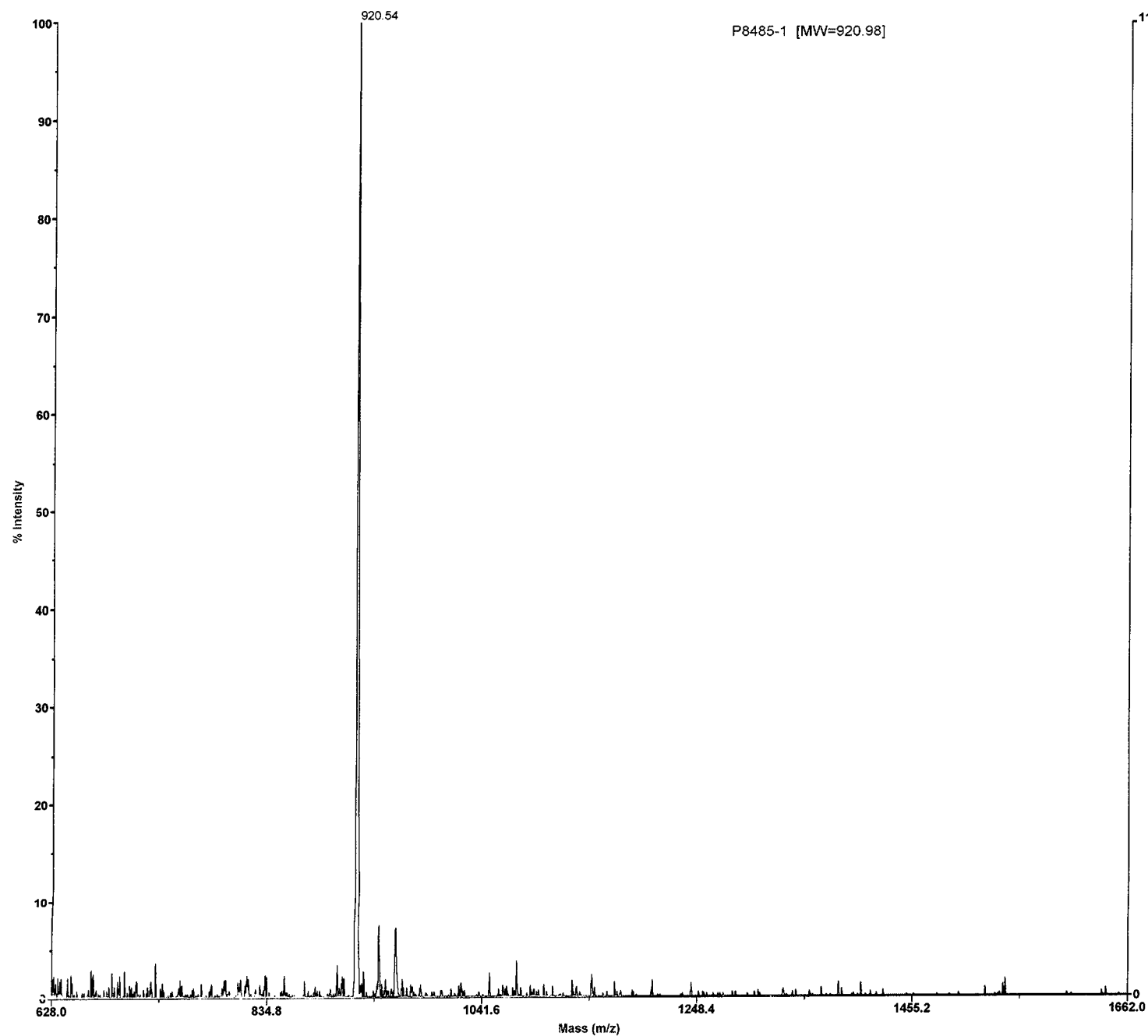


Biosyn. Lot#	Cat#/Peptide Pool	Sequence	Calculated Mass	Observed Purity	Peptide Content
P8485-1	9808 CEF Control Peptide Pool	VSDGGPNLY	920.98	>97%	87.6%
P8485-2	9808 CEF Control Peptide Pool	CTELKLSDY	1071.22	>90%	80.3%
P8485-3	9808 CEF Control Peptide Pool	GILGFVFTL	966.20	>97%	88.0%
P8485-4	9808 CEF Control Peptide Pool	FMYSDFHFI	1206.39	>81%	82.2%
P8485-5	9808 CEF Control Peptide Pool	CLGGLLTMV	906.18	>84%	87.3%
P8485-6	9808 CEF Control Peptide Pool	GLCTLVAML	920.21	>95%	87.6%
P8485-7	9808 CEF Control Peptide Pool	NLVPMVATV	943.18	>88%	87.8%
P8485-8	9808 CEF Control Peptide Pool	KTGGPIYKR	1019.21	>96%	66.1%
P8485-9	9808 CEF Control Peptide Pool	RVLSFIKGTK	1148.42	>92%	68.7%
P8485-10	9808 CEF Control Peptide Pool	ILRGSAHK	980.19	>87%	65.1%
P8485-11	9808 CEF Control Peptide Pool	RVRAYTYSK	1143.31	>92%	68.6%
P8485-12	9808 CEF Control Peptide Pool	RLRAEAQVK	1070.27	>93%	67.1%
P8485-13	9808 CEF Control Peptide Pool	SIIPSGPLK	911.12	>96%	77.6%
P8485-14	9808 CEF Control Peptide Pool	AVFDRKSDAK	1136.28	>97%	68.4%
P8485-15	9808 CEF Control Peptide Pool	IVTDFSVIK	1021.23	>93%	79.6%
P8485-16	9808 CEF Control Peptide Pool	ATIGTAMYK	955.14	>98%	78.5%
P8485-17	9808 CEF Control Peptide Pool	DYCNVLNKEF	1244.39	>95%	82.6%
P8485-18	9808 CEF Control Peptide Pool	LPFDKTTVM	1051.28	>82%	80.1%
P8485-19	9808 CEF Control Peptide Pool	RPPIFIRRL	1167.48	>94%	69.0%
P8485-20	9808 CEF Control Peptide Pool	ELRSRYWAI	1193.37	>84%	75.2%
P8485-21	9808 CEF Control Peptide Pool	RAKFKQLL	1003.26	>92%	65.7%
P8485-22	9808 CEF Control Peptide Pool	FLRGRAYGL	1052.25	>96%	72.8%
P8485-23	9808 CEF Control Peptide Pool	QAKWRLQTL	1143.36	>80%	74.4%
P8485-24	9808 CEF Control Peptide Pool	SDEEEAIVAYTL	1339.42	>95%	91.1%
P8485-25	9808 CEF Control Peptide Pool	SRYWAIATR	1208.39	>95%	69.7%
P8485-26	9808 CEF Control Peptide Pool	ASCMGLIY	857.06	>98%	86.7%
P8485-27	9808 CEF Control Peptide Pool	RRIYDLIEL	1190.41	>96%	75.2%
P8485-28	9808 CEF Control Peptide Pool	YPLHEQHGM	1111.25	>80%	73.9%
P8485-29	9808 CEF Control Peptide Pool	IPSINVHHY	1079.23	>96%	73.3%
P8485-30	9808 CEF Control Peptide Pool	EENLLDFVRF	1281.44	>93%	83.1%
P8485-31	9808 CEF Control Peptide Pool	EFFWDANDIY	1319.39	>92%	91.0%
P8485-32	9808 CEF Control Peptide Pool	TPRVTGGGAM	946.10	>80%	78.3%

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 920.4, 1152]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 615 -- 1800 Da
Number of laser shots: 100/spectrum
Laser intensity: 1910
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 16.922
Bin size: 2 nsec
Number of data points: 5975
Vertical scale: 500 mV
Vertical offset: -2%
Input bandwidth: 150 MHz

Sample well: 32
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.plt
Lab name: PE Biosystems

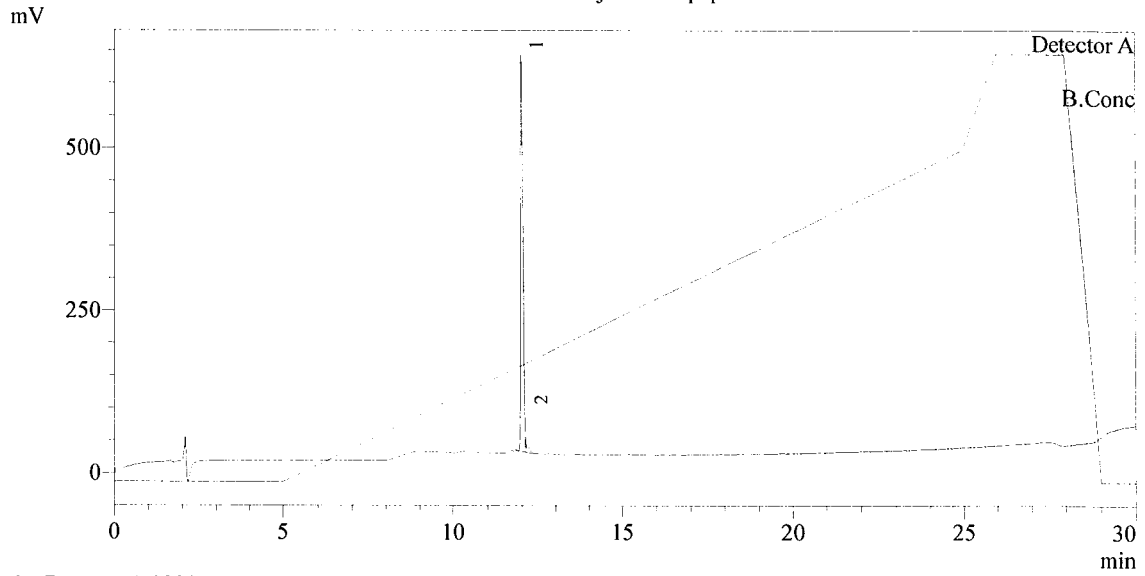
Absolute x-position: 6309.17
Absolute y-position: 33696.5
Relative x-position: -358.326
Relative y-position: 1628.96
Shots in spectrum: 30
Source pressure: 5.21e-007
Mirror pressure: 0
TC2 pressure: 0.01801
TIS gate width: 30
TIS flight length: 940

Sample Information

Acquired by : System Administrator
Sample Name : P8485-1
Sample ID : P8485-1
Data Filename : P8485-1.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 5:12:37 PM
Data Processed : 8/17/2018 5:44:51 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

P8485-1 C:\LabSolutions\Data\Project1\Anapep25\P8485-1.lcd



1 Detector A / 220nm

PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	12.012	2712065	610158	97.640	97.556
2	12.108	67949	14749	2.360	2.444
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: VSDGGPNLY

Lot# P8485-1

ID#:

Project #:

Mol Wt: 920.98

Amount injected: 72.89 ngs

Amount Recovered: 63.853 ngs

Percent Recovery: 87.6%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

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	64.123	87.08	5.584	64.12	0.9
R	0	0.000	156.19	0.000	0.00	0.0
G	2	143.423	57.05	8.182	71.71	2.0
D/N	2	137.669	114.10	15.708	68.83	1.9
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	0	0.000	71.08	0.000	0.00	0.0
P	1	71.336	97.12	6.928	71.34	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	1	73.486	163.18	11.991	73.49	1.0
M	0	0.000	131.20	0.000	0.00	0.0
V	1	73.071	99.13	7.244	73.07	1.0
I	0	0.000	113.16	0.000	0.00	0.0
L	1	72.602	113.16	8.216	72.60	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				63.853		

Performed by:

R. Mancini

09/25/2018

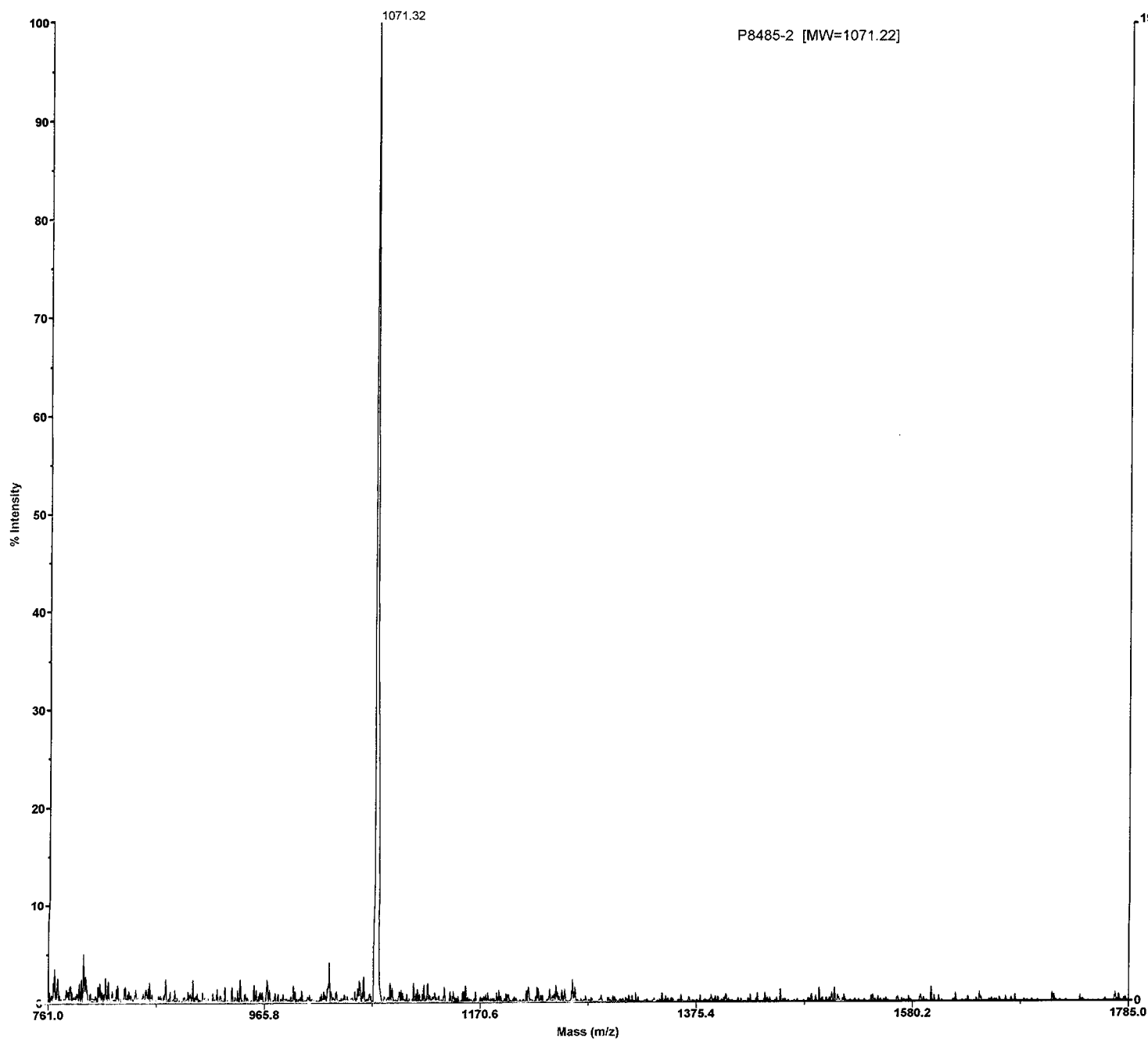
Verified by:

Nousa Bazani

09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 1071.5, 1917]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 620 -- 2000 Da
Number of laser shots: 100/spectrum
Laser intensity: 2010
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 17.004
Bin size: 2 nsec
Number of data points: 6724
Vertical scale: 500 mV
Vertical offset: -2%
Input bandwidth: 150 MHz

Sample well: 33
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.pt
Lab name: PE Biosystems

Absolute x-position: 10900.1
Absolute y-position: 33212.5
Relative x-position: -847.35
Relative y-position: 1144.96
Shots in spectrum: 30
Source pressure: 4.265e-007
Mirror pressure: 0
TC2 pressure: 0.01764
TIS gate width: 30
TIS flight length: 940

