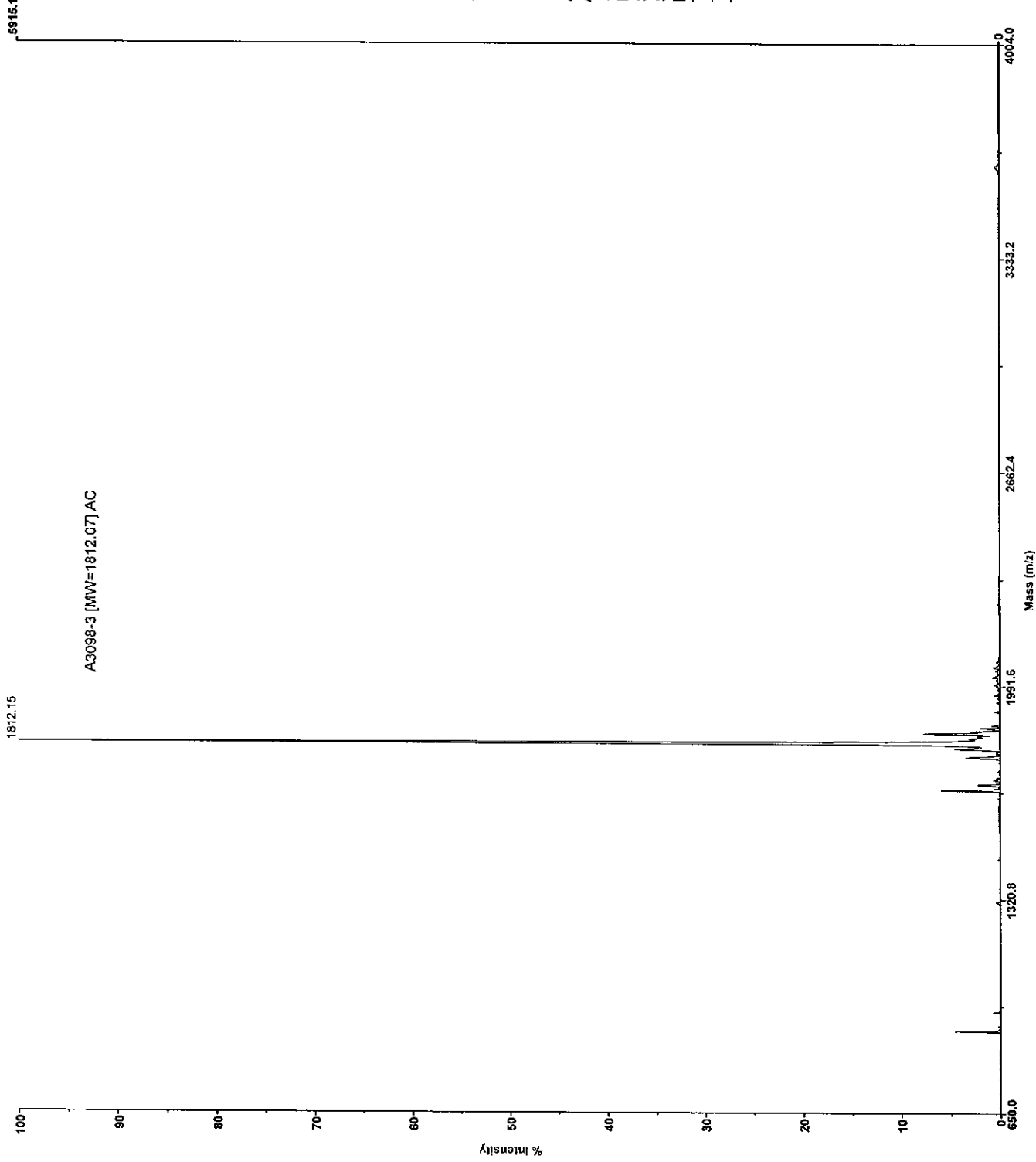
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	15.552	441842	57088	4.256	4.237
2	15.801	9643789	1231538	91.821	92.468
3	16.202	142498	13303	0.992	1.366
4	17.179	201208	39315	2.931	1.929
Total				100.000	100.000

Applied Biosystems Voyager System 1099

Voyager Spec #1=>SM5=>NR(2.00)=>AdvBC(32,0.5,0.1)[BP = 1812.0, 5915]



Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Manual

Accelerating voltage: 20000 V
Grid voltage: 95%
Guide wire 0: 0.05%
Extraction delay time: 150 nsec

Acquisition mass range: 650 -- 4000 Da
Number of laser shots: 100/spectrum
Laser intensity: 1670
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 16.782
Bin size: 2 nsec
Number of data points: 12334
Vertical scale: 200 mV
Vertical offset: 0%
Input bandwidth: 500 MHz

Sample well: 02
Plate ID: 100 WELL PLATE
Serial number: 1099
Instrument name: Voyager-DE
Plate type filename: C:\VOYAGER\100 well plate.pt
Lab name: BioSynthesis, Inc

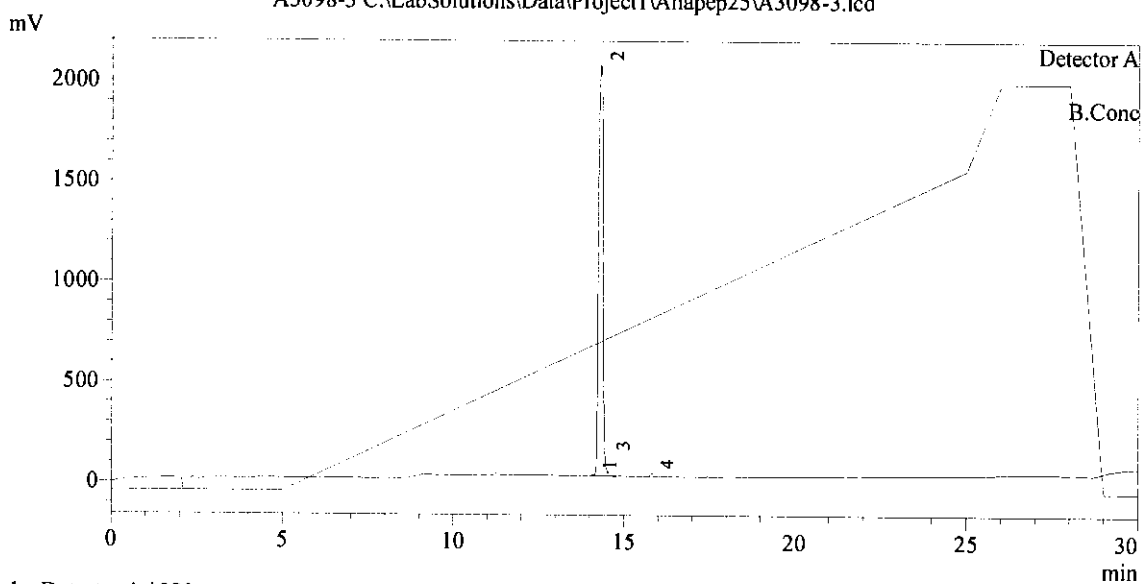
Absolute x-position: 6952.74
Absolute y-position: 47273.9
Relative x-position: 285.241
Relative y-position: -33.6052
Shots in spectrum: 47
Source pressure: 1.597e-006
Mirror pressure: 0
TC2 pressure: 0.001
TIS gate width: 30
TIS flight length: 940

Sample Information

Acquired by : System Administrator
 Sample Name : A3098-3
 Sample ID : A3098-3
 Data Filename : A3098-3.lcd
 Method Filename : ANAPEP25_FORM_ID.lsr.lcm
 Date Acquired : 11/15/2019 1:53:14 PM
 Data Processed : 11/15/2019 2:25:27 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID : CD-339 / EQ-332

Chromatogram

A3098-3 C:\LabSolutions\Data\Project1\Anapep25\A3098-3.lcd



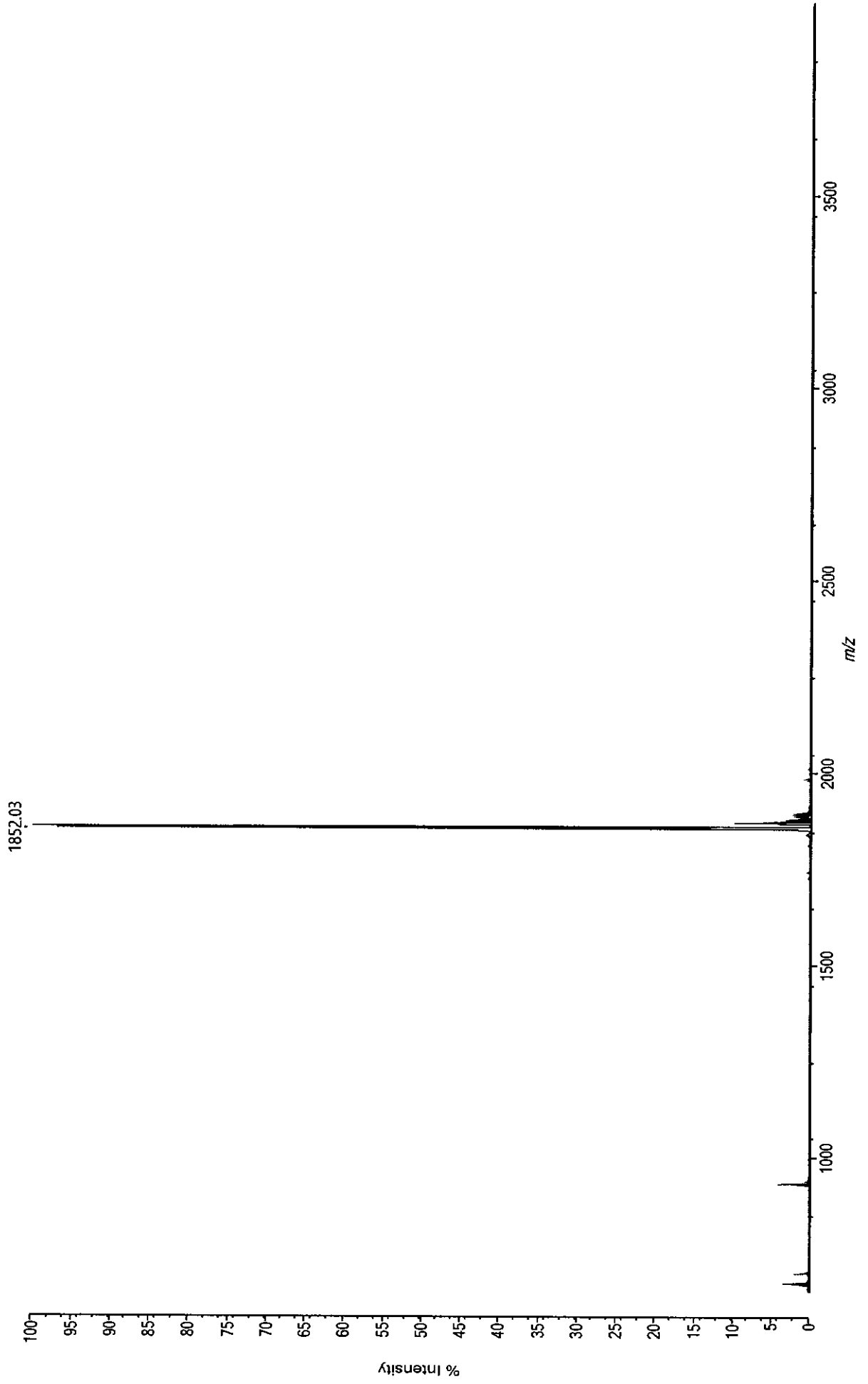
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	14.132	47788	7152	0.343	0.251
2	14.301	18765472	2043206	97.955	98.667
3	14.525	99388	19988	0.958	0.523
4	15.817	106388	15509	0.744	0.559
Total				100.000	100.000

Data: A3098-4 [MW=1852.23] CB_0002:D2 Thursday, November 14, 2019 2:26:44 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 2:28:27 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

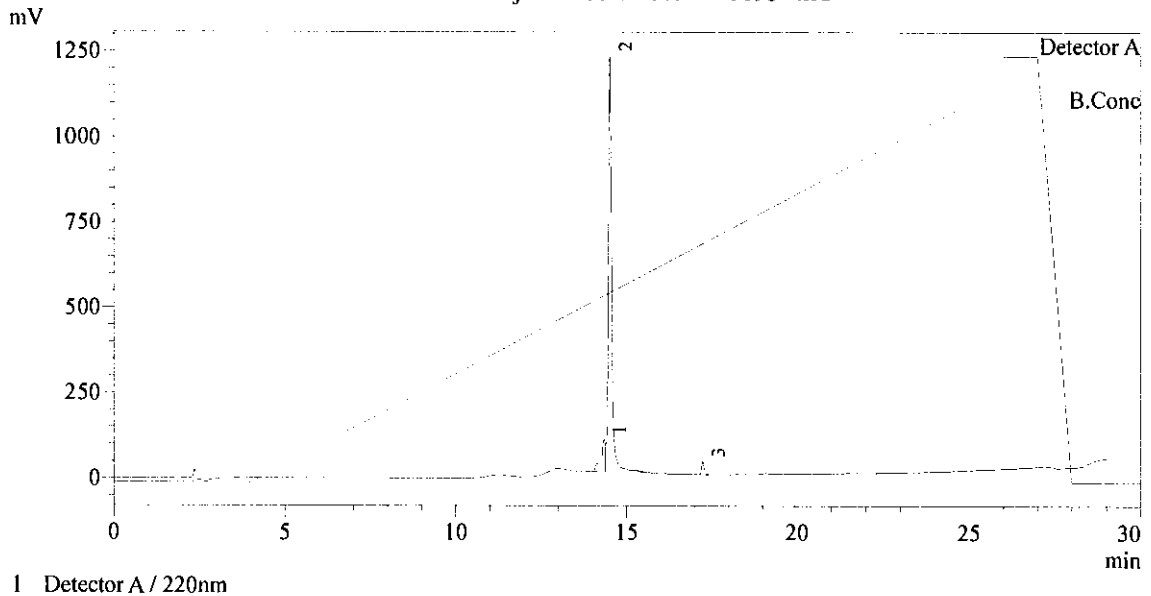
Processed data (averaged) : 162.0 mV [sum=1024.9 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A3098-4
 Sample ID : A3098-4
 Data Filename : A3098-4.lcd
 Method Filename : ANAPEP_29.lcm
 Date Acquired : 11/14/2019 4:40:58 PM
 Data Processed : 11/14/2019 5:10:08 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 A3098-4 Default Project - 4-334/4-1484 - A3098-4.lcd



1 Detector A / 220nm

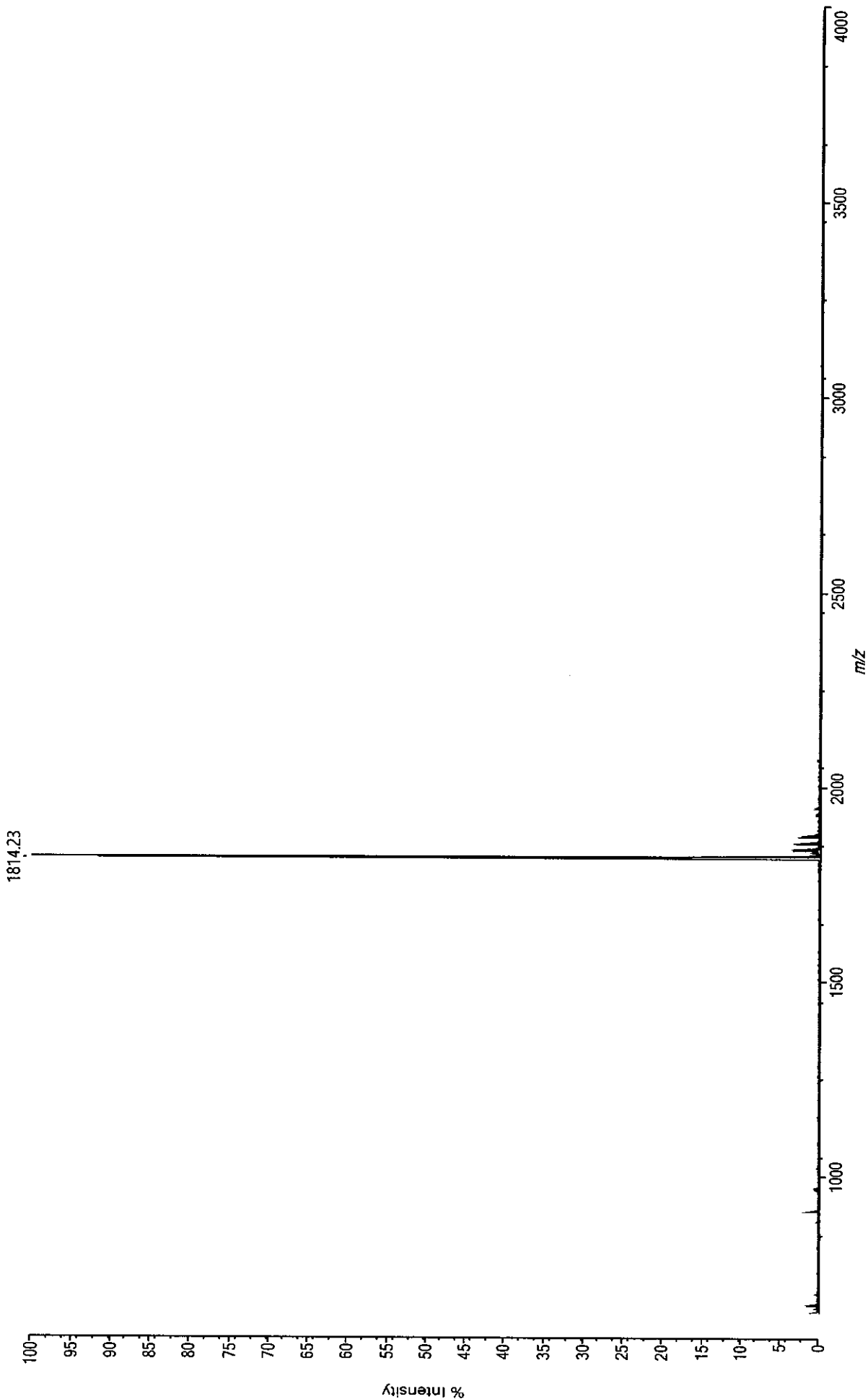
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	14.337	867025	93939	6.966	9.142
2	14.524	8421407	1216901	90.241	88.795
3	17.244	195659	37661	2.793	2.063
Total				100.000	100.000

Data: A3098-5 [MW=1814.25] CB_0002:E2 Thursday, November 14, 2019 2:26:44 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 2:28:27 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

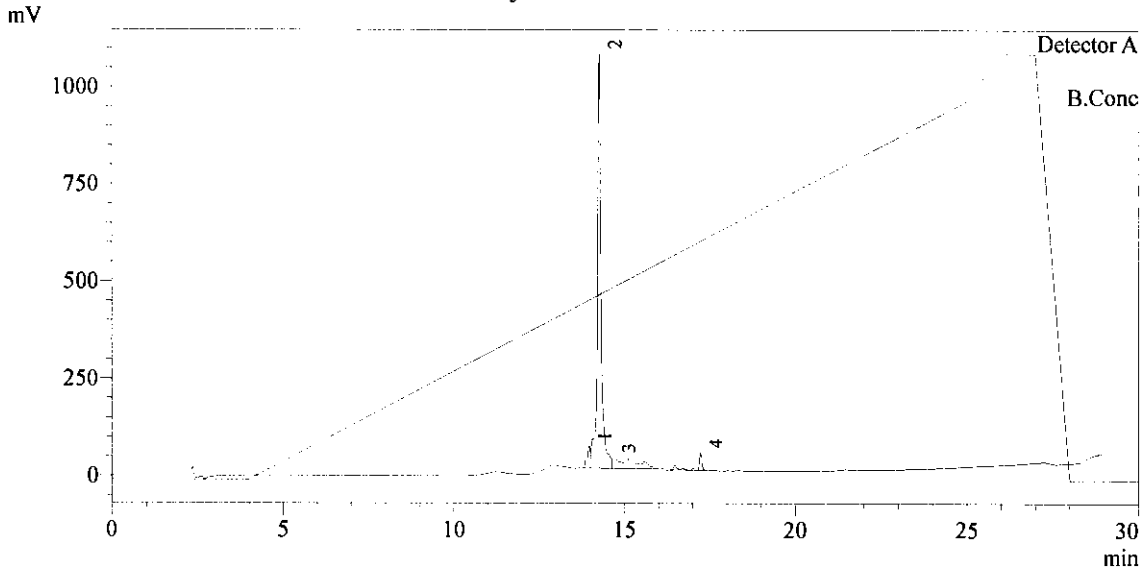
Processed data (averaged) : 103.1 mV [sum=652.3 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A3098-5
 Sample ID : A3098-5
 Data Filename : A3098-5.lcd
 Method Filename : ANAPEP_29.lcm
 Date Acquired : 11/14/2019 5:15:11 PM
 Data Processed : 11/14/2019 5:44:20 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID : CD-347 / EQ-349

Chromatogram
 A3098-5 Default Project - 4-334/4-1485 - A3098-5.lcd



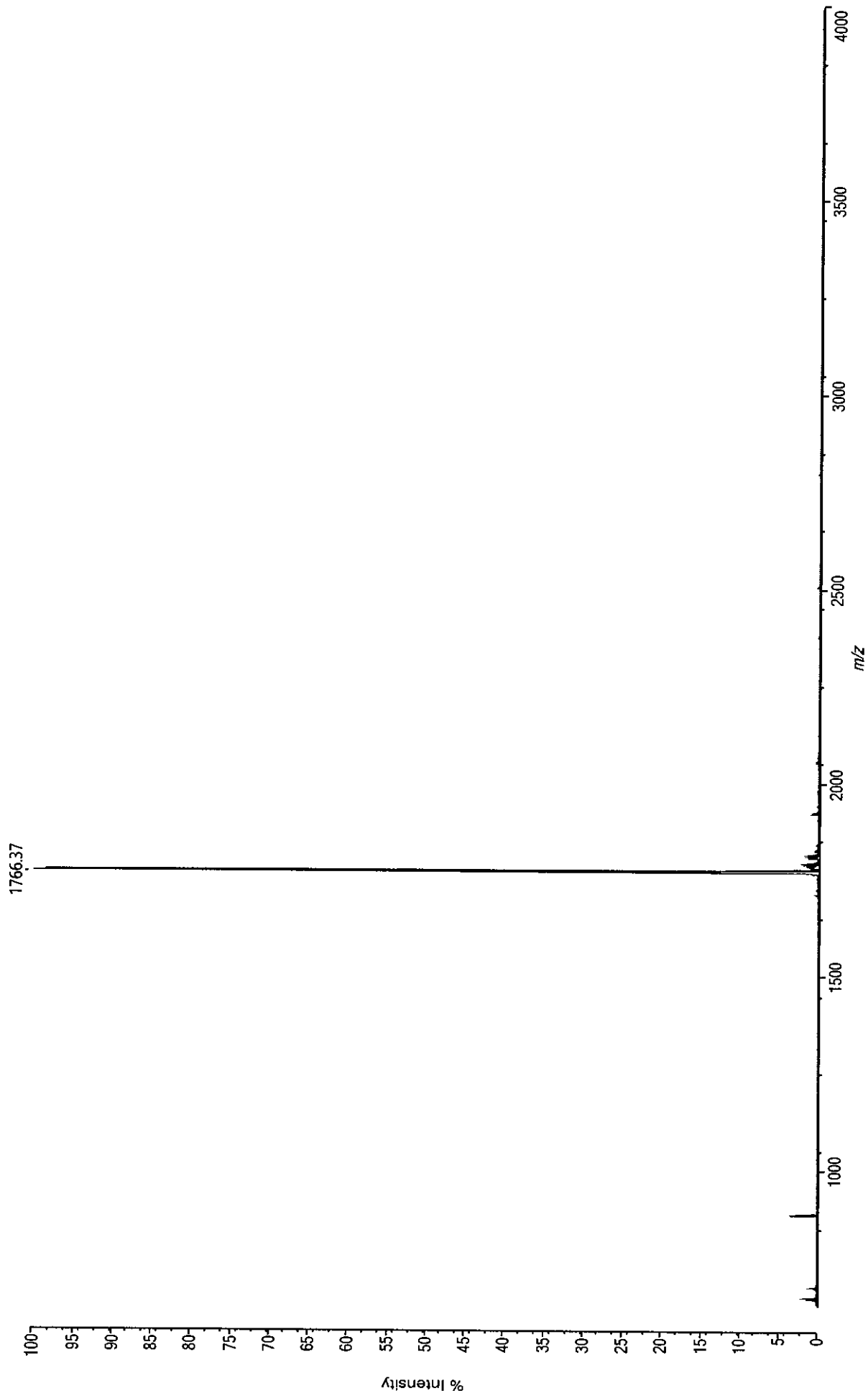
1 Detector A / 220nm

PeakTable

Peak#	Ret. Time	Area	Height	Height %	Area %
1	13.963	385532	57380	4.805	3.876
2	14.271	8096780	1065230	89.206	81.404
3	14.671	1117217	27297	2.286	11.232
4	17.236	346901	44222	3.703	3.488
Total				100.000	100.000

