

## Certificate of Analysis

### Peptide Sequence (N-terminus to C-terminus):

[Acetyl] WQEWERKVDLFLEENITALLEEAQIQQEK NMYELQ [Amide]

<b>Peptide Name:</b>	Cat # 9774 SIVmac251 C34 Peptide	<b>Lot No.:</b> P3062-1
<b>Client Project No.:</b>	Lot 150279	
<b>Modification(s):</b>	N/A	<b>Qty:</b> 10 mg
<b>Additional Instructions(s):</b>	20 x 0.5 mg	<b>Counter-ion:</b> Trifluoroacetate

### Quality Control Specifications

**Format:** White Powder

**Mass Spectrometry Analysis: Voyager-DE RP**

Calculated Mass: MW = 4323.84  
Observed Mass: MH - = 4323.32

**Purity Level Analysis: RP-HPLC**

Guaranteed Purity: >80%  
Observed Purity: >97%

**Amino Acid Analysis:** Yes

**Endotoxin Services:**

Endotoxin Testing: No  
Endotoxin Removal: No

**Solubility Test:** No

**Other Data:** No

### General Solubility Guidelines

Peptides shorter than 5 residues are usually soluble in water or aqueous buffer, unless the entire sequence consists of hydrophobic amino acids such as W, L, I, F, M, V, Y.

Hydrophilic peptides containing >25% charged residues like D, K, R, H, E and <25% hydrophobic amino acids are usually soluble in water or aqueous buffer.

Hydrophobic peptides containing  $\geq 50\%$  hydrophobic residues may be insoluble or only partly soluble in aqueous solutions. In this case, we recommend using organic solvents like DMSO. In such cases dissolve the peptide in the smallest possible volume of 100% DMSO and subsequently add water/buffer until the desired concentration is achieved. If DMSO interferes with your experimental system, DMF (dimethylformamide) or acetonitrile can serve as alternative solvents.

Peptides containing a very high (>75%) proportion of D, E, H, K, N, Q, R, S, T, Y are capable of building intermolecular hydrogen bonds (cross-linking), thus forming gels in aqueous solutions. These peptides should either be treated according to instructions for hydrophobic peptides (see above) or by changing the pH value if possible.

Note: Peptides containing the amino acids Cys, Met, and Trp are susceptible to oxidation; therefore, oxygen-free solvents should be used.

### Handling Storage

All Bio-Synthesis peptides are supplied lyophilized. Peptide containing vial should be tightly capped at all time. Repeated freeze-thaw cycles should be avoided for lyophilized peptides or peptide in solutions.

The lyophilized peptide and peptide solutions should be stored at  $-20\text{ }^{\circ}\text{C}$  when not in use. For long-term storage (over one year), it is recommended that peptides be stored at  $-80\text{ }^{\circ}\text{C}$ .

Prepared by: Lan Nguyen Approved by: Mousa Bazgani Date: 9/28/2015

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## Amino Acid Analysis Data Sheet

Sequence [Acetyl] WQEWERK VDFLEENITALLLEEAIQQEK NMYELQ [Amide]  
 Lot# P3062-1  
 Name Cat # 9774 SIVmac251 C34 Peptide  
 Mol Wt 4323.84  
 Amount injected 1000ngs  
 Amount Recovered 901.2ngs  
 % Pep. Recovery 90.12%