Acquired: 19:40:00, August 21, 2018

Printed: 19:41, August 21, 2018

C:\VOYAGER\Data\P2018\P8485-2_0001.dat

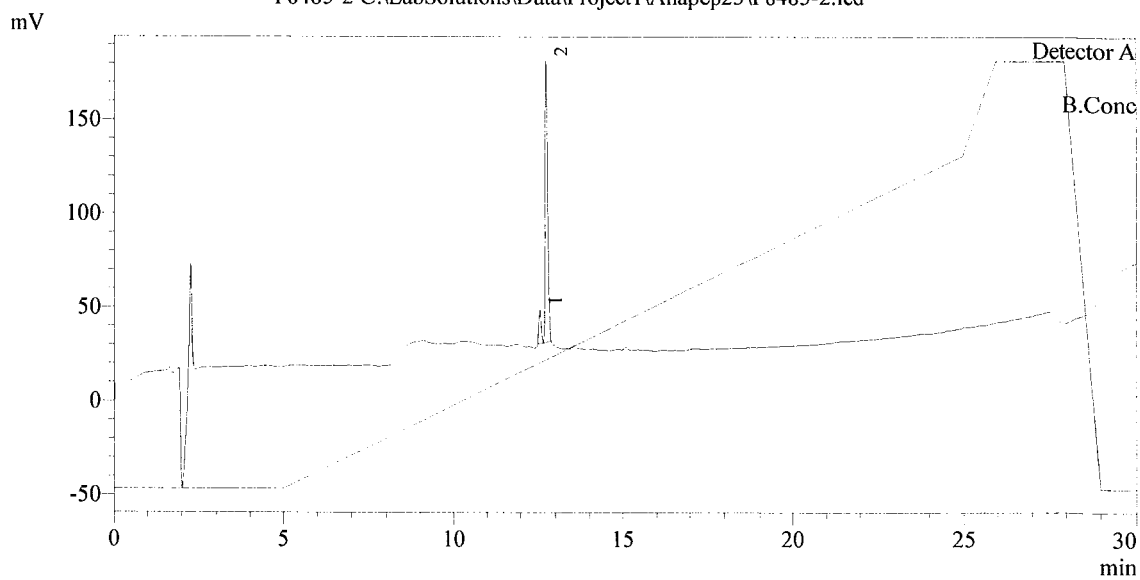
Sample Information

Acquired by : System Administrator
Sample Name : P8485-2
Sample ID : P8485-2
Data Filename : P8485-2.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 5:45:22 PM
Data Processed : 8/17/2018 6:17:36 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

P8485-2 C:\LabSolutions\Data\Project1\Ana pep25\P8485-2.lcd



PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	12.559	84544	17826	10.619	9.992
2	12.762	761552	150038	89.381	90.008
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: CTELKLSDY

Lot# P8485-2

ID#:

Project #:

Mol Wt: 1,071.22

Amount injected: 61.28 ngs

Amount Recovered: 49.211 ngs

Percent Recovery: 80.3%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

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	50.437	87.08	4.392	50.44	1.0
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	45.774	114.10	5.223	45.77	0.9
E/Q	1	46.007	128.13	5.895	46.01	0.9
T	1	49.909	101.11	5.046	49.91	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	1	0.000	103.14	0.000	0.00	0.0
K	1	53.062	128.18	6.801	53.06	1.0
Y	1	61.281	163.18	10.000	61.28	1.2
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	104.751	113.16	11.854	52.38	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				49.211		

Performed by:

R. Monchi

09/25/2018

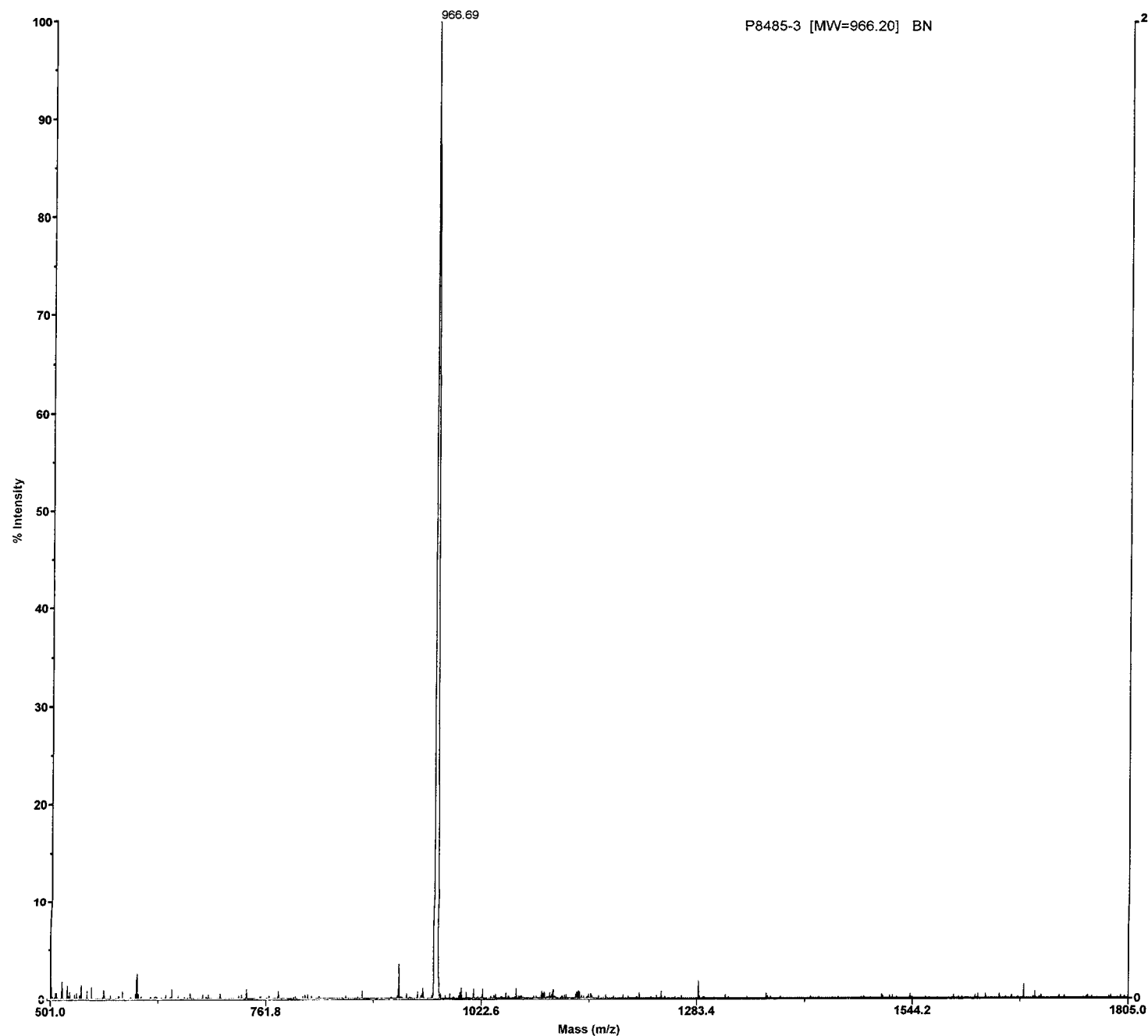
Verified by:

Mouza Barzani

09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM3[BP = 966.5, 21148]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 300 nsec

Acquisition mass range: 500 -- 1800 Da
Number of laser shots: 100/spectrum
Laser intensity: 1910
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 15.286
Bin size: 2 nsec
Number of data points: 6820
Vertical scale: 500 mV
Vertical offset: -1.2%
Input bandwidth: 150 MHz

Sample well: 14
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.plt
Lab name: PE Biosystems

Absolute x-position: 17485.7
Absolute y-position: 43142.9
Relative x-position: 658.224
Relative y-position: 915.379
Shots in spectrum: 10
Source pressure: 8.513e-007
Mirror pressure: 0
TC2 pressure: 0.01982
TIS gate width: 30
TIS flight length: 940

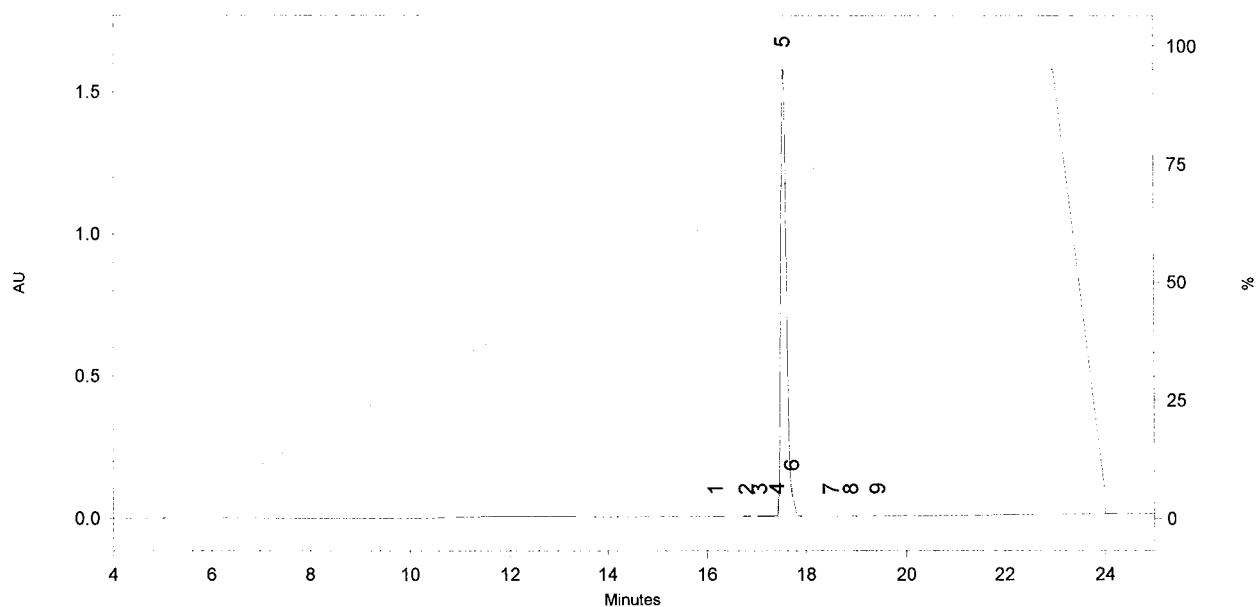
Acquired: 19:31:00, August 17, 2018

Printed: 19:33, August 17, 2018

C:\VOYAGER\Data\P2018\P8485-3_0001.dat

HPLC Report

Sample: P8485-3
 Method: C:\32Karat\Projects\Default\Methods\ANAP2.met
 File Name: C:\32Karat\Projects\Default\Data\P8485-3A
 Solvent: A: 0.05 % TFA in H₂O; B: 0.05 % TFA in ACN
 Column: Onyx Monolithic C18, 100x 3.00mm 3u Flow Rate: 1.0ml/min.
 Run Time: 8/18/2018 12:34:49 AM
 HPLC ID #: CD-159/EQ-066



Det 166 Results

Pk #	Time	Area	Area %
1	16.167	1262	0.01
2	16.792	18292	0.15
3	17.058	7007	0.06
4	17.408	18547	0.15
5	17.550	12206213	97.18
6	17.708	299826	2.39
7	18.492	3311	0.03
8	18.883	522	0.00
9	19.425	5493	0.04

Totals		12560473	100.00
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Amino Acid Analysis Data Sheet

Sequence: GILGFVFTL

Lot# P8485-3

ID#:

Project #:

Mol Wt: 966.20

Amount injected: 31.96 ngs

Amount Recovered: 28.126 ngs

Percent Recovery: 88.0%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

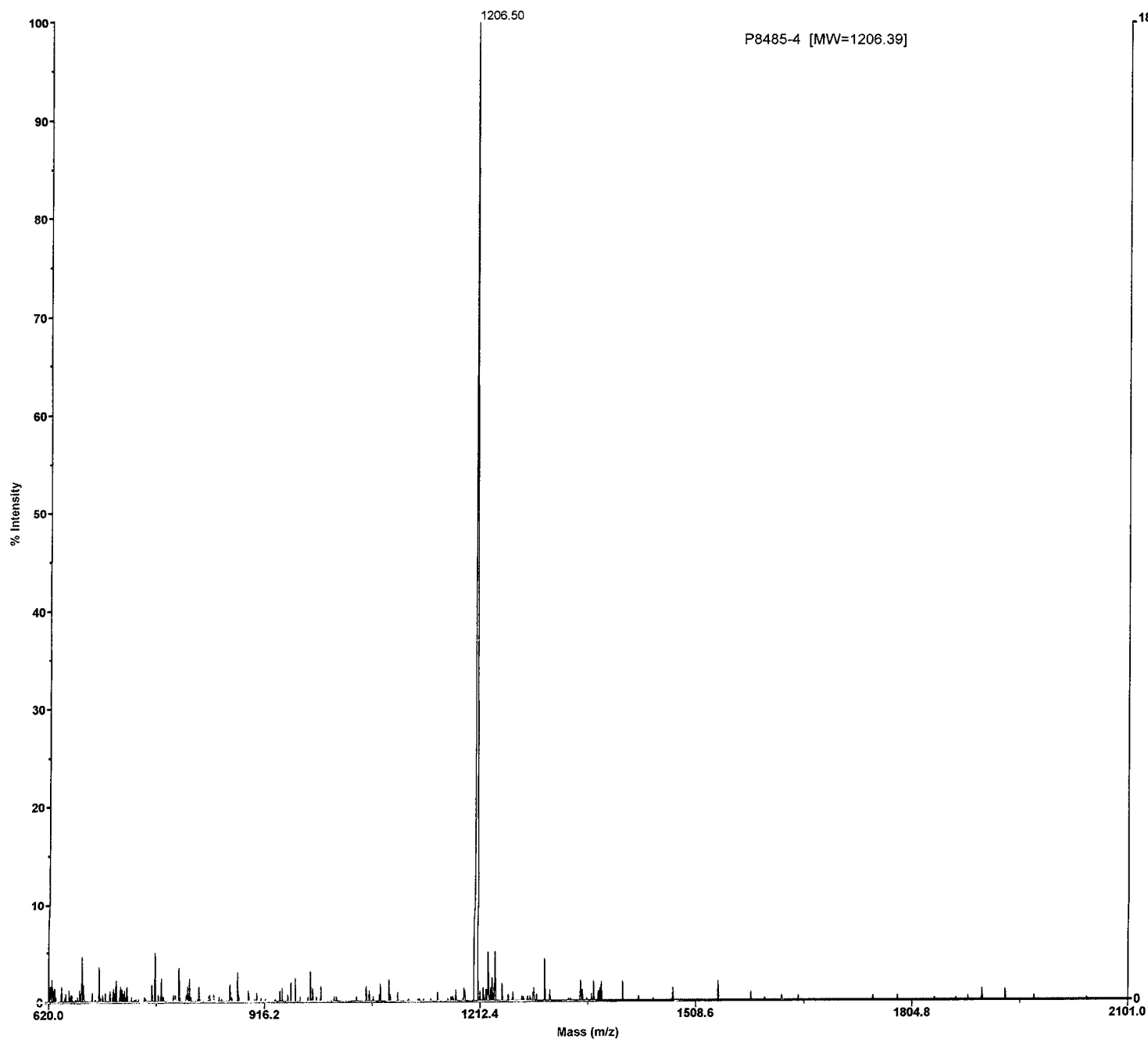
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	0	0.000	87.08	0.000	0.00	0.0
R	0	0.000	156.19	0.000	0.00	0.0
G	2	61.350	57.05	3.500	30.68	2.1
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	1	32.771	101.11	3.313	32.77	1.1
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	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	1	26.907	99.13	2.667	26.91	0.9
I	1	25.889	113.16	2.930	25.89	0.9
L	2	59.326	113.16	6.713	29.66	2.0
F	2	61.163	147.18	9.002	30.58	2.1
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				28.126		

Performed by: *R. Monachini* 09/25/2018

Verified by: *Mousa Bazani* 09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 1206.5, 1831]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 620 – 2100 Da
Number of laser shots: 100/spectrum
Laser intensity: 1948
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 17.004
Bin size: 2 nsec
Number of data points: 7099
Vertical scale: 500 mV
Vertical offset: -2%
Input bandwidth: 150 MHz

Sample well: 34
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.pt
Lab name: PE Biosystems

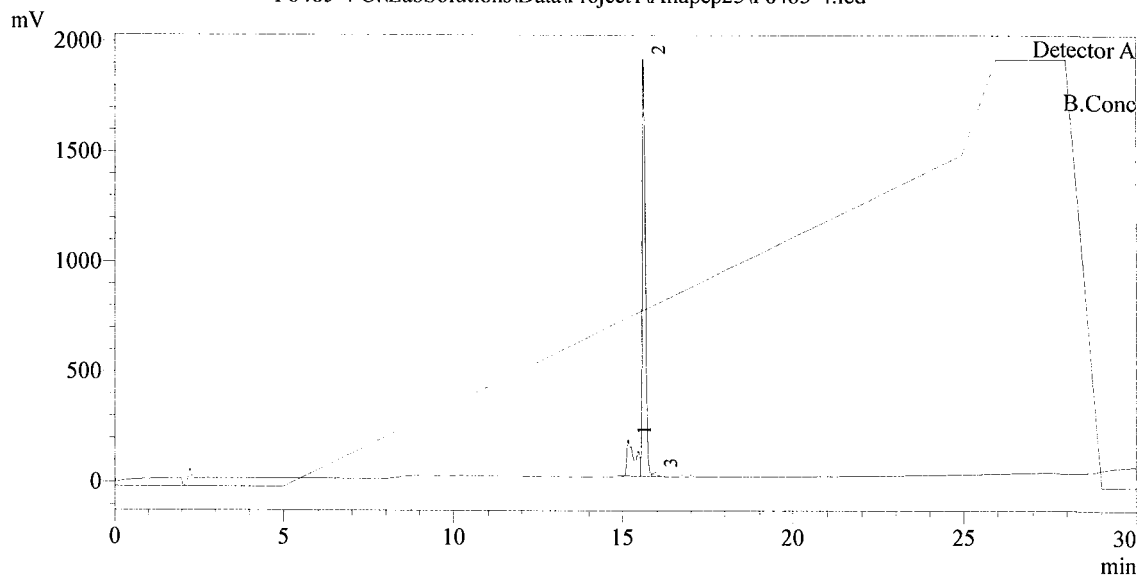
Absolute x-position: 16398.7
Absolute y-position: 31106.7
Relative x-position: -428.77
Relative y-position: -960.785
Shots in spectrum: 14
Source pressure: 3.4e-007
Mirror pressure: 0
TC2 pressure: 0.0174
TIS gate width: 30
TIS flight length: 940

