

# Parallel Glyco-SPOT Synthesis of Glycopeptide Libraries

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## Data S1

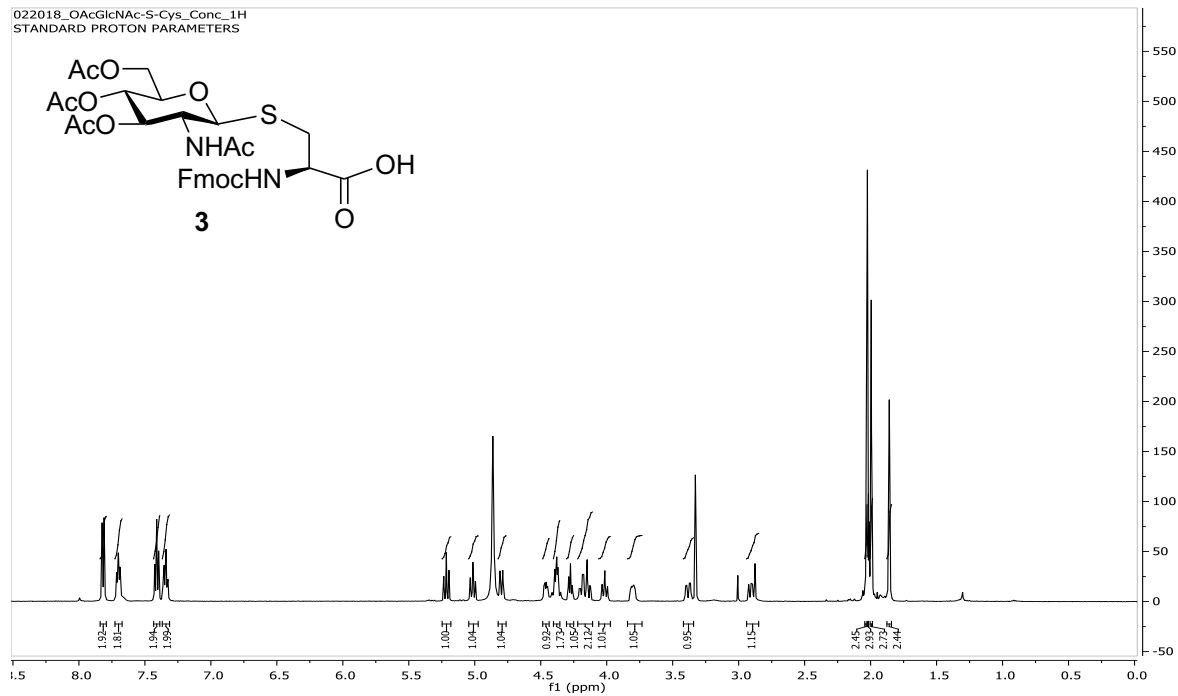
### Chemical Characterization- Related to Figure 7

#### Contents

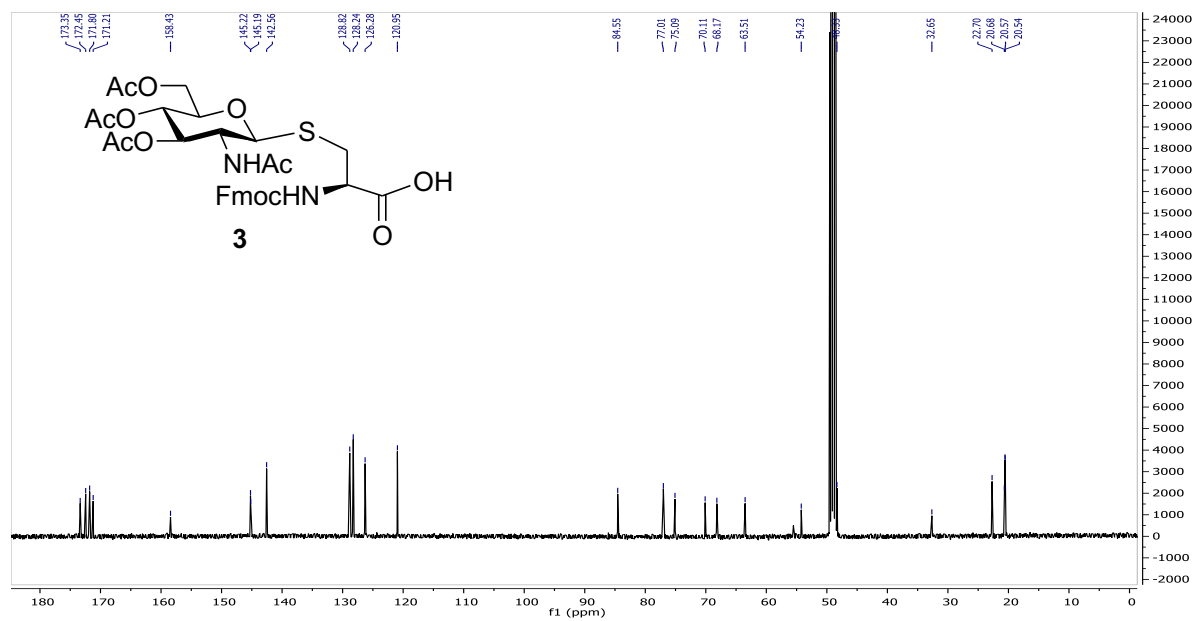
NMR Spectra for Synthesized Cys-linked FPGAs .....	2
MALDI Spectra For Glycopeptides.....	5
Note About MALDI Spectra:.....	5
MALDI Spectra for all Peptides.....	6
GlycoPeptide 1 library (GP1) .....	6
GlycoPeptide 2 library (GP2) .....	18
HPLC Chromatography For Glycopeptides.....	38
GP1 Library HPLC Chromatography .....	38
GP2 Library HPLC Chromatography .....	50
Orbitrap Characterization of GP2 Library .....	69
MS spectra of GP2.01-GP.40 by high-resolution C18-RP-LC-MS.....	69
References .....	74

# NMR Spectra for Synthesized Cys-linked FPGAs

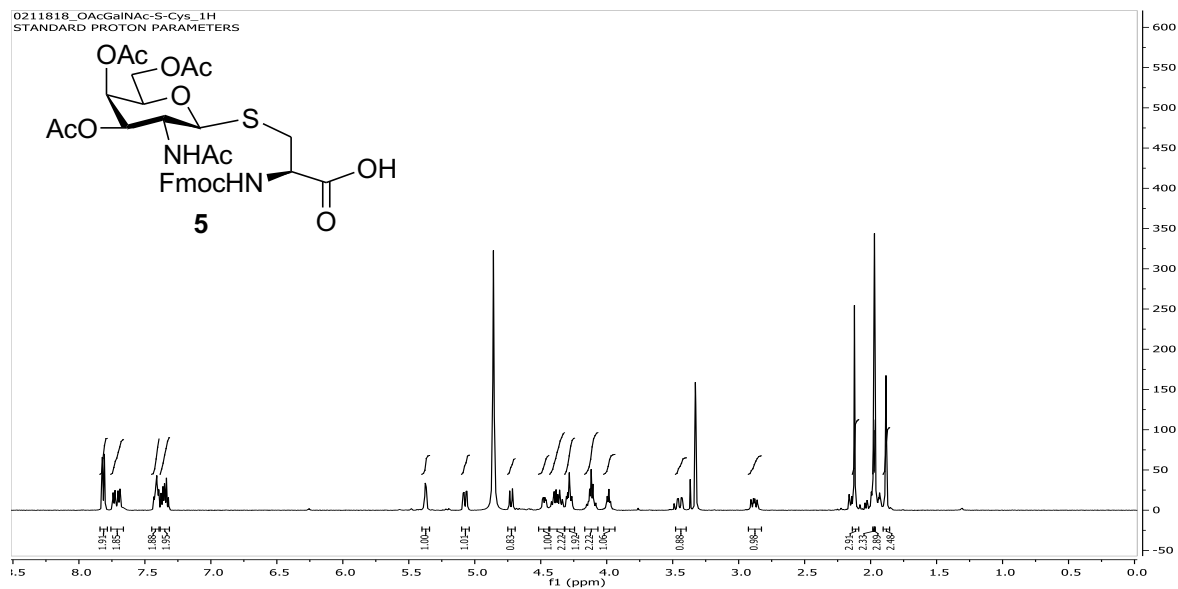
## <sup>1</sup>H NMR Spectrum of 3:



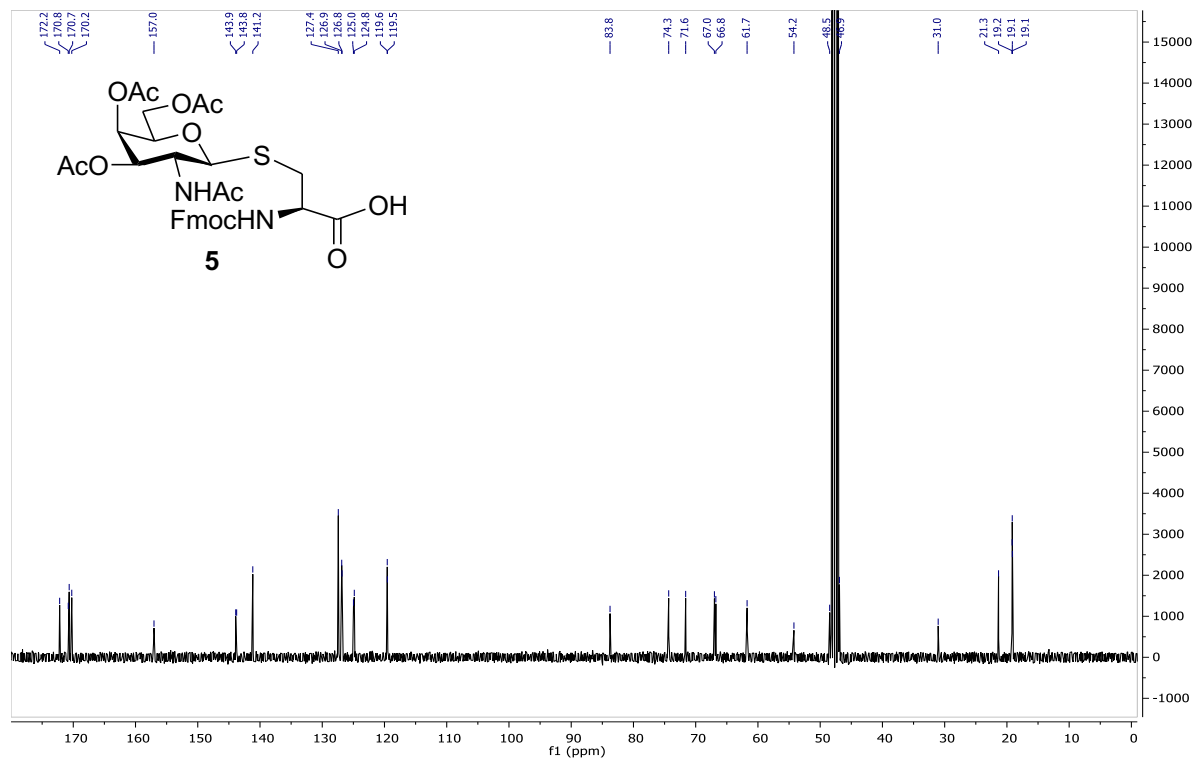
## <sup>13</sup>C NMR Spectrum of 3:



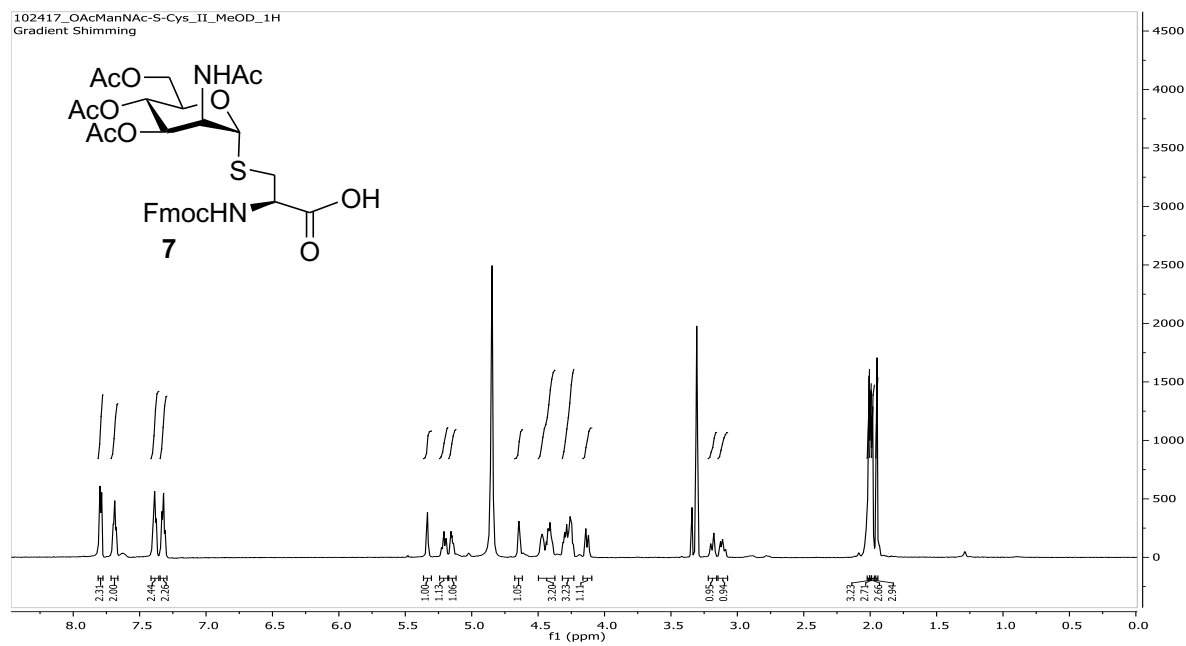
# <sup>1</sup>H NMR Spectrum of 5:



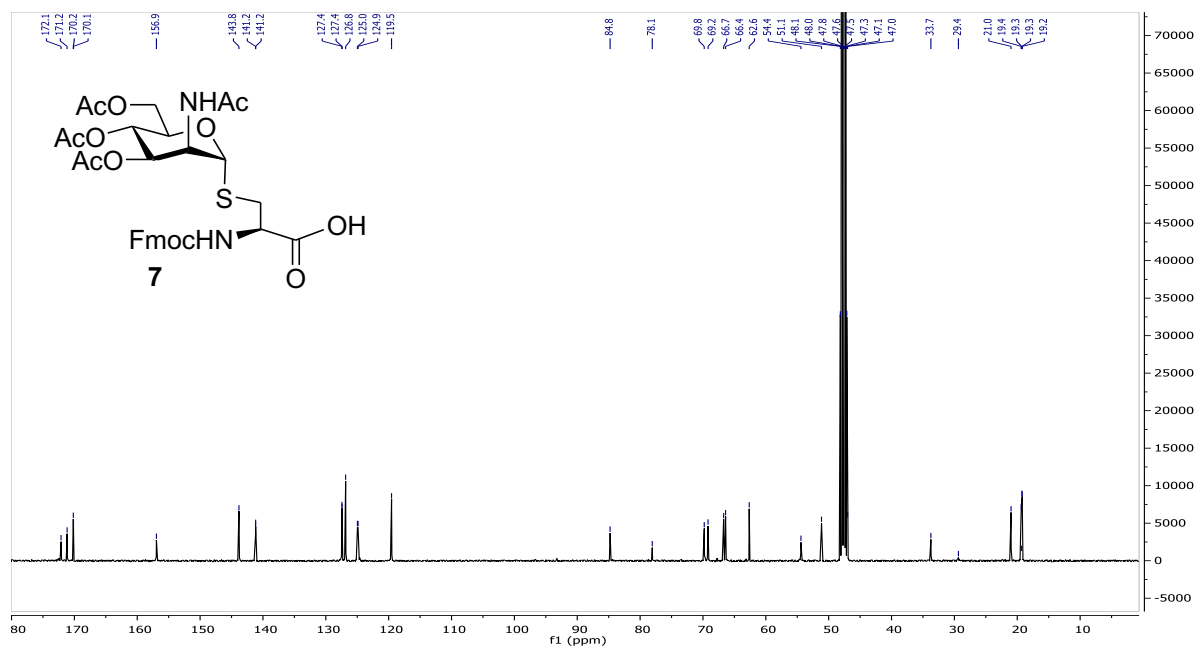
# <sup>13</sup>C NMR Spectrum of 5:



# <sup>1</sup>H NMR Spectrum of 7:



# <sup>13</sup>C NMR Spectrum of 7:





## MALDI Spectra For Glycopeptides

### Notes About MALDI Spectra:

To perform MALDI experiments, 1  $\mu\text{L}$  of glycopeptide was mixed with 1  $\mu\text{L}$  of MALDI matrix solution of  $\alpha$ -Cyano-4-hydroxycinnamic acid (HCCA) or 2,5-dihydroxybenzoic acid (for larger glycans). The matrix, once dried, was analyzed on a Bruker ultrafleXtreme MALDI TOF/TOF machine in positive mode. Only peaks with signal to noise ratio > 5 were annotated below.

In some cases a loss of 169 m/z was observed from the  $[\text{M}+\text{H}]^+$  peak as a result of metastable peak formed by the loss of HexNAc during time-of-flight as has been reported previously (Huberty et al., 1993). This is especially noticed in the case of O-linked glycans.

In case of GP1 library, which was released and deacetylated using sodium bicarbonate and water alone (no methanol), some peptides showed peaks of  $[\text{M}+126]^+$  peak. We suspect this is resistant peracetylated glycopeptide (where +126 Da would correspond to 3 Acetyl groups on the GlcNAc), which for some reason co-eluted in our HPLC semi-prep. We estimate this is <10% in most cases based on signal intensity. We did not further attempt purification or chemical treatment due to the small scale of synthesis, to avoid losses. This phenomenon was not observed when using methanol:water with sodium bicarbonate which is the preferred method of release used in the GP2 library. As we mentioned we used the GP1 library to learn and optimize the method.

In addition, where methanol:water method was used for release, a  $[\text{M}+14]^+$  peak was also observed due to the formation of methyl ester at the C-terminus of the peptide as discussed in Figure 3. Special cases for assignments are also highlighted along with the spectra in the list below.

## MALDI Spectra for all Peptides

GlycoPeptide 1 library (GP1)

Spectrum: 1

Peptide ID: GP1.1 (Acetylated)

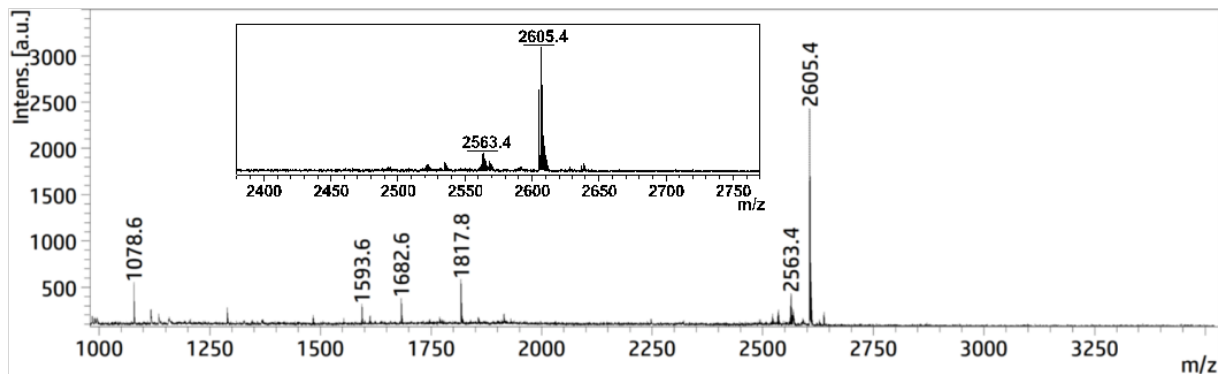
Internal ID: MBGP-04

Purification Level: Crude (initial release)

Sequence: AcNH-KTSTTATPPV{[3Ac][4Ac][6Ac]GlcNAcb1-S}QASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+$  = 2605.5

Notes: Release with  $NaHCO_3$  in water is very mild and can release the glycopeptide with the Acetyls intact.



Spectrum: 2

Peptide ID: GP1.1 (Prototypical Peptide)

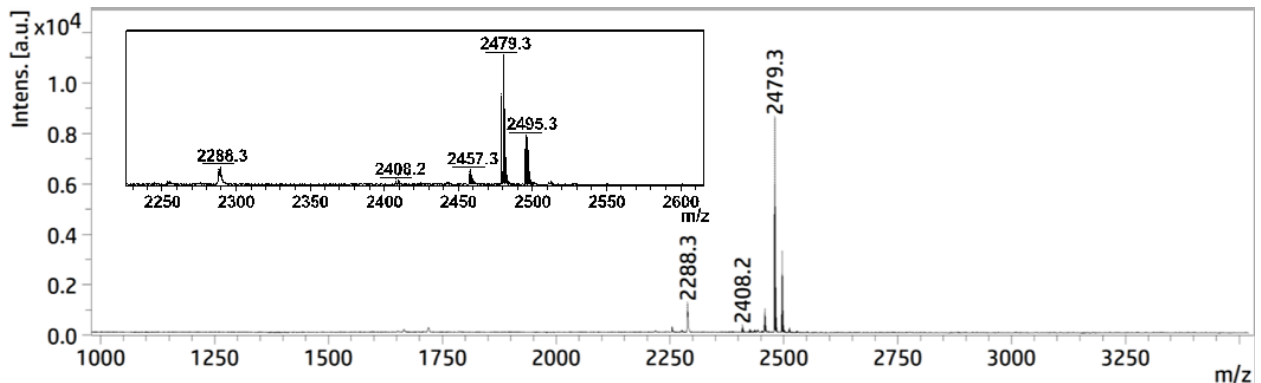
Internal ID: MBGP-04

Purification Level: HPLC Purified

Sequence: AcNH-KTSTTATPPV{GlcNAcb1-S}QASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+$  = 2479.3

Notes: After treatment with  $NaHCO_3$  2 times. Note in-source fragmentation shows a loss of m/z 169 (from  $[M+H]$  mass) in most spectra.