Data: A3098-6 [MW=1765.22] CB_0002:F2 Thursday, November 14, 2019 2:26:44 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 2:28:27 PM
Shimadzu MALDI-8020; Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

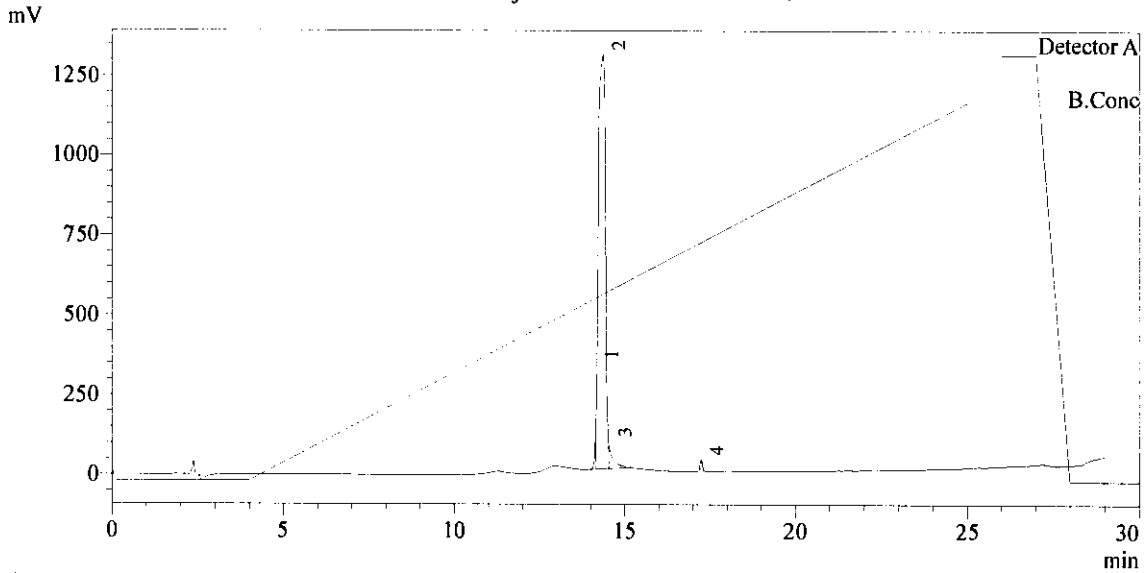
Processed data (averaged) : 176.2 mV [sum=1114.4 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A3098-6
 Sample ID : A3098-6
 Data Filename : A3098-6.lcd
 Method Filename : ANAPEP_29.lcm
 Date Acquired : 11/14/2019 5:49:25 PM
 Data Processed : 11/14/2019 6:18:33 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 A3098-6 Default Project - 4-334/4-1486 - A3098-6.lcd



1 Detector A / 220nm

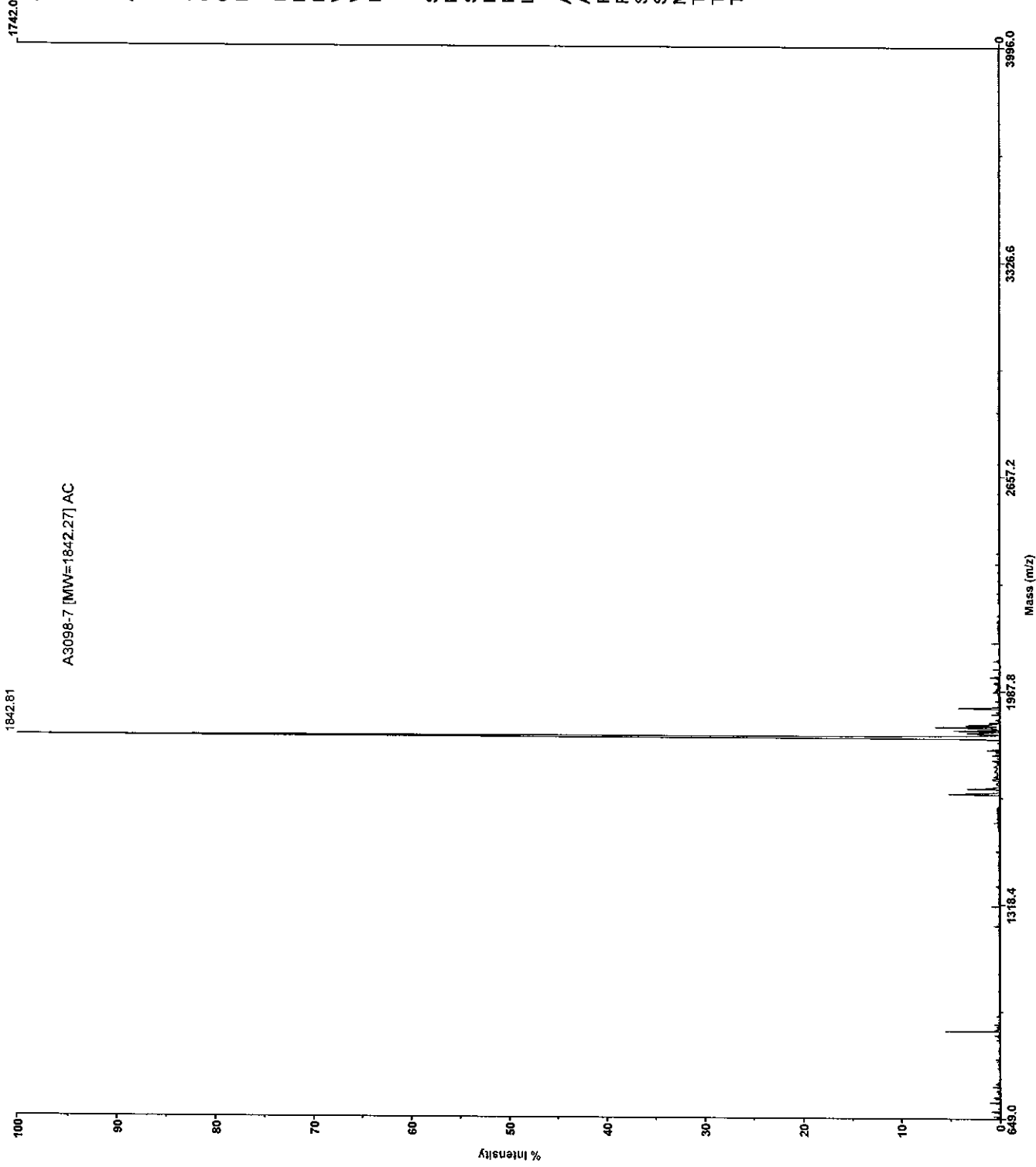
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	14.154	391279	141130	9.185	2.004
2	14.358	18384427	1297327	84.434	94.172
3	14.546	622360	68224	4.440	3.188
4	17.242	124061	29820	1.941	0.635
Total				100.000	100.000

Applied Biosystems Voyager System 1099

Voyager Spec #1=>SM5=>NR(2.00)=>AdvBC(32,0,5,0,1)=>AdvBC(20,0,5,0,1)[BP = 1842.7, 1742]



Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Manual

Accelerating voltage: 20000 V
Grid voltage: 95%
Guide wire 0: 0.05%
Extraction delay time: 150 nsec

Acquisition mass range: 650 -- 4000 Da
Number of laser shots: 100/spectrum
Laser intensity: 1670
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 16.774
Bin size: 2 nsec
Number of data points: 12330
Vertical scale: 200 mV
Vertical offset: 0%
Input bandwidth: 500 MHz

Sample well: 09
Plate ID: 100 WELL PLATE
Serial number: 1099
Instrument name: Voyager-DE
Plate type filename: C:\VOYAGER\100 well plate.pt
Lab name: BioSynthesis, Inc

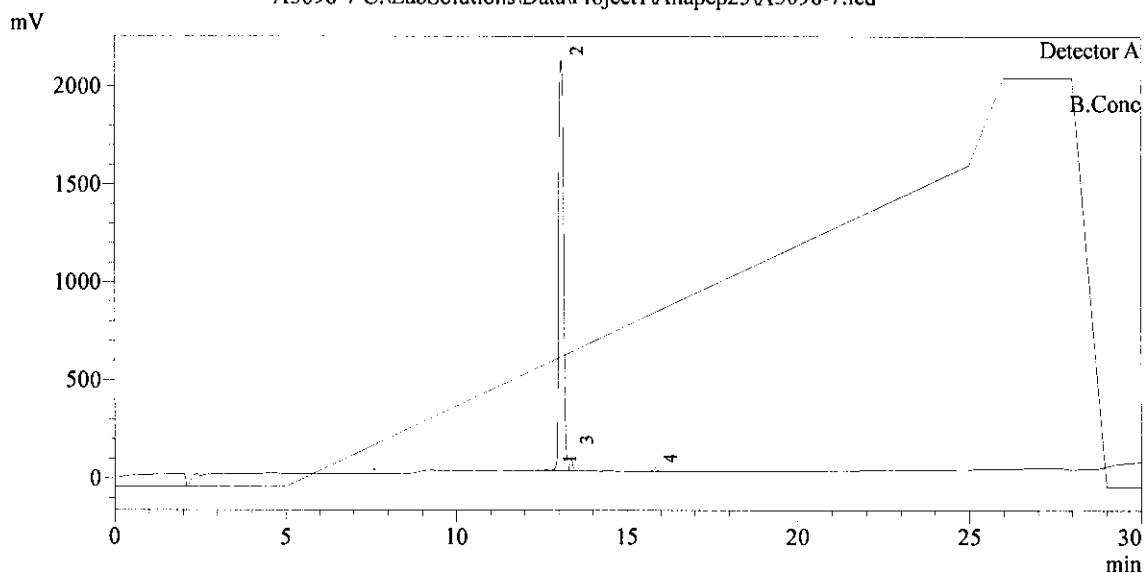
Absolute x-position: 41565.3
Absolute y-position: 47192.6
Relative x-position: -662.198
Relative y-position: -114.926
Shots in spectrum: 35
Source pressure: 8.56e-007
Mirror pressure: 0
TC2 pressure: 0.001
TIS gate width: 30
TIS flight length: 940

Sample Information

Acquired by : System Administrator
 Sample Name : A3098-7
 Sample ID : A3098-7
 Data Filename : A3098-7.lcd
 Method Filename : ANAPEP25_FORM_ID.lsr.lcm
 Date Acquired : 11/15/2019 2:26:03 PM
 Data Processed : 11/15/2019 2:58:17 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram

A3098-7 C:\LabSolutions\Data\Project I\Anapep25\A3098-7.lcd



1 Detector A / 220nm

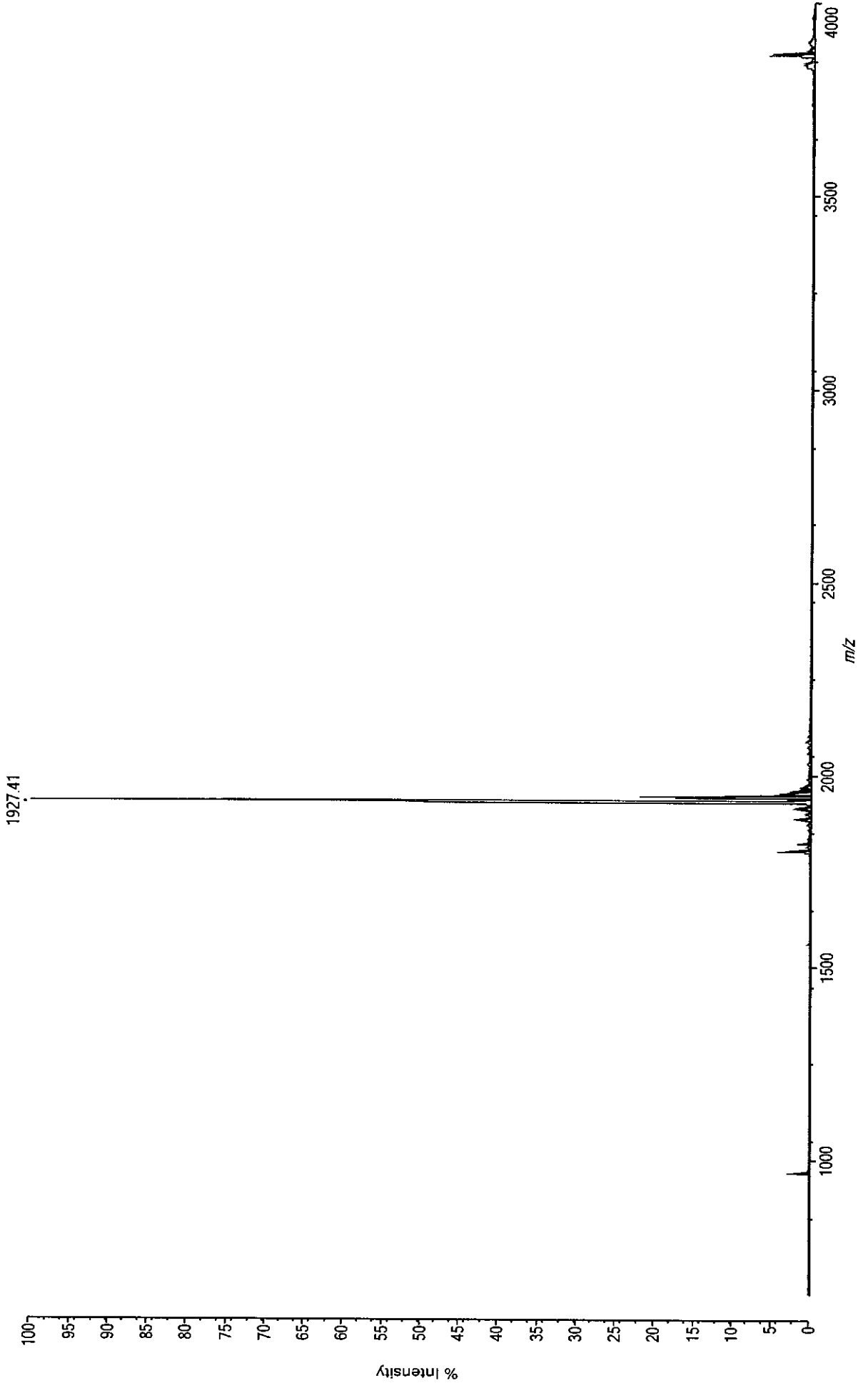
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	12.858	54603	4668	0.215	0.258
2	13.081	20659479	2091431	96.152	97.621
3	13.363	325729	60963	2.803	1.539
4	15.825	123240	18074	0.831	0.582
Total				100.000	100.000

Data: A3098-8 [MW=1928.27] C8_0002:H2 Thursday, November 14, 2019 2:26:44 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 2:30:54 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

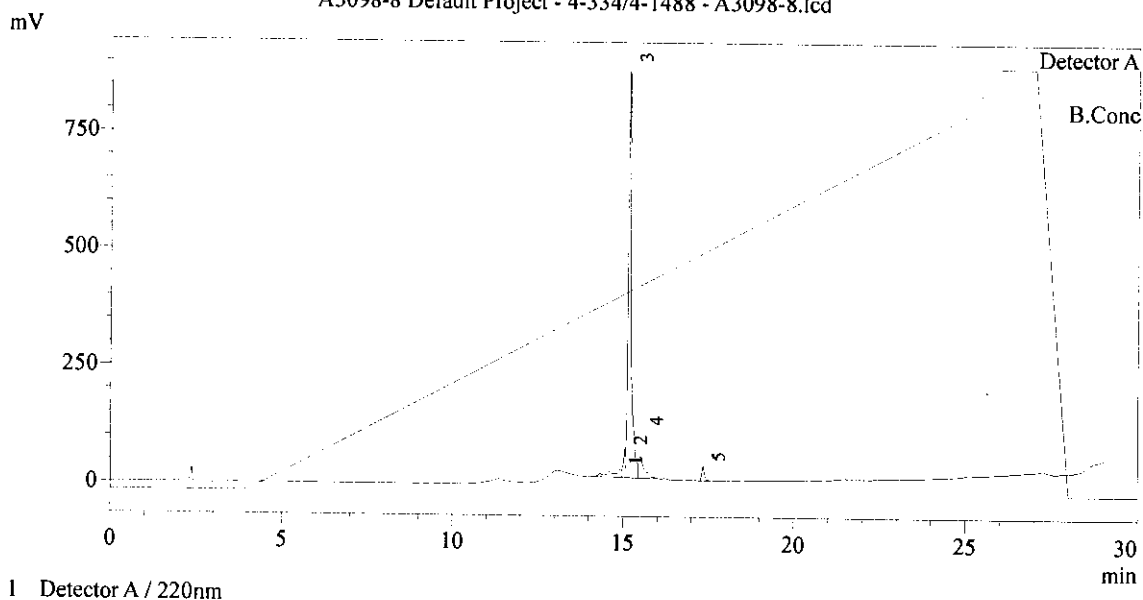
Processed data (averaged) : 804.0 mV [sum=5084.8 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A3098-8
 Sample ID : A3098-8
 Data Filename : A3098-8.lcd
 Method Filename : ANAPEP_29.lcm
 Date Acquired : 11/14/2019 6:57:51 PM
 Data Processed : 11/14/2019 7:27:01 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 A3098-8 Default Project - 4-334/4-1488 - A3098-8.lcd



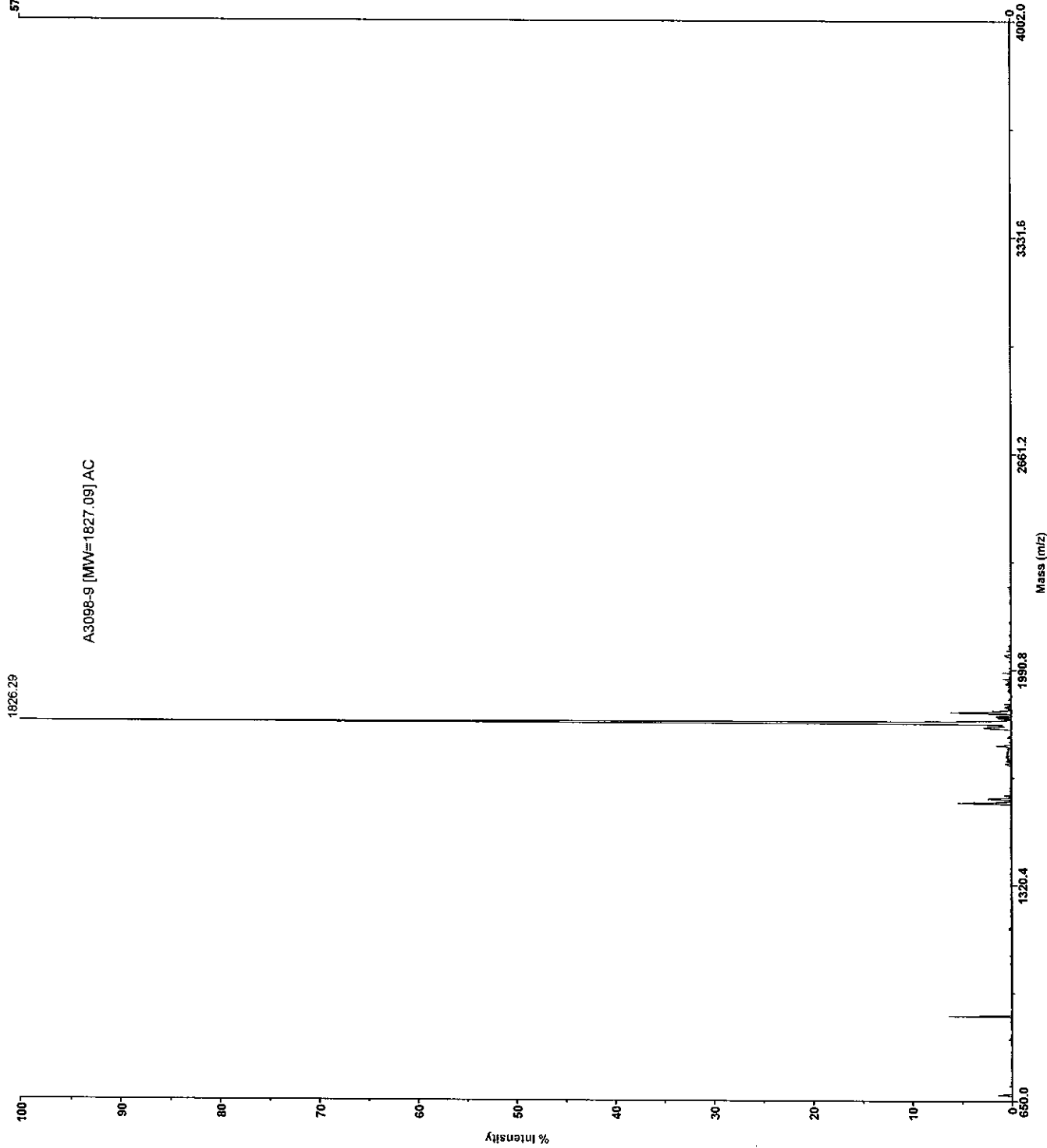
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	14.912	339190	16030	1.557	4.945
2	15.053	265878	60226	5.849	3.876
3	15.158	5585661	877382	85.213	81.430
4	15.520	505647	45137	4.384	7.372
5	17.338	163100	30863	2.997	2.378
Total				100.000	100.000

Applied Biosystems Voyager System 1099

Voyager Spec #1=>SM5=>NR(2.00)=>AdvBC(20,0.5,0.1)[BP = 1826.3, 5786]



Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Manual

Accelerating voltage: 20000 V
Grid voltage: 95%
Guide wire 0: 0.05%
Extraction delay time: 150 nsec

Acquisition mass range: 650 - 4000 Da
Number of laser shots: 100/spectrum
Laser intensity: 1770
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 16.786
Bin size: 2 nsec
Number of data points: 12336
Vertical scale: 200 mV
Vertical offset: 0%
Input bandwidth: 500 MHz

Sample well: 12
Plate ID: 100 WELL PLATE
Serial number: 1099
Instrument name: Voyager-DE
Plate type filename: C:\VOYAGER\100 well plate.plt
Lab name: BioSynthesis, Inc