Sample Information

Acquired by : System Administrator
Sample Name : P8485-4
Sample ID : P8485-4
Data Filename : P8485-4.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 6:18:07 PM
Data Processed : 8/17/2018 6:50:20 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

P8485-4 C:\LabSolutions\Data\Project1\Ana pep25\P8485-4.lcd



1 Detector A / 220nm

PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	15.174	2539255	163776	7.903	17.521
2	15.633	11820748	1890535	91.227	81.565
3	15.952	132424	18041	0.871	0.914
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: FMYSDFHFI

Lot# P8485-4

ID#:

Project #:

Mol Wt: 1,206.39

Amount injected: 60.48 ngs

Amount Recovered: 49.714 ngs

Percent Recovery: 82.2%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

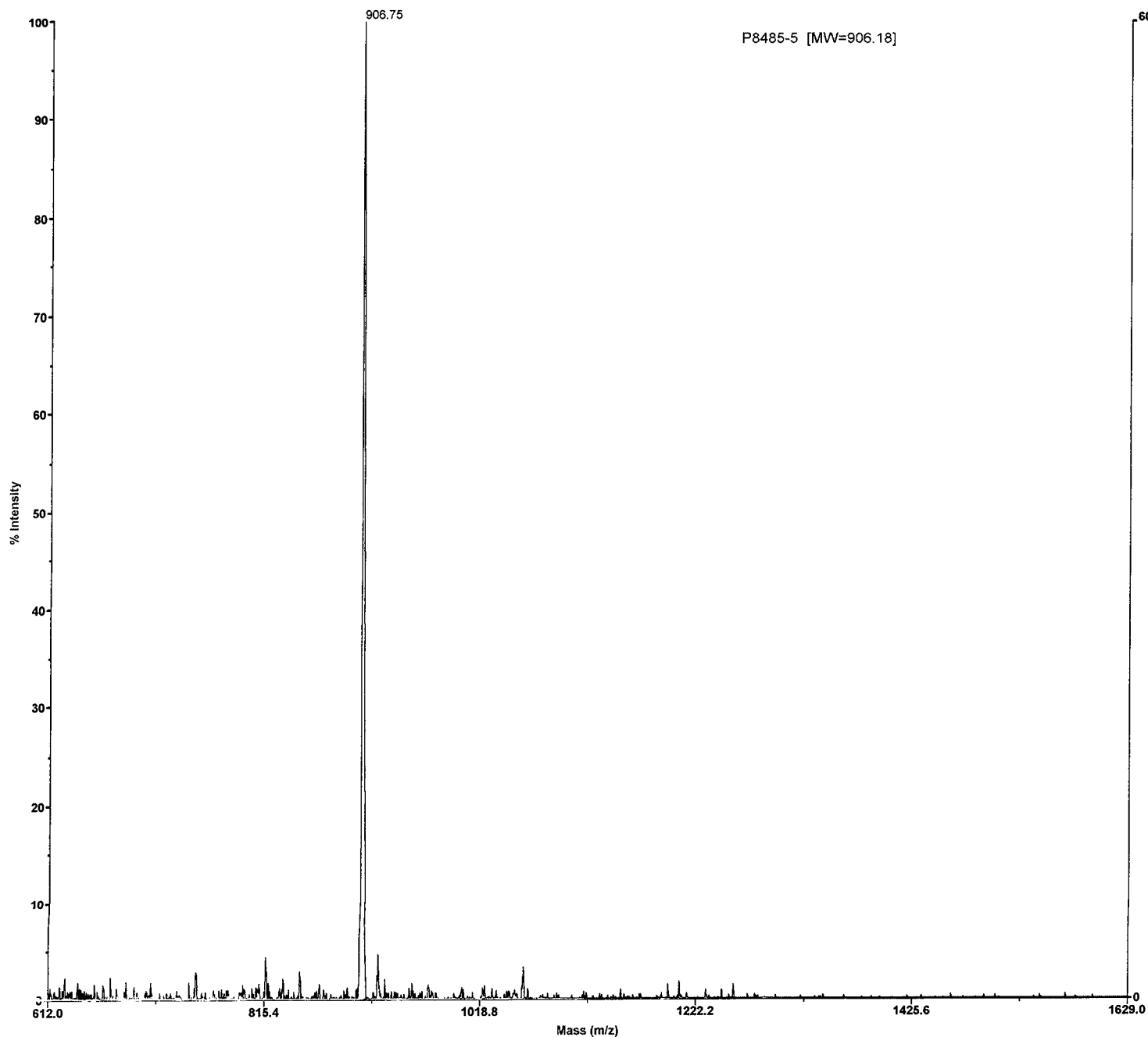
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	41.909	137.14	5.747	41.91	1.0
S	1	40.889	87.08	3.561	40.89	1.0
R	0	0.000	156.19	0.000	0.00	0.0
G	0	0.000	57.05	0.000	0.00	0.0
D/N	1	42.135	114.10	4.808	42.14	1.0
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	0	0.000	101.11	0.000	0.00	0.0
A	0	0.000	71.08	0.000	0.00	0.0
P	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	1	43.213	163.18	7.051	43.21	1.0
M	1	43.502	131.20	5.707	43.50	1.0
V	0	0.000	99.13	0.000	0.00	0.0
I	1	38.095	113.16	4.311	38.10	0.9
L	0	0.000	113.16	0.000	0.00	0.0
F	3	125.889	147.18	18.528	41.96	3.0
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				49.714		

Performed by: *R. Monachini* 09/25/2018

Verified by: *Moussa Bazani* 09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 906.4, 6021]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 500 – 1800 Da
Number of laser shots: 100/spectrum
Laser intensity: 2000
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 15.278
Bin size: 2 nsec
Number of data points: 6808
Vertical scale: 500 mV
Vertical offset: -2%
Input bandwidth: 150 MHz

Sample well: 35
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.plt
Lab name: PE Biosystems

Absolute x-position: 22699.1
Absolute y-position: 30856.9
Relative x-position: 791.58
Relative y-position: -1210.55
Shots in spectrum: 10
Source pressure: 3.114e-007
Mirror pressure: 0
TC2 pressure: 0.0174
TIS gate width: 30
TIS flight length: 940

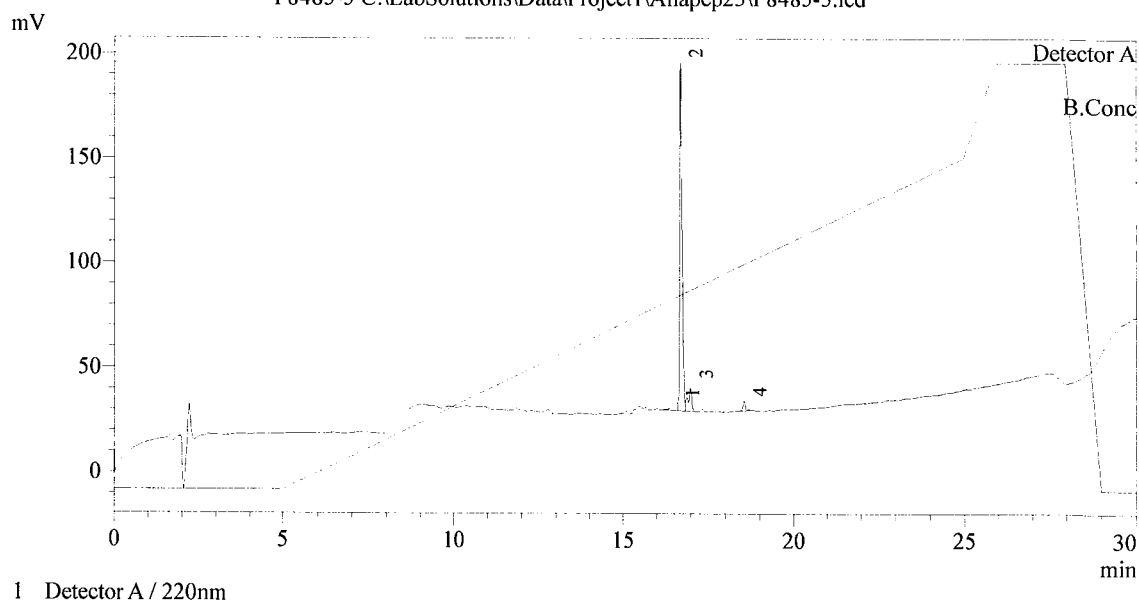
Sample Information

Acquired by : System Administrator
Sample Name : P8485-5
Sample ID : P8485-5
Data Filename : P8485-5.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 6:50:52 PM
Data Processed : 8/17/2018 7:23:06 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

P8485-5 C:\LabSolutions\Data\Project1\Anapep25\P8485-5.lcd



PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	16.597	39909	3762	2.028	4.277
2	16.730	788690	166257	89.634	84.515
3	16.997	81934	10929	5.892	8.780
4	18.560	22660	4537	2.446	2.428
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: CLGGLTMV

Lot# P8485-5

ID#:

Project #:

Mol Wt: 906.18

Amount injected: 86.4 ngs

Amount Recovered: 75.424 ngs

Percent Recovery: 87.3%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

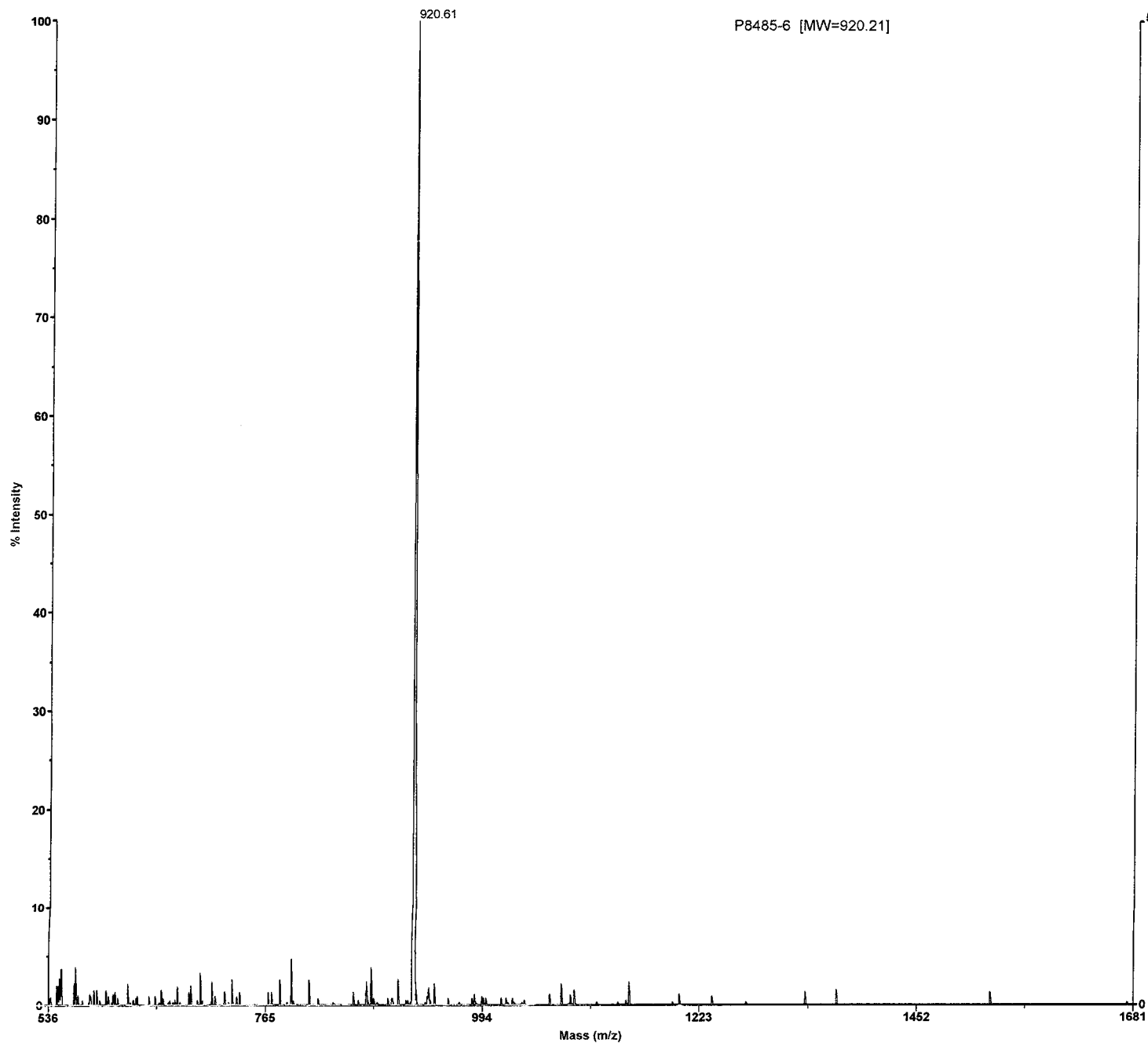
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	0	0.000	87.08	0.000	0.00	0.0
R	0	0.000	156.19	0.000	0.00	0.0
G	2	193.310	57.05	11.028	96.66	2.0
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	1	92.760	101.11	9.379	92.76	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	1	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	97.811	131.20	12.833	97.81	1.0
V	1	100.579	99.13	9.970	100.58	1.0
I	0	0.000	113.16	0.000	0.00	0.0
L	3	284.671	113.16	32.213	94.89	2.9
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				75.424		

Performed by: *R. Monachini* 09/25/2018

Verified by: *Mousa Bazani* 09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM7[BP = 920.7, 508]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 500 -- 1800 Da
Number of laser shots: 100/spectrum
Laser intensity: 1900
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 15.272
Bin size: 2 nsec
Number of data points: 6804
Vertical scale: 500 mV
Vertical offset: -2%
Input bandwidth: 150 MHz

Sample well: 36
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.plt
Lab name: PE Biosystems

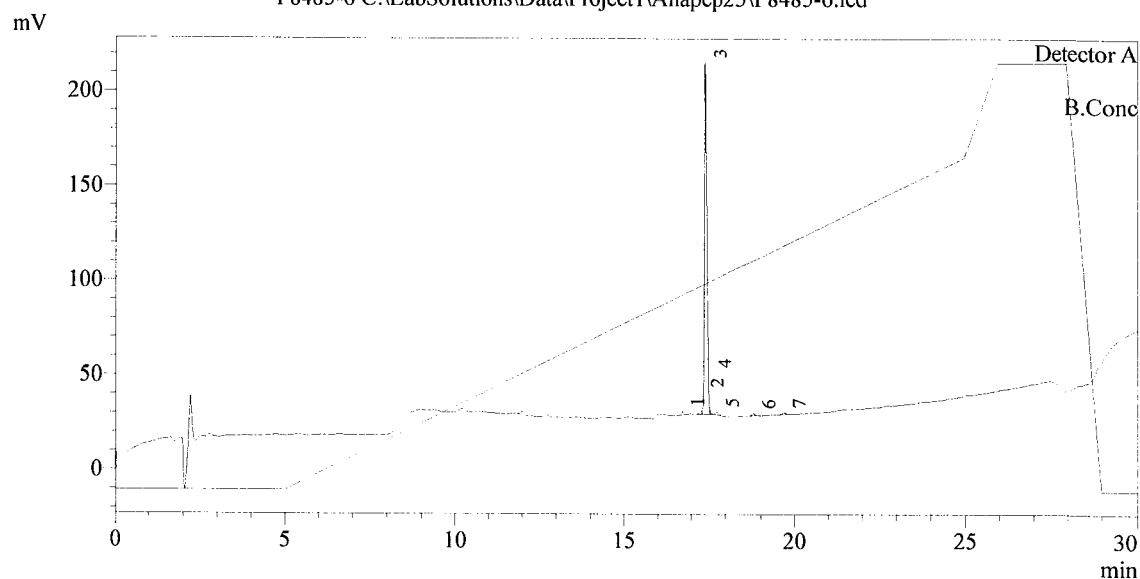
Absolute x-position: 26832.7
Absolute y-position: 32734.6
Relative x-position: -154.823
Relative y-position: 667.148
Shots in spectrum: 30
Source pressure: 3.019e-007
Mirror pressure: 0
TC2 pressure: 0.01743
TIS gate width: 30
TIS flight length: 940