Spectrum: 3

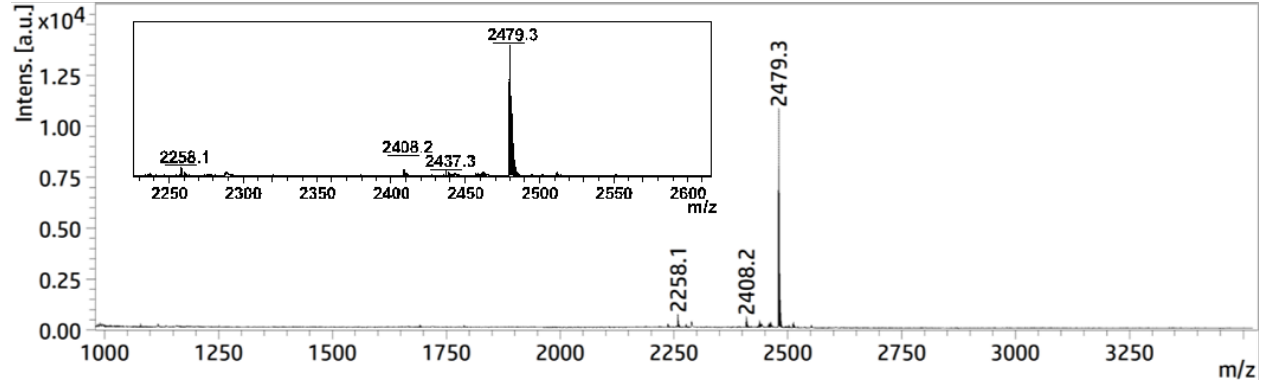
Peptide ID: GP1.1HPLC

Internal ID: MBGP-05-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPPV{GlcNAc1-S}QASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2479.3$



Spectrum: 4

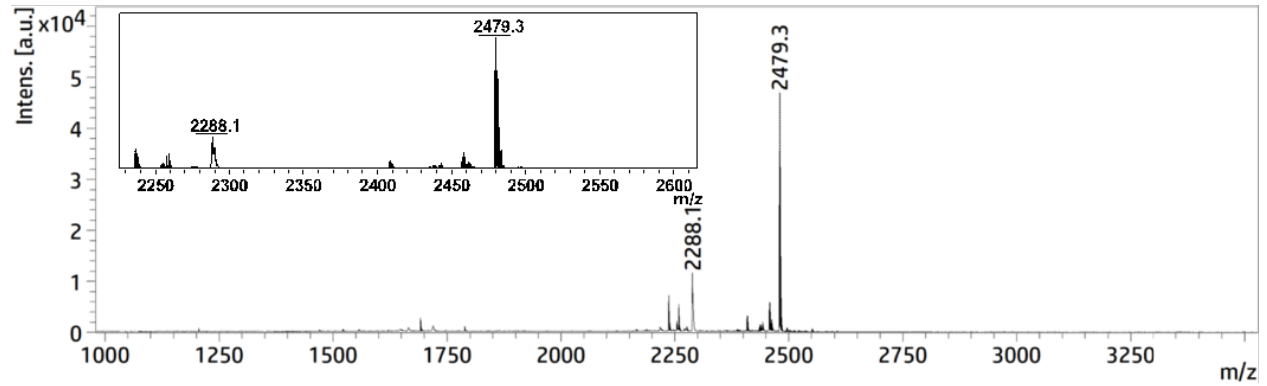
Peptide ID: GP1.1SepPak

Internal ID: MBGP-05-SepPak

Purification Level: SepPak purified

Sequence: AcNH-KTSTTATPPV{GlcNAc1-S}QASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2479.3$



Spectrum: 5

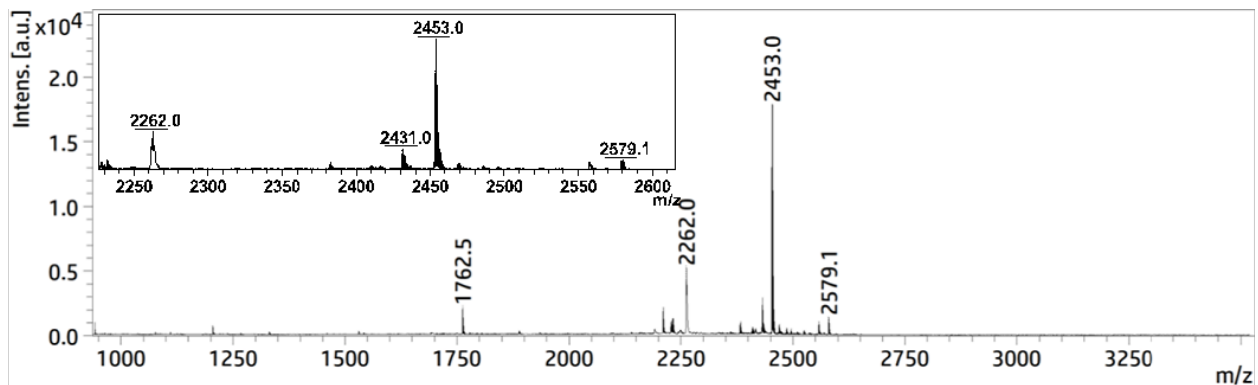
Peptide ID: GP1.2

Internal ID: MBGP-08-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPAV{GlcNAc1-S}QASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2453.5$



Spectrum: 6

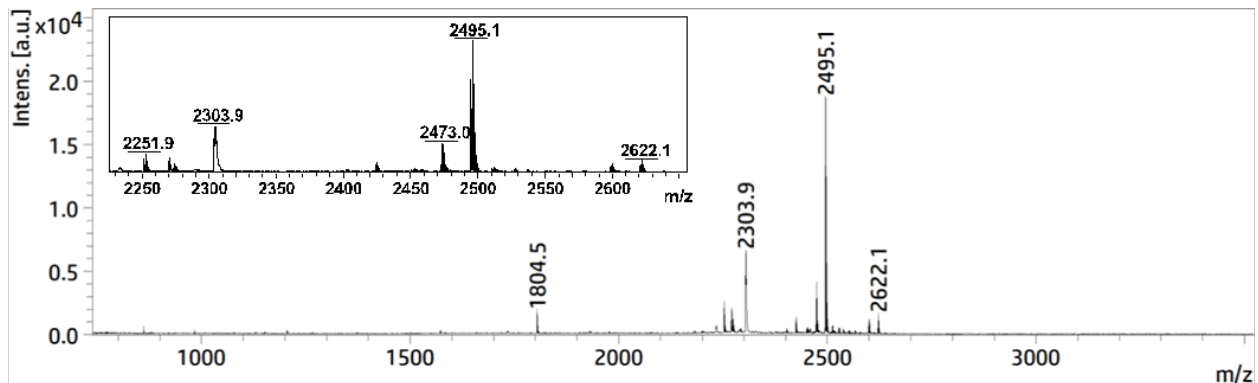
Peptide ID: GP1.3

Internal ID: MBGP-09-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPLV{GlcNAc1-S}QASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2495.3$



Spectrum: 7

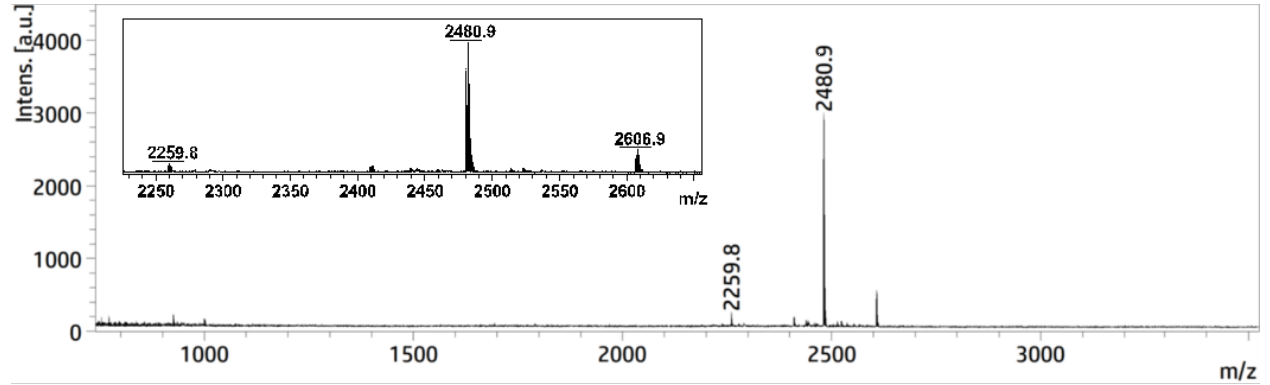
Peptide ID: GP1.4

Internal ID: MBGP-10-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPPT{GlcNAc1-S}QASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2481.2$



Spectrum: 8

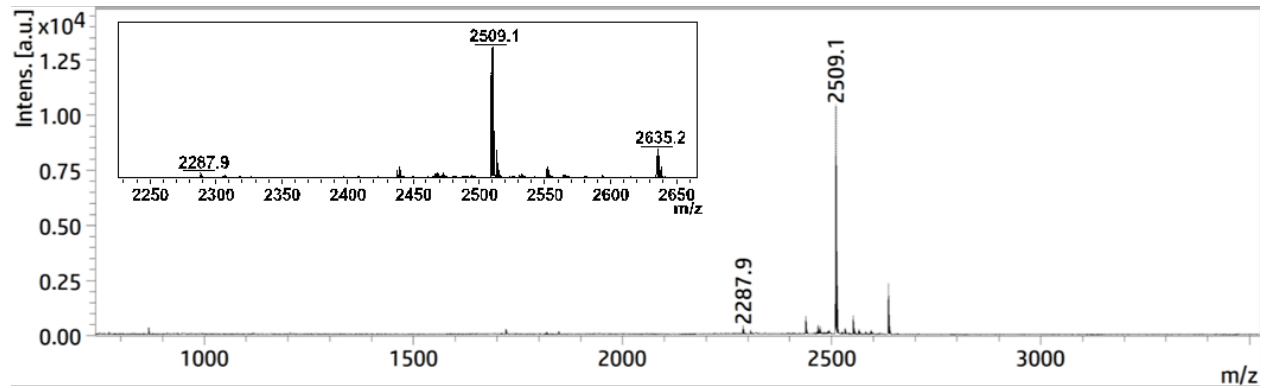
Peptide ID: GP1.5

Internal ID: MBGP-11-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPPE{GlcNAc1-S}QASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2509.3$