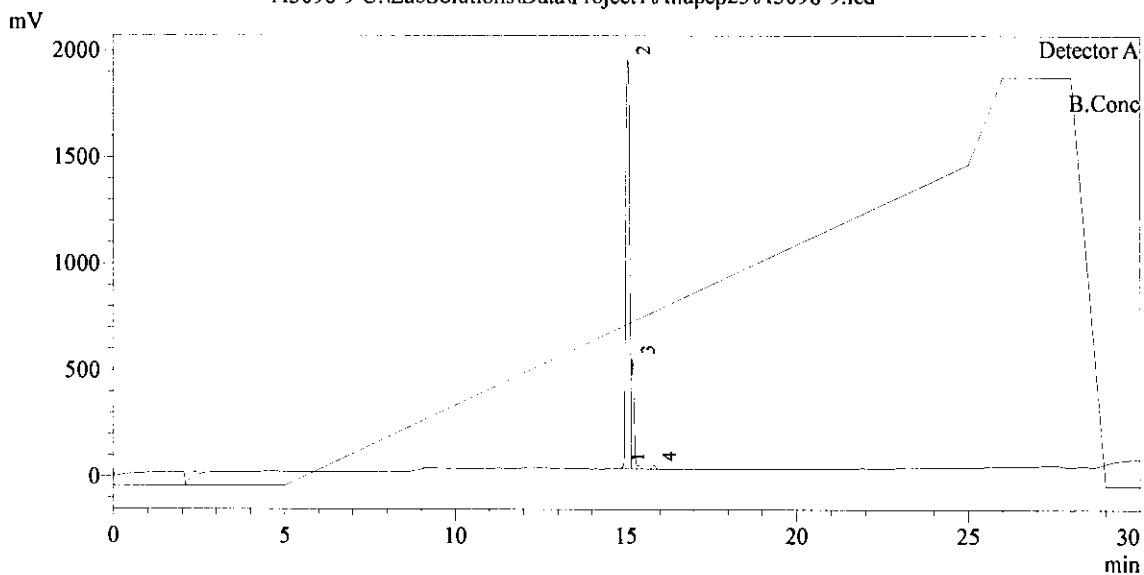
Absolute x-position: 6780.32
Absolute y-position: 41670.1
Relative x-position: 112.821
Relative y-position: -557.371
Shots in spectrum: 16
Source pressure: 6.234e-007
Mirror pressure: 0
TC2 pressure: 0.001
TIS gate width: 30
TIS flight length: 940

Sample Information

Acquired by : System Administrator
 Sample Name : A3098-9
 Sample ID : A3098-9
 Data Filename : A3098-9.lcd
 Method Filename : ANAPEP25_FORM_ID.lsr.lcm
 Date Acquired : 11/15/2019 2:58:51 PM
 Data Processed : 11/15/2019 3:31:04 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram

A3098-9 C:\LabSolutions\Data\Project1\Anapep25\A3098-9.lcd



1 Detector A / 220nm

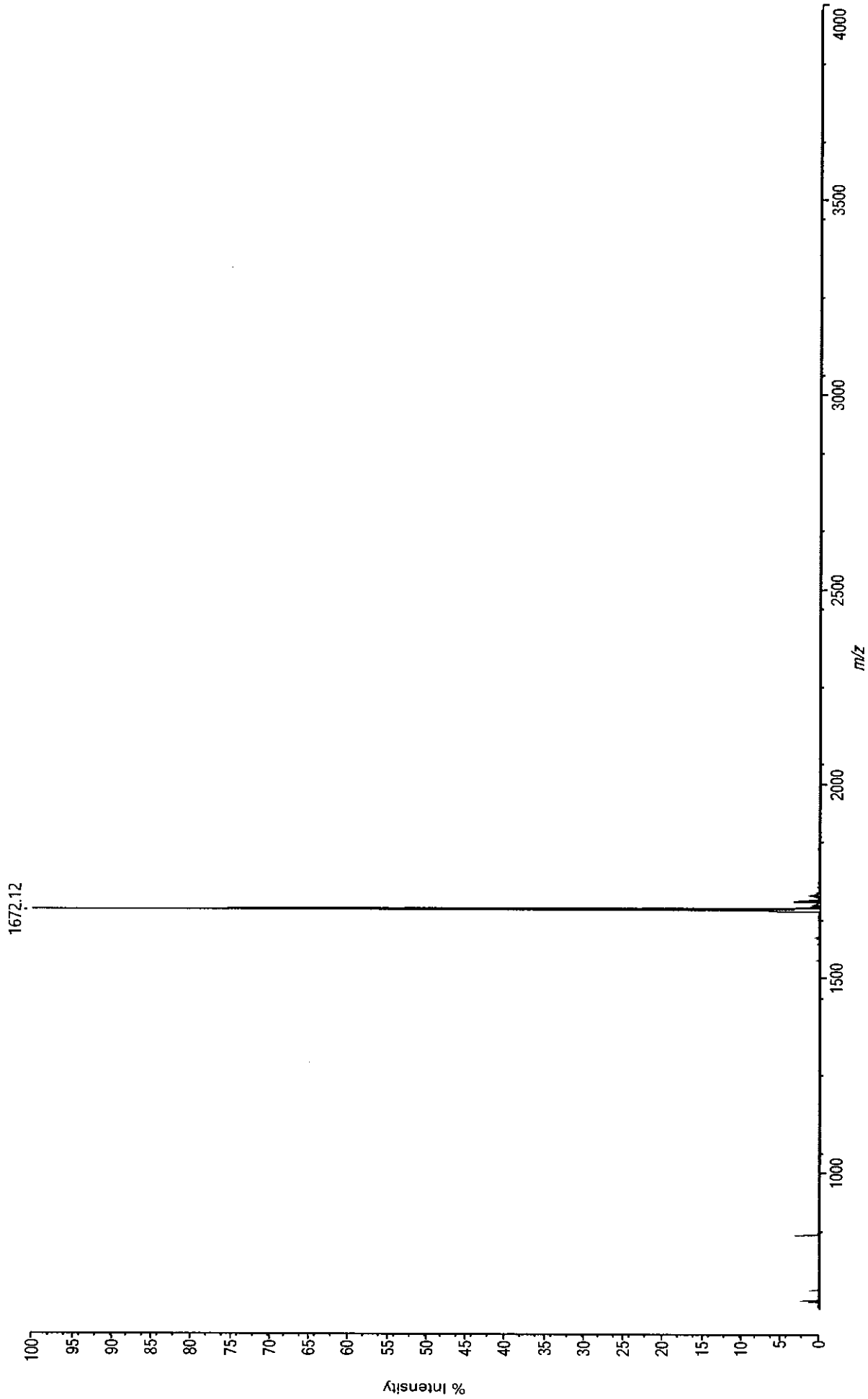
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	14.892	33247	7823	0.318	0.180
2	15.057	15754949	1921625	78.132	85.419
3	15.190	2555971	514241	20.909	13.858
4	15.812	100232	15785	0.642	0.543
Total				100.000	100.000

Data: A3098-10 [MW=1671.93] CB_0002:J2 Thursday, November 14, 2019 2:26:44 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 2:30:54 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

Processed data (averaged) : 359.3 mV [sum=2272.3 mV], Smoothed = 10, profiles # 1 - 50

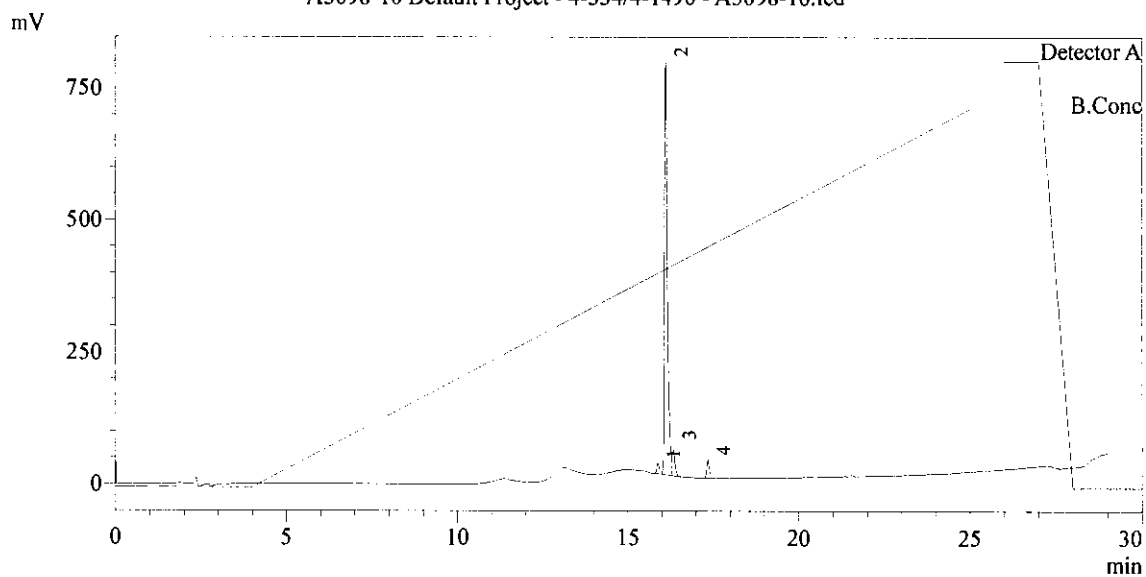


Sample Information

Acquired by : System Administrator
 Sample Name : A3098-10
 Sample ID : A3098-10
 Data Filename : A3098-10.lcd
 Method Filename : ANAPEP_29.lcm
 Date Acquired : 11/14/2019 8:06:22 PM
 Data Processed : 11/14/2019 8:35:31 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram

A3098-10 Default Project - 4-334/4-1490 - A3098-10.lcd



1 Detector A / 220nm

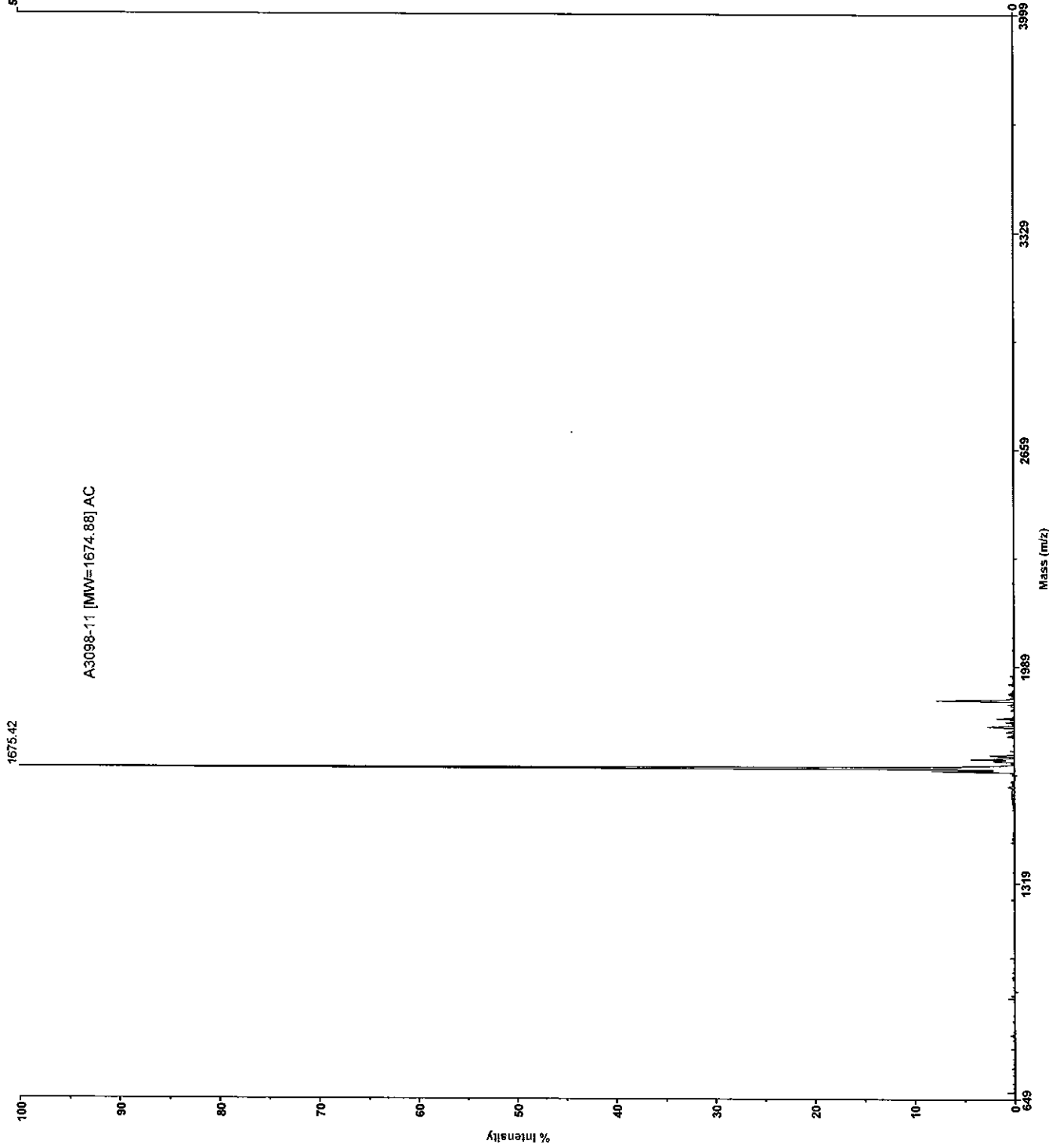
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	15.889	121021	19170	2.169	2.331
2	16.125	4634863	782016	88.470	89.286
3	16.347	254668	47927	5.422	4.906
4	17.351	180473	34819	3.939	3.477
Total				100.000	100.000

Applied Biosystems Voyager System 1099

Voyager Spec #1=>SM5=>NR(2.00)=>AdvBC(20.0.5.0.1)[BP = 1675.4, 5055]



Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Manual
Accelerating voltage: 20000 V
Grid voltage: 95%
Guide wire 0: 0.05%
Extraction delay time: 150 nsec
Acquisition mass range: 650 – 4000 Da
Number of laser shots: 100/spectrum
Laser intensity: 1670
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 16.782
Bin size: 2 nsec
Number of data points: 12334
Vertical scale: 200 mV
Vertical offset: 0%
Input bandwidth: 500 MHz

Sample well: 19
Plate ID: 100 WELL PLATE
Serial number: 1099
Instrument name: Voyager-DE
Plate type filename: C:\VOYAGER\100 well plate.plt
Lab name: BioSynthesis, Inc

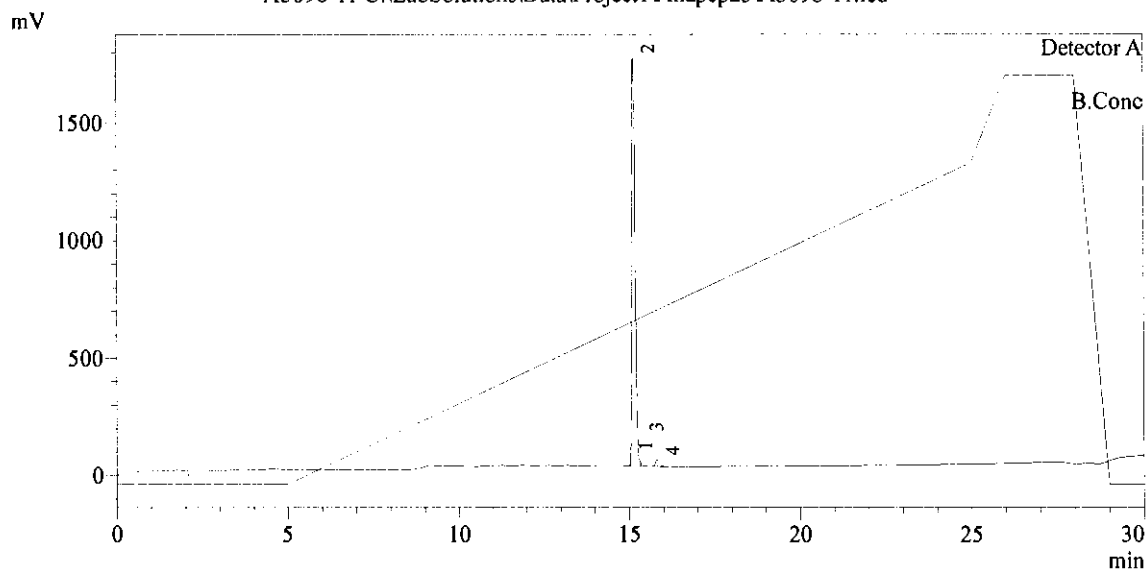
Absolute x-position: 42451.7
Absolute y-position: 41614.2
Relative x-position: 224.217
Relative y-position: -613.274
Shots in spectrum: 26
Source pressure: 4.825e-007
Mirror pressure: 0
TC2 pressure: 0.001
TIS gate width: 30
TIS flight length: 940

Sample Information

Acquired by : System Administrator
 Sample Name : A3098-11
 Sample ID : A3098-11
 Data Filename : A3098-11.lcd
 Method Filename : ANAPEP25_FORM_ID.lsr.lcm
 Date Acquired : 11/15/2019 3:31:37 PM
 Data Processed : 11/15/2019 4:03:51 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram

A3098-11 C:\LabSolutions\Data\Project1\Anapep25\A3098-11.lcd



1 Detector A / 220nm

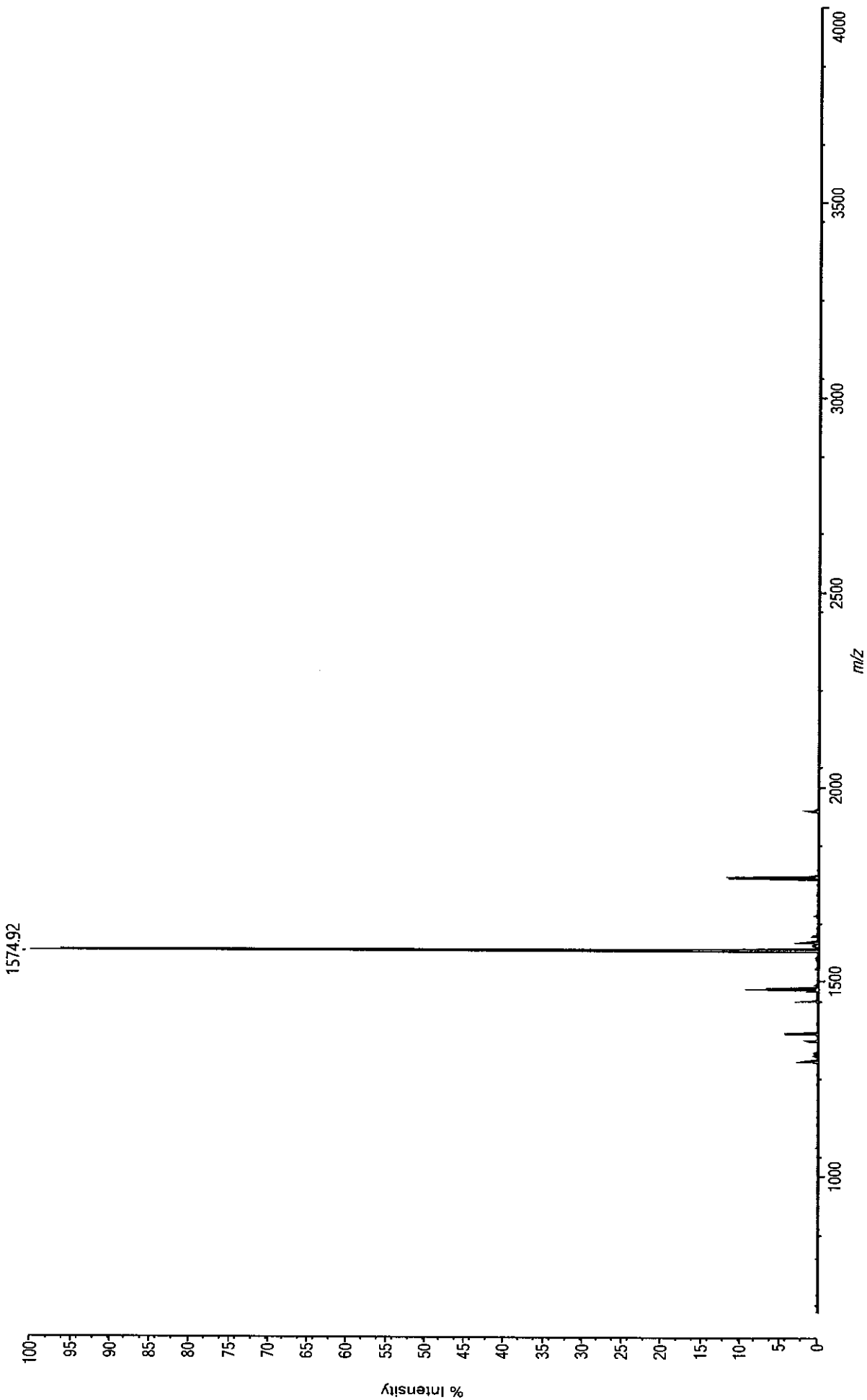
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	15.025	36031	6498	0.364	0.282
2	15.135	12492568	1737713	97.337	97.624
3	15.350	41152	12554	0.703	0.322
4	15.816	226923	28486	1.596	1.773
Total				100.000	100.000

Data: A3098-12 [MW=1573.76] CB_0001:81 Thursday, November 14, 2019 2:32:23 PM Cal:Named Calibration "TOFMIX_8/27/2019" by MALDI Solutions Admin on Tuesday, August 27, 2019 4:32:14 PM (Origin...
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

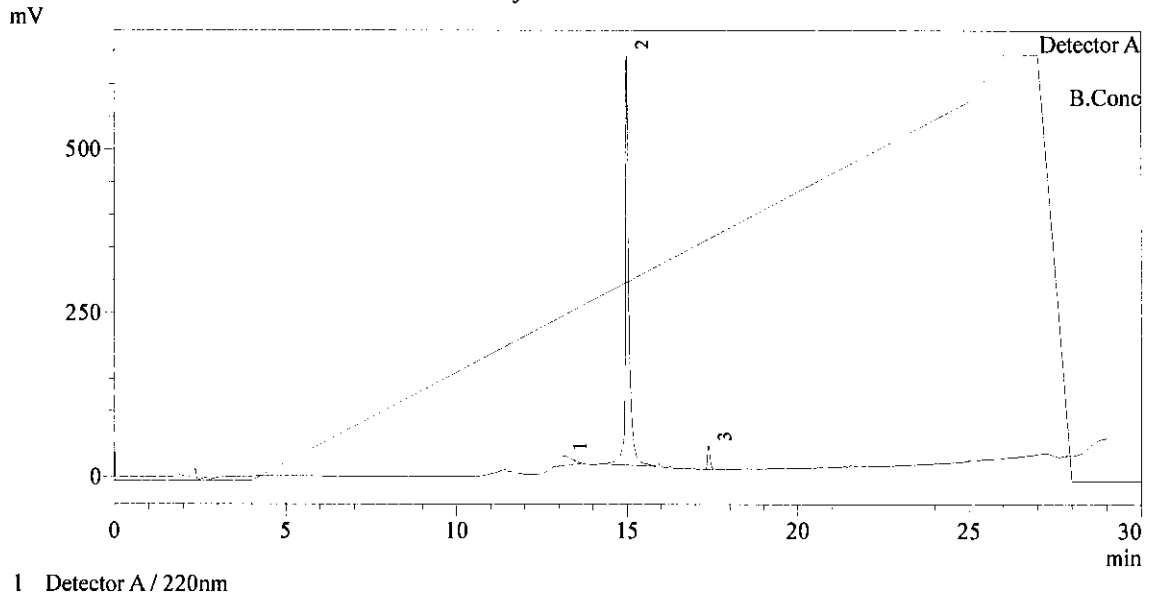
Processed data (averaged) : 577.3 mV [sum=3651.0 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A3098-12
 Sample ID : A3098-12
 Data Filename : A3098-12.lcd
 Method Filename : ANAPEP_29.lcm
 Date Acquired : 11/14/2019 9:14:47 PM
 Data Processed : 11/14/2019 9:43:55 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 A3098-12 Default Project - 4-334/4-1492 - A3098-12.lcd