Sample Information

Acquired by : System Administrator
Sample Name : P8485-6
Sample ID : P8485-6
Data Filename : P8485-6.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 7:23:37 PM
Data Processed : 8/17/2018 7:55:51 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

P8485-6 C:\LabSolutions\Data\Project1\Ana pep25\P8485-6.lcd



1 Detector A / 220nm

PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	16.740	8773	1797	0.927	0.954
2	17.308	7966	1756	0.905	0.866
3	17.426	880332	185549	95.681	95.747
4	17.542	2254	1593	0.822	0.245
5	17.768	8588	1388	0.716	0.934
6	18.793	6765	1203	0.621	0.736
7	19.703	4754	637	0.329	0.517
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: GLCTLVAML

Lot# P8485-6

ID#:

Project #:

Mol Wt: 920.21

Amount injected: 61.36 ngs

Amount Recovered: 53.747 ngs

Percent Recovery: 87.6%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

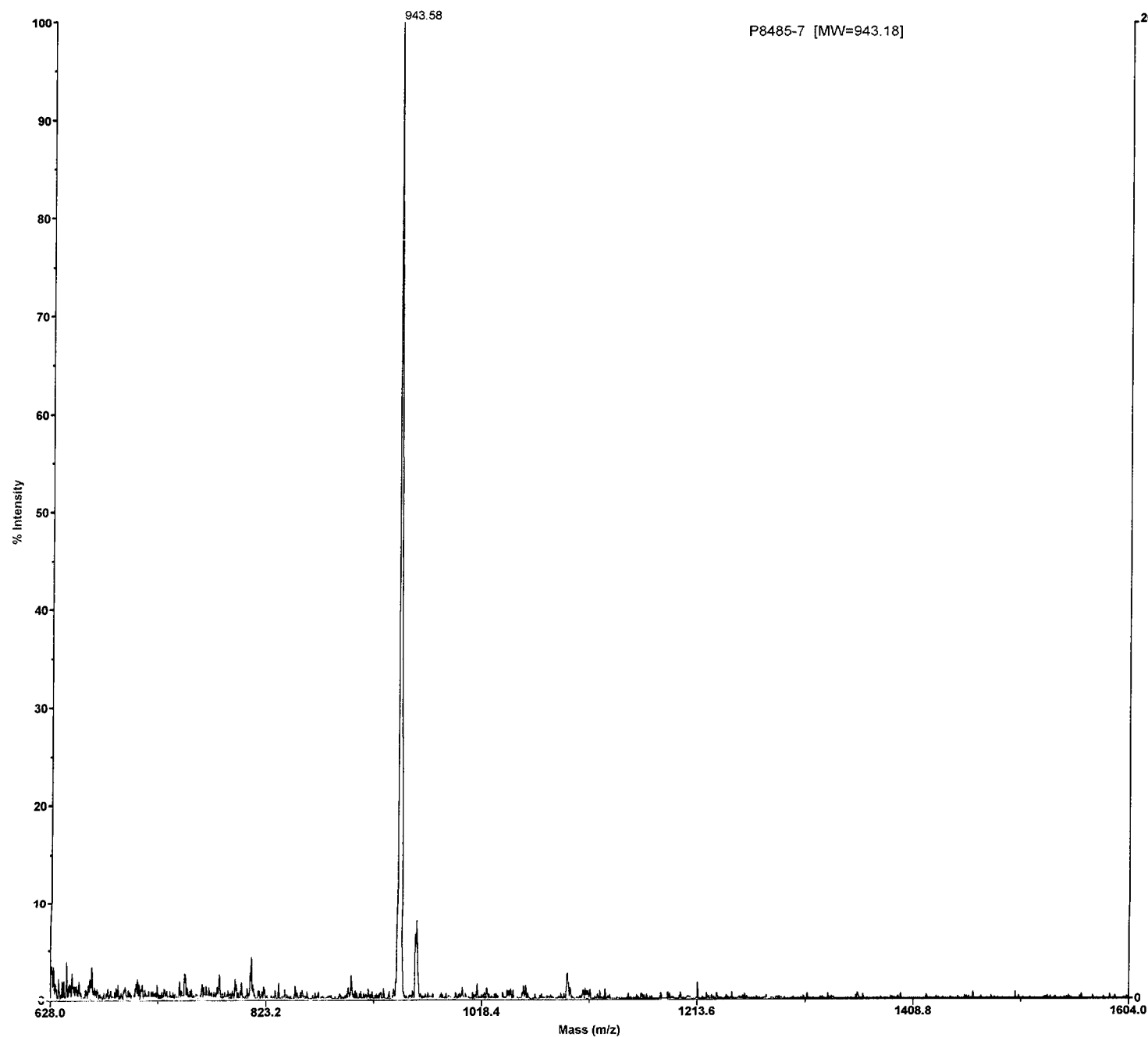
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	0	0.000	87.08	0.000	0.00	0.0
R	0	0.000	156.19	0.000	0.00	0.0
G	1	71.850	57.05	4.099	71.85	1.1
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	1	65.153	101.11	6.588	65.15	1.0
A	1	59.535	71.08	4.232	59.54	0.9
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	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	72.518	131.20	9.514	72.52	1.1
V	1	68.909	99.13	6.831	68.91	1.0
I	0	0.000	113.16	0.000	0.00	0.0
L	3	198.684	113.16	22.483	66.23	2.9
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				53.747		

Performed by: *R. Monicchi* 09/25/2018

Verified by: *Moussa Bazani* 09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 943.3, 2637]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 500 -- 1800 Da
Number of laser shots: 100/spectrum
Laser intensity: 2000
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 15.27
Bin size: 2 nsec
Number of data points: 6804
Vertical scale: 500 mV
Vertical offset: -2%
Input bandwidth: 150 MHz

Sample well: 37
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.pt
Lab name: PE Biosystems

Absolute x-position: 30942.1
Absolute y-position: 31184.5
Relative x-position: -1125.41
Relative y-position: -882.968
Shots in spectrum: 34
Source pressure: 2.785e-007
Mirror pressure: 0
TC2 pressure: 0.01743
TIS gate width: 30
TIS flight length: 940

Acquired: 19:55:00, August 21, 2018

Printed: 19:56, August 21, 2018

C:\VOYAGER\Data\P2018\P8485-7_0001.dat

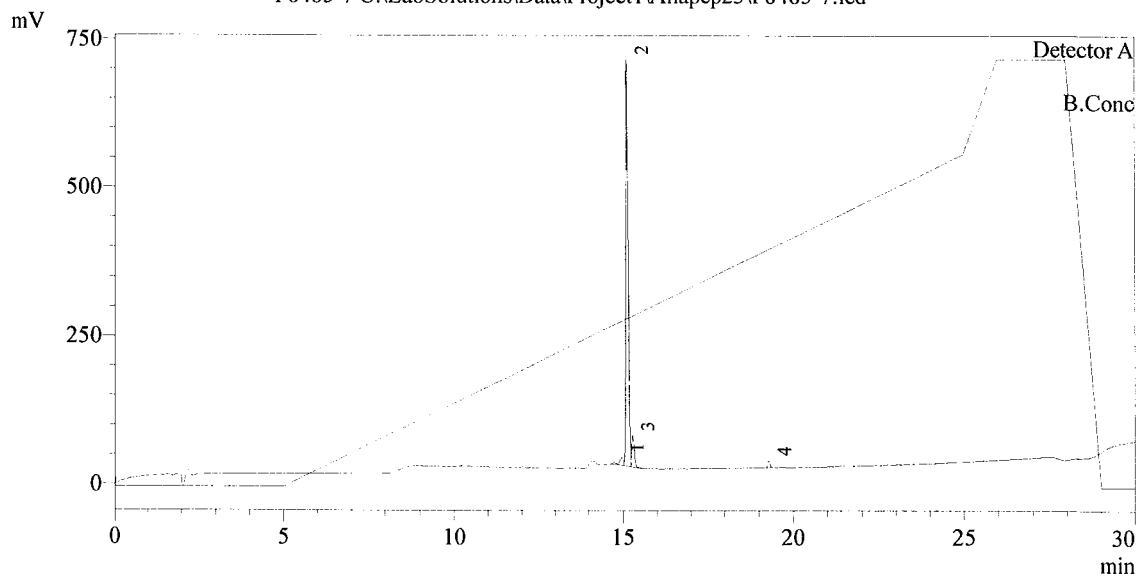
Sample Information

Acquired by : System Administrator
Sample Name : P8485-7
Sample ID : P8485-7
Data Filename : P8485-7.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 7:56:23 PM
Data Processed : 8/17/2018 8:28:37 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

P8485-7 C:\LabSolutions\Data\Project I\Anapep25\P8485-7.lcd



1 Detector A / 220nm

PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	14.954	100555	13059	1.714	2.776
2	15.123	3200373	685419	89.983	88.348
3	15.274	270129	52178	6.850	7.457
4	19.296	51387	11068	1.453	1.419
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: NLVPMVATV

Lot# P8485-7

ID#:

Project #:

Mol Wt: 943.18

Amount injected: 134.98 ngs

Amount Recovered: 118.516 ngs

Percent Recovery: 87.8%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

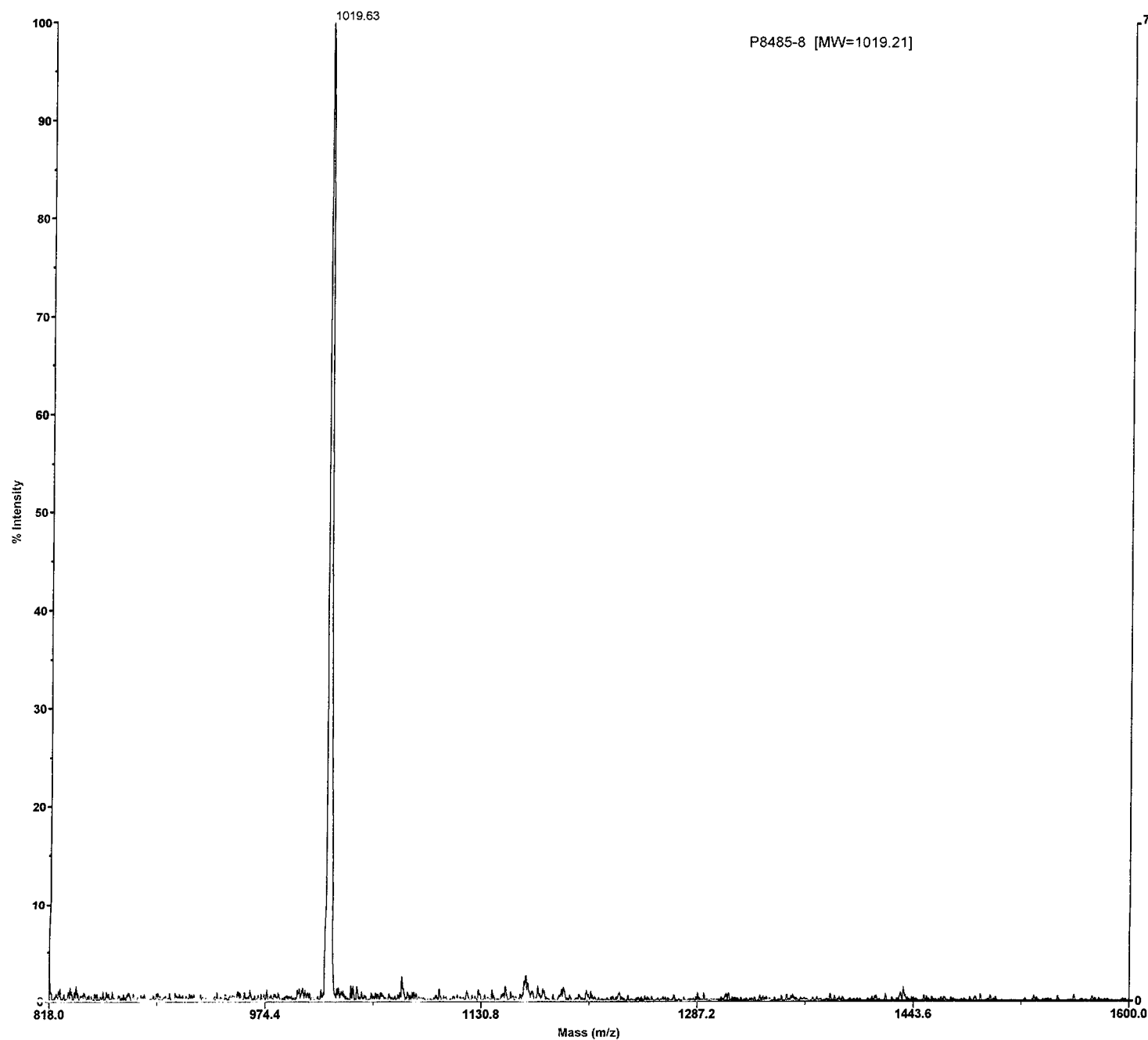
AA	AA in sequence	AA found in pmoles	MW	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	0	0.000	87.08	0.000	0.00	0.0
R	0	0.000	156.19	0.000	0.00	0.0
G	0	0.000	57.05	0.000	0.00	0.0
D/N	1	100.459	114.10	11.462	100.46	0.8
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	1	125.390	101.11	12.678	125.39	1.0
A	1	114.747	71.08	8.156	114.75	0.9
P	1	142.055	97.12	13.796	142.06	1.1
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	1	130.763	131.20	17.156	130.76	1.0
V	3	404.892	99.13	40.137	134.96	3.2
I	0	0.000	113.16	0.000	0.00	0.0
L	1	133.703	113.16	15.130	133.70	1.1
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				118.516		

Performed by: *R. Monicchi* 09/25/2018

Verified by: *Mousa Bazani* 09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 1019.5, 7546]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 620 -- 1800 Da
Number of laser shots: 150/spectrum
Laser intensity: 2000
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 17.004
Bin size: 2 nsec
Number of data points: 5946
Vertical scale: 500 mV
Vertical offset: -2%
Input bandwidth: 150 MHz

Sample well: 38
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.pt
Lab name: PE Biosystems

Absolute x-position: 38796.2
Absolute y-position: 32760.1
Relative x-position: 1648.72
Relative y-position: 692.62
Shots in spectrum: 18
Source pressure: 2.99e-007
Mirror pressure: 0
TC2 pressure: 0.01747
TIS gate width: 30
TIS flight length: 940

Acquired: 19:57:00, August 21, 2018

Printed: 19:58, August 21, 2018

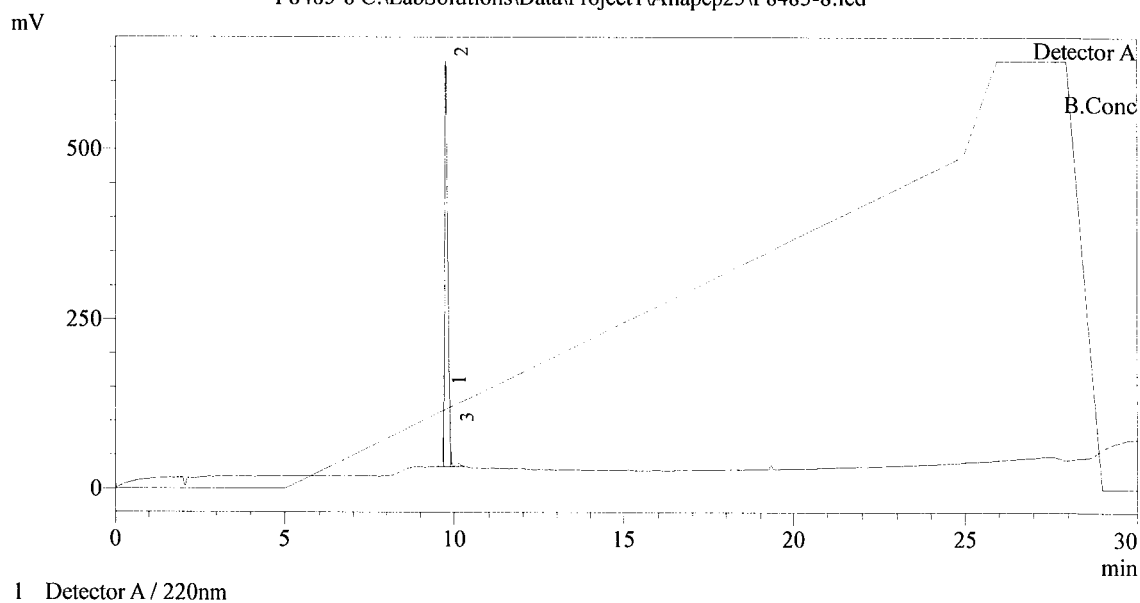
C:\VOYAGER\Data\2018\P8485-8_0001.dat

Sample Information

Acquired by : System Administrator
Sample Name : P8485-8
Sample ID : P8485-8
Data Filename : P8485-8.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 8:29:10 PM
Data Processed : 8/17/2018 9:01:23 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