Spectrum: 9

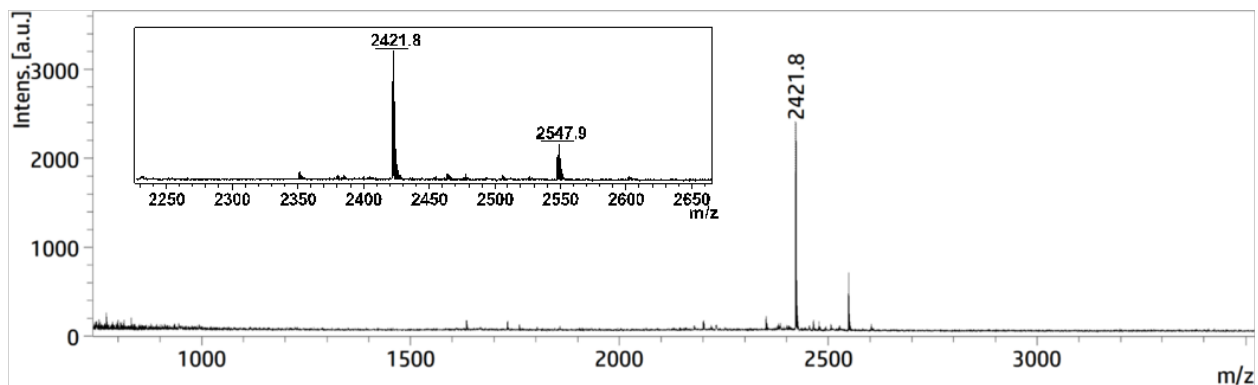
Peptide ID: GP1.6

Internal ID: MBGP-12-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPPV{GlcNAc1-S}AASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2422.0$



Spectrum: 10

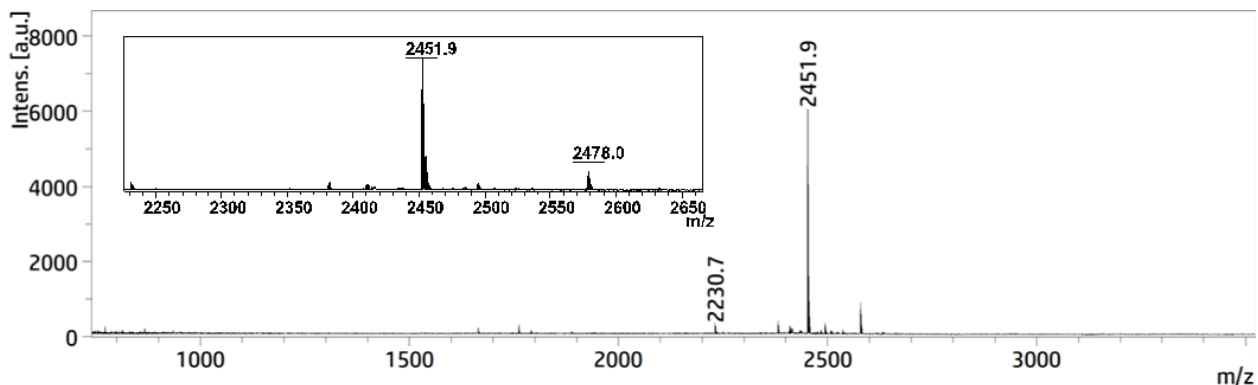
Peptide ID: GP1.7

Internal ID: MBGP-13-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPPV{GlcNAc1-S}TASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2452.0$



Spectrum: 11

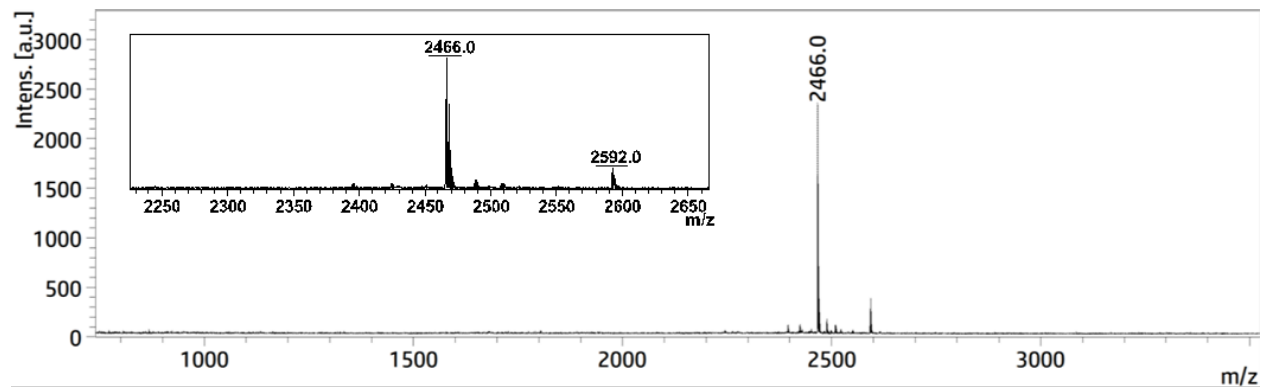
Peptide ID: GP1.8

Internal ID: MBGP-14-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPPV{GlcNAc1-S}DASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2466.0$



Spectrum: 12

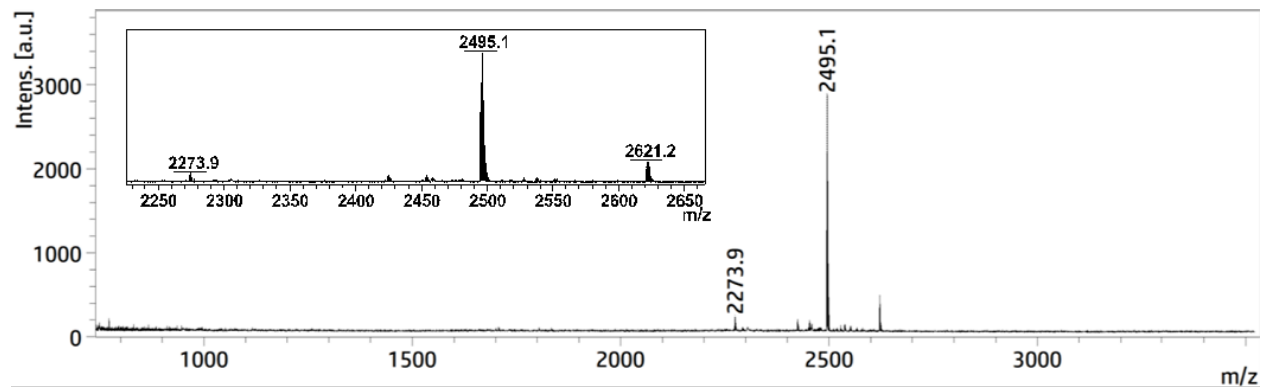
Peptide ID: GP1.9

Internal ID: MBGP-15-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPPV{GlcNAc1-S}QSSSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2495.1$



Spectrum: 13

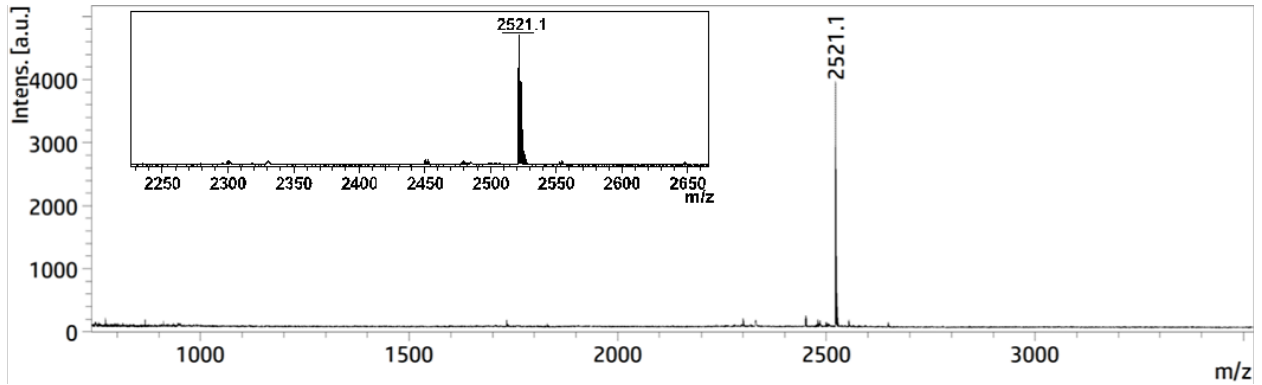
Peptide ID: GP1.10

Internal ID: MBGP-16-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPPV{GlcNAc1-S}QLSSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2521.1$



Spectrum: 14

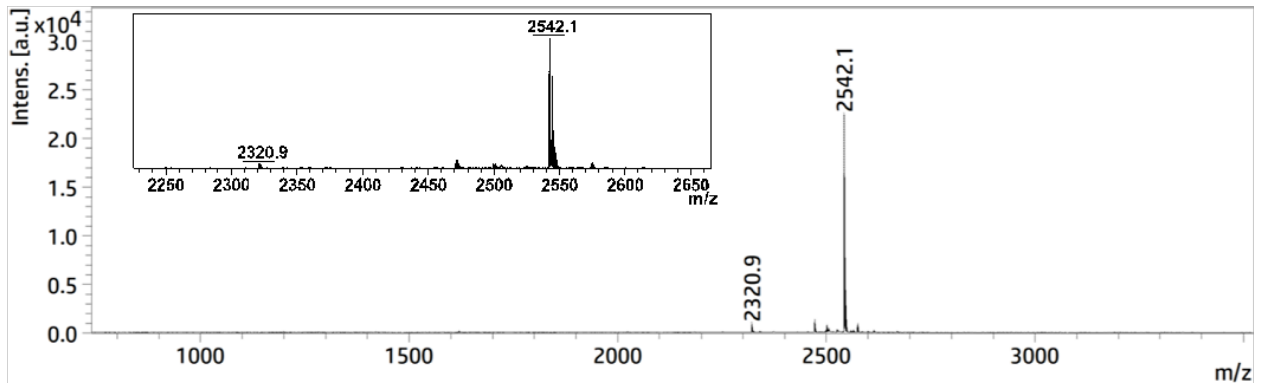
Peptide ID: GP1.11

Internal ID: MBGP-17-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTRTPPV{GlcNAc1-S}QASSTTTSTWA-COOH

Calculated Mass  $[M+H]^+ = 2542.2$





Spectrum: 15

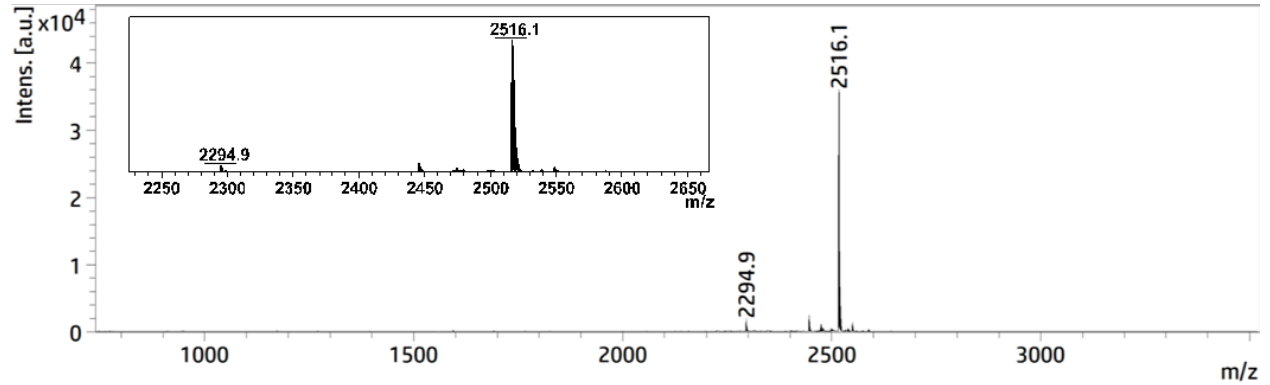
Peptide ID: GP1.12

Internal ID: MBGP-18-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATRPV{GlcNAc1-S}QASSTTTSTWA-COOH