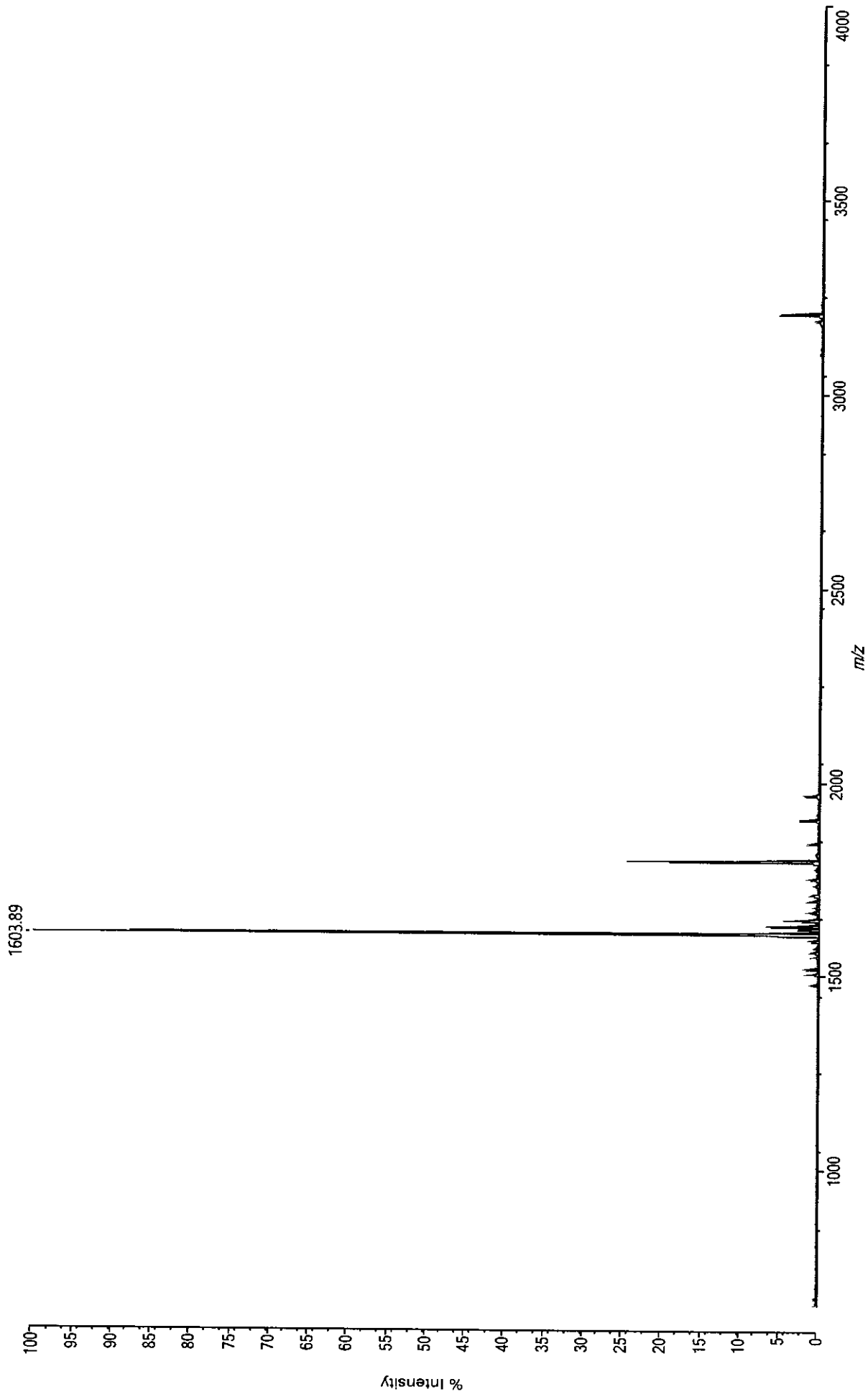
Peak Table

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	13.167	396314	14184	2.096	7.795
2	15.000	4502463	626852	92.641	88.562
3	17.395	185202	35609	5.263	3.643
Total				100.000	100.000

Data: A3098-13 [MW=1603.83] CB_0001.C1 Thursday, November 14, 2019 2:32:23 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 2:34:41 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

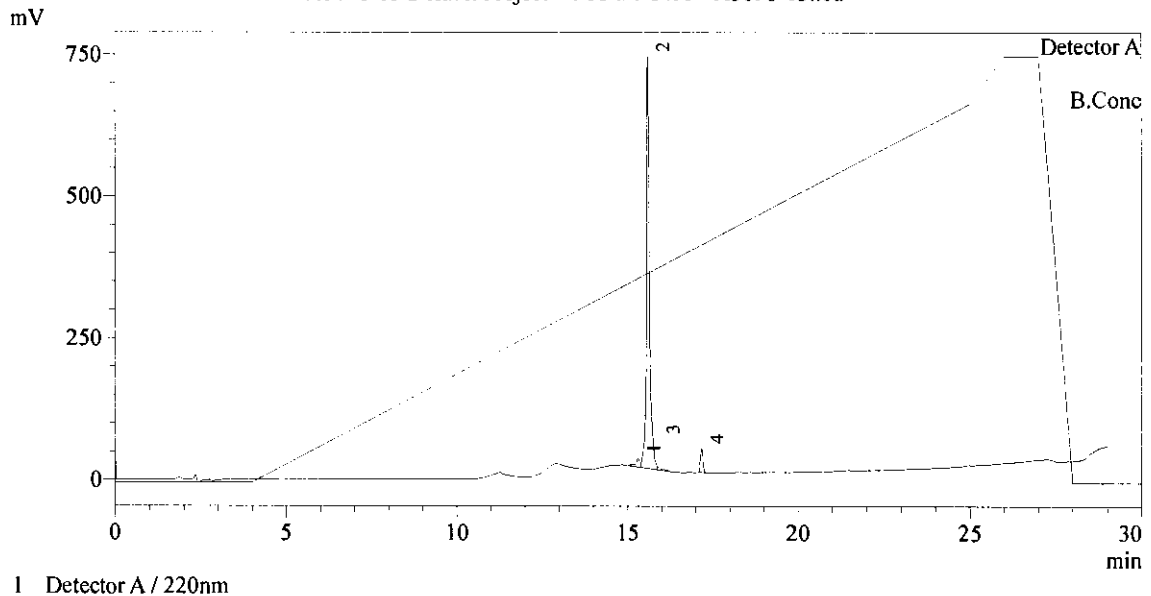
Processed data (averaged) : 885.9 mV [sum=5603.0 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A3098-13
 Sample ID : A3098-13
 Data Filename : A3098-13.lcd
 Method Filename : ANAPEP_29.lcm
 Date Acquired : 11/14/2019 9:49:00 PM
 Data Processed : 11/14/2019 10:18:08 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID : CD-347 / EQ-349

Chromatogram
 A3098-13 Default Project - 4-334/4-1493 - A3098-13.lcd



I Detector A / 220nm

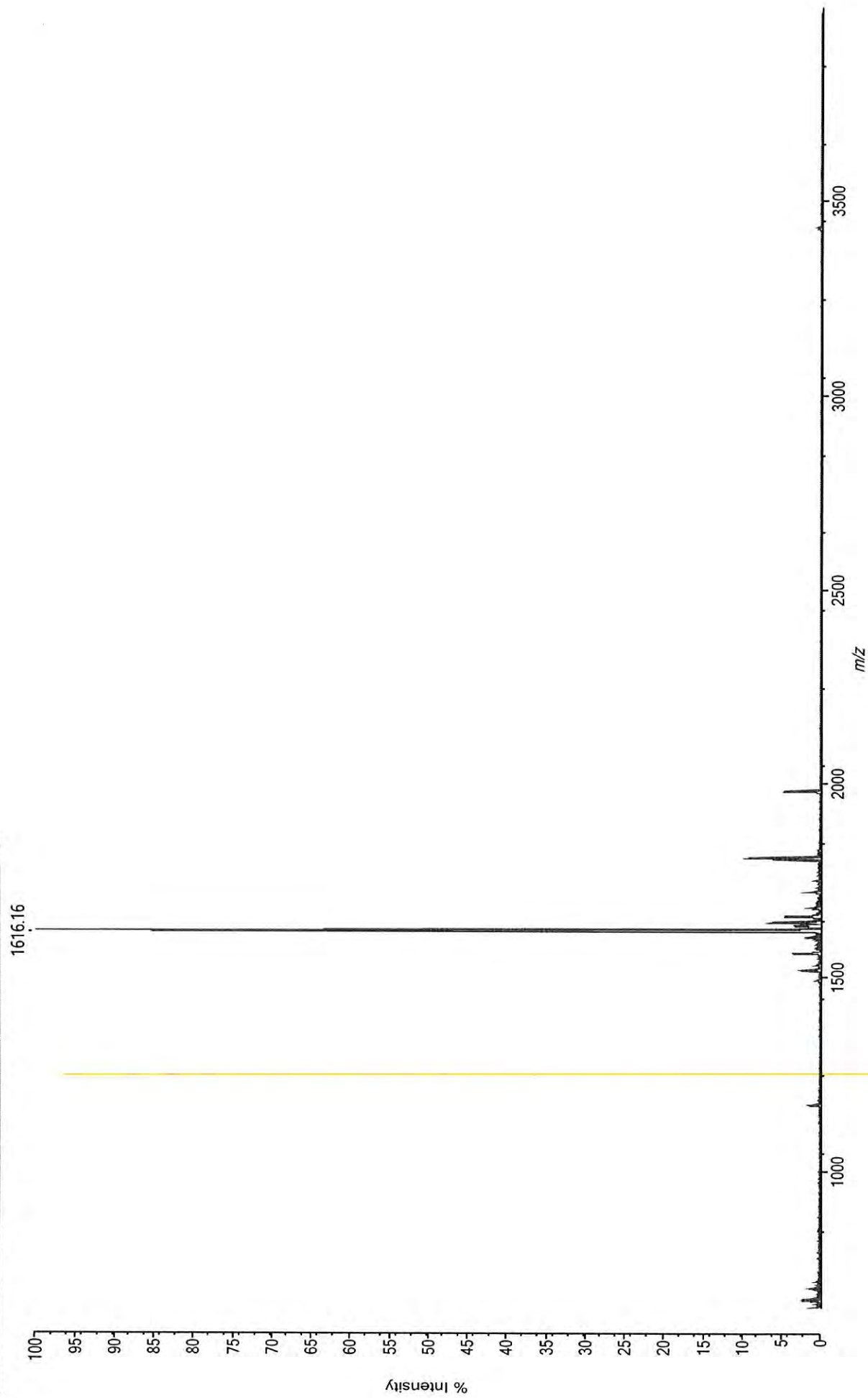
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	15.300	119006	15782	1.998	2.459
2	15.594	4462883	726483	91.958	92.216
3	15.879	48459	5448	0.690	1.001
4	17.169	209238	42302	5.355	4.323
Total				100.000	100.000

Data: A3098-14 [MW=1616.82] CB_0001:A3 Friday, November 15, 2019 10:47:21 AM Cal:Custom Calibration by MALDI Solutions Admin on Friday, November 15, 2019 10:48:52 AM
Shimadzu MALDI-8020: Tuning_Linear, Power 36, P.Ext at 7622.00 (bin 237)

Processed data (averaged) : 269.7 mV [sum=1705.7 mV], Smoothed = 5, profiles # 1 - 50

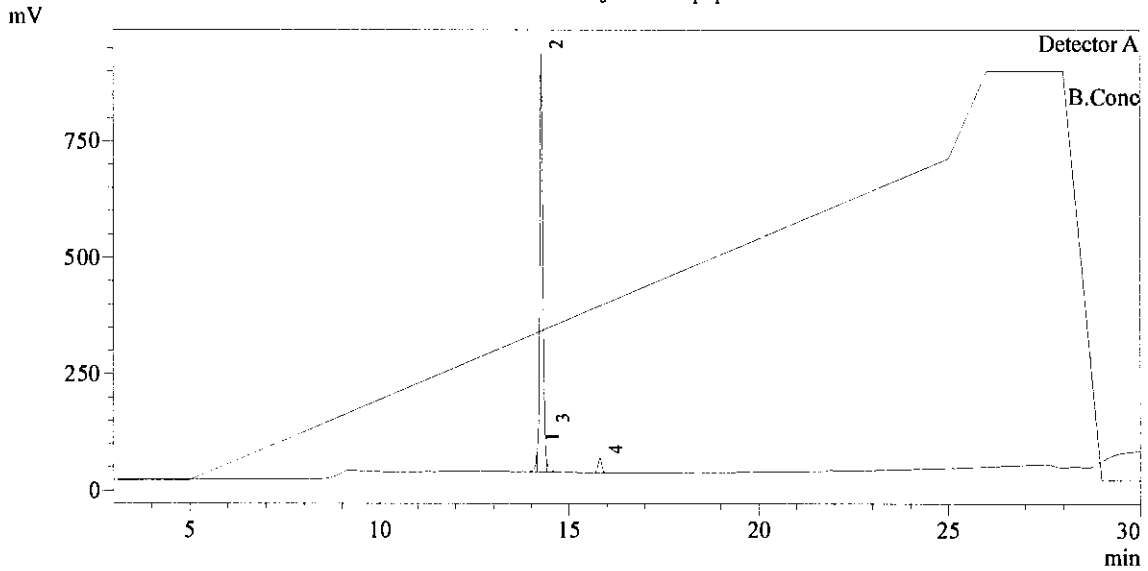


Sample Information

Acquired by : System Administrator
 Sample Name : A3098-14
 Sample ID : A3098-14
 Data Filename : A3098-14.lcd
 Method Filename : ANAPEP25_FORM_ID.lsr.lcm
 Date Acquired : 11/16/2019 2:27:43 AM
 Data Processed : 11/16/2019 2:59:57 AM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID : CD-339 / EQ-332

Chromatogram

A3098-14 C:\LabSolutions\Data\Project1\Anapep25\A3098-14.lcd



1 Detector A / 220nm

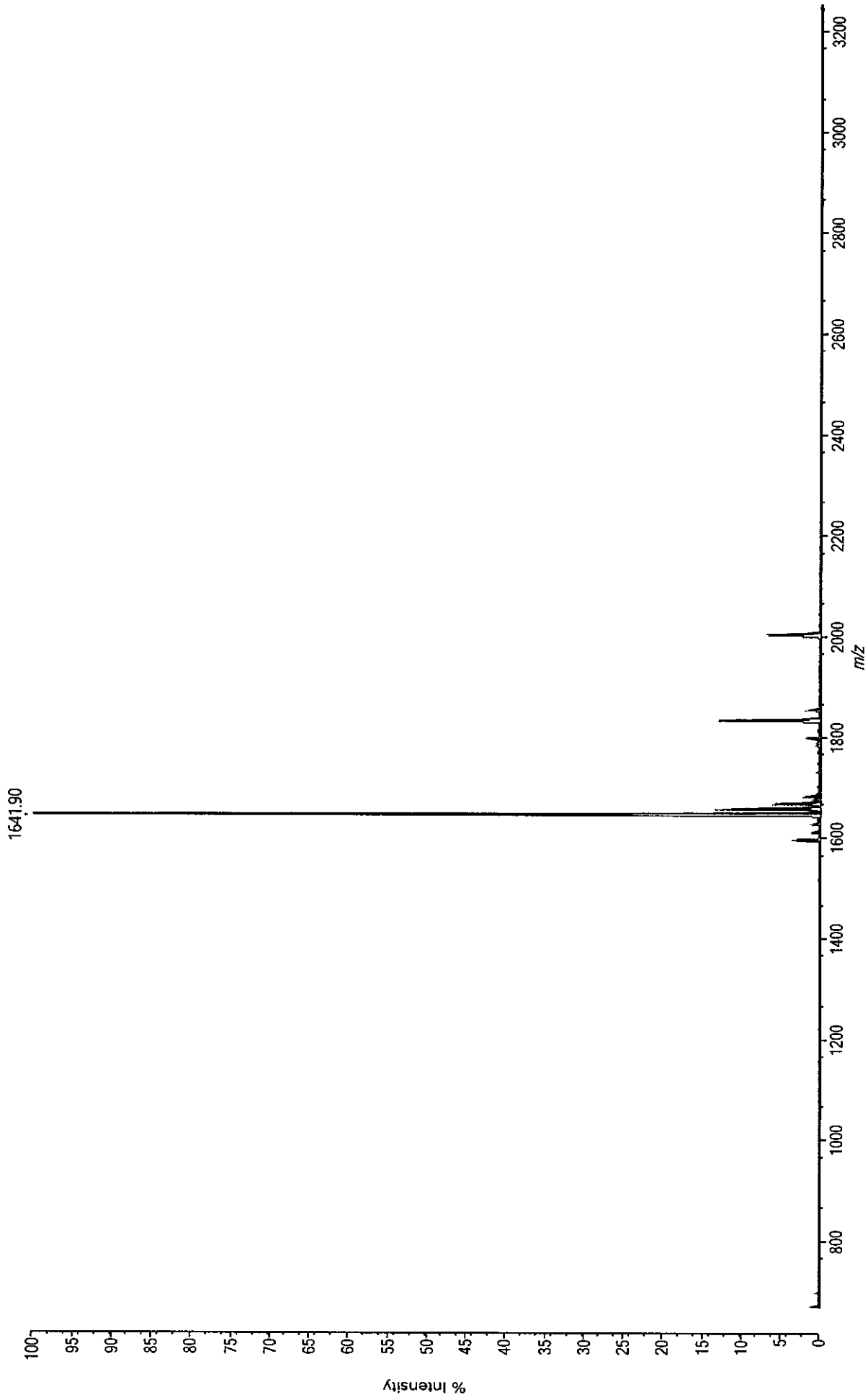
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	14.142	111757	33130	3.382	1.891
2	14.270	5514458	898011	91.675	93.308
3	14.425	74445	17632	1.800	1.260
4	15.820	209303	30786	3.143	3.542
Total				100.000	100.000

Data: A3098-15 [MW=1641.92] CB_0001:E1 Thursday, November 14, 2019 2:32:23 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 2:34:41 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

Processed data (averaged) : 846.5 mV [sum=5353.6 mV], Smoothed = 10, profiles # 1 - 50

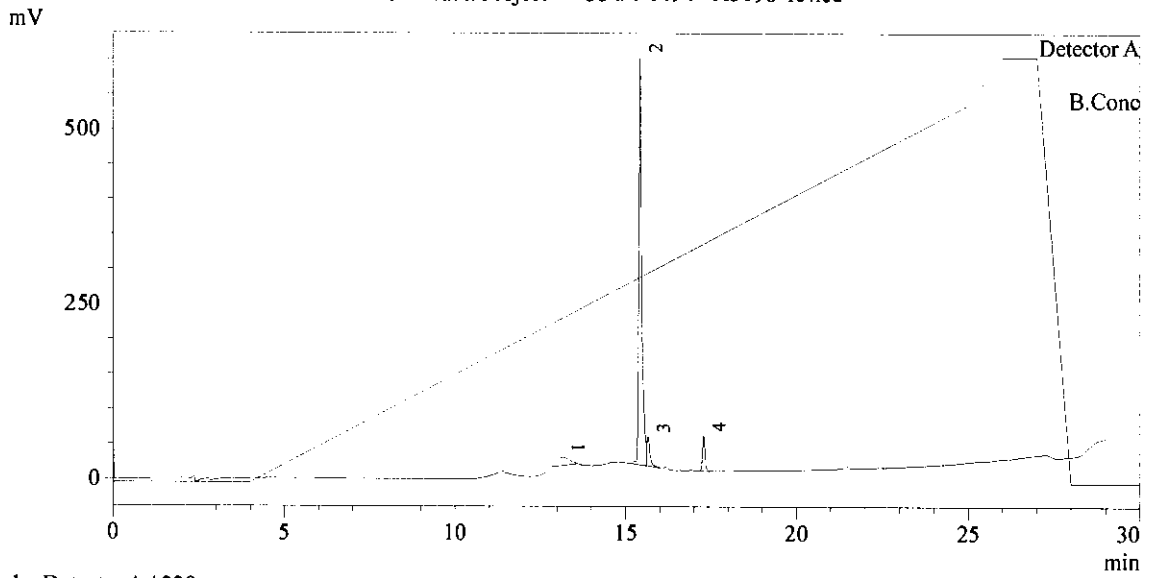


Sample Information

Acquired by : System Administrator
 Sample Name : A3098-15
 Sample ID : A3098-15
 Data Filename : A3098-15.lcd
 Method Filename : ANAPEP_29.lcm
 Date Acquired : 11/14/2019 10:23:14 PM
 Data Processed : 11/14/2019 10:52:24 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram

A3098-15 Default Project - 4-334/4-1494 - A3098-15.lcd



1 Detector A / 220nm

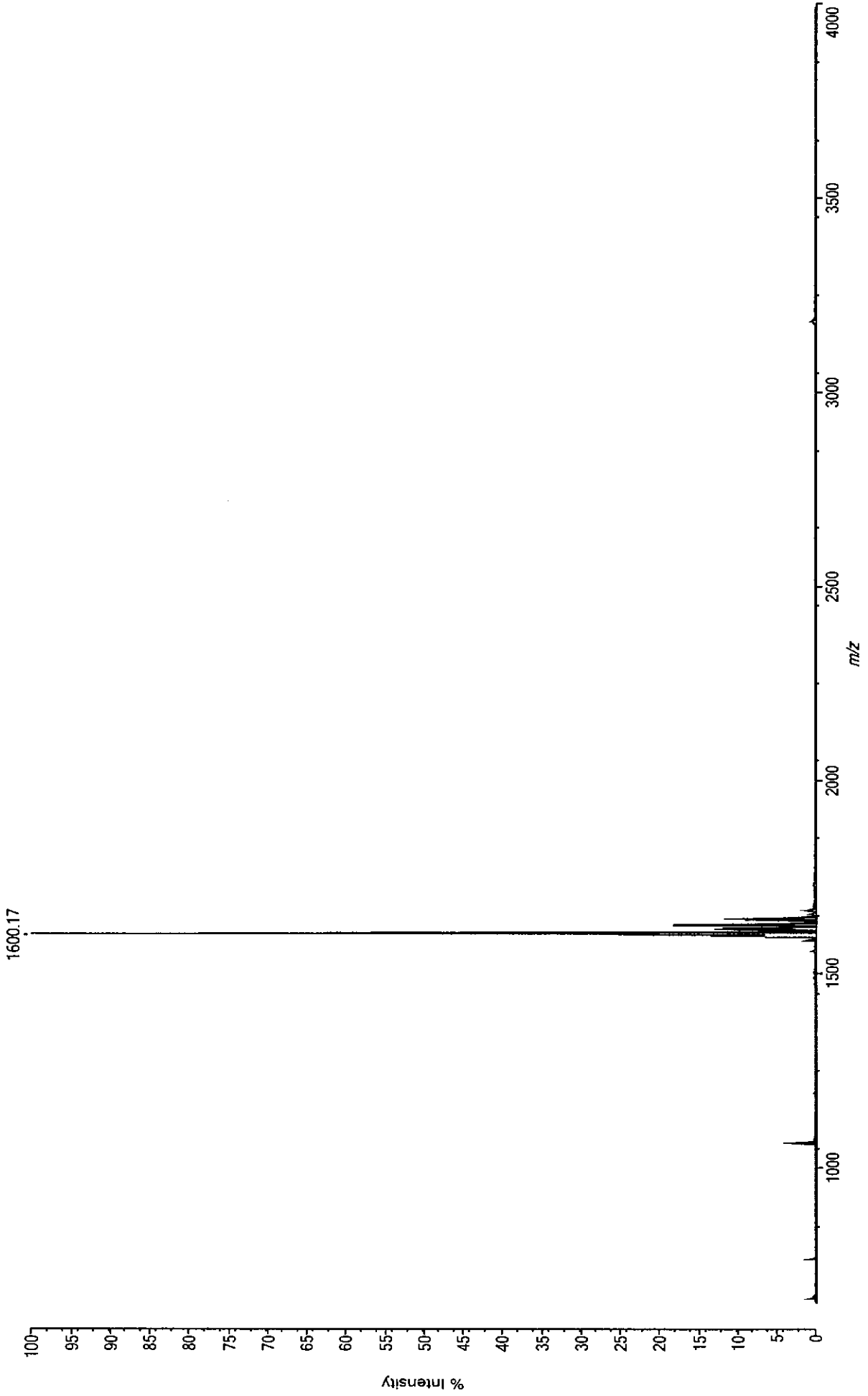
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	13.140	293007	11651	1.700	6.924
2	15.412	3439646	582697	85.029	81.281
3	15.652	248717	41028	5.987	5.877
4	17.281	250408	49913	7.284	5.917
Total				100.000	100.000