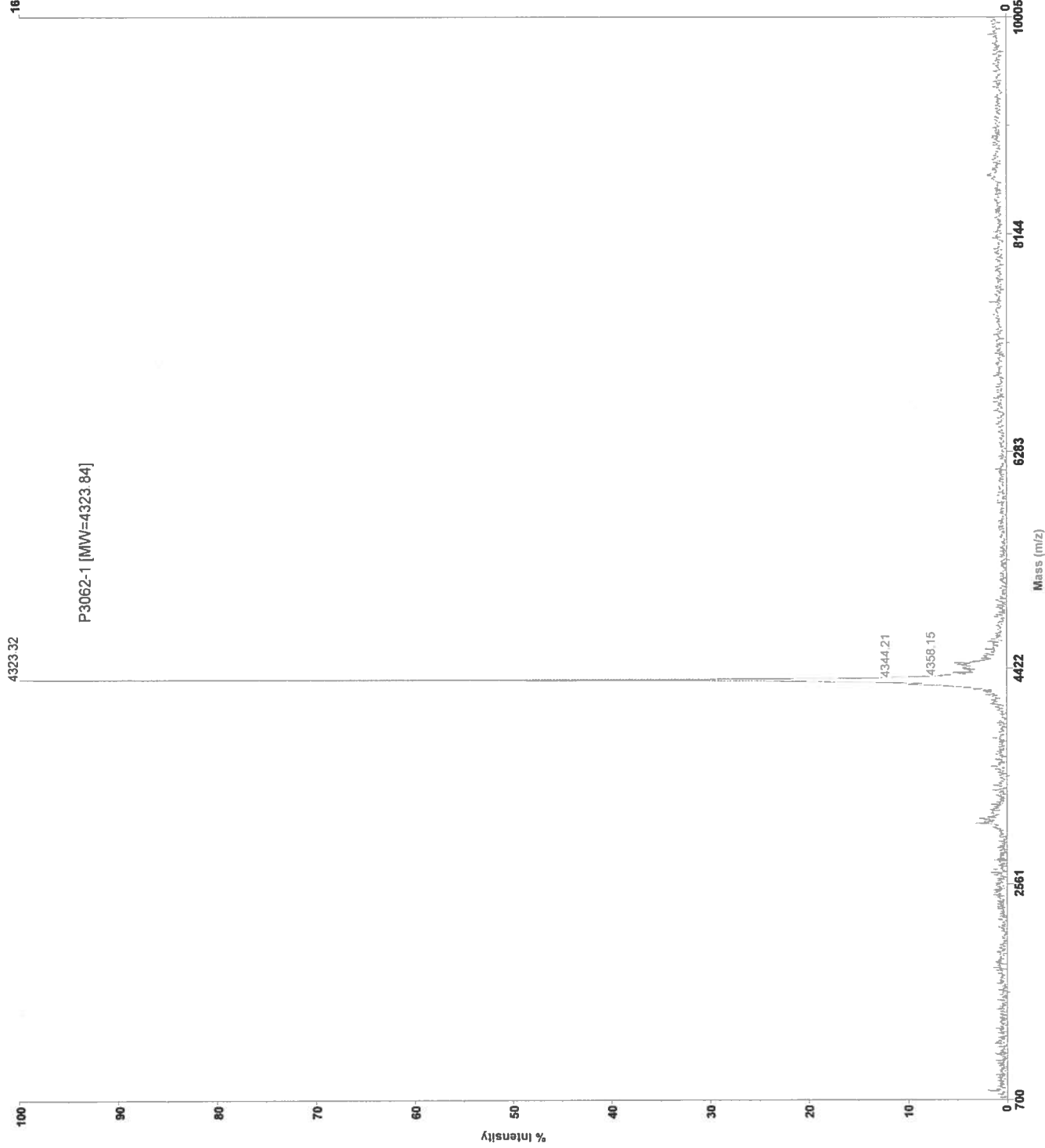
AA	AA in sequence	AA found in pmoles	M W	Amt in ngs	Ave. AA in pmoles	Experimental AA found
D/N	3	662.697	114.1	75.614	220.90	3.0
S	0	0.000	87.08	0.000	0.00	0.0
E/Q	13	2926.984	128.13	375.034	225.15	13.1
G	0	0.000	57.05	0.000	0.00	0.0
H	0	0.000	137.14	0.000	0.00	0.0
R	1	220.990	156.19	34.516	220.99	1.0
T	1	201.307	101.11	20.354	201.31	0.9
A	2	421.511	71.08	29.961	210.76	1.9
P	0	0.000	97.12	0.000	0.00	0.0
C	0	0.000	103.14	0.000	0.00	0.0
Y	1	205.923	163.18	33.603	205.92	0.9
V	1	199.878	99.13	19.814	199.88	0.9
M	1	214.199	131.2	28.103	214.20	1.0
K	2	416.818	128.18	53.428	208.41	1.9
I	2	399.478	113.16	45.205	199.74	1.8
L	4	880.535	113.16	99.641	220.13	3.9
F	1	223.484	147.18	32.892	223.48	1.0
W	2	0.000	186.22	0.000	0.00	0.0
			<b>Pep. Recovered</b>	<b>848.165</b>		
			<b>Trp adjusted</b>	<b>901.153</b>		