P8485-8 C:\LabSolutions\Data\Project1\Anapep25\P8485-8.lcd



PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	9.700	96847	32581	5.033	2.508
2	9.804	3710481	597449	92.291	96.079
3	9.925	54597	17326	2.676	1.414
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: KTGGPIYKR

Lot# P8485-8

ID#:

Project #:

Mol Wt: 1,019.21

Amount injected: 105.27 ngs

Amount Recovered: 69.583 ngs

Percent Recovery: 66.1%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

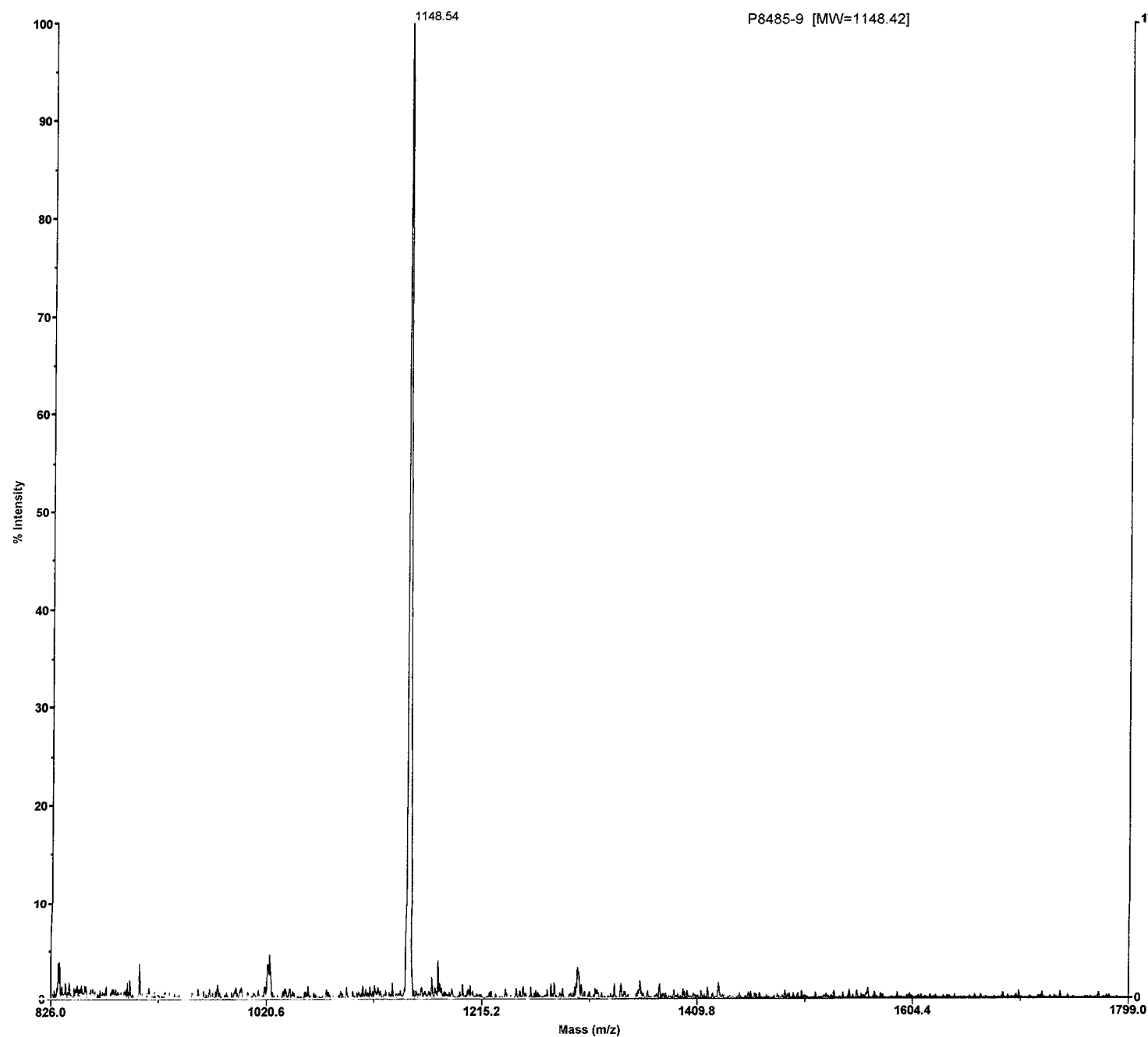
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	0	0.000	87.08	0.000	0.00	0.0
R	1	71.450	156.19	11.160	71.45	1.0
G	2	143.091	57.05	8.163	71.55	2.1
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	1	72.451	101.11	7.326	72.45	1.0
A	0	0.000	71.08	0.000	0.00	0.0
P	1	65.232	97.12	6.335	65.23	0.9
C	0	0.000	103.14	0.000	0.00	0.0
K	2	136.267	128.18	17.467	68.13	2.0
Y	1	68.880	163.18	11.240	68.88	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	69.743	113.16	7.892	69.74	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				69.583		

Performed by: *R. Mancini* 09/25/2018

Verified by: *Moussa Bazani* 09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 1148.4, 1766]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 625 -- 2000 Da
Number of laser shots: 150/spectrum
Laser intensity: 2100
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 17.072
Bin size: 2 nsec
Number of data points: 6690
Vertical scale: 500 mV
Vertical offset: -2%
Input bandwidth: 150 MHz

Sample well: 39
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.plt
Lab name: PE Biosystems

Absolute x-position: 43216.9
Absolute y-position: 33155
Relative x-position: 989.433
Relative y-position: 1087.54
Shots in spectrum: 46
Source pressure: 2.668e-007
Mirror pressure: 0
TC2 pressure: 0.01752
TIS gate width: 30
TIS flight length: 940

Acquired: 20:00:00, August 21, 2018

Printed: 20:01, August 21, 2018

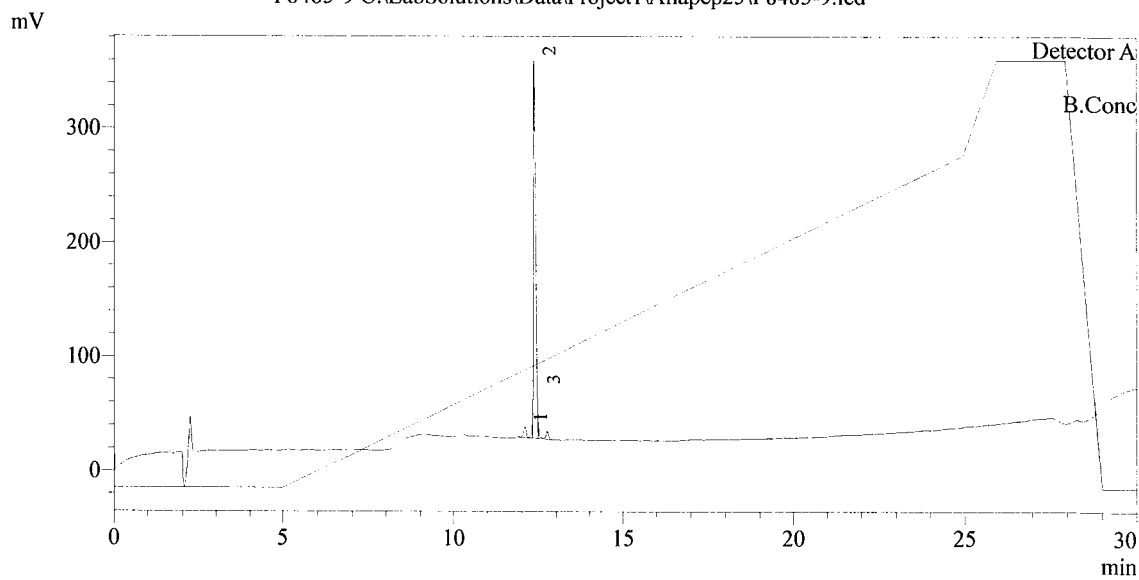
C:\VOYAGER\Data\P2018\P8485-9_0001.dat

Sample Information

Acquired by : System Administrator
Sample Name : P8485-9
Sample ID : P8485-9
Data Filename : P8485-9.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 9:01:55 PM
Data Processed : 8/17/2018 9:34:08 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

P8485-9 C:\LabSolutions\Data\Project1\Anapep25\P8485-9.lcd



PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	12.085	65988	9242	2.631	4.075
2	12.381	1496572	331013	94.227	92.421
3	12.475	56746	11038	3.142	3.504
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: RVLSFIKGTK

Lot# P8485-9

ID#:

Project #:

Mol Wt: 1,148.42

Amount injected: 100.68 ngs

Amount Recovered: 69.169 ngs

Percent Recovery: 68.7%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

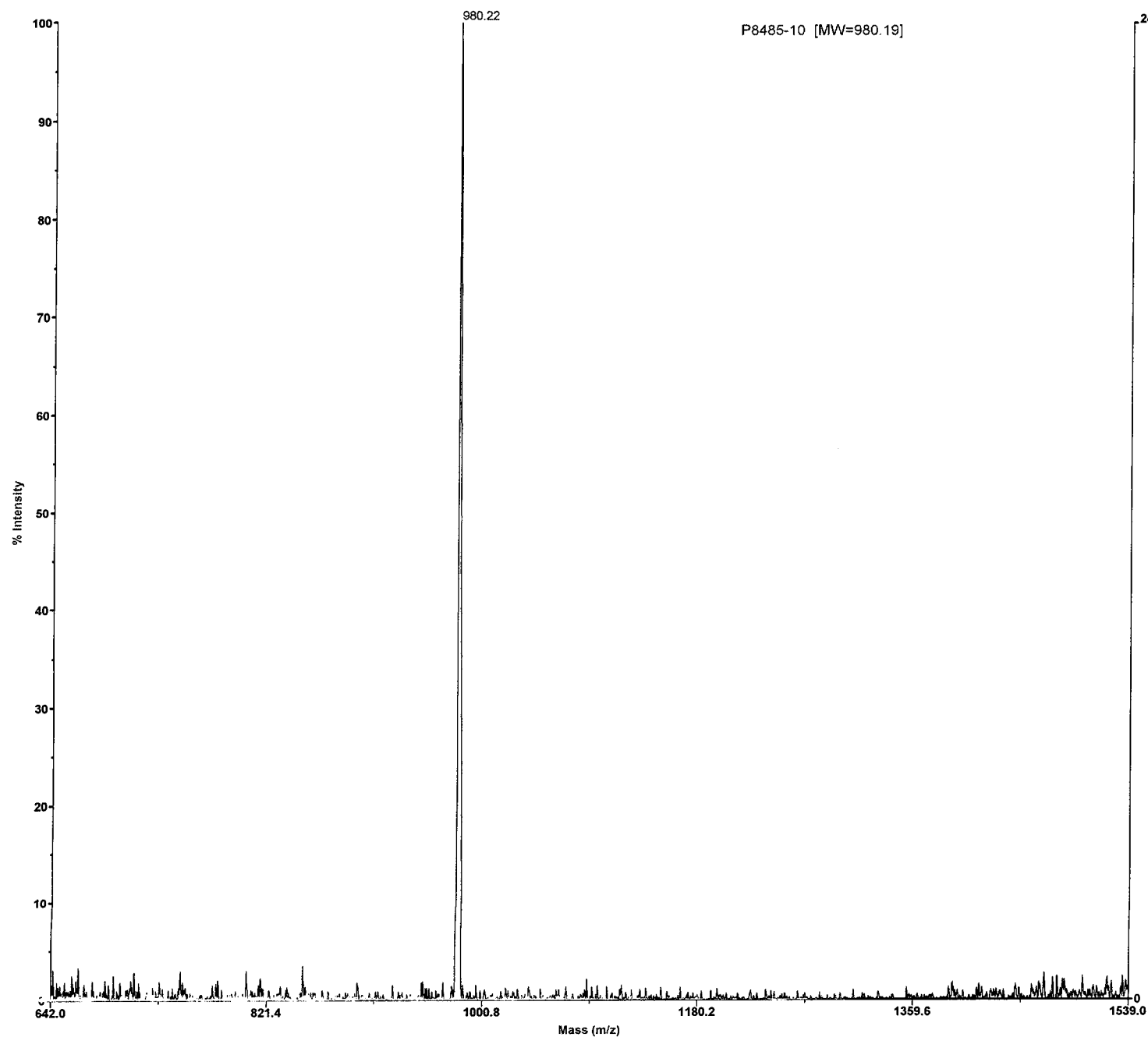
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	1	64.559	87.08	5.622	64.56	1.0
R	1	55.739	156.19	8.706	55.74	0.9
G	1	72.970	57.05	4.163	72.97	1.2
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	1	67.477	101.11	6.823	67.48	1.1
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	117.314	128.18	15.037	58.66	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	1	58.977	99.13	5.846	58.98	0.9
I	1	52.602	113.16	5.952	52.60	0.8
L	1	60.983	113.16	6.901	60.98	1.0
F	1	68.749	147.18	10.118	68.75	1.1
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				69.169		

Performed by: *R. Minichini* 09/25/2018

Verified by: *Nousa Bazani* 09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 980.1, 2450]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 610 -- 2000 Da
Number of laser shots: 100/spectrum
Laser intensity: 2000
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 16.86
Bin size: 2 nsec
Number of data points: 6791
Vertical scale: 500 mV
Vertical offset: -2%
Input bandwidth: 150 MHz

Sample well: 42
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.plt
Lab name: PE Biosystems

Absolute x-position: 5860.61
Absolute y-position: 27057
Relative x-position: -806.894
Relative y-position: 69.4885
Shots in spectrum: 22
Source pressure: 2.538e-007
Mirror pressure: 0
TC2 pressure: 0.01759
TIS gate width: 30
TIS flight length: 940

Acquired: 20:03:00, August 21, 2018

Printed: 20:03, August 21, 2018

C:\VOYAGER\Data\2018\P8485-10_0001.dat

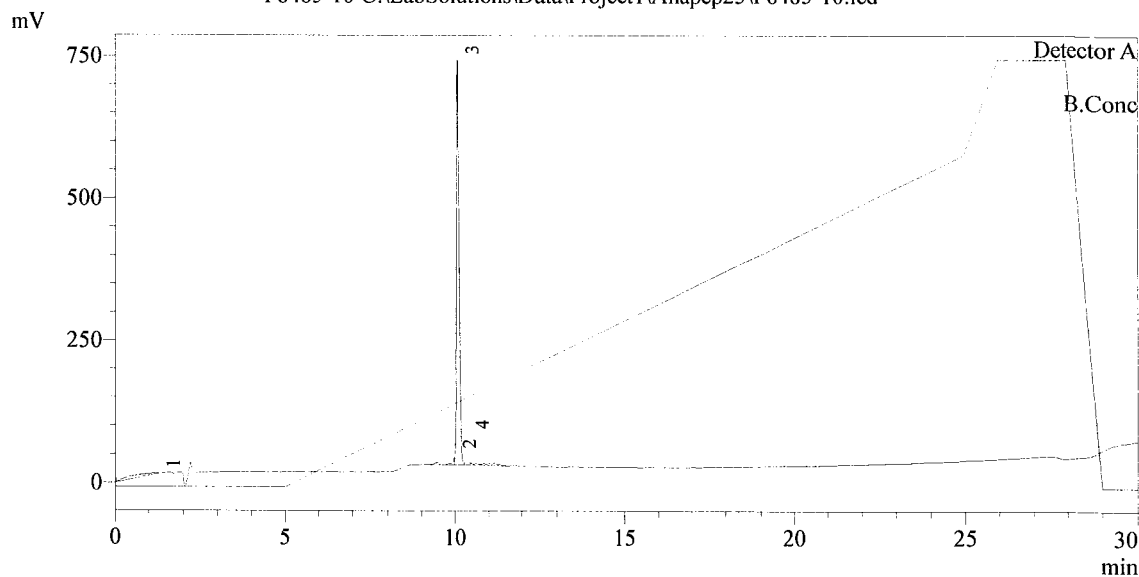
Sample Information

Acquired by : System Administrator
Sample Name : P8485-10
Sample ID : P8485-10
Data Filename : P8485-10.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 9:34:39 PM
Data Processed : 8/17/2018 10:06:53 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

P8485-10 C:\LabSolutions\Data\Project1\Anapep25\P8485-10.lcd



PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	1.258	252586	702	0.096	5.725
2	9.983	84596	10526	1.437	1.917
3	10.109	3865648	712584	97.271	87.621
4	10.361	208963	8761	1.196	4.736
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: ILRGSAVHK

Lot# P8485-10

ID#:

Project #:

Mol Wt: 980.19

Amount injected: 96.47 ngs

Amount Recovered: 62.804 ngs

Percent Recovery: 65.1%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

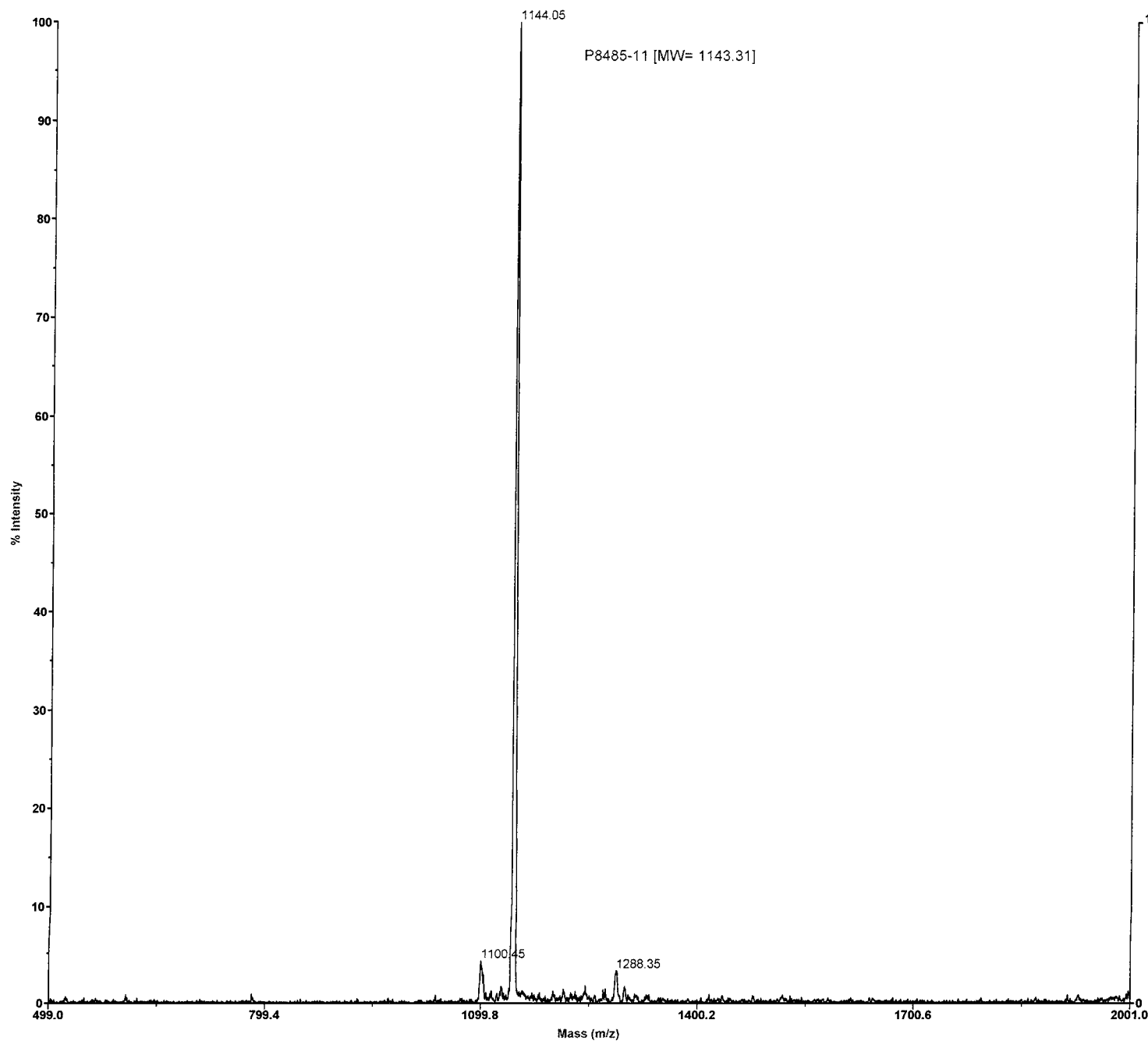
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	1	65.524	137.14	8.986	65.52	1.0
S	1	62.483	87.08	5.441	62.48	1.0
R	1	66.623	156.19	10.406	66.62	1.0
G	1	67.140	57.05	3.830	67.14	1.0
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	0	0.000	101.11	0.000	0.00	0.0
A	1	63.316	71.08	4.501	63.32	1.0
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	1	67.532	128.18	8.656	67.53	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	1	67.016	99.13	6.643	67.02	1.0
I	1	61.713	113.16	6.983	61.71	0.9
L	1	65.017	113.16	7.357	65.02	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				62.804		

Performed by: *R. Monicelli* 09/25/2018

Verified by: *Moussa Bazani* 09/25/2018

Applied Biosystems Voyager System 1099

Voyager Spec #1=>SM5[BP = 1144.2, 15040]



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

Accelerating voltage: 20000 V
Grid voltage: 92%
Guide wire 0: 0.01%
Extraction delay time: 300 nsec

Acquisition mass range: 500 -- 2200 Da
Number of laser shots: 100/spectrum
Laser intensity: 1741
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 14.568
Bin size: 2 nsec
Number of data points: 7947
Vertical scale: 200 mV
Vertical offset: 0%
Input bandwidth: 150 MHz

Sample well: 13
Plate ID: 100 WELL PLATE
Serial number: 1099
Instrument name: Voyager-DE
Plate type filename: C:\VOYAGER\100 well plate.ptt
Lab name: BioSynthesis, Inc

Absolute x-position: 11732.8
Absolute y-position: 40836.2
Relative x-position: -14.6559
Relative y-position: -1391.33
Shots in spectrum: 21
Source pressure: 2.481e-007
Mirror pressure: 0
TC2 pressure: 0.001
TIS gate width: 30
TIS flight length: 940

Acquired: 09:32:00, August 20, 2018

Printed: 09:33, August 20, 2018

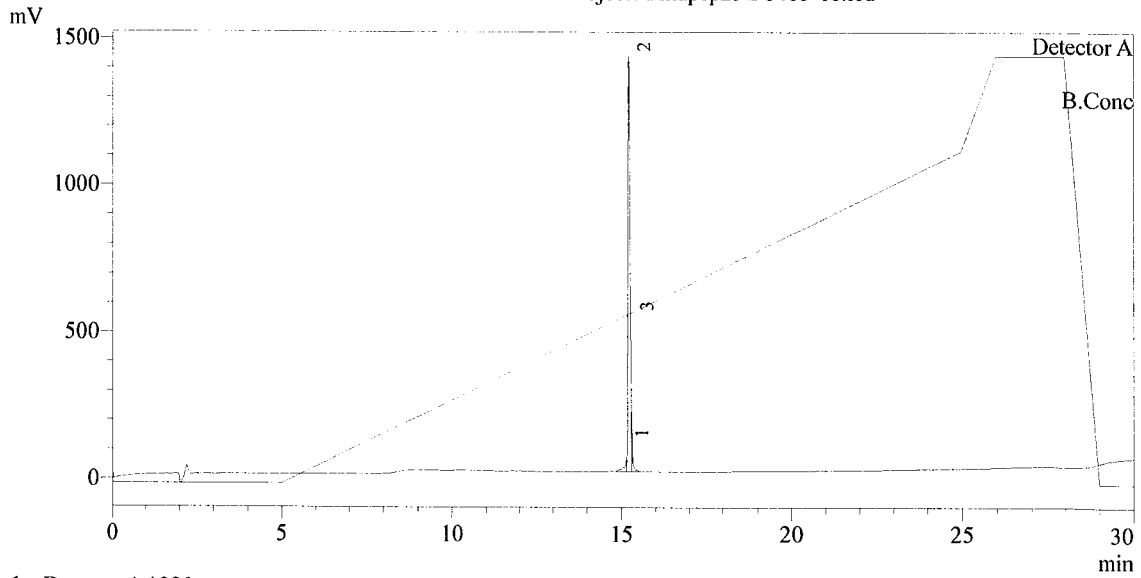
C:\VOYAGER\Data\PEPTIDE 2018 1\P8485-11_0001.dat

Sample Information

Acquired by : System Administrator
Sample Name : P8485-11
Sample ID : P8485-11
Data Filename : P8485-11.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 10:07:26 PM
Data Processed : 8/17/2018 10:39:39 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

P8485-11 C:\LabSolutions\Data\Project1\Anapep25\P8485-11.lcd



PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	15.150	225257	36088	2.243	3.378
2	15.236	6144161	1413559	87.864	92.137
3	15.308	299073	159153	9.893	4.485
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: RVRAYTYSK

Lot# P8485-11

ID#:

Project #:

Mol Wt: 1,143.31

Amount injected: 121.8 ngs

Amount Recovered: 83.554 ngs

Percent Recovery: 68.6%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

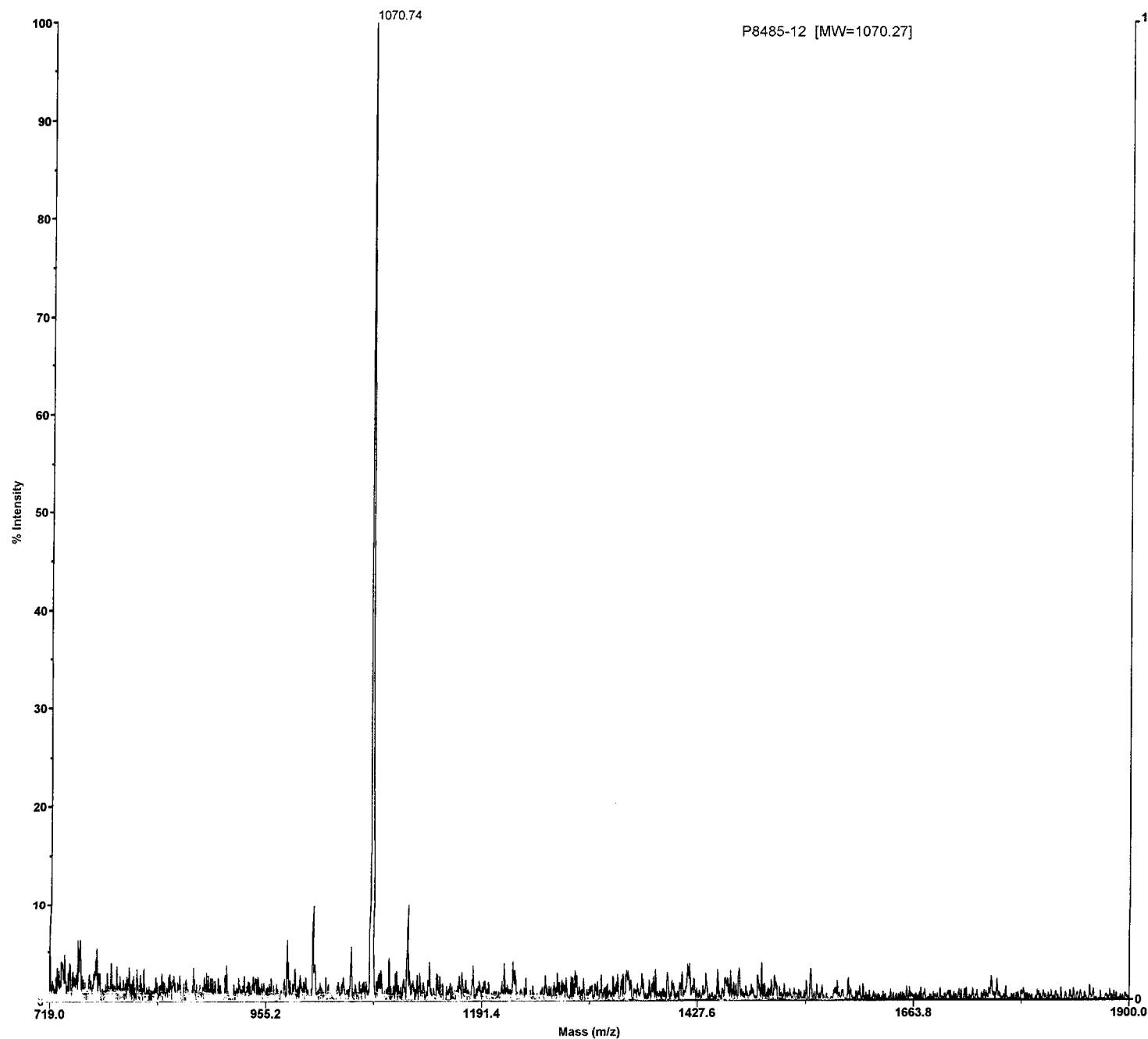
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	1	77.775	87.08	6.773	77.78	1.0
R	2	138.369	156.19	21.612	69.18	1.9
G	0	0.000	57.05	0.000	0.00	0.0
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	1	79.197	101.11	8.008	79.20	1.1
A	1	76.694	71.08	5.451	76.69	1.0
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	1	80.369	128.18	10.302	80.37	1.1
Y	2	156.323	163.18	25.509	78.16	2.1
M	0	0.000	131.20	0.000	0.00	0.0
V	1	59.517	99.13	5.900	59.52	0.8
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				83.554		

Performed by: *R. Mancini* 09/25/2018

Verified by: *Moussa Bazani* 09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 1070.7, 1491]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 610 -- 2000 Da
Number of laser shots: 100/spectrum
Laser intensity: 2000
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 16.872
Bin size: 2 nsec
Number of data points: 6795
Vertical scale: 500 mV
Vertical offset: -1.1%
Input bandwidth: 150 MHz

Sample well: 13
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.pt
Lab name: PE Biosystems

Absolute x-position: 11387.3
Absolute y-position: 44621.8
Relative x-position: -360.206
Relative y-position: 2394.28
Shots in spectrum: 46
Source pressure: 2.522e-007
Mirror pressure: 0
TC2 pressure: 0.01843
TIS gate width: 30
TIS flight length: 940

Acquired: 20:59:00, August 21, 2018

Printed: 21:00, August 21, 2018

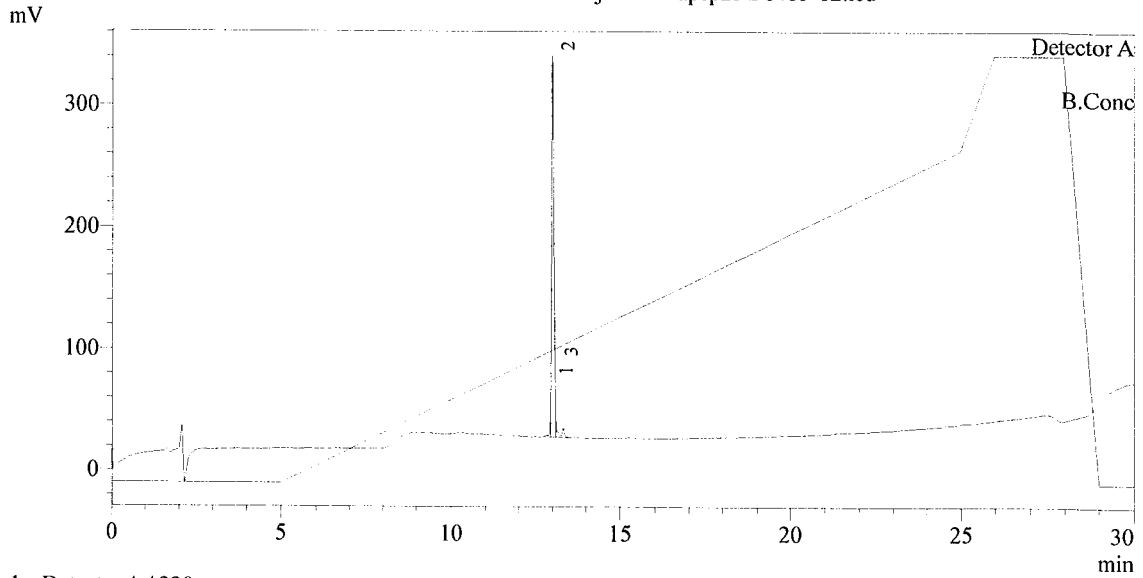
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Sample Information

Acquired by : System Administrator
Sample Name : P8485-12
Sample ID : P8485-12
Data Filename : P8485-12.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 10:40:12 PM
Data Processed : 8/17/2018 11:12:25 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

P8485-12 C:\LabSolutions\Data\Project1\Anapep25\P8485-12.lcd



PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	12.942	27012	8856	2.629	1.792
2	13.020	1414424	313177	92.980	93.840
3	13.108	65833	14787	4.390	4.368
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: RLRAEAQVK

Lot# P8485-12

ID#:

Project #:

Mol Wt: 1,070.27

Amount injected: 121.08 ngs

Amount Recovered: 81.248 ngs

Percent Recovery: 67.1%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

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	167.784	156.19	26.206	83.89	2.2
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	2	151.015	128.13	19.350	75.51	2.0
T	0	0.000	101.11	0.000	0.00	0.0
A	2	149.935	71.08	10.657	74.97	2.0
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	1	71.318	128.18	9.142	71.32	0.9
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	69.638	99.13	6.903	69.64	0.9
I	0	0.000	113.16	0.000	0.00	0.0
L	1	79.450	113.16	8.991	79.45	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				81.248		