Data: A3098-16 [MW=1599.77] CB_0001.F1 Thursday, November 14, 2019 2:32:23 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 2:34:41 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

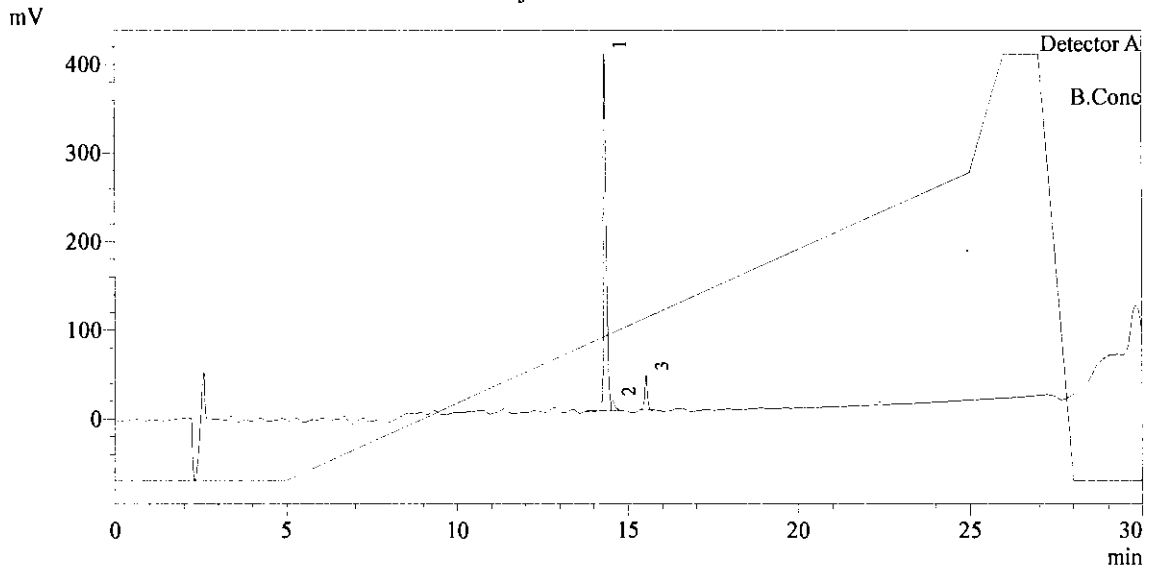
Processed data (averaged) : 1063.2 mV [sum=6724.0 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A2098-16
 Sample ID : A2098-16
 Data Filename : A2098-16.lcd
 Method Filename : ANAPEP_28.lcm
 Date Acquired : 11/15/2019 9:37:46 AM
 Data Processed : 11/15/2019 10:07:57 AM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 A2098-16 Default Project - 3-170/3-406 - A2098-16.lcd



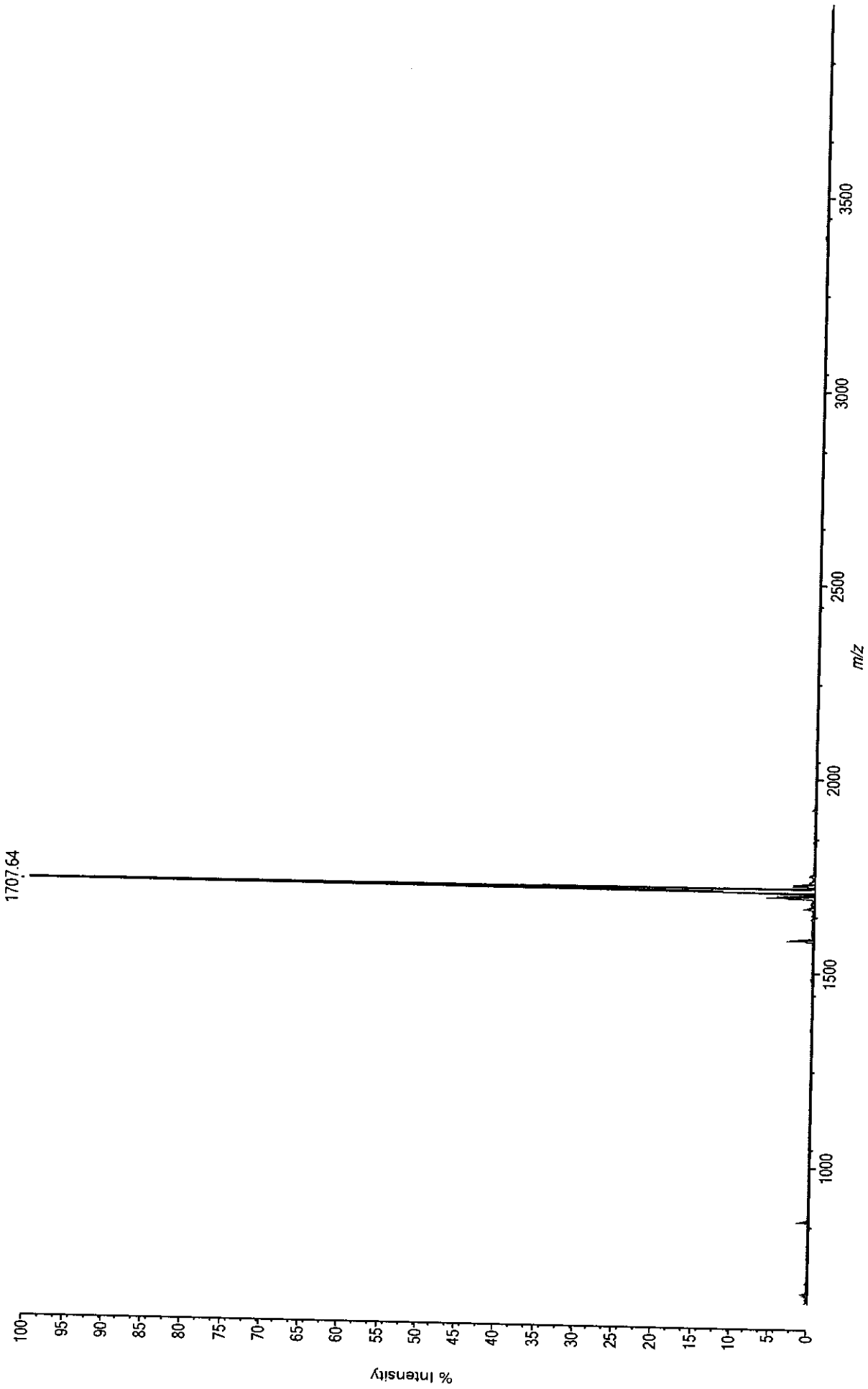
1 Detector A / 220nm

PeakTable

Peak#	Ret. Time	Area	Height	Height %	Area %
1	14.337	2390824	402417	89.038	89.235
2	14.564	76246	10900	2.412	2.846
3	15.534	212160	38642	8.550	7.919
Total				100.000	100.000

Data: A309B-17 [MW=1707.86] CB_0001:83 Friday, November 15, 2019 10:49:06 AM Cal:Custom Calibration by MALDI Solutions Admin on Friday, November 15, 2019 10:50:14 AM
Shimadzu MALDI-8020: Tuning Linear, Power 36, P.Ext at 7622.00 (bin 237)

Processed data (averaged) : 408.0 mV [sum=2580.4 mV]. Smoothed = 15, profiles # 1 - 50

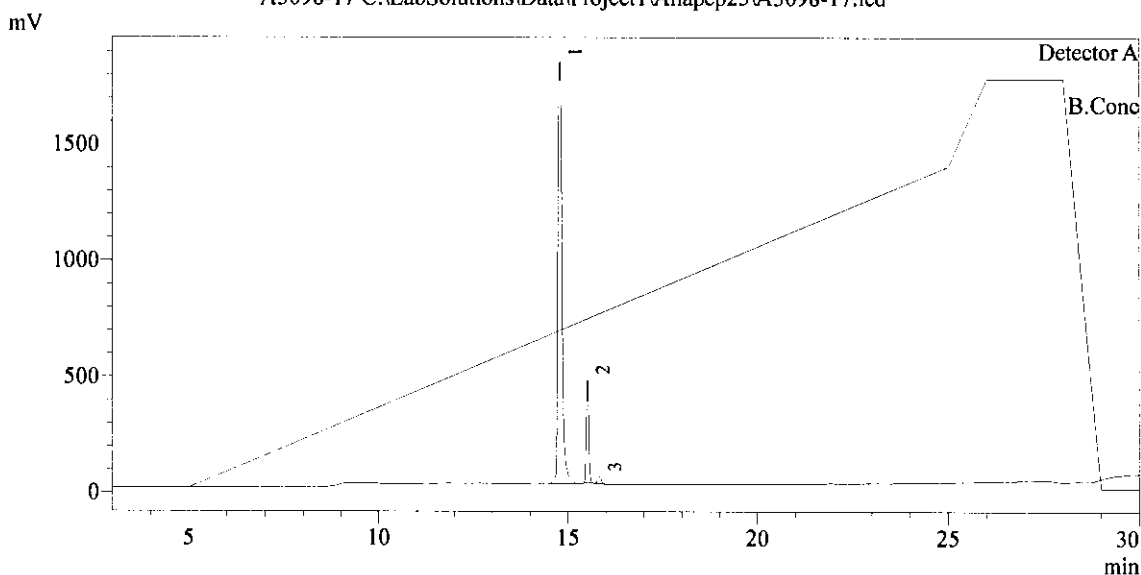


Sample Information

Acquired by : System Administrator
 Sample Name : A3098-17
 Sample ID : A3098-17
 Data Filename : A3098-17.lcd
 Method Filename : ANAPEP25_FORM_ID.lsr.lcm
 Date Acquired : 11/16/2019 3:00:32 AM
 Data Processed : 11/16/2019 3:32:45 AM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram

A3098-17 C:\LabSolutions\Data\Project1\Anapep25\A3098-17.lcd



1 Detector A / 220nm

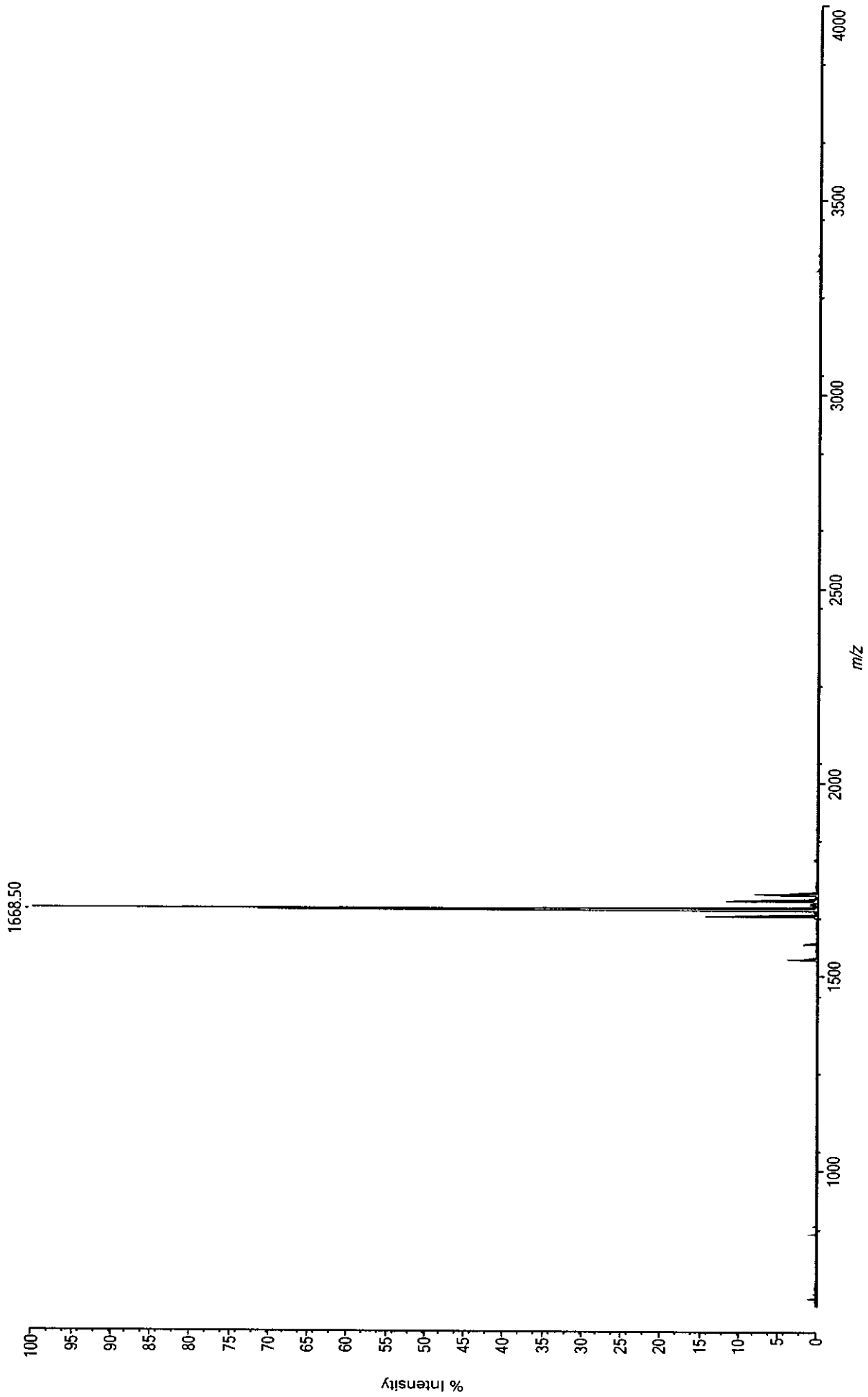
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	14.780	13876163	1819686	79.164	85.656
2	15.512	2126783	447062	19.449	13.128
3	15.835	196884	31871	1.387	1.215
Total				100.000	100.000

Data: A3098-18 [MW=1667.8] CB_0001:H1 Thursday, November 14, 2019 2:32:23 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 2:34:41 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

Processed data (averaged) : 419.7 mV [sum=2654.7 mV], Smoothed = 10, profiles # 1 - 50

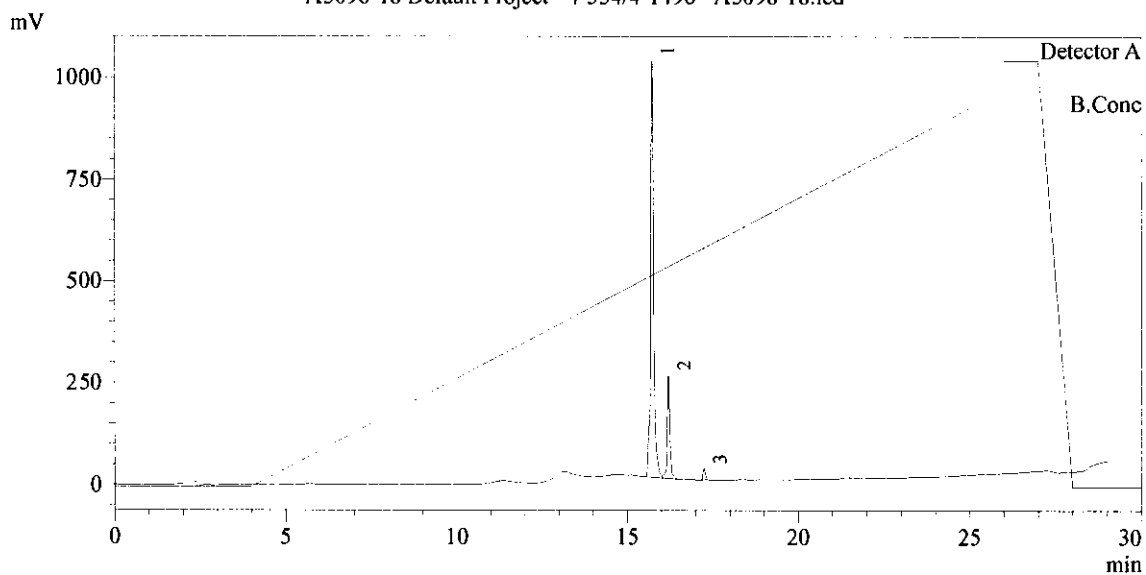


Sample Information

Acquired by : System Administrator
 Sample Name : A3098-18
 Sample ID : A3098-18
 Data Filename : A3098-18.lcd
 Method Filename : ANAPEP_29.lcm
 Date Acquired : 11/14/2019 11:31:41 PM
 Data Processed : 11/15/2019 12:00:49 AM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram

A3098-18 Default Project - 4-334/4-1496 - A3098-18.lcd



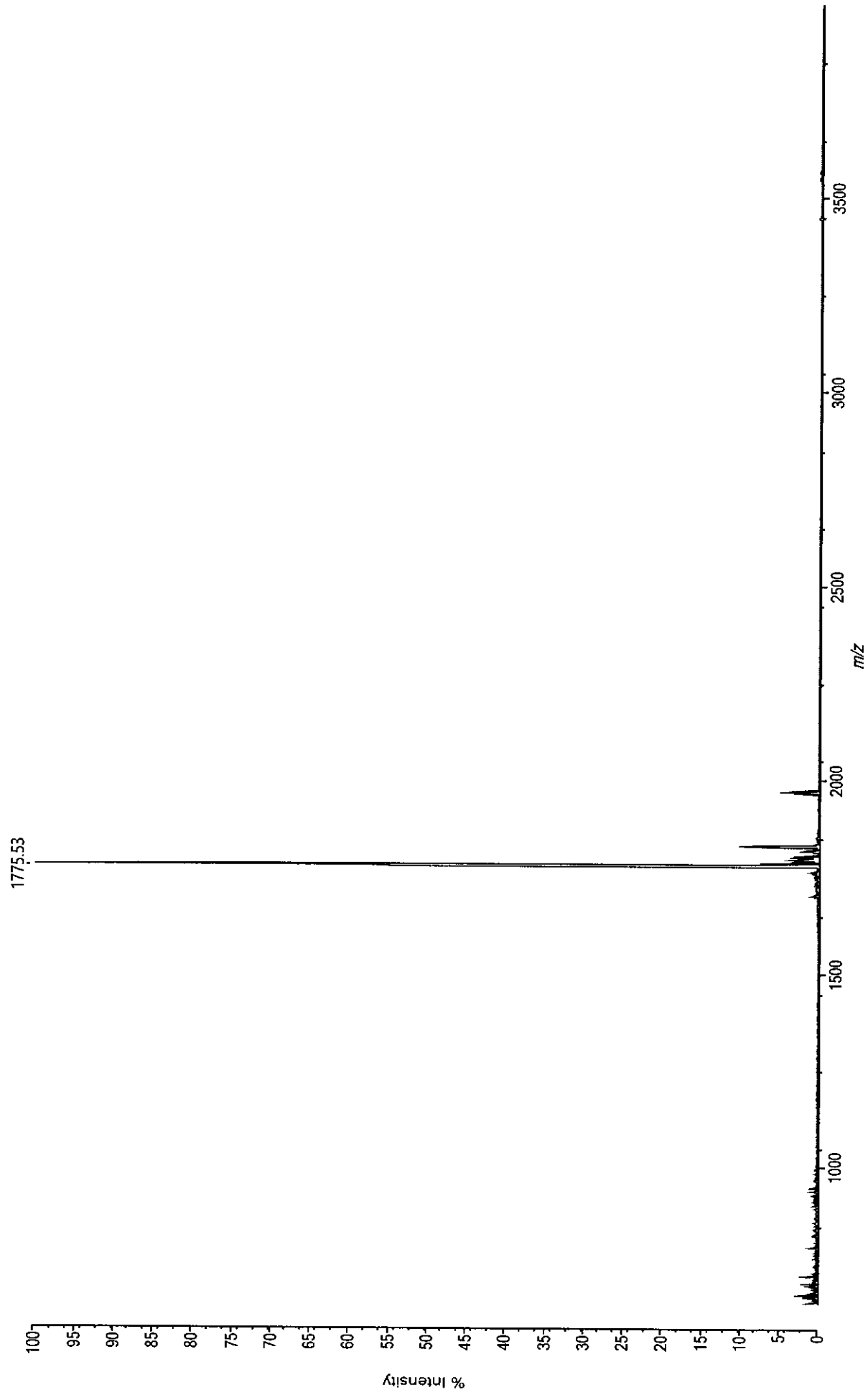
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	15.736	6266353	1023426	78.389	80.799
2	16.208	1356487	254501	19.493	17.491
3	17.250	132604	27655	2.118	1.710
Total				100.000	100.000

Data: A3098-19 [MW=1775.01] CB_0001:C3 Friday, November 15, 2019 10:50:28 AM Cal:Custom Calibration by MALDI Solutions Admin on Friday, November 15, 2019 10:51:19 AM
Shimadzu MALDI-8020: Tuning Linear, Power 36, P.Ext at 7622.00 (bin 237)

Processed data (averaged) : 147.4 mV [sum=932.5 mV], Smoothed = 15, profiles # 1 - 50

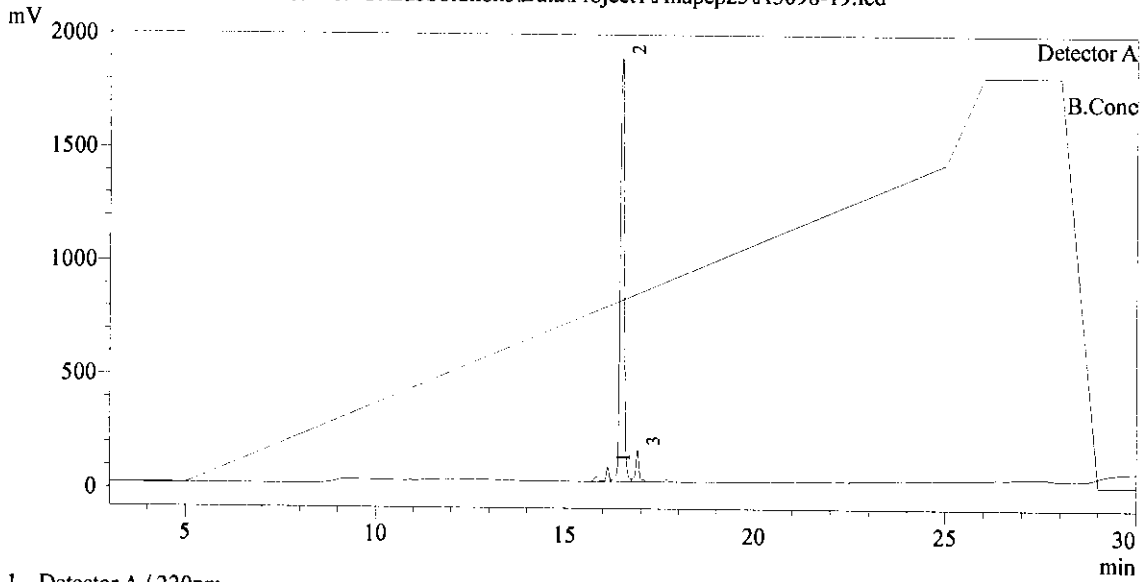


Sample Information

Acquired by : System Administrator
 Sample Name : A3098-19
 Sample ID : A3098-19
 Data Filename : A3098-19.lcd
 Method Filename : ANAPEP25_FORM_ID.Isr.lcm
 Date Acquired : 11/16/2019 3:33:20 AM
 Data Processed : 11/16/2019 4:05:33 AM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram

A3098-19 C:\LabSolutions\Data\Project1\Anapep25\A3098-19.lcd



1 Detector A / 220nm

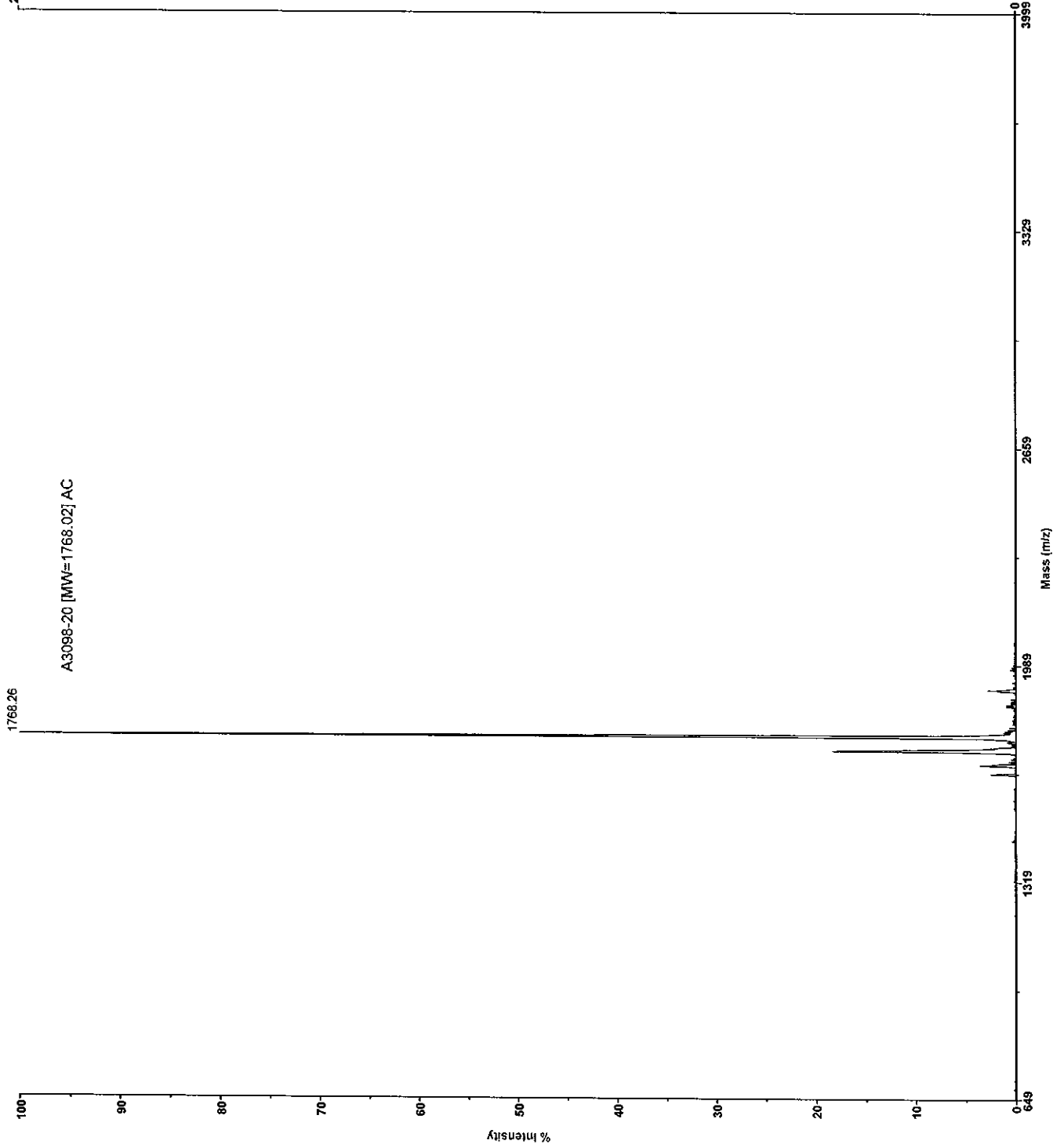
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	16.117	458211	63130	3.060	2.969
2	16.481	14126485	1862610	90.287	91.539
3	16.902	847475	137240	6.653	5.492
Total				100.000	100.000

Applied Biosystems Voyager System 1099

Voyager Spec #1=>SM5=>NR(2.00)=>AdvBC(32,0.5,0.1)=>AdvBC(25,0.5,0.1)=>AdvBC(20,0.5,0.1)[BP = 1768.0, 2165]



Mode of operation: Linear
Extraction mode: Delayed
Polarity: Negative
Acquisition control: Manual

Accelerating voltage: 20000 V
Grid voltage: 95%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 650 -- 4000 Da
Number of laser shots: 100/spectrum
Laser intensity: 1763
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 16.77
Bin size: 2 nsec
Number of data points: 12324
Vertical scale: 200 mV
Vertical offset: 0%
Input bandwidth: 500 MHz

Sample well: 33
Plate ID: 100 WELL PLATE
Serial number: 1099
Instrument name: Voyager-DE
Plate type filename: C:\VOYAGER\100 well plate.plt
Lab name: BioSynthesis, Inc

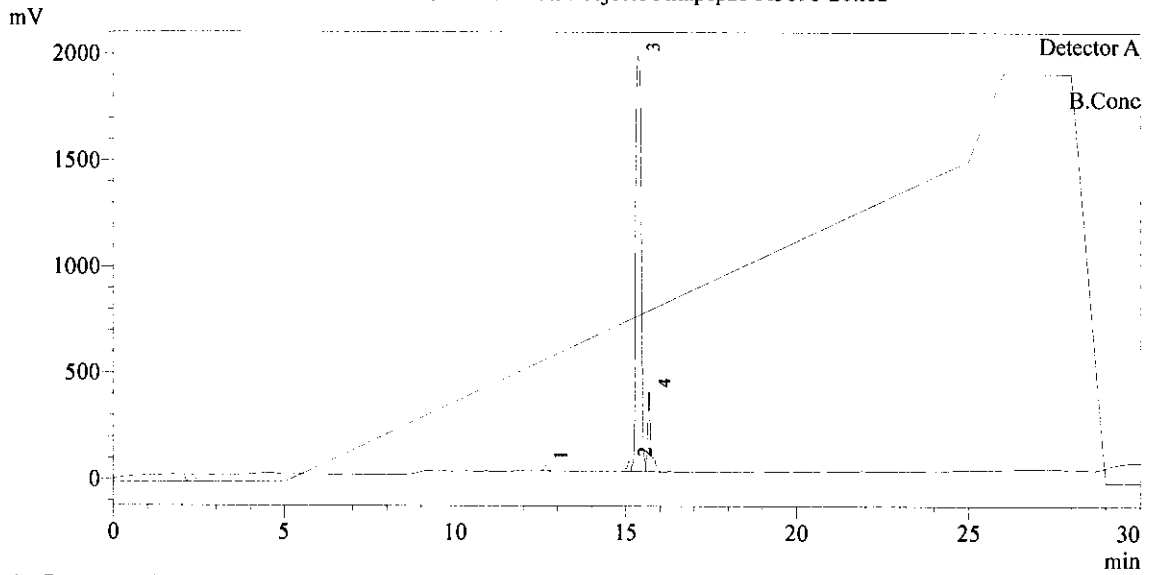
Absolute x-position: 11847.3
Absolute y-position: 32800.7
Relative x-position: 99.7894
Relative y-position: 733.181
Shots in spectrum: 71
Source pressure: 4.557e-007
Mirror pressure: 0
TC2 pressure: 0.001
TIS gate width: 30
TIS flight length: 940

Sample Information

Acquired by : System Administrator
 Sample Name : A3098-20
 Sample ID : A3098-20
 Data Filename : A3098-20.lcd
 Method Filename : ANAPEP25_FORM_ID.lsr.lcm
 Date Acquired : 11/14/2019 9:30:02 PM
 Data Processed : 11/14/2019 10:02:15 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram

A3098-20 C:\LabSolutions\Data\Project1\Anapep25\A3098-20.lcd



1 Detector A / 220nm

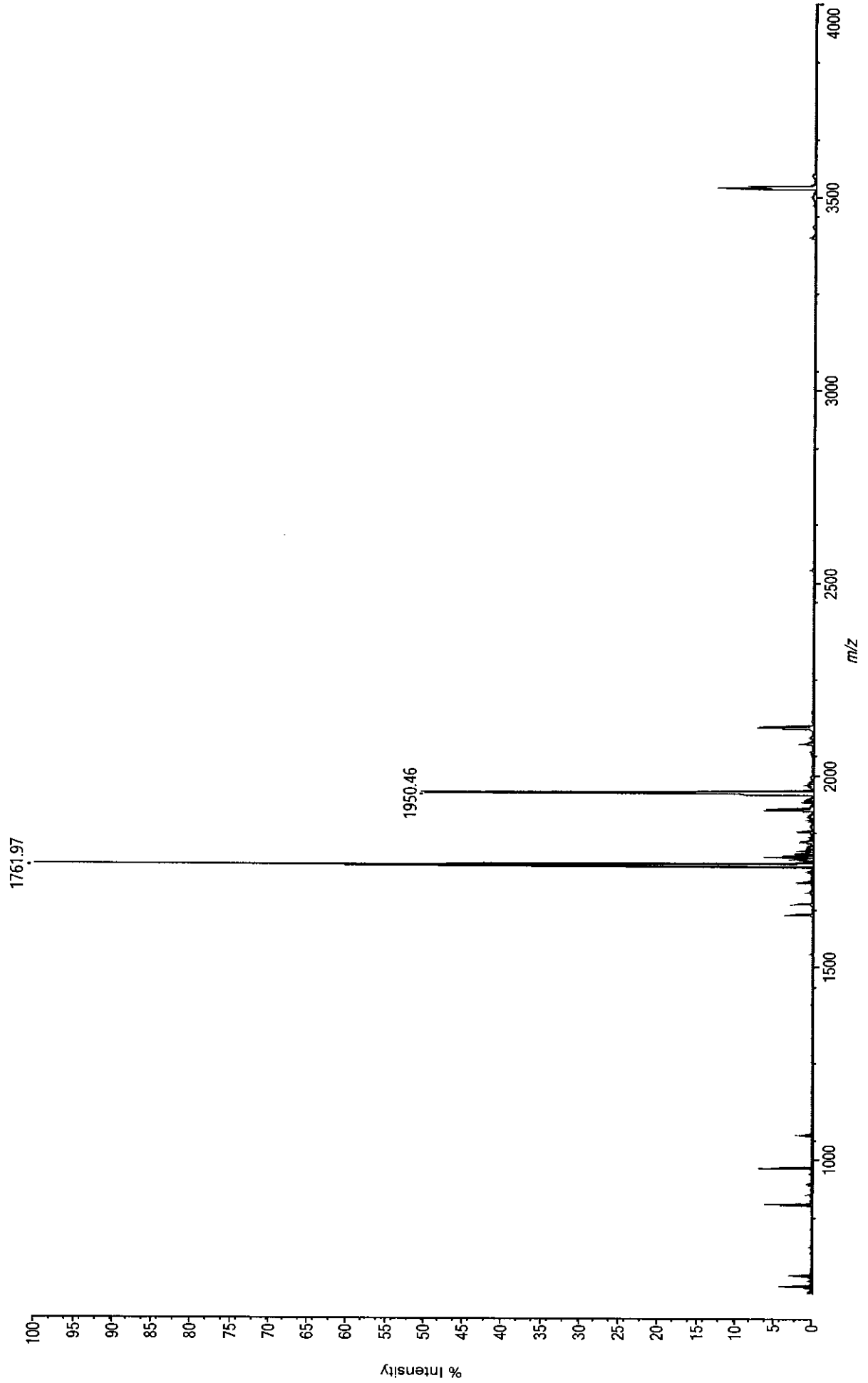
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	12.647	149478	26963	1.123	0.608
2	15.087	298617	47658	1.984	1.215
3	15.351	21646177	1953128	81.327	88.038
4	15.674	2492941	373811	15.565	10.139
Total				100.000	100.000

Data: A3098-21 [MW=1760.09] CB_0001.A1 Thursday, November 14, 2019 4:02:03 PM Cal:Named Calibration "TOFMIX_8/27/2019" by MALDI Solutions Admin on Tuesday, August 27, 2019 4:32:14 PM (Origin... Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

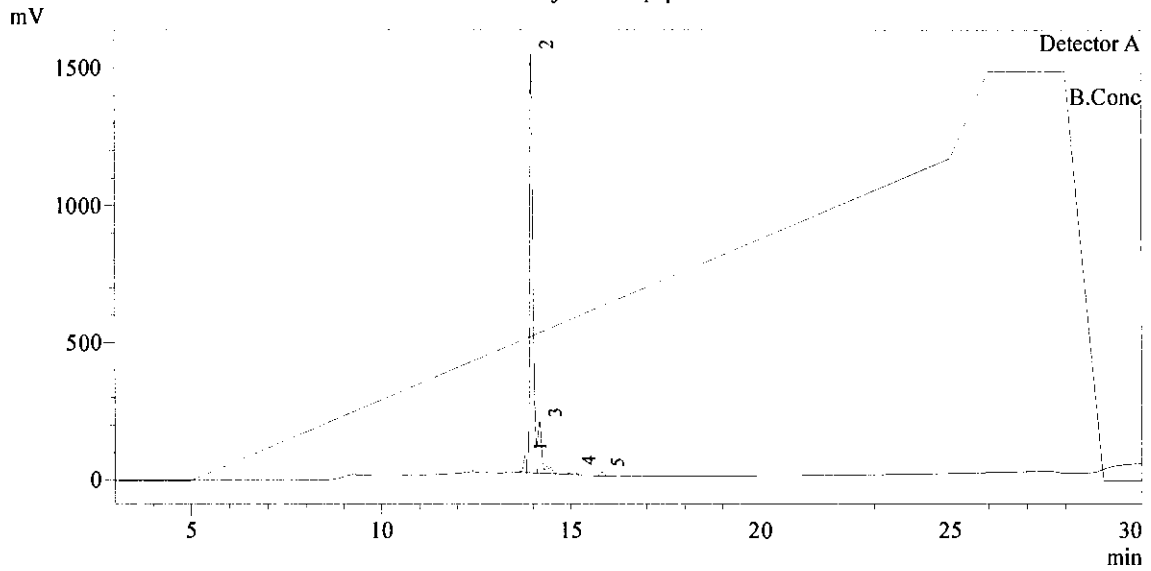
Processed data (averaged) : 510.8 mV [sum=3230.9 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A3098-21
 Sample ID : A3098-21
 Data Filename : A3098-21.lcd
 Method Filename : ANAPEP25_FORM_ID.lsr.lcm
 Date Acquired : 11/15/2019 10:36:20 AM
 Data Processed : 11/15/2019 11:08:34 AM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 C:\LabSolutions\Data\Project1\Anapep25\A3098-21.lcd



1 Detector A / 220nm

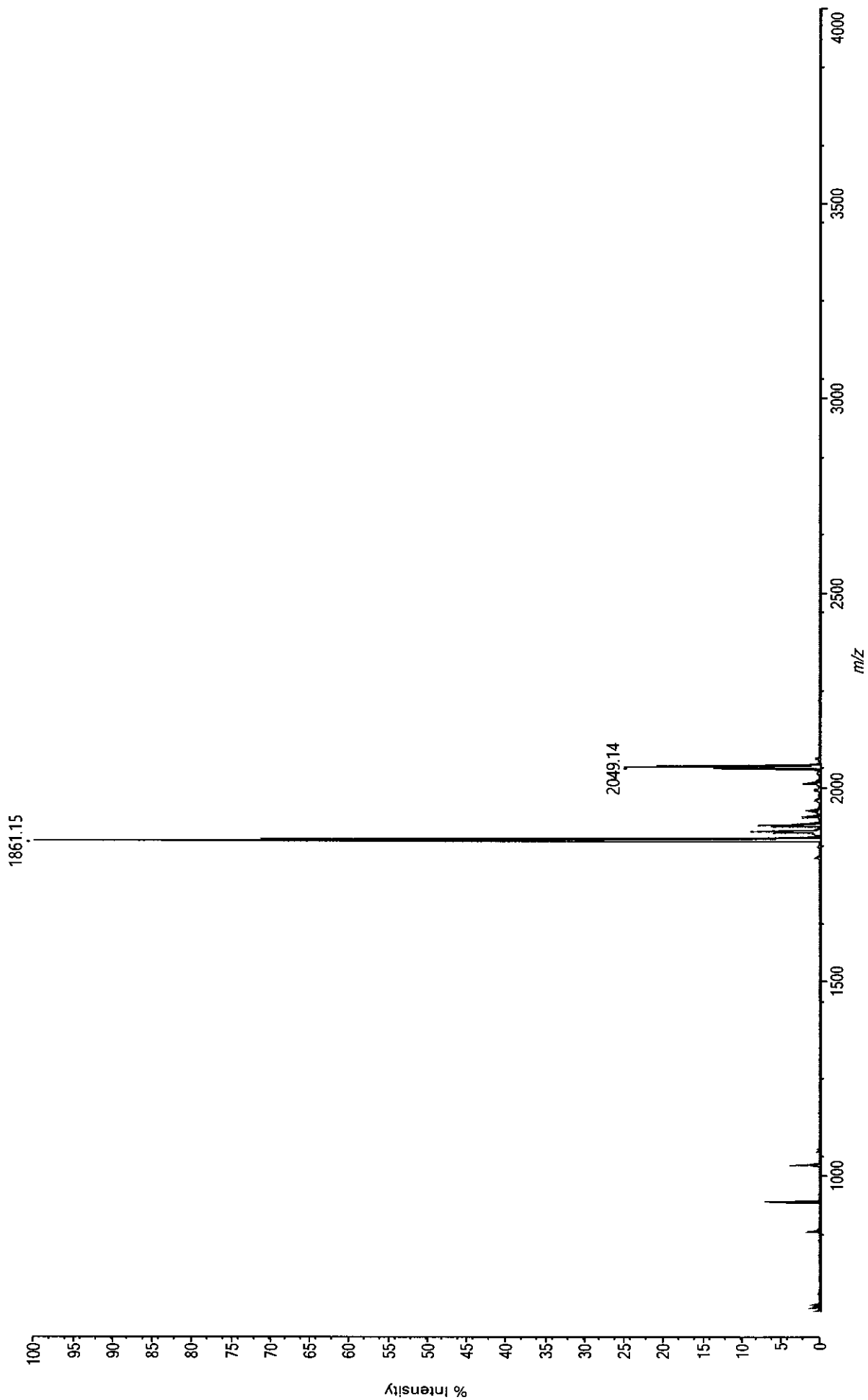
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	13.781	314032	60387	3.351	2.824
2	13.966	9075758	1523852	84.573	81.628
3	14.171	1492867	186350	10.342	13.427
4	15.062	143026	17327	0.962	1.286
5	15.825	92726	13900	0.771	0.834
Total				100.000	100.000

Data: A3098-22 [MW=1861.16] CB_0001:A4 Monday, November 18, 2019 8:56:53 AM Cal:Named Calibration "TOFMIX_8/27/2019" by MALDI Solutions Admin on Tuesday, August 27, 2019 4:32:14 PM (Original)
Shimadzu MALDI-8020: Tuning Linear, Power 25, P.Ext at 700.00 (bin 72)

Processed data (averaged) : 700.6 mV [sum=4430.9 mV], Smoothed = 15, profiles # 1 - 50

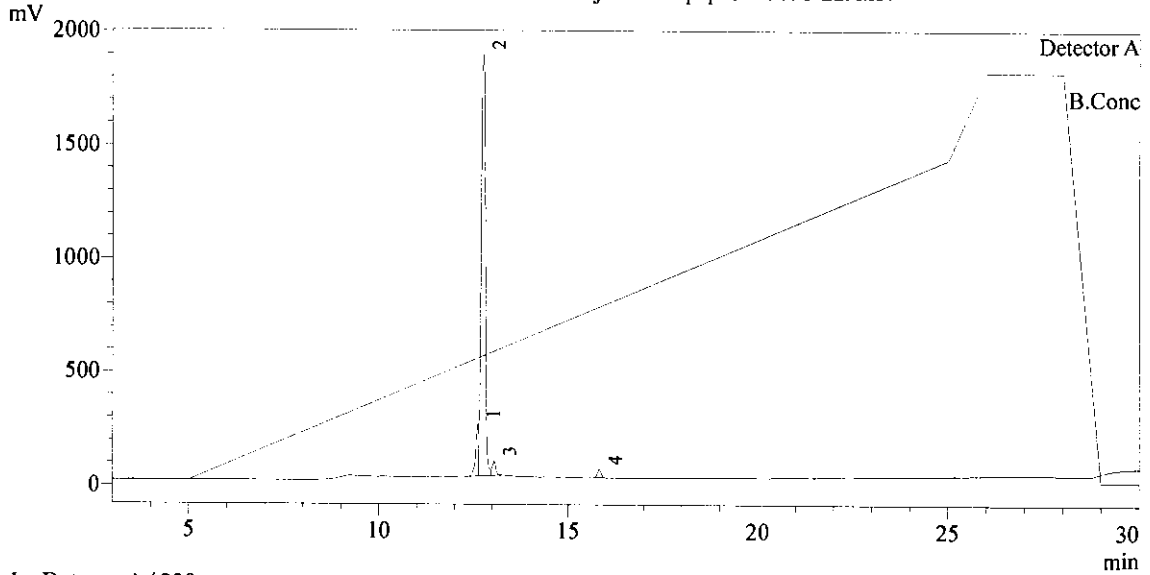


Sample Information

Acquired by : System Administrator
 Sample Name : A3098-22
 Sample ID : A3098-22
 Data Filename : A3098-22A.lcd
 Method Filename : ANAPEP25_FORM_ID.lsr.lcm
 Date Acquired : 11/16/2019 6:17:15 AM
 Data Processed : 11/16/2019 6:49:29 AM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram

A3098-22 C:\LabSolutions\Data\Project1\Anapep25\A3098-22A.lcd



1 Detector A / 220nm

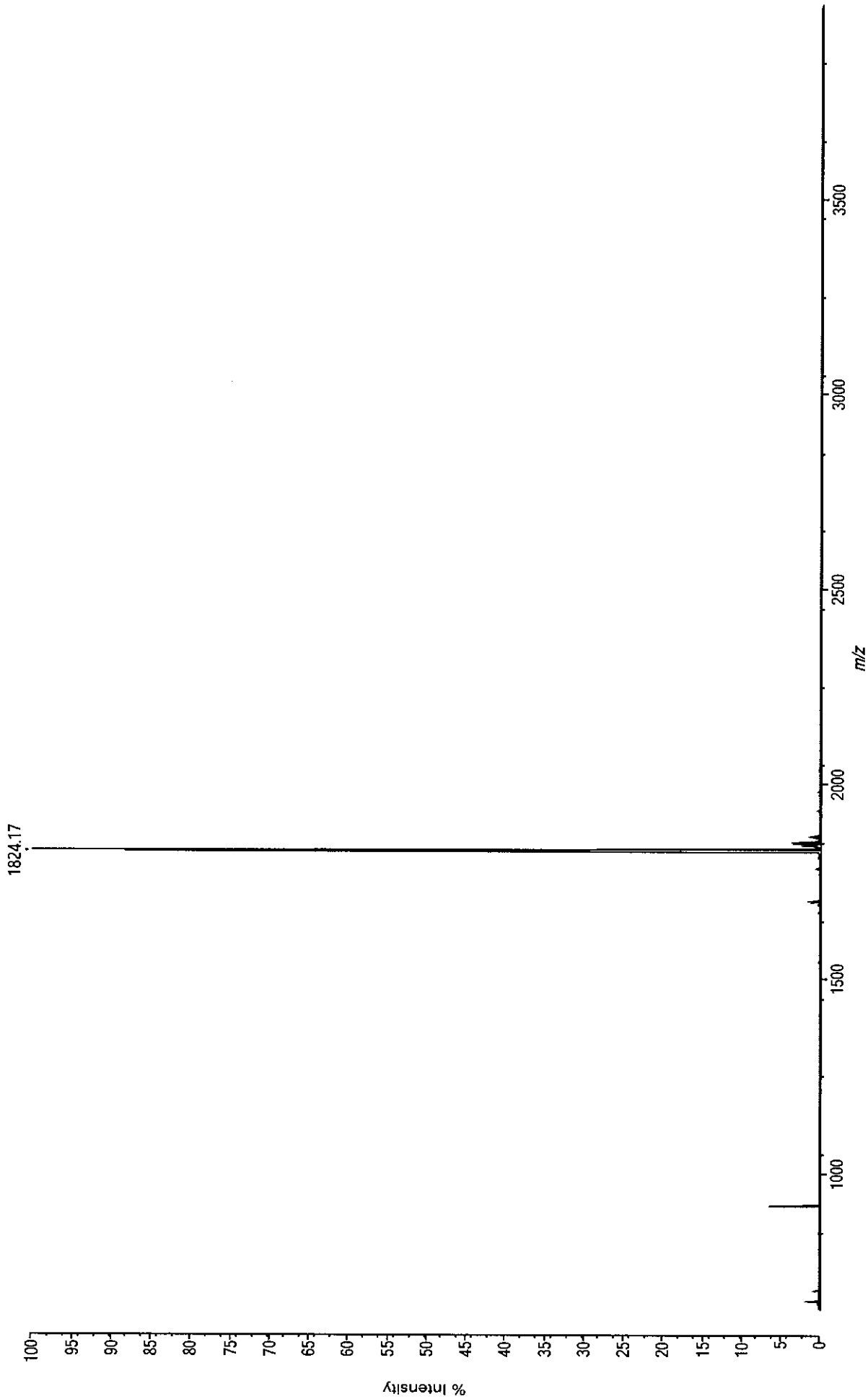
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	12.615	1189230	230294	10.535	7.359
2	12.754	14288687	1857094	84.953	88.424
3	13.046	438226	62778	2.872	2.712
4	15.829	243225	35856	1.640	1.505
Total				100.000	100.000

Data: A3098-23 [MW=1824.08] CB_0001:C1 Thursday, November 14, 2019 4:02:03 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 4:04:17 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

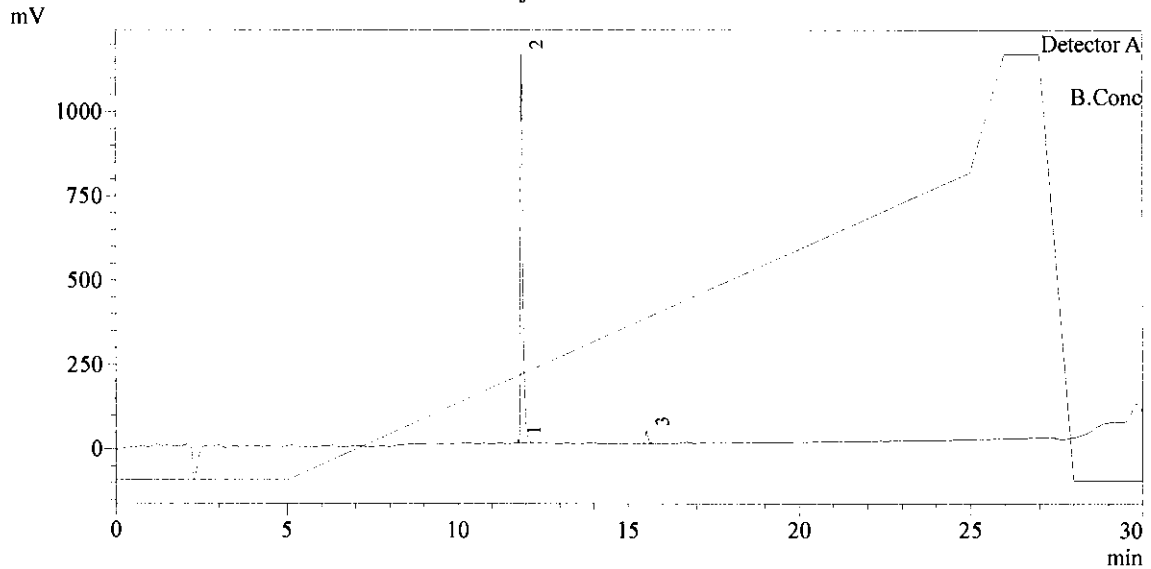
Processed data (averaged) : 1175.7 mV [sum=7436.1 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A2098-23
 Sample ID : A2098-23
 Data Filename : A2098-23.lcd
 Method Filename : ANAPEP_28.lcm
 Date Acquired : 11/15/2019 11:18:57 AM
 Data Processed : 11/15/2019 11:49:08 AM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 A2098-23 Default Project - 3-171/3-409 - A2098-23.lcd



I Detector A / 220nm

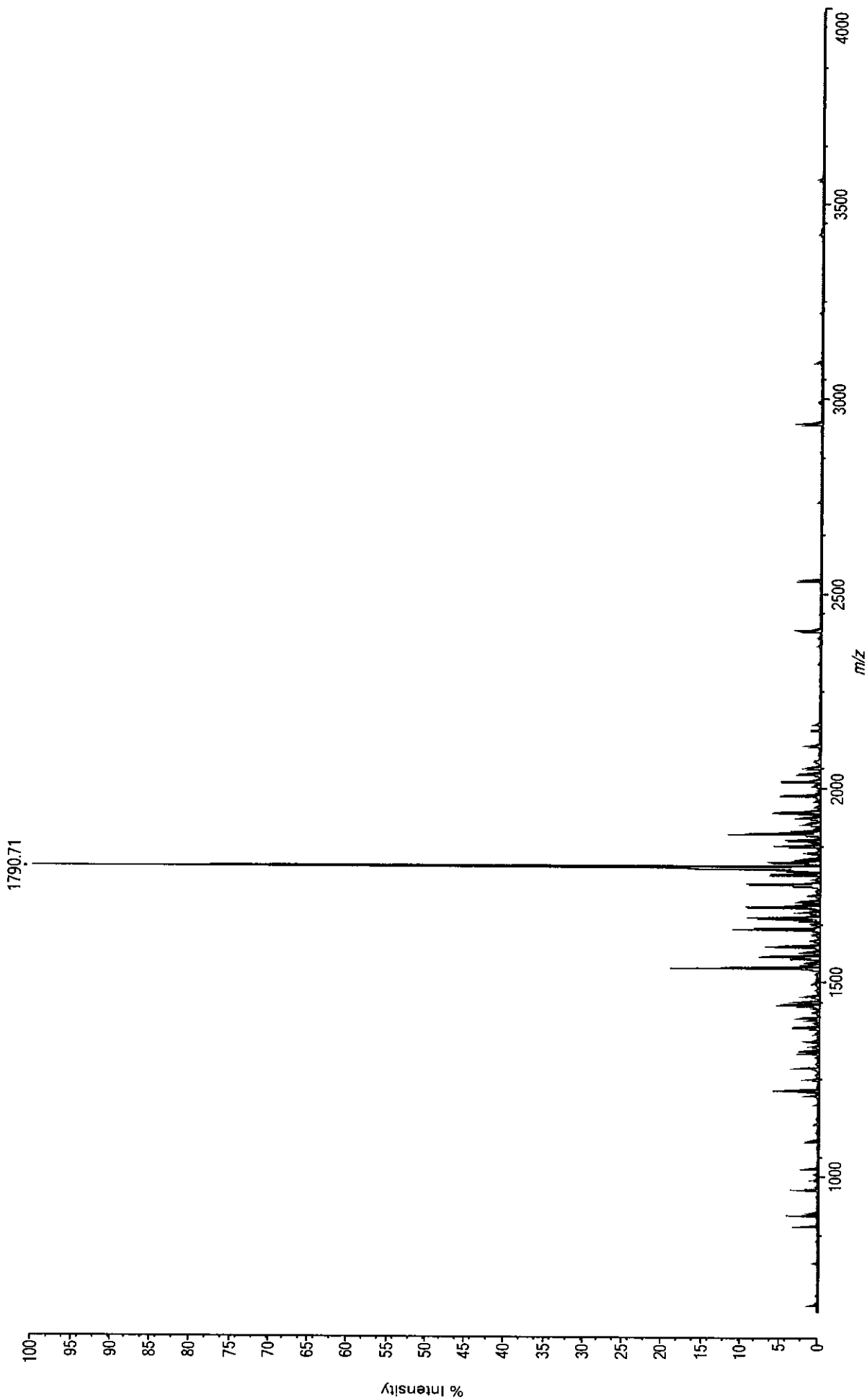
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	11.782	26085	10045	0.837	0.442
2	11.876	5682094	1153508	96.076	96.278
3	15.541	193585	37066	3.087	3.280
Total				100.000	100.000

Data: A3098-24 [MW=1789.96] CB_0001:D1 Thursday, November 14, 2019 4:02:03 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 4:04:17 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

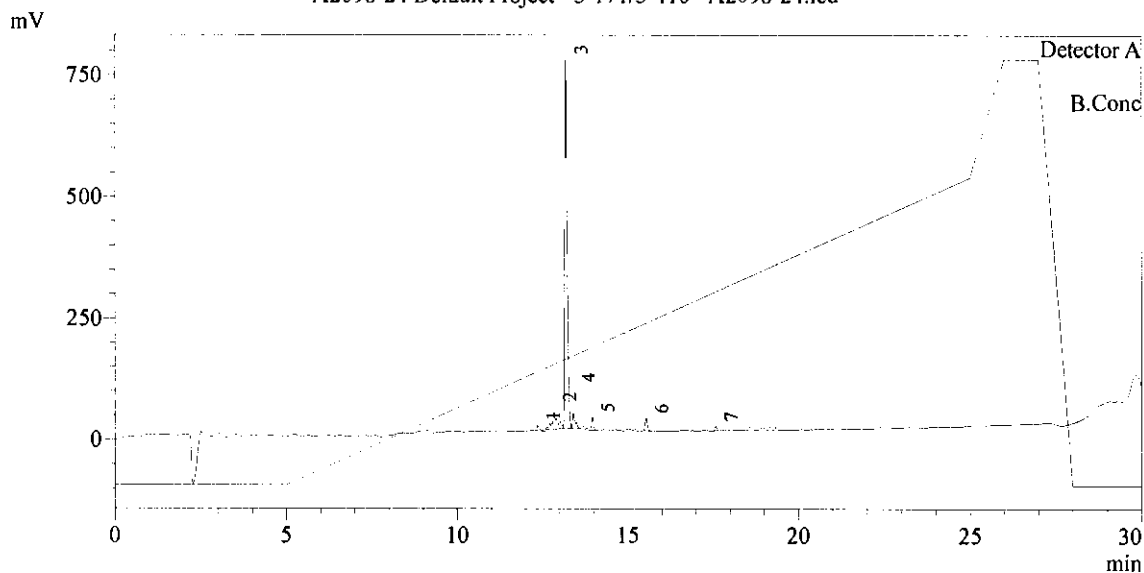
Processed data (averaged): 1453.0 mV [sum=9189.9 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A2098-24
 Sample ID : A2098-24
 Data Filename : A2098-24.lcd
 Method Filename : ANAPEP_28.lcm
 Date Acquired : 11/15/2019 11:50:54 AM
 Data Processed : 11/15/2019 12:21:05 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 A2098-24 Default Project - 3-171/3-410 - A2098-24.lcd



1 Detector A / 220nm

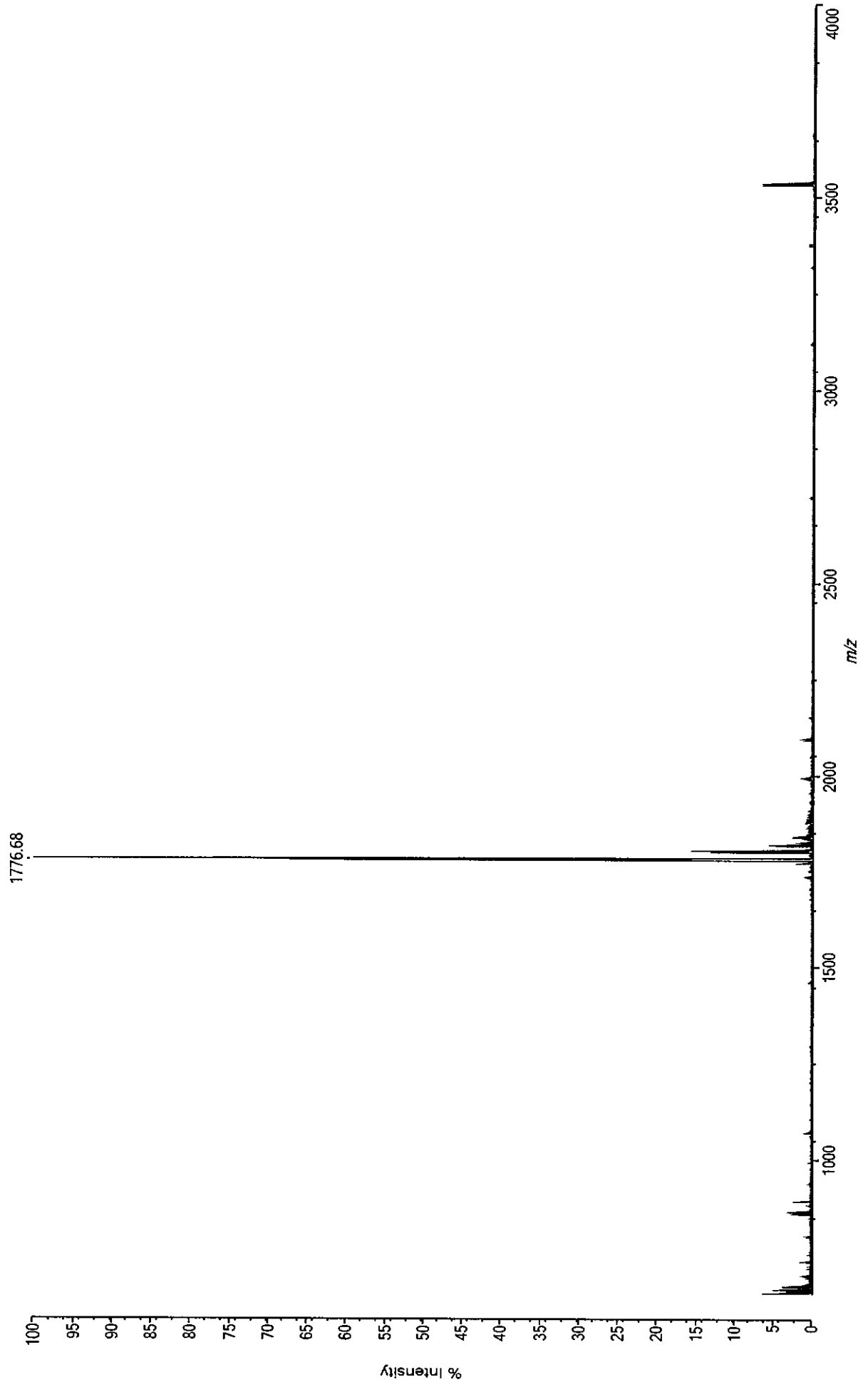
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	12.366	47858	10909	1.215	1.070
2	12.840	374552	34052	3.792	8.376
3	13.185	3643475	760271	84.665	81.481
4	13.398	154071	31244	3.479	3.446
5	13.967	101780	27449	3.057	2.276
6	15.537	118049	25296	2.817	2.640
7	17.581	31780	8751	0.974	0.711
Total				100.000	100.000

Data: A3098-25 [MW=1775.94] CB_0001:E1 Thursday, November 14, 2019 4:02:03 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 4:04:17 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

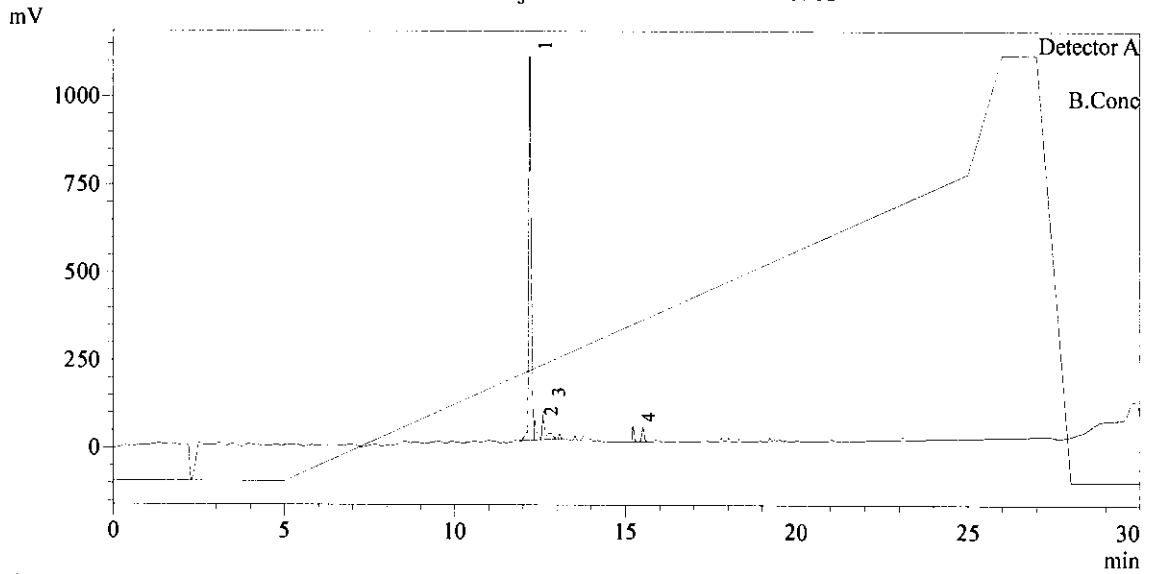
Processed data (averaged) : 62.5 mV [sum=395.4 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A2098-25
 Sample ID : A2098-25
 Data Filename : A2098-25.lcd
 Method Filename : ANAPEP_28.lcm
 Date Acquired : 11/15/2019 12:22:52 PM
 Data Processed : 11/15/2019 12:53:00 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 A2098-25 Default Project - 3-171/3-411 - A2098-25.lcd



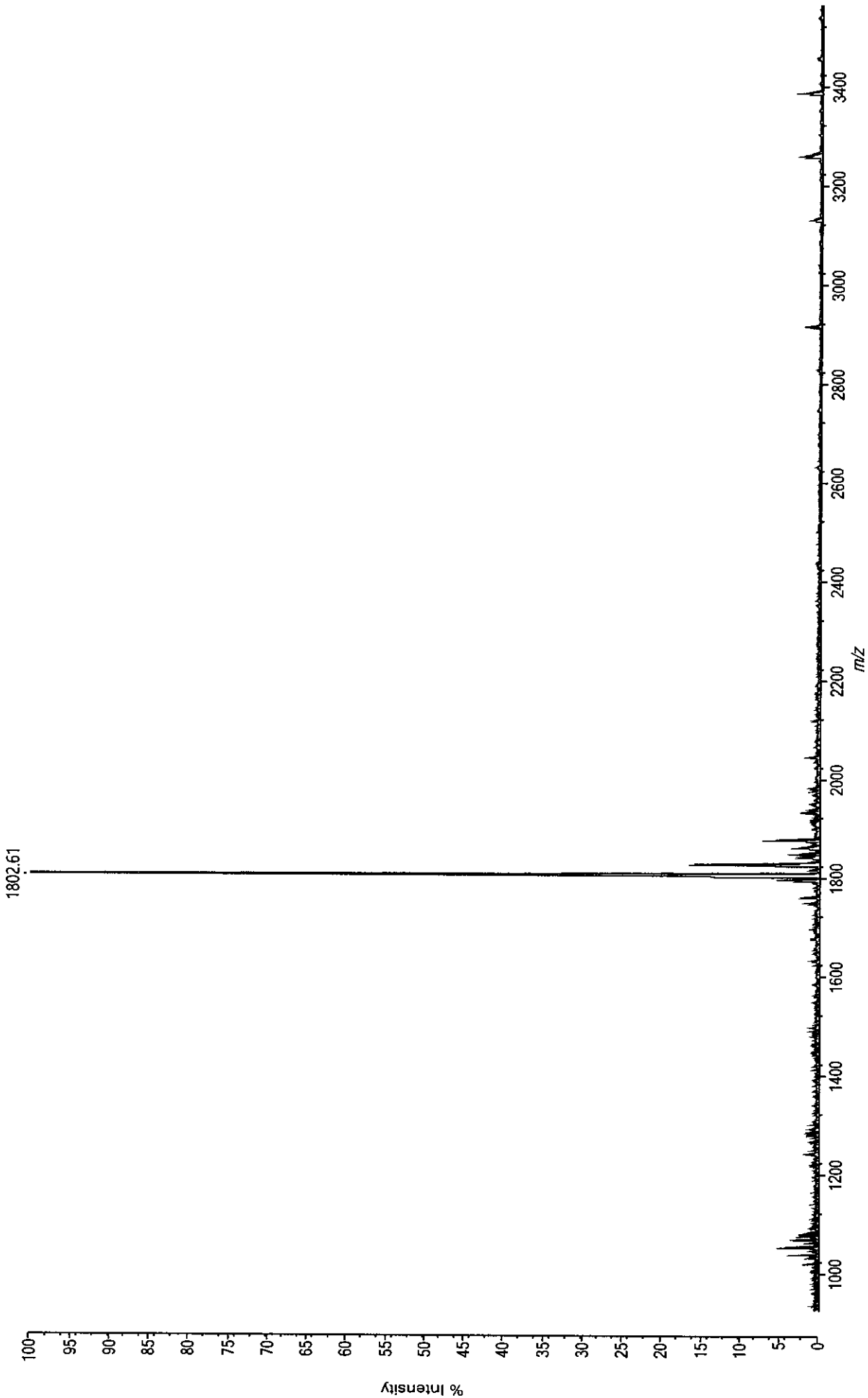
1 Detector A / 220nm

PeakTable

Peak#	Ret. Time	Area	Height	Height %	Area %
1	12.197	5717097	1095527	86.558	81.820
2	12.350	278649	54971	4.343	3.988
3	12.577	607616	71731	5.667	8.696
4	15.220	384029	43431	3.432	5.496
Total				100.000	100.000

Data: A3098-26 [MW=1802.07] CB_0001:F1 Thursday, November 14, 2019 4:02:03 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 4:05:47 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

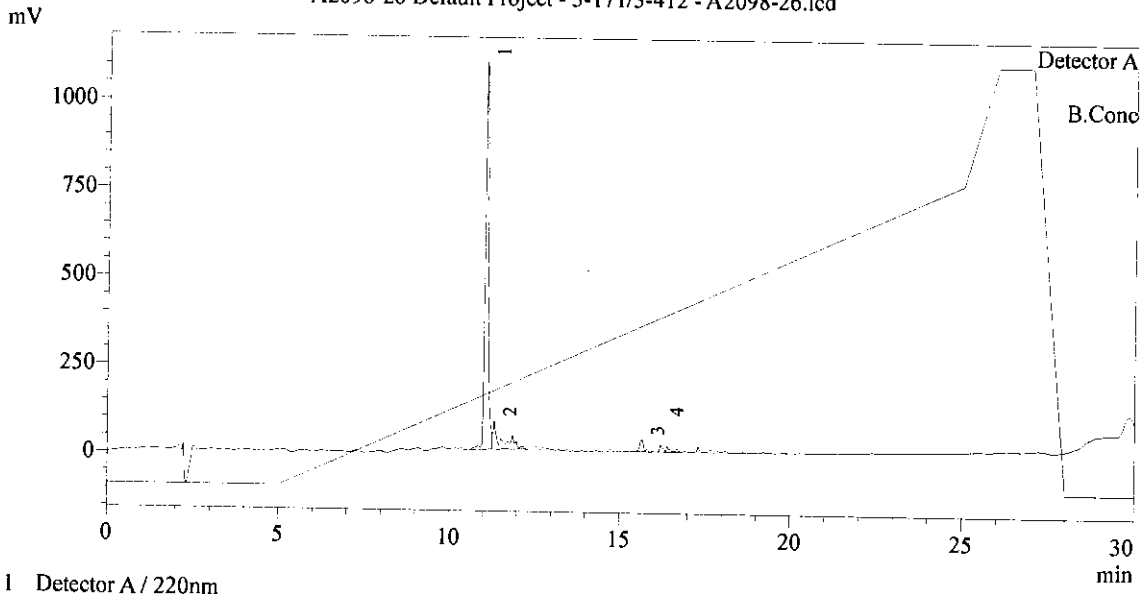
Processed data (averaged) : 77.8 mV [sum=491.8 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A2098-26
 Sample ID : A2098-26
 Data Filename : A2098-26.lcd
 Method Filename : ANAPEP_28.lcm
 Date Acquired : 11/15/2019 12:54:48 PM
 Data Processed : 11/15/2019 1:24:56 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID : CD-347 / EQ-349