Calculated Mass  $[M+H]^+$  = 2515.8



Spectrum: 16

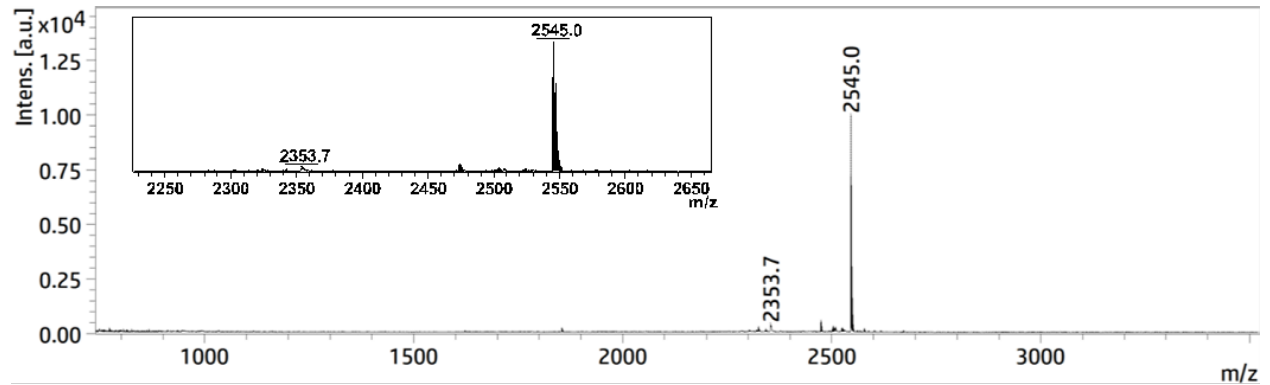
Peptide ID: GP1.13

Internal ID: MBGP-19-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPYV{GlcNAc1-S}QASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+$  = 2545.1



Spectrum: 17

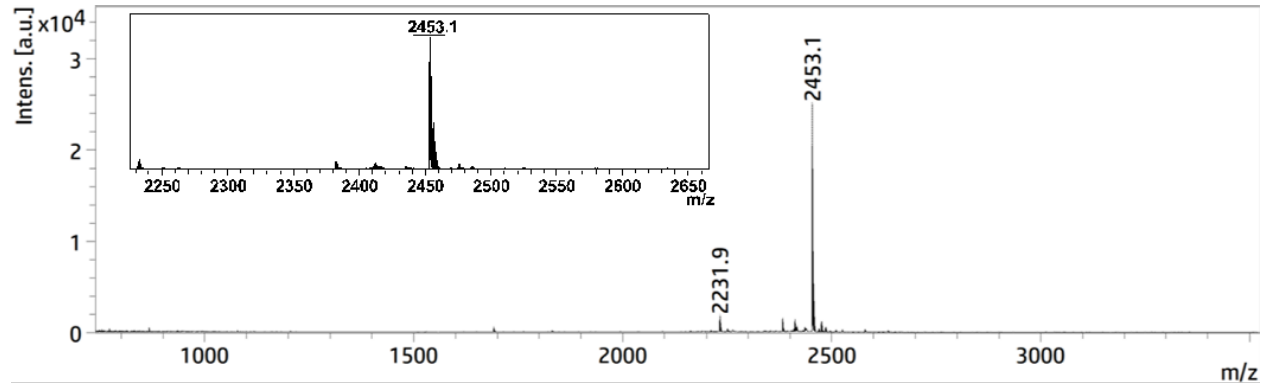
Peptide ID: GP1.14

Internal ID: MBGP-20-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATAPV{GlcNAc1-S}QASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2453.0$



Spectrum: 18

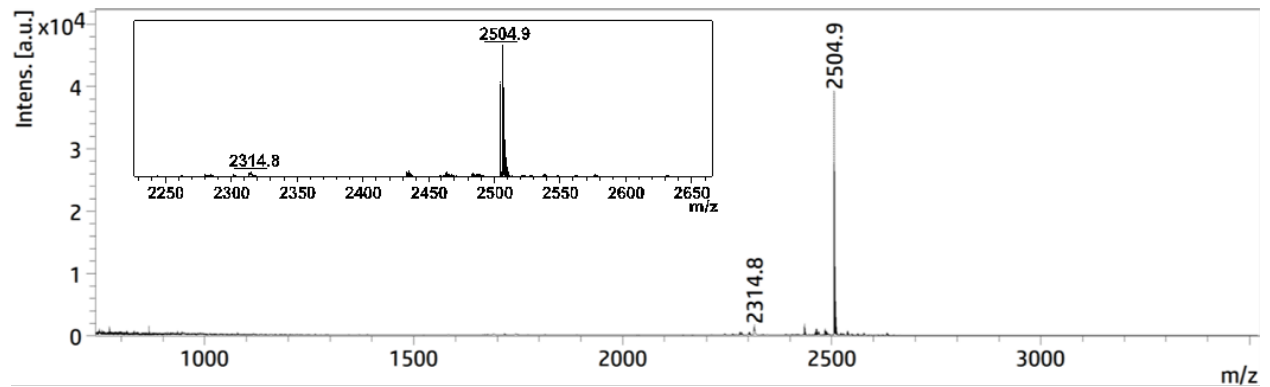
Peptide ID: GP1.15

Internal ID: MBGP-21-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPPV{GlcNAc1-S}QPSSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2505.1$



Spectrum: 19

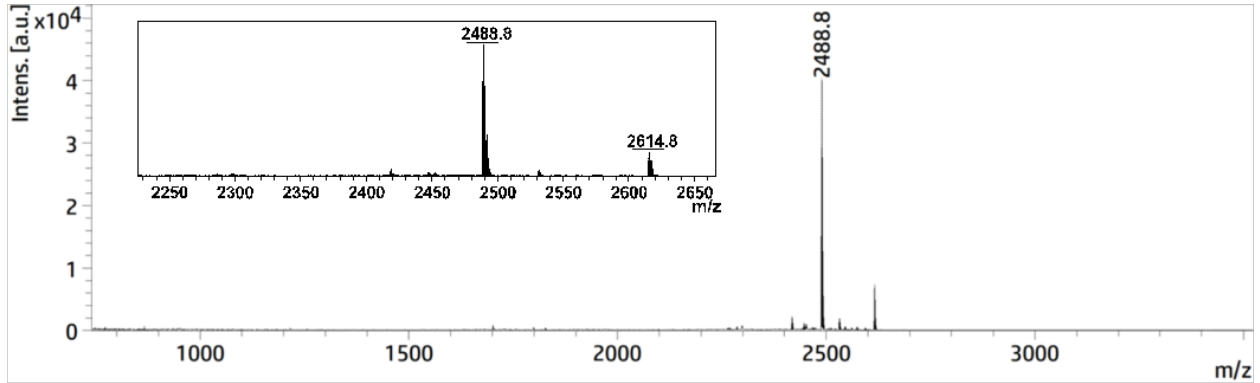
Peptide ID: GP1.16

Internal ID: MBGP-22-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPPV{GlcNAc1-S}QAPSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2489.1$



Spectrum: 20

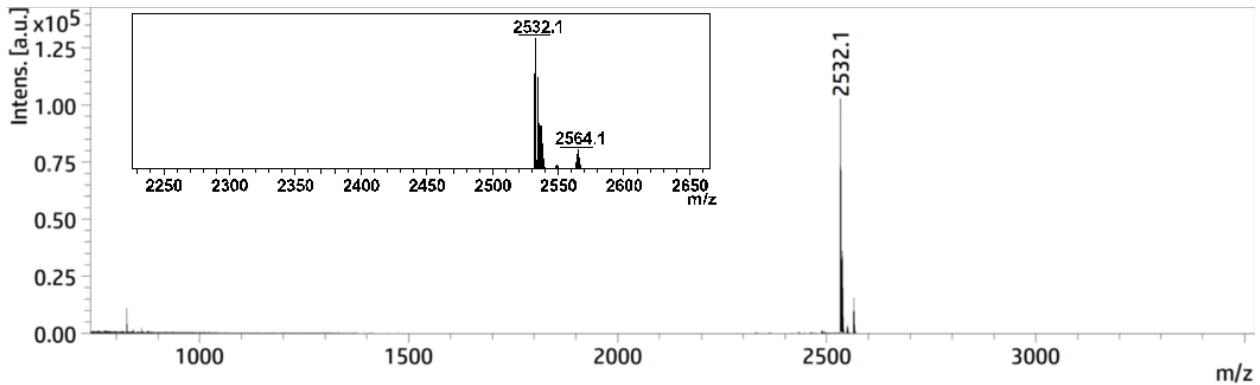
Peptide ID: GP1.17

Internal ID: MBGP-23-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATRSV{GlcNAc1-S}QPSSTTTSTWA-COOH

Calculated Mass  $[M+H]^+ = 2531.9$



Spectrum: 21

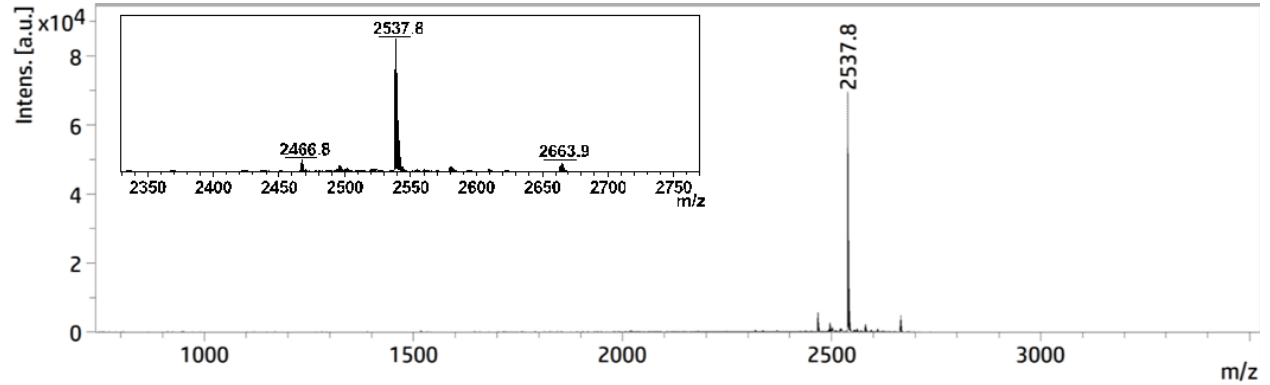
Peptide ID: GP1.18

Internal ID: MBGP-24-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTARPPV{GlcNAc1-S}QPSSTTTSTWA-COOH