Performed by:

R. Mancini

09/25/2018

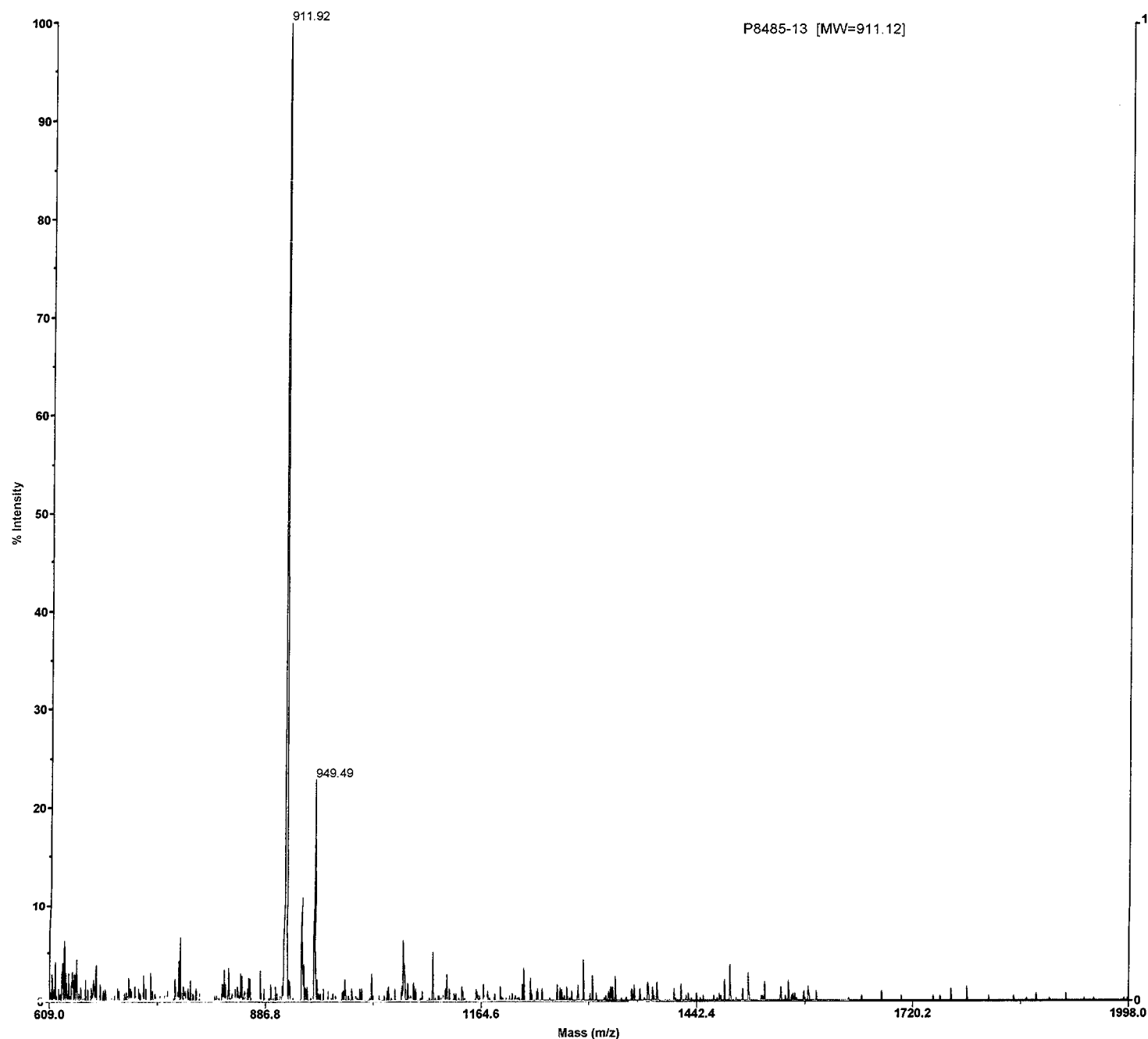
Verified by:

Nousa Bazani

09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 911.9, 1000]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 610 -- 2000 Da
Number of laser shots: 100/spectrum
Laser intensity: 1900
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 16.872
Bin size: 2 nsec
Number of data points: 6795
Vertical scale: 500 mV
Vertical offset: -1.1%
Input bandwidth: 150 MHz

Sample well: 14
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.pt
Lab name: PE Biosystems

Absolute x-position: 18470.1
Absolute y-position: 41426.6
Relative x-position: 1642.62
Relative y-position: -800.892
Shots in spectrum: 22
Source pressure: 2.295e-007
Mirror pressure: 0
TC2 pressure: 0.01862
TIS gate width: 30
TIS flight length: 940

Acquired: 21:05:00, August 21, 2018

Printed: 21:06, August 21, 2018

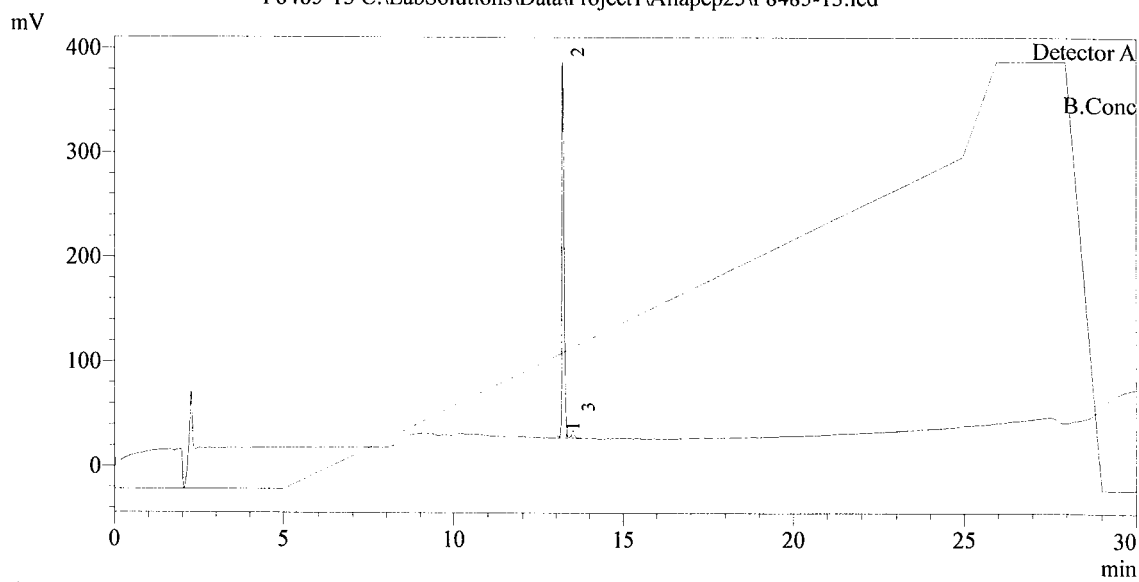
C:\VOYAGER\Data\2018\P8485-13_0001.dat

Sample Information

Acquired by : System Administrator
Sample Name : P8485-13
Sample ID : P8485-13
Data Filename : P8485-13.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 11:12:55 PM
Data Processed : 8/17/2018 11:45:09 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

P8485-13 C:\LabSolutions\Data\Project1\Anapec25\P8485-13.lcd



1 Detector A / 220nm

PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	13.055	10803	1891	0.512	0.650
2	13.223	1599694	360182	97.491	96.215
3	13.519	52122	7379	1.997	3.135
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: SIIPSGPLK

Lot# P8485-13

ID#:

Project #:

Mol Wt: 911.12

Amount injected: 66.77 ngs

Amount Recovered: 51.816 ngs

Percent Recovery: 77.6%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

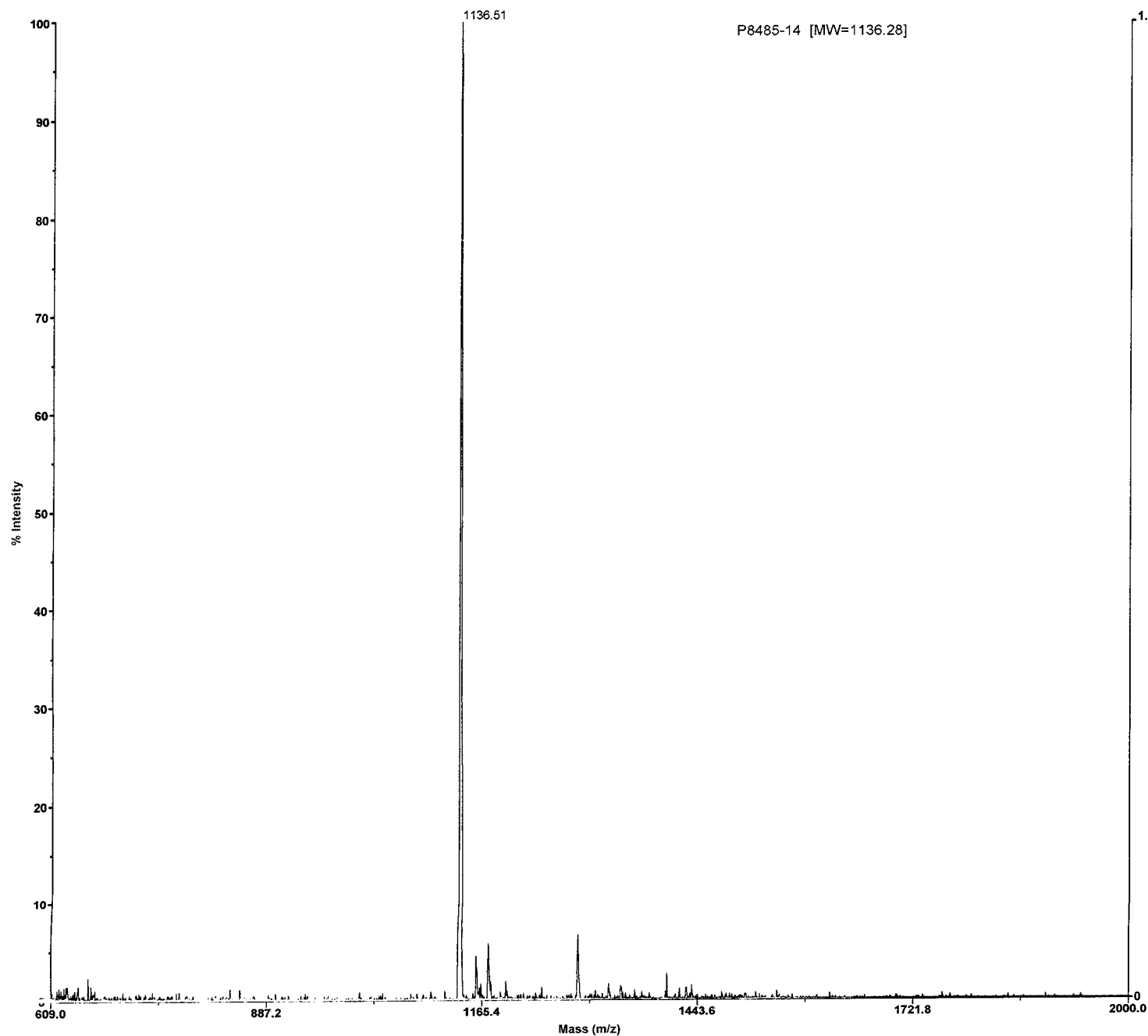
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	2	121.701	87.08	10.598	60.85	1.8
R	0	0.000	156.19	0.000	0.00	0.0
G	1	71.377	57.05	4.072	71.38	1.0
D/N	0	0.000	114.10	0.000	0.00	0.0
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	0	0.000	101.11	0.000	0.00	0.0
A	0	0.000	71.08	0.000	0.00	0.0
P	2	140.918	97.12	13.686	70.46	2.1
C	0	0.000	103.14	0.000	0.00	0.0
K	1	70.073	128.18	8.982	70.07	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	2	58.400	113.16	6.609	29.20	0.9
L	1	69.549	113.16	7.870	69.55	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				51.816		

Performed by: *R. Mancini* 09/25/2018

Verified by: *Moussa Bazani* 09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 1136.3, 13420]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 610 -- 2000 Da
Number of laser shots: 100/spectrum
Laser intensity: 1900
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 16.884
Bin size: 2 nsec
Number of data points: 6799
Vertical scale: 500 mV
Vertical offset: -1.1%
Input bandwidth: 150 MHz

Sample well: 15
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.ptt
Lab name: PE Biosystems

Absolute x-position: 23095.1
Absolute y-position: 41917.6
Relative x-position: 1187.62
Relative y-position: -309.886
Shots in spectrum: 10
Source pressure: 1.998e-007
Mirror pressure: 0
TC2 pressure: 0.01872
TIS gate width: 30
TIS flight length: 940

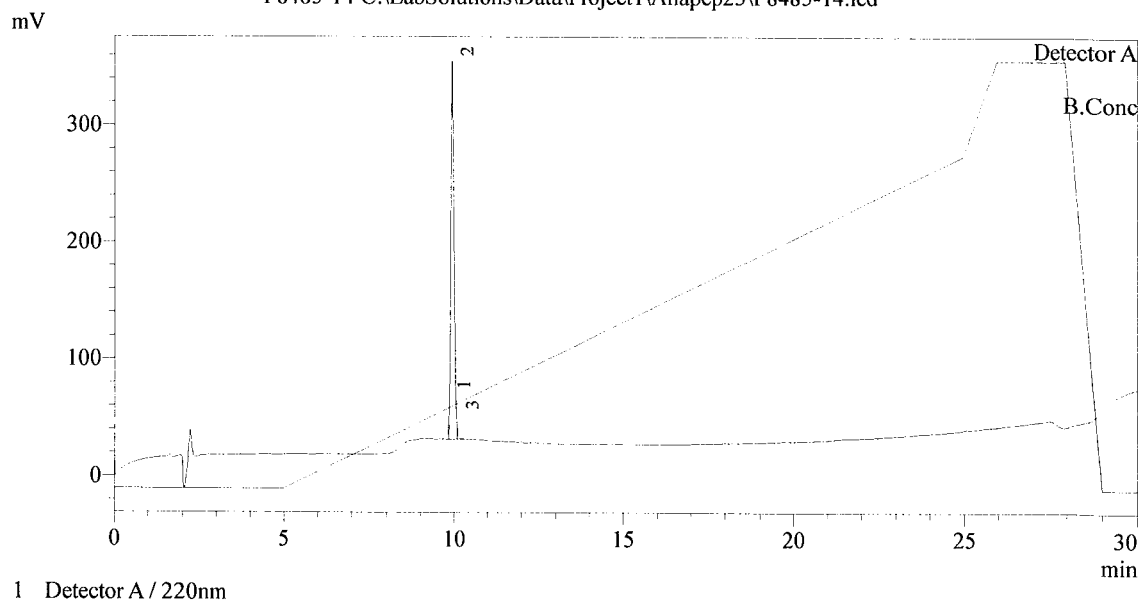
Sample Information

Acquired by : System Administrator
Sample Name : P8485-14
Sample ID : P8485-14
Data Filename : P8485-14.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/17/2018 11:45:41 PM
Data Processed : 8/18/2018 12:17:55 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

P8485-14 C:\LabSolutions\Data\Project1\Anapep25\P8485-14.lcd



PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	9.842	38591	9419	2.764	1.769
2	9.961	2126831	323594	94.949	97.470
3	10.100	16621	7797	2.288	0.762
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: AVFDRKSDAK

Lot# P8485-14

ID#:

Project #:

Mol Wt: 1,136.28

Amount injected: 116.48 ngs

Amount Recovered: 79.675 ngs

Percent Recovery: 68.4%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Ile bond is only partially hydrolyzed and result in lower recovery of Ile