Chromatogram
 A2098-26 Default Project - 3-171/3-412 - A2098-26.lcd



1 Detector A / 220nm

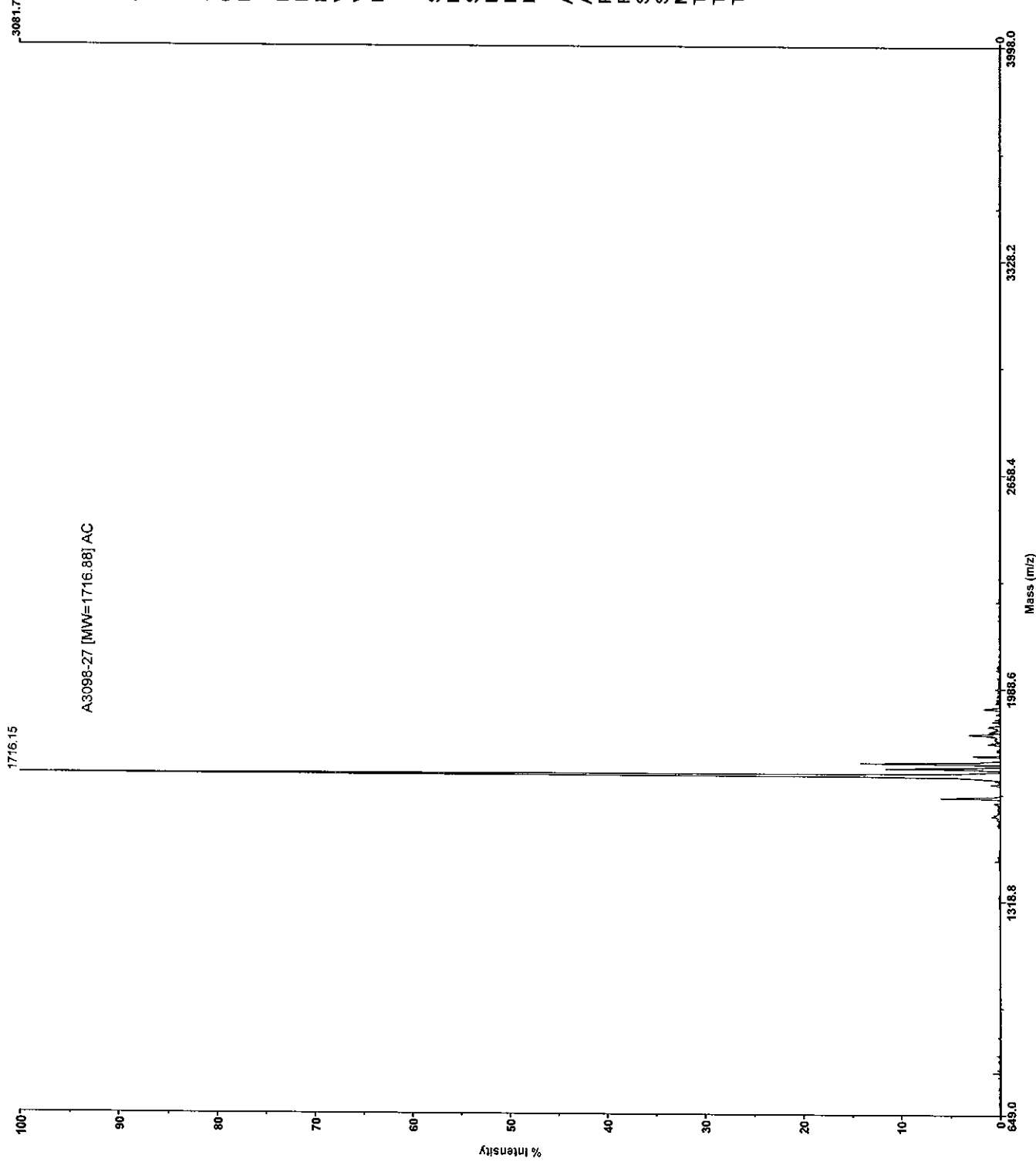
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	11.040	7492807	1097194	89.270	80.780
2	11.325	1273834	80425	6.544	13.733
3	15.660	262503	32174	2.618	2.830
4	16.206	246410	19278	1.568	2.657
Total				100.000	100.000

Applied Biosystems Voyager System 1099

Voyager Spec #1=>SM5=>NR(2.00)=>AdvBC(20,0.5,0.1)[BP = 1716.3, 3082]



Mode of operation: Linear
Extraction mode: Delayed
Polarity: Negative
Acquisition control: Manual

Accelerating voltage: 20000 V
Grid voltage: 95%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 650 -- 4000 Da
Number of laser shots: 100/spectrum
Laser intensity: 1863
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 16.772
Bin size: 2 nsec
Number of data points: 12327
Vertical scale: 200 mV
Vertical offset: 0%
Input bandwidth: 500 MHz

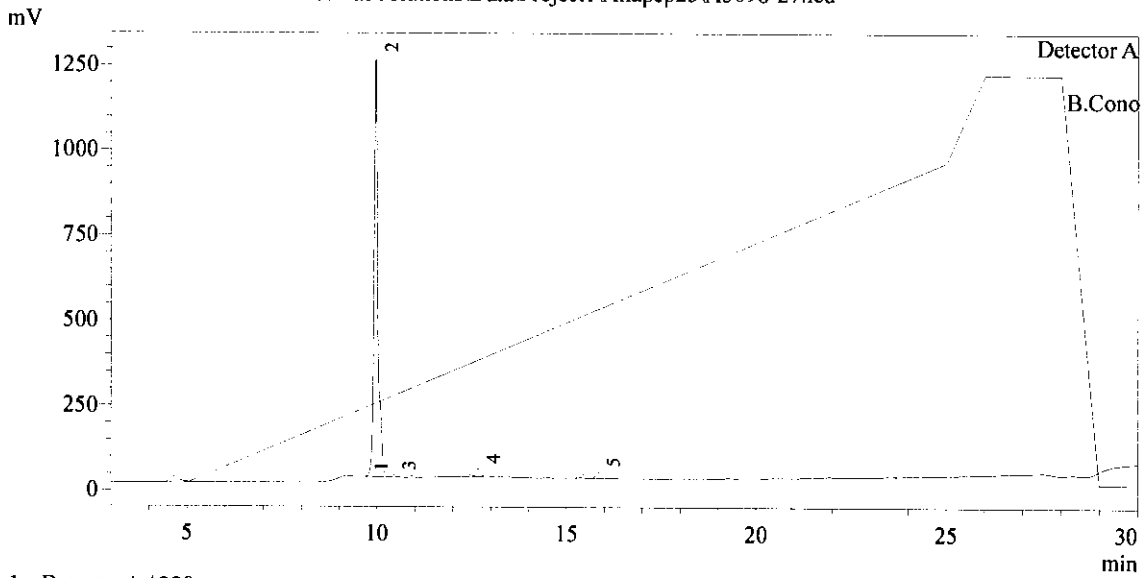
Sample well: 44
Plate ID: 100 WELL PLATE
Serial number: 1099
Instrument name: Voyager-DE
Plate type filename: C:\VOYAGER\100 well plate.plt
Lab name: BioSynthesis, Inc

Absolute x-position: 15992.3
Absolute y-position: 26874.6
Relative x-position: -835.244
Relative y-position: -112.853
Shots in spectrum: 25
Source pressure: 2.923e-007
Mirror pressure: 0
TC2 pressure: 0.001
TIS gate width: 30
TIS flight length: 940

Sample Information

Acquired by : System Administrator
 Sample Name : A3098-27
 Sample ID : A3098-27
 Data Filename : A3098-27.lcd
 Method Filename : ANAPEP25_FORM_ID.lsr.lcm
 Date Acquired : 11/14/2019 10:02:49 PM
 Data Processed : 11/14/2019 10:35:03 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 C:\LabSolutions\Data\Project1\Anapep25\A3098-27.lcd



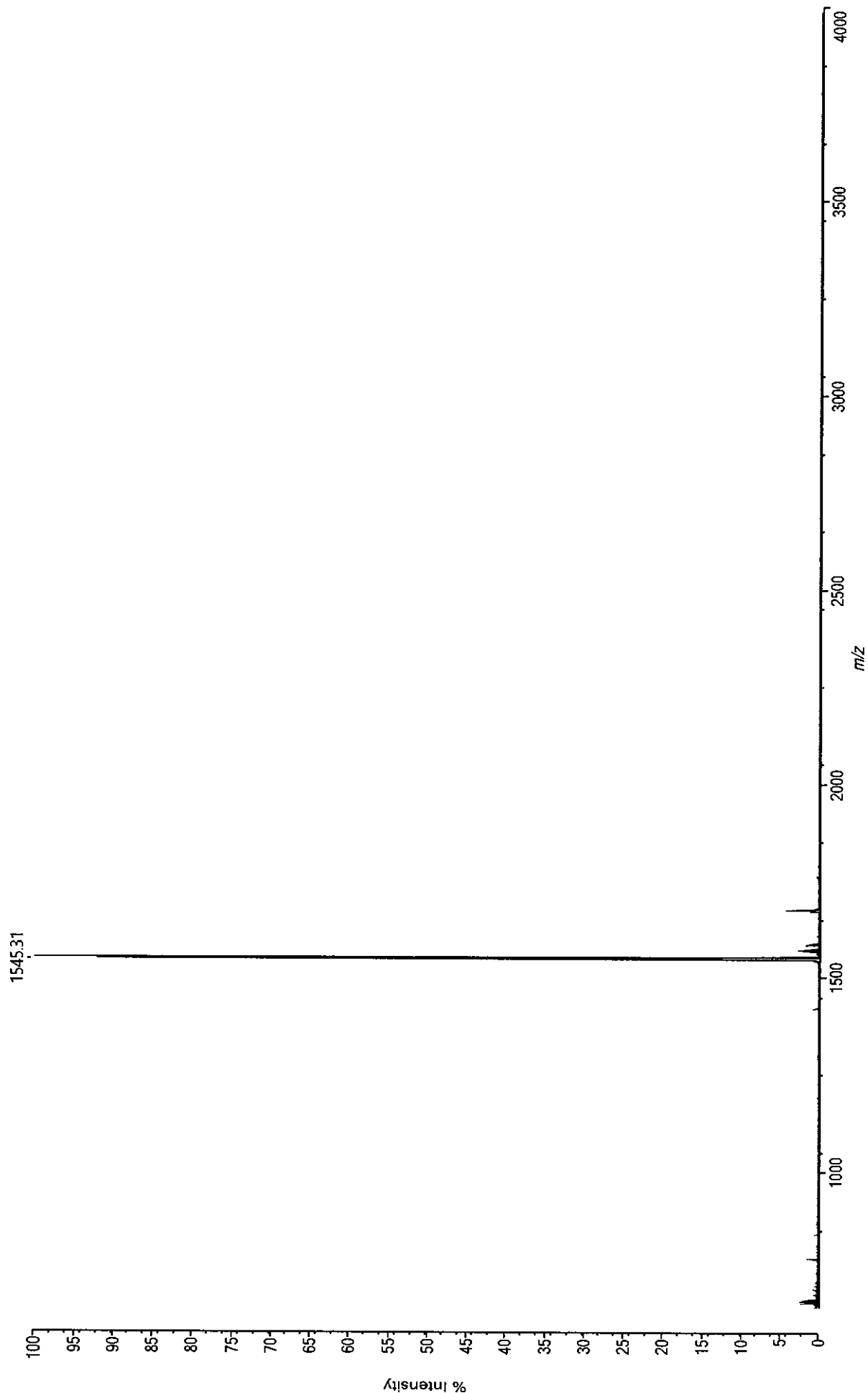
1 Detector A / 220nm

PeakTable

Peak#	Ret. Time	Area	Height	Height %	Area %
1	9.700	2780	929	0.072	0.030
2	9.953	8881387	1233488	96.086	95.403
3	10.438	37966	6003	0.468	0.408
4	12.662	197795	24055	1.874	2.125
5	15.829	189448	19259	1.500	2.035
Total				100.000	100.000

Data: A3098-28 [MW=1545.72] CB_0001:G1 Thursday, November 14, 2019 4:02:03 PM Cal:Custom Calibration by MALDI Solutions Admin on Thursday, November 14, 2019 4:05:47 PM
Shimadzu MALDI-8020: Tuning Linear, Power 30, P.Ext at 1852.00 (bin 117)

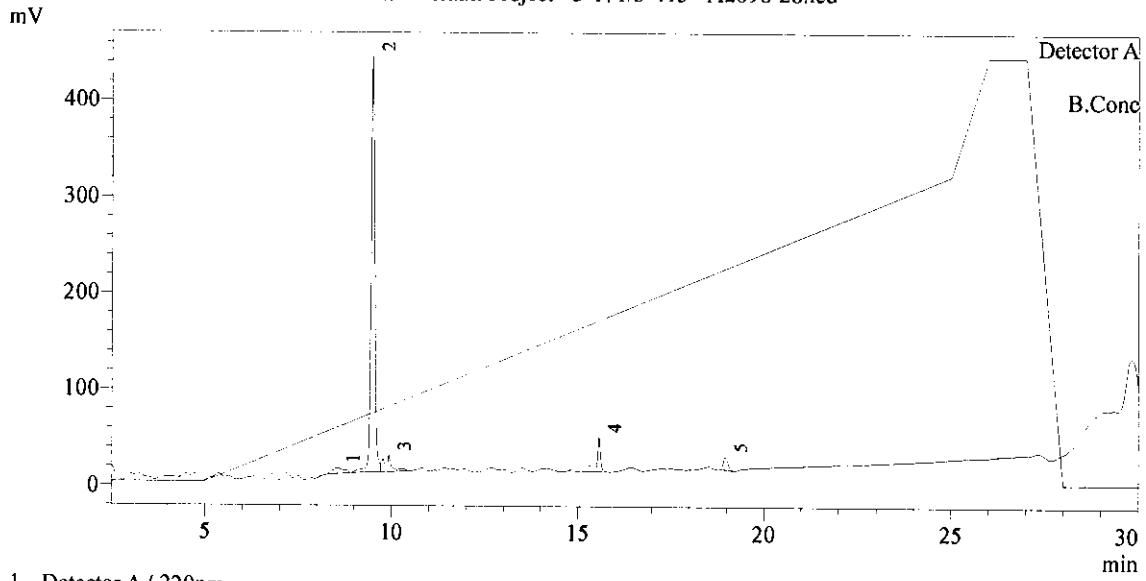
Processed data (averaged) : 103.7 mV [sum=655.6 mV], Smoothed = 10, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A2098-28
 Sample ID : A2098-28
 Data Filename : A2098-28.lcd
 Method Filename : ANAPEP_28.lcm
 Date Acquired : 11/15/2019 1:26:42 PM
 Data Processed : 11/15/2019 1:56:51 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 A2098-28 Default Project - 3-171/3-413 - A2098-28.lcd



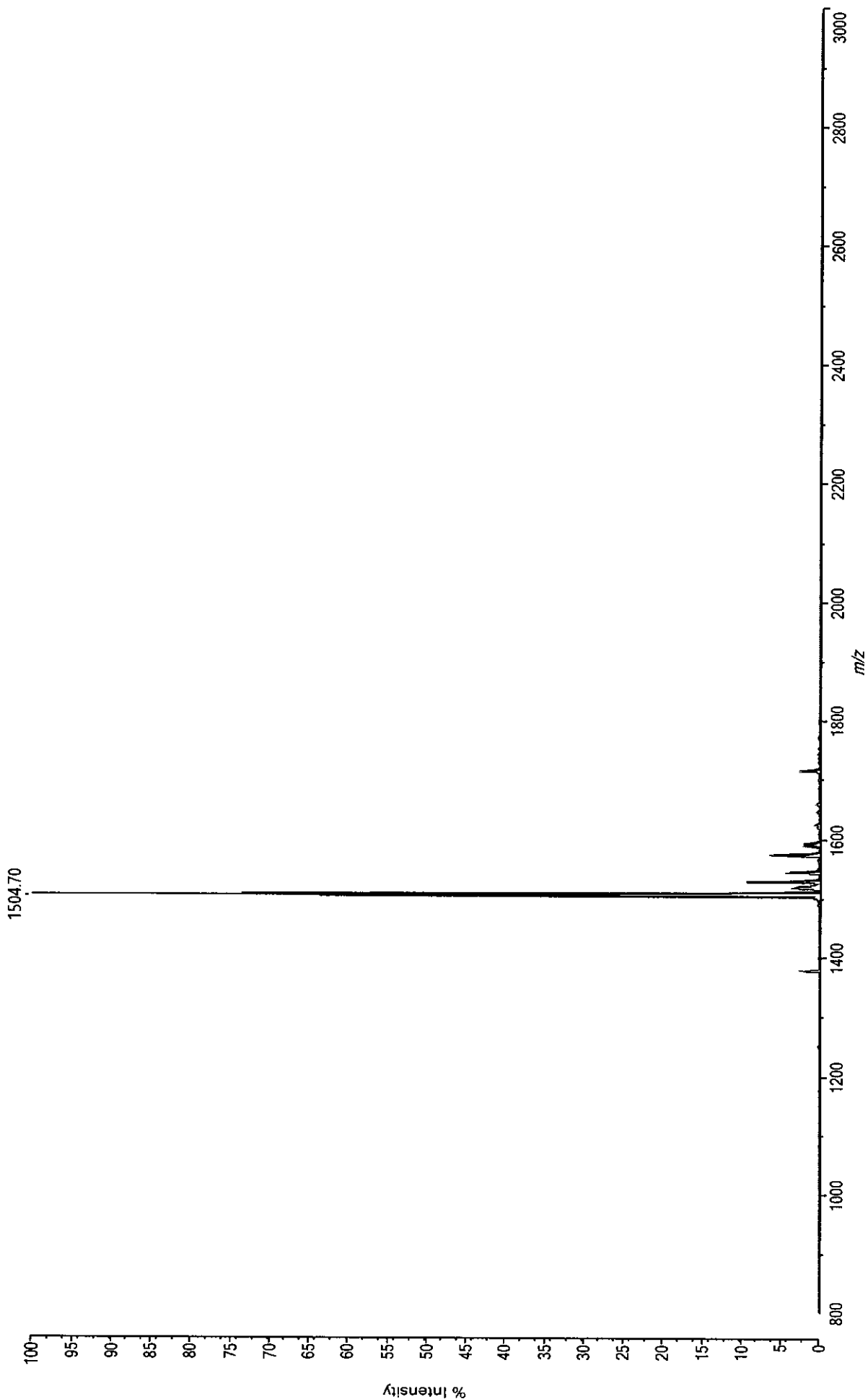
PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	8.554	127144	5862	1.166	3.382
2	9.481	3014726	431629	85.825	80.195
3	9.932	236682	16633	3.307	6.296
4	15.578	267414	35519	7.063	7.114
5	18.969	113259	13272	2.639	3.013
Total				100.000	100.000

Data: A3098-29 [MW=1504.58] PS_0001:F1 Tuesday, November 19, 2019 12:28:28 PM Cal:Custom Calibration by MALDI Solutions Admin on Tuesday, November 19, 2019 12:31:05 PM
Shimadzu MALDI-8020: Tuning Linear, Power 27, P.Ext at 1504.00 (bin 105)

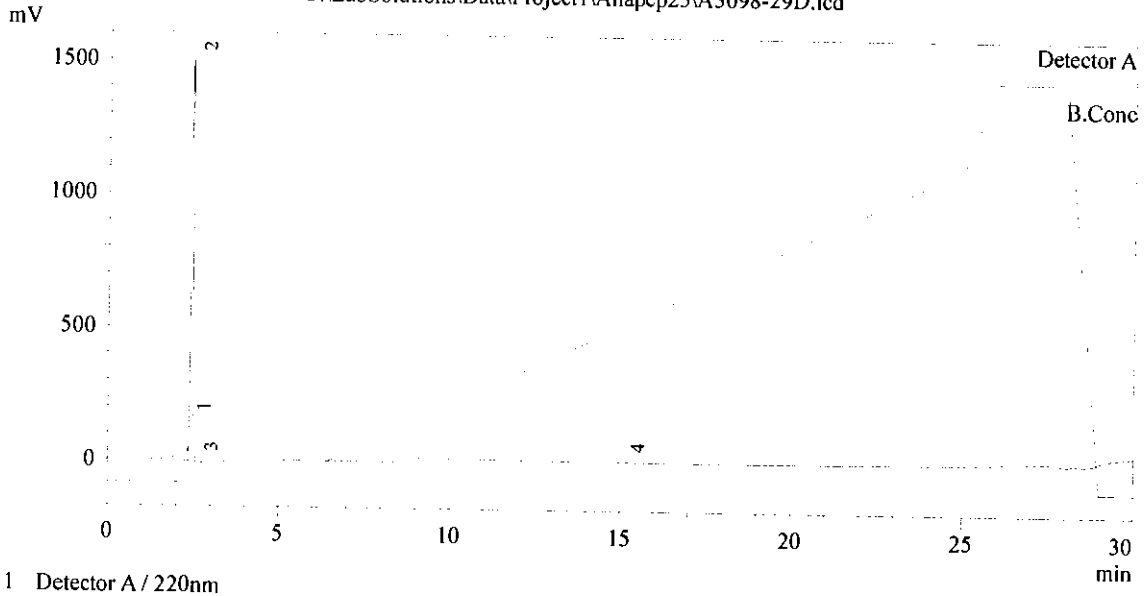
Processed data (averaged) : 804.4 mV [sum=5087.2 mV], Smoothed = 15, profiles # 1 - 50



Sample Information

Acquired by : System Administrator
 Sample Name : A3098-29
 Sample ID : A3098-29
 Data Filename : A3098-29D.lcd
 Method Filename : ANAPEP25_FORM_ID.lsr.lcm
 Date Acquired : 11/22/2019 11:36:58 AM
 Data Processed : 11/22/2019 12:09:12 PM
 Column: 250X4.6mm 5u C18 120A
 Solvent: A:0.05%TFA in Water; B: 0.05 % TFA in ACN
 ID :

Chromatogram
 C:\LabSolutions\Data\Project I\Anapep25\A3098-29D.lcd



1 Detector A / 220nm

PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	2.342	168133	46444	2.902	2.321
2	2.413	6799642	1518653	94.895	93.849
3	2.567	100697	15158	0.947	1.390
4	15.077	176798	20089	1.255	2.440
Total				100.000	100.000

Data: A3098-30 [MW=1477.47] PS_0001:A4 Wednesday, November 20, 2019 11:08:57 AM Cal:Named Calibration "TOFMIX_8/27/2019" by MALDI SolutionsAdmin on Tuesday, August 27, 2019 4:32:14 PM (Or...

Shimadzu MALDI-8020: Tuning Linear, Power 28, P.Ext at 1477.00 (bin 104)

Processed data (averaged) : 473.0 mV [sum=2991.4 mV], Smoothed = 15, profiles # 1 - 50