Calculated Mass  $[M+H]^+ = 2537.9$



Spectrum: 22

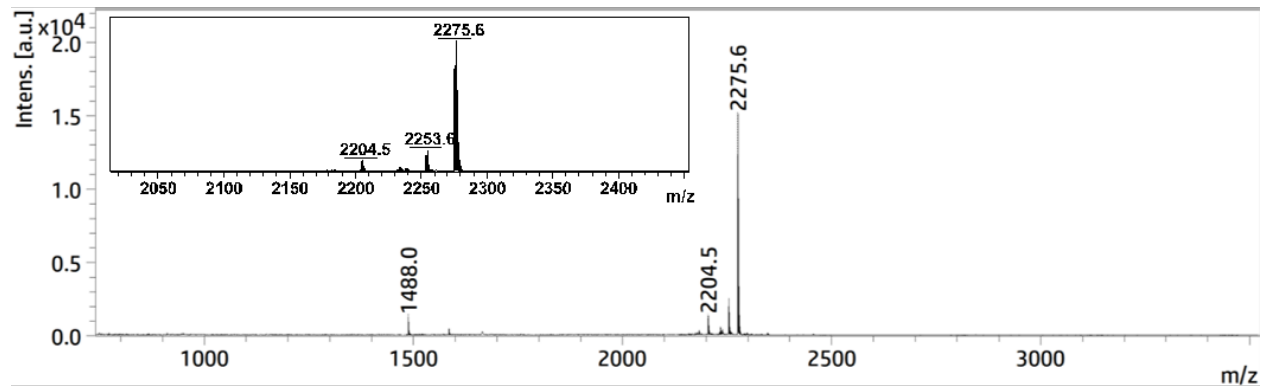
Peptide ID: GP1.19 (non-glycosylated)

Internal ID: MBGP-25-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTATPPVSQASSTTTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2275.9$



Spectrum: 23

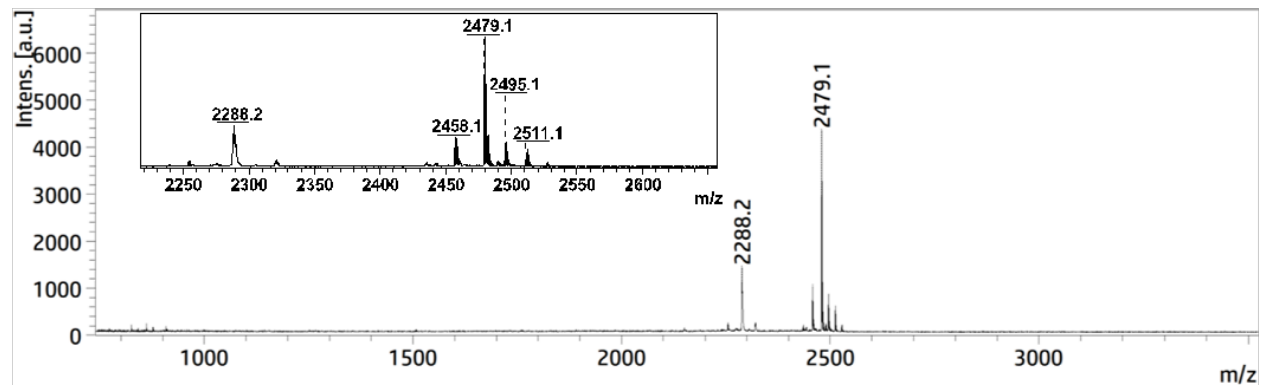
Peptide ID: GP1.20 (Scrambled Sequence)

Internal ID: MBGP-26-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KPSTTASPTT{GlcNAc1-S}QATSSTTVTWA-COOH

Calculated Mass  $[M+Na]^+ = 2479.1$



Spectrum: 24

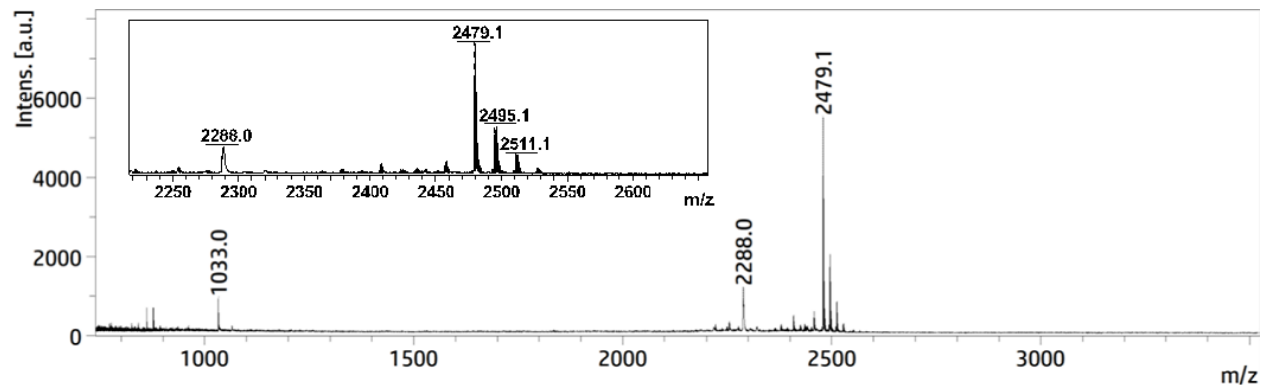
Peptide ID: GP1.21 (Reversed Sequence)

Internal ID: MBGP-27-HPLC

Purification Level: HPLC purified

Sequence: AcNH-KTSTTTSSAQ{GlcNAc1-S}VPPTATTSTWA-COOH

Calculated Mass  $[M+Na]^+ = 2479.1$



GlycoPeptide 2 library (GP2)

Note- minor peaks for peptides ending with  $-OCH_3$  ( $-COOMe$ ) C-terminus also observed with +14 Da caused due to using methanol:water mixture which results in better cleavage but forms ester at C-terminus.