Performed by: *R. Manicki* 10/12/2015

Verified by: *Moussa Bazani* 10/12/2015

# Applied Biosystems Voyager System 1054

Voyager Spec #1=>BC=>NF1.0=>BC=>SM9[BP = 4323.7, 1657]



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

Accelerating voltage: 20000 V  
Grid voltage: 94%  
Guide wire 0: 0.05%  
Extraction delay time: 400 nsec

Acquisition mass range: 700 -- 10000 Da  
Number of laser shots: 100/spectrum  
Laser intensity: 1432  
Laser Rep Rate: 3.0 Hz  
Calibration type: Default  
Calibration matrix: a-Cyano-4-hydroxycinnamic acid  
Low mass gate: Off

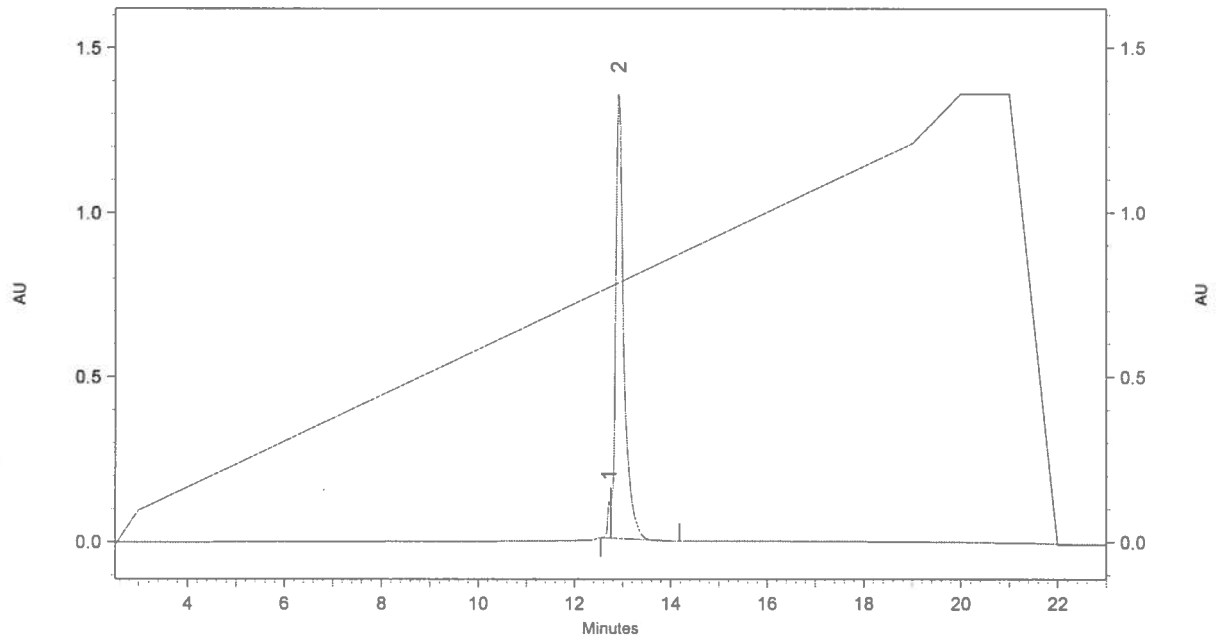
Digitizer start time: 17.262  
Bin size: 2 nsec  
Number of data points: 23838  
Vertical scale: 200 mV  
Vertical offset: 0%  
Input bandwidth: 500 MHz

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

Absolute x-position: 12006  
Absolute y-position: 41406.7  
Relative x-position: 258.483  
Relative y-position: -820.761  
Shots in spectrum: 26  
Source pressure: 5.436e-007  
Mirror pressure: 0  
TC2 pressure: 0.00984  
TIS gate width: 30  
TIS flight length: 940

# HPLC REPORT

Sample ID: P3062-1  
Method: D:\32Karat\Methods\Monolithic\_1.met  
File Name: D:\32Karat\Projects\Default\Data\P3062-1  
Column: Monolithic C18, 100X3mm, 120A, Flow Rate: 1ml min.  
Wavelength: 220nm  
HPLC ID# CD-069



Pk #	Retention Time	Area	Area Percent
1	12.717	408944	2.535
2	12.917	15721083	97.465

Totals		16130027	100.000
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