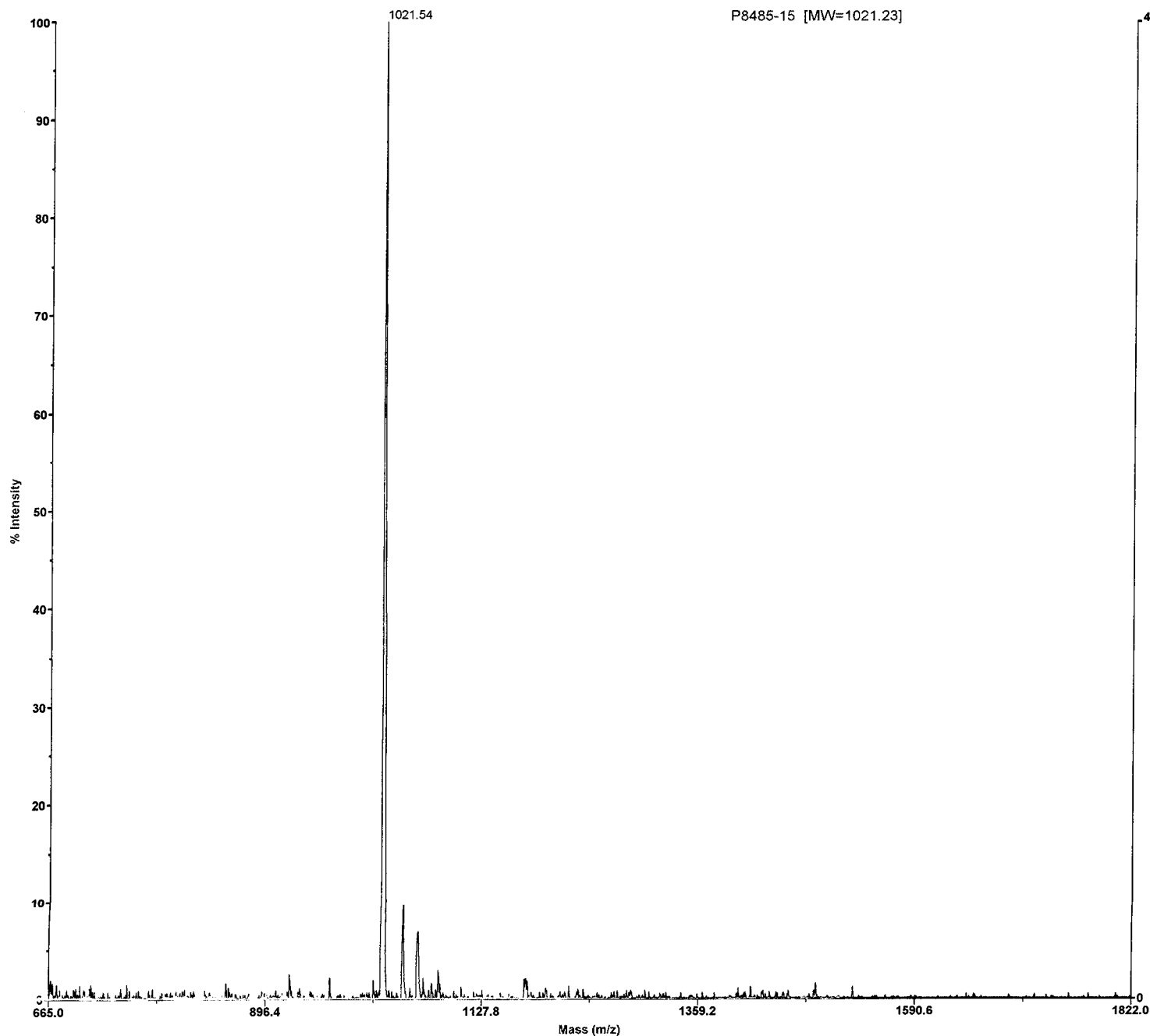
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	1	67.711	87.08	5.896	67.71	1.0
R	1	77.740	156.19	12.142	77.74	1.1
G	0	0.000	57.05	0.000	0.00	0.0
D/N	2	150.436	114.10	17.165	75.22	2.2
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	0	0.000	101.11	0.000	0.00	0.0
A	2	149.289	71.08	10.611	74.64	2.2
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	155.755	128.18	19.965	77.88	2.2
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	55.174	99.13	5.469	55.17	0.8
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	57.251	147.18	8.426	57.25	0.8
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				79.675		

Performed by: *R. Mancini* 09/25/2018

Verified by: *Mousa Bazani* 09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 1021.3, 4999]



Mode of operation:	Linear
Extraction mode:	Delayed
Polarity:	Positive
Acquisition control:	Manual
Accelerating voltage:	20000 V
Grid voltage:	91%
Guide wire O:	0.05%
Extraction delay time:	100 nsec
Acquisition mass range:	610 -- 2000 Da
Number of laser shots:	100/spectrum
Laser intensity:	1900
Laser Rep Rate:	3.0 Hz
Calibration type:	Default
Calibration matrix:	a-Cyano-4-hydroxycinnamic acid
Low mass gate:	Off
Digitizer start time:	16.886
Bin size:	2 nsec
Number of data points:	6801
Vertical scale:	500 mV
Vertical offset:	-1.1%
Input bandwidth:	150 MHz
Sample well:	16
Plate ID:	100 WELL PLATE
Serial number:	1054
Instrument name:	Voyager-DE RP
Plate type filename:	C:\VOYAGER\100 well plate.plt
Lab name:	PE Biosystems
Absolute x-position:	26131.7
Absolute y-position:	43295.5
Relative x-position:	-855.823
Relative y-position:	1067.97
Shots in spectrum:	18
Source pressure:	1.99e-007
Mirror pressure:	0
TC2 pressure:	0.01872
TIS gate width:	30
TIS flight length:	940

Acquired: 21:22:00, August 21, 2018

Printed: 21:22, August 21, 2018

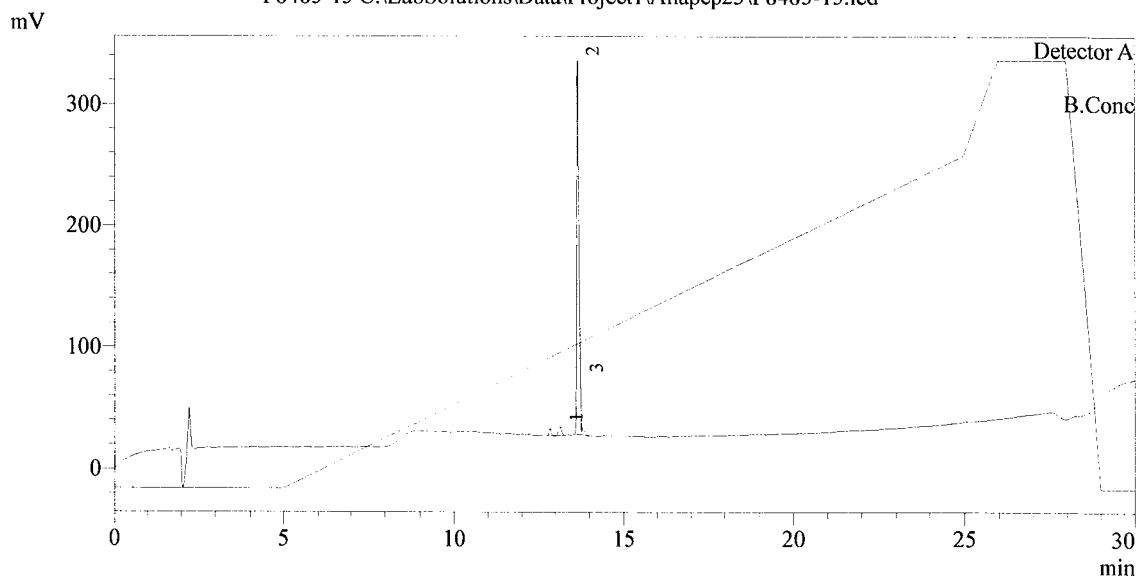
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Sample Information

Acquired by : System Administrator
Sample Name : P8485-15
Sample ID : P8485-15
Data Filename : P8485-15.lcd
Method Filename : ANAPEP_25HEAT.lcm
Date Acquired : 8/18/2018 12:18:26 AM
Data Processed : 8/18/2018 12:50:39 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

P8485-15 C:\LabSolutions\Data\Project1\Anapep25\P8485-15.lcd



1 Detector A / 220nm

PeakTable

Detector A 220nm

Peak#	Ret. Time	Area	Height	Height %	Area %
1	13.166	65857	7154	2.192	4.437
2	13.683	1388273	307708	94.278	93.528
3	13.775	30208	11522	3.530	2.035
Total				100.000	100.000

Amino Acid Analysis Data Sheet

Sequence: IVTDFSVIK

Lot# P8485-15

ID#:

Project #:

Mol Wt: 1,021.23

Amount injected: 38.57 ngs

Amount Recovered: 30.704 ngs

Percent Recovery: 79.6%

Notes: Cys and Trp are destroyed during HCl hydrolysis and are not included in analysis
Ile-Val bond is only partially hydrolyzed and result in lower recovery of Ile and Val

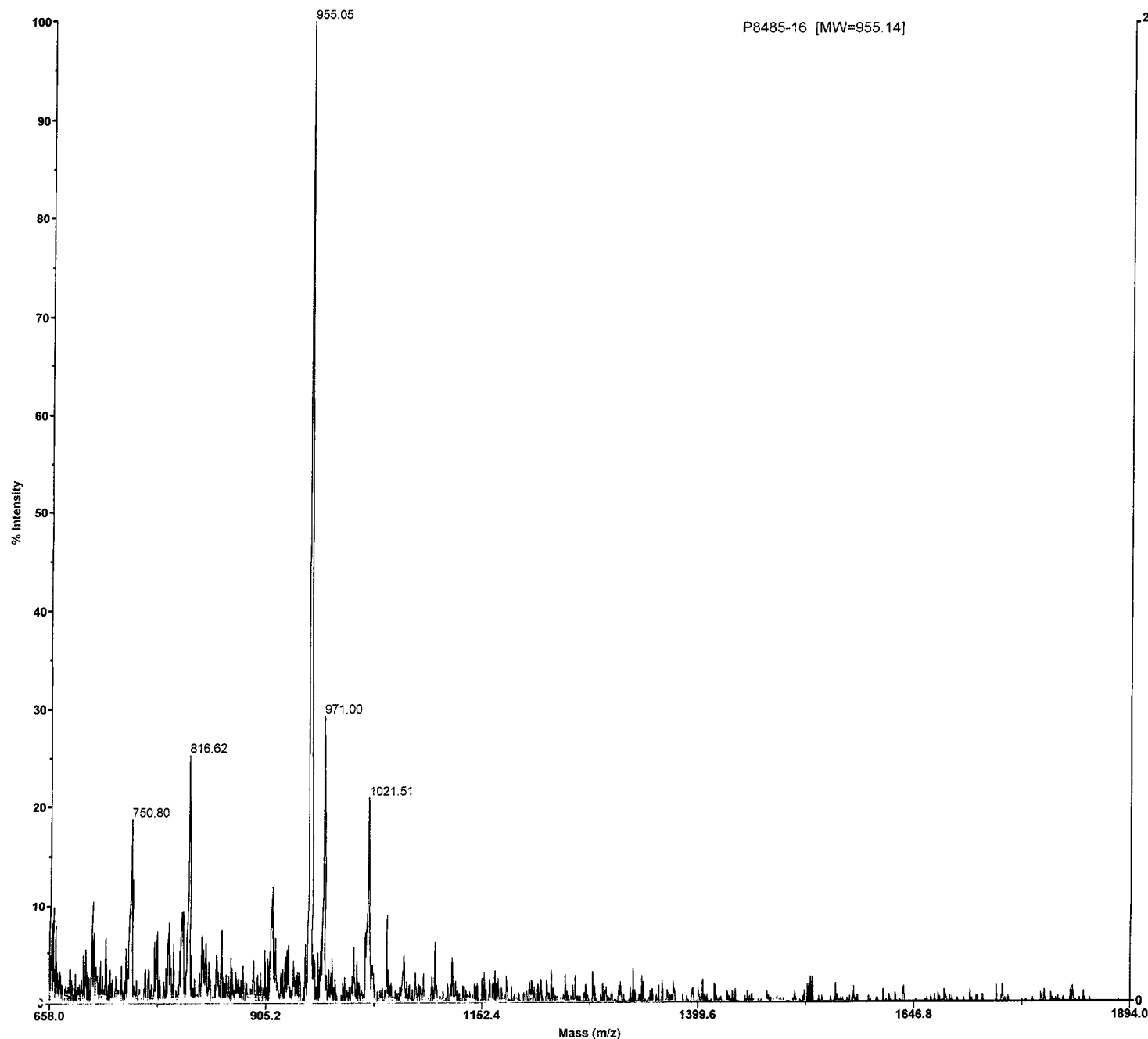
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
H	0	0.000	137.14	0.000	0.00	0.0
S	1	40.672	87.08	3.542	40.67	0.9
R	0	0.000	156.19	0.000	0.00	0.0
G	0	0.000	57.05	0.000	0.00	0.0
D/N	1	42.499	114.10	4.849	42.50	1.0
E/Q	0	0.000	128.13	0.000	0.00	0.0
T	1	43.688	101.11	4.417	43.69	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	1	39.508	128.18	5.064	39.51	0.9
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	2	29.457	99.13	2.920	14.73	0.7
I	2	22.984	113.16	2.601	11.49	0.5
L	0	0.000	113.16	0.000	0.00	0.0
F	1	49.672	147.18	7.311	49.67	1.1
W	0	0.000	186.22	0.000	0.00	0.0
Pep. Recovered				30.704		

Performed by: *R. Mancini* 09/25/2018

Verified by: *Moussa Bazani* 09/25/2018

Applied Biosystems Voyager System 1054

Voyager Spec #1=>SM5[BP = 955.1, 2221]



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

Accelerating voltage: 20000 V
Grid voltage: 91%
Guide wire 0: 0.05%
Extraction delay time: 100 nsec

Acquisition mass range: 610 -- 2000 Da
Number of laser shots: 100/spectrum
Laser intensity: 2000
Laser Rep Rate: 3.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic acid
Low mass gate: Off

Digitizer start time: 16.888
Bin size: 2 nsec
Number of data points: 6802
Vertical scale: 500 mV
Vertical offset: -1.1%
Input bandwidth: 150 MHz

Sample well: 17
Plate ID: 100 WELL PLATE
Serial number: 1054
Instrument name: Voyager-DE RP
Plate type filename: C:\VOYAGER\100 well plate.pt
Lab name: PE Biosystems

Absolute x-position: 33216.6
Absolute y-position: 42923.5
Relative x-position: 1149.07
Relative y-position: 695.97
Shots in spectrum: 14
Source pressure: 1.839e-007
Mirror pressure: 0
TC2 pressure: 0.01857
TIS gate width: 30
TIS flight length: 940

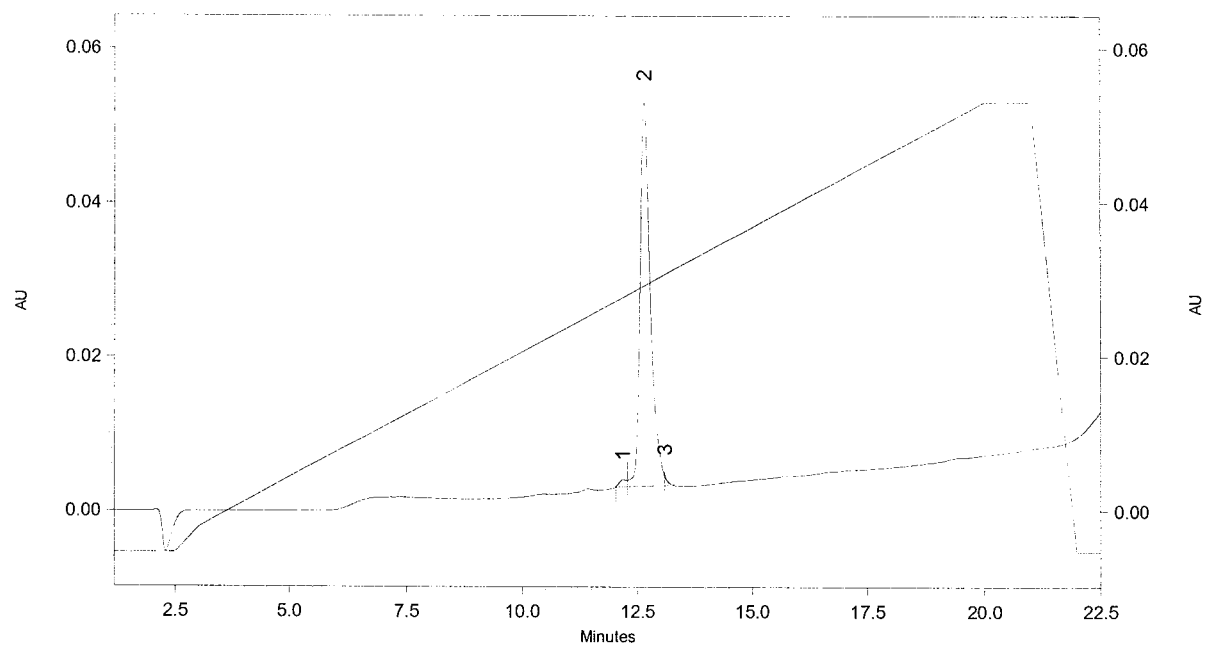
Acquired: 21:30:00, August 21, 2018

Printed: 21:31, August 21, 2018

C:\VOYAGER\Data\P2018\P8485-16_0002.dat

HPLC Report

Sample ID: P8485-16
 Method: D:\32Karat\Methods\Monolithic_1.met
 File Name: D:\32Karat\Projects\Default\Data\P8485-16
 Wavelength: 220nm
 HPLC ID#: CD-069/EQ-380



Pk #	Retention Time	Area	Area Percent
1	12.183	9871	1.229
2	12.667	788507	98.152
3	13.117	4971	0.619

Totals		803349	100.000
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