Spectrum: 25

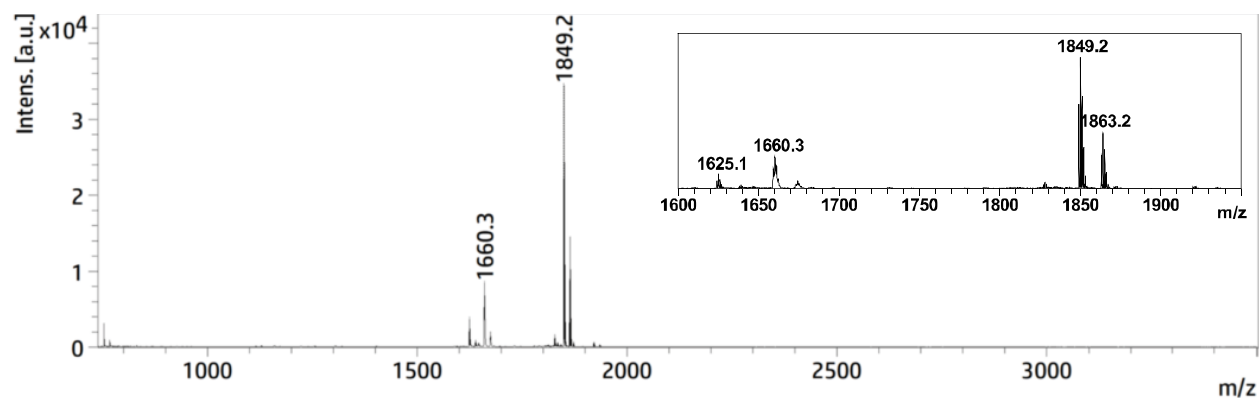
Peptide ID: GP2.1

Internal ID: GP2.1

Purification Level: SepPak C18 purified

Sequence: FINH-KVPS{GalNAca1-T}PPTPSPSA-COOH

Calculated Mass  $[M+Na]^+ = 1849.4$



Spectrum: 26

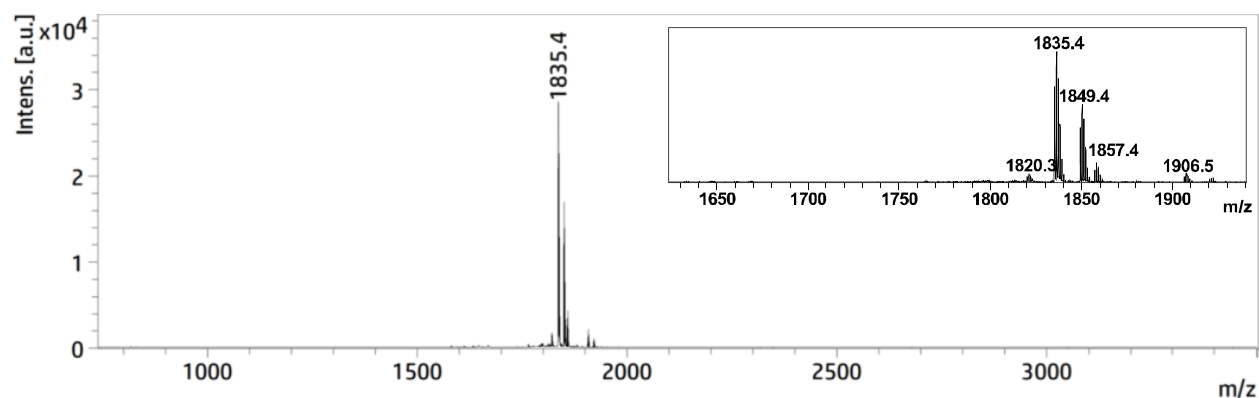
Peptide ID: GP2.2

Internal ID: GP2.2

Purification Level: SepPak C18 purified

Sequence: FINH-KVPS{GalNAca1-S}PPTPSPSA-COOH

Calculated Mass  $[M+Na]^+ = 1835.4$

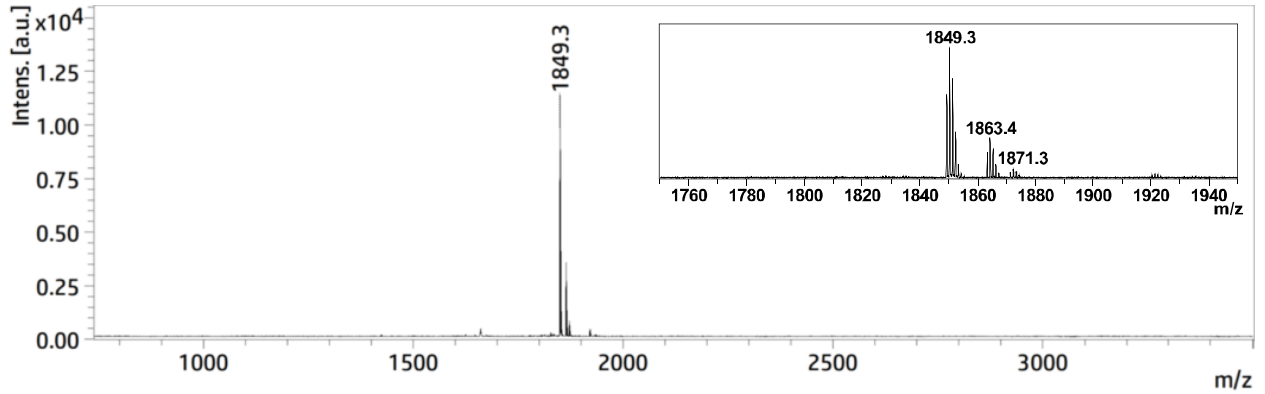


Spectrum: 27

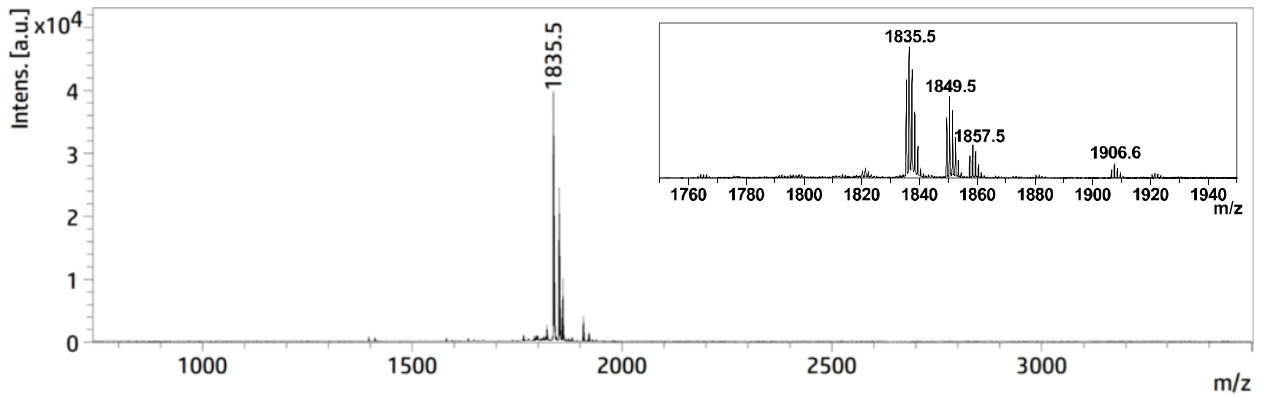
Peptide ID: GP2.3

Internal ID: GP2.3

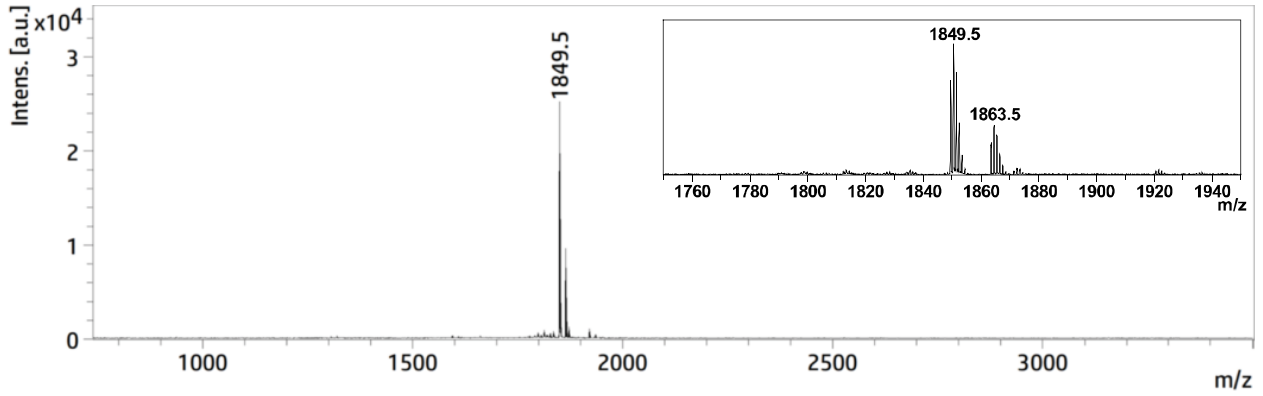
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPP{GalNAca1-T}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1849.4$



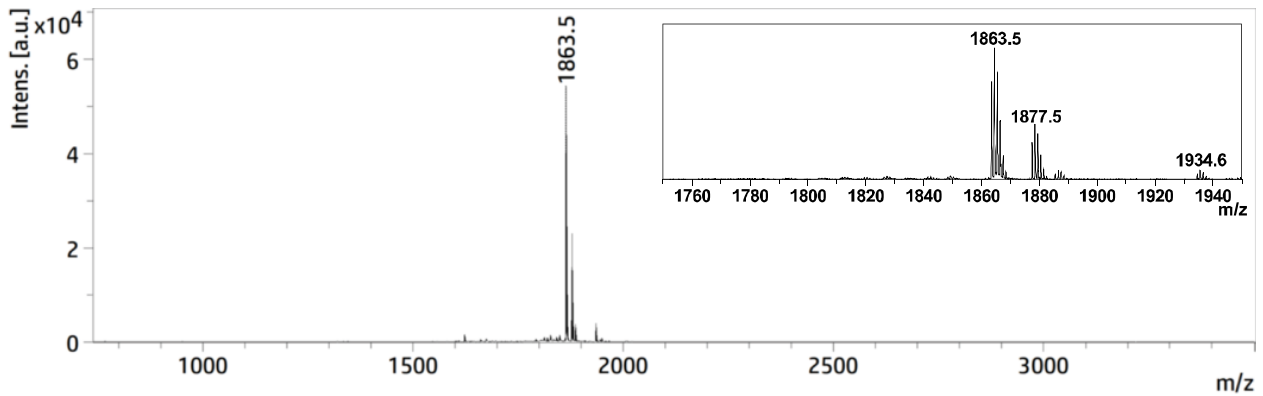
Spectrum: 28  
Peptide ID: GP2.4  
Internal ID: GP2.4  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPP{GalNAca1-S}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1835.4$



Spectrum: 29  
Peptide ID: GP2.5  
Internal ID: GP2.5  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPPTP{GaINAc1-S}PSA-COOH  
Calculated Mass  $[M+Na]^+ = 1849.4$

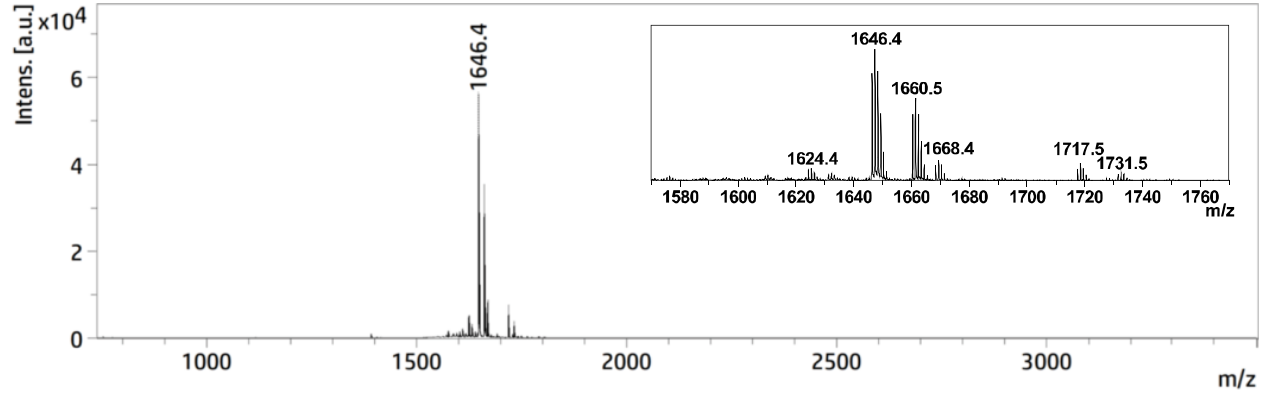


Spectrum: 30  
Peptide ID: GP2.6  
Internal ID: GP2.6  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPPTP{GaINAc1-T}PSA-COOH  
Calculated Mass  $[M+Na]^+ = 1863.4$

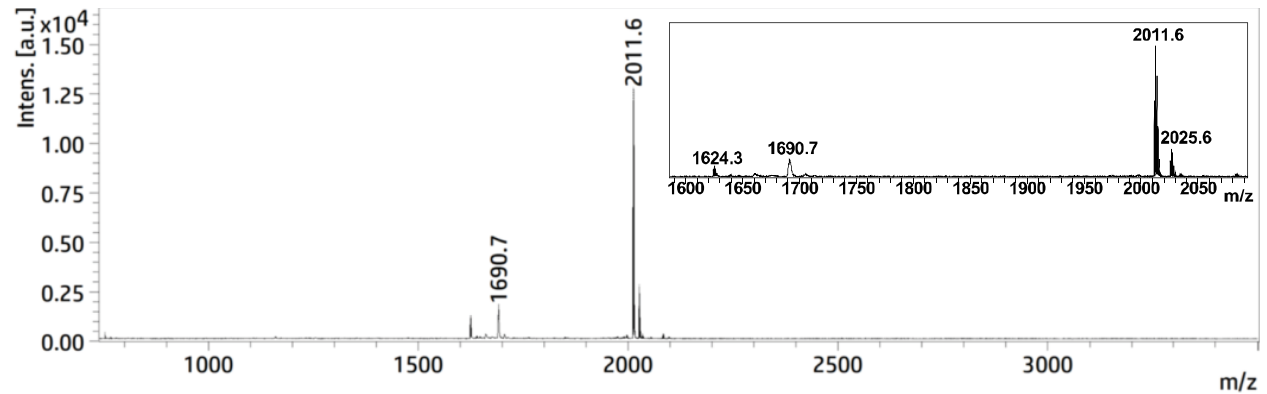




Spectrum: 31  
Peptide ID: GP2.7  
Internal ID: GP2.7  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPPTSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1646.2$



Spectrum: 32  
Peptide ID: GP2.8  
Internal ID: GP2.8  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPS{Galb1-3GalNAca1-T}PPTSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 2011.6$



Spectrum: 33

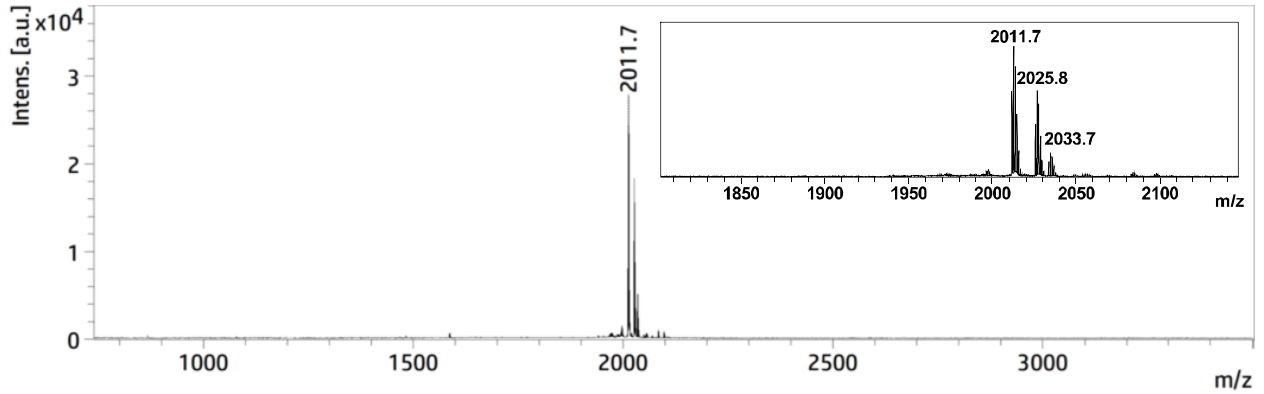
Peptide ID: GP2.9

Internal ID: GP2.9

Purification Level: SepPak C18 purified

Sequence: FINH-KVPSTPP{Galb1-3GalNAca1-T}PSPSA-COOH

Calculated Mass  $[M+Na]^+ = 2011.6$



Spectrum: 34

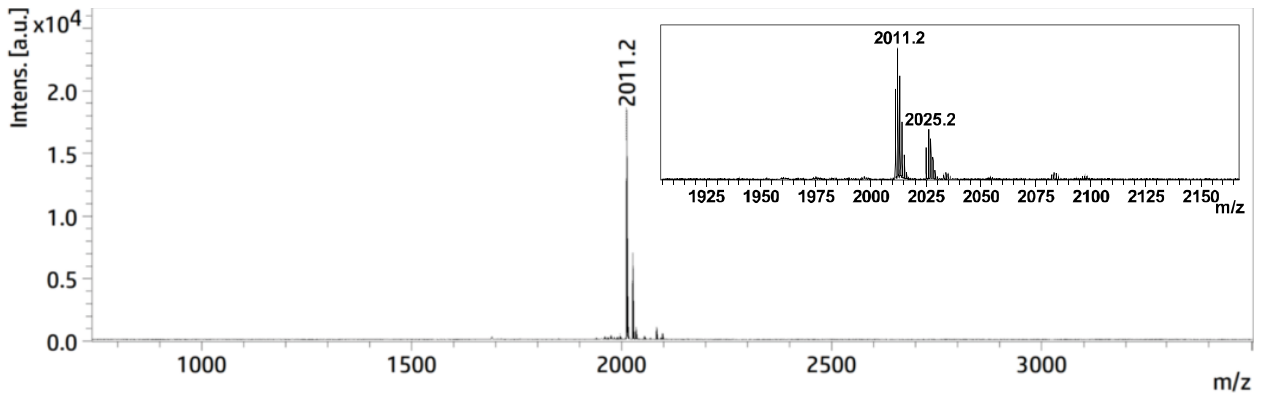
Peptide ID: GP2.10

Internal ID: GP2.10

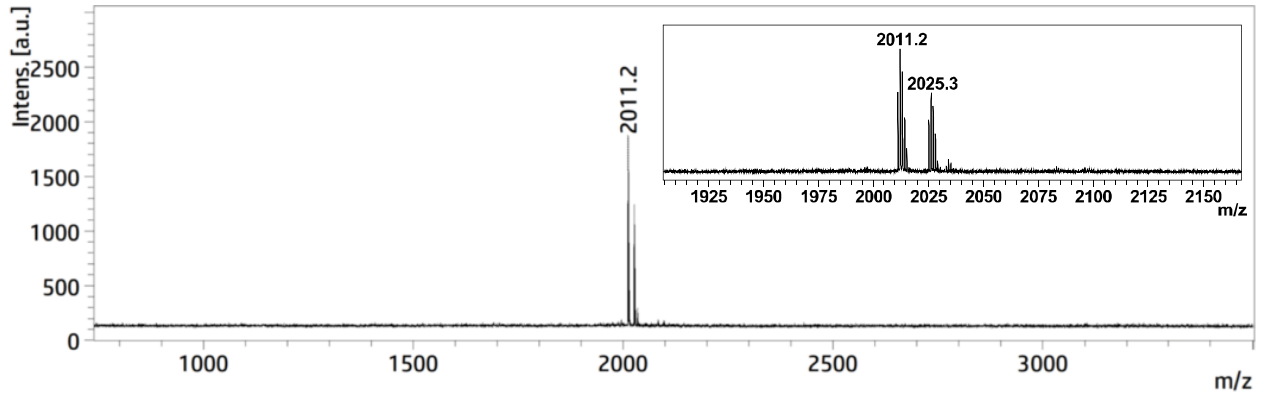
Purification Level: SepPak C18 purified

Sequence: FINH-KVPSTPPTP{Galb1-3GalNAca1-S}PSA-COOH

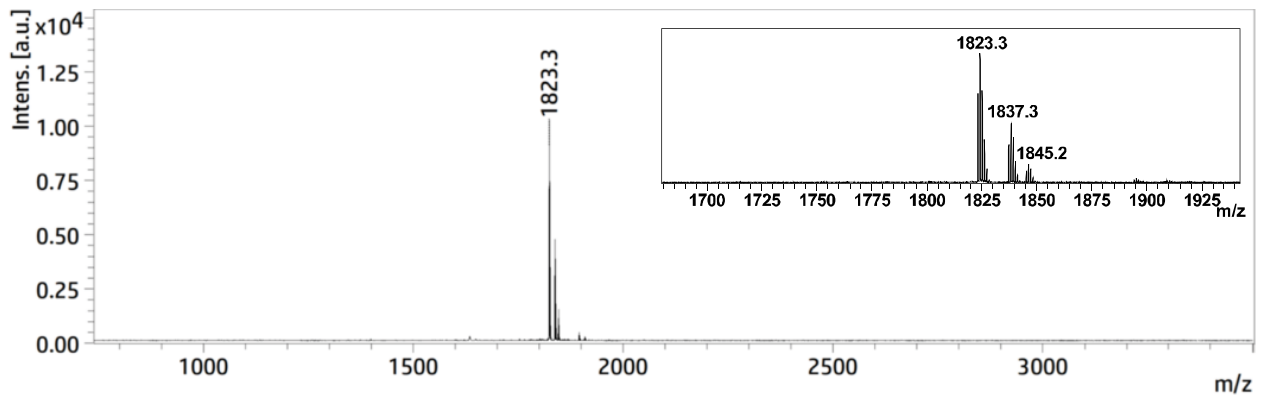
Calculated Mass  $[M+Na]^+ = 2011.6$



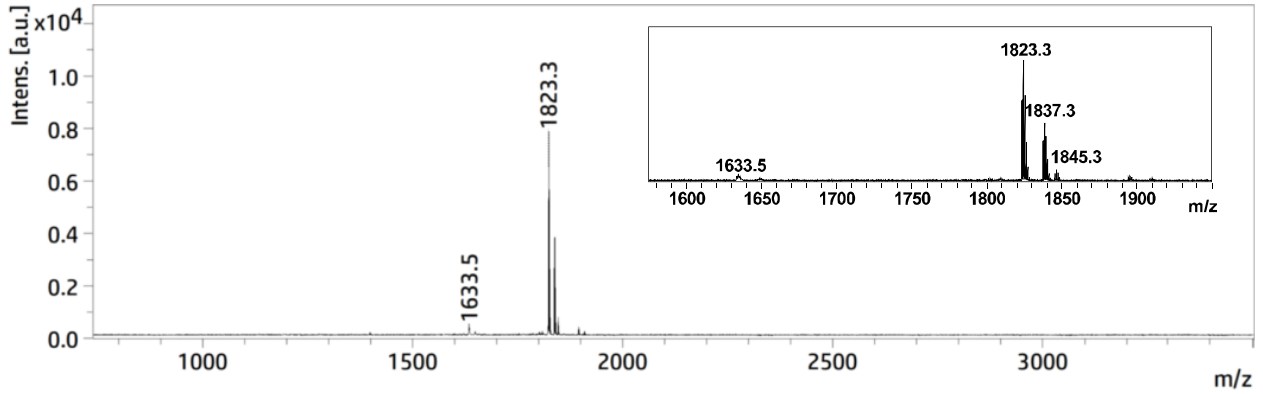
Spectrum: 35  
Peptide ID: GP2.11  
Internal ID: GP2.11  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPP{Galb1-3GalNAca1-T}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 2011.6$



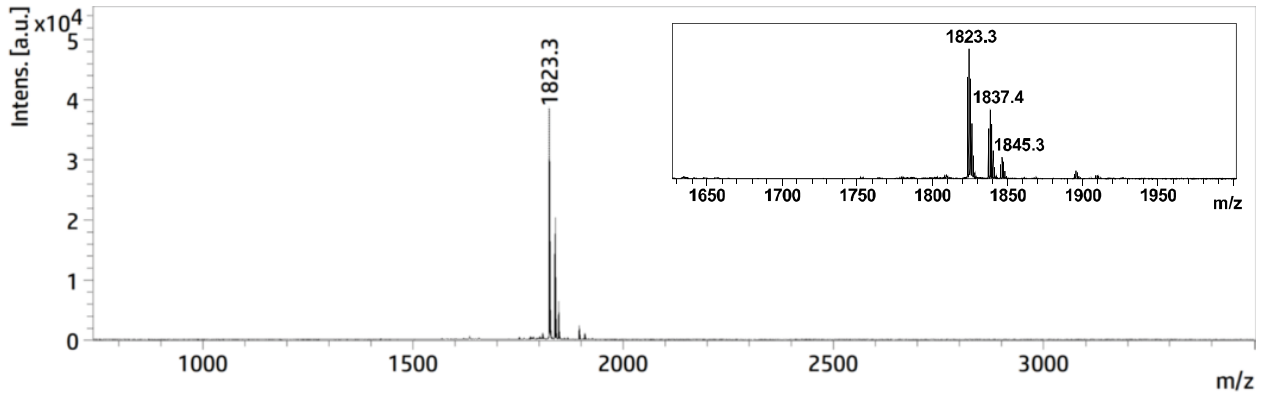
Spectrum: 36  
Peptide ID: GP2.12  
Internal ID: GP2.12  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTAP{GalNAca1-T}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1822.9$



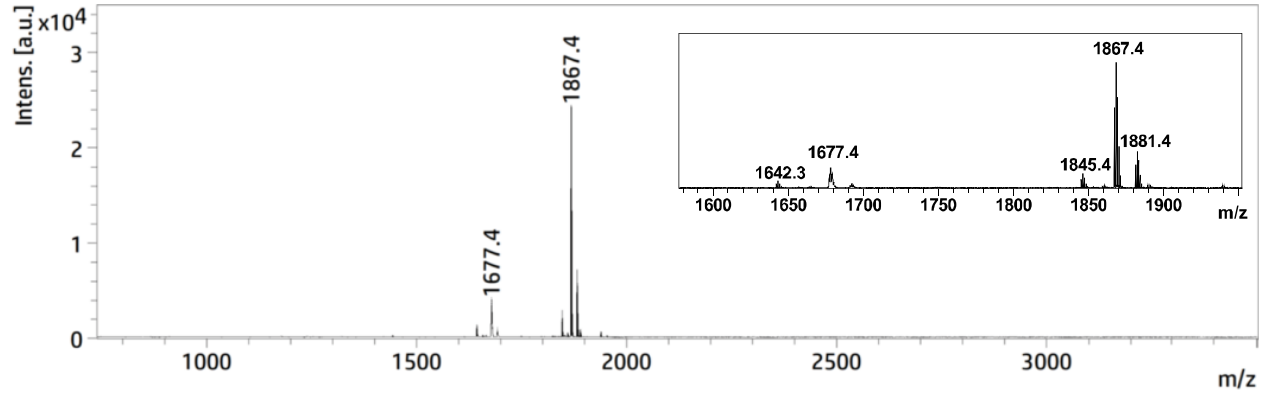
Spectrum: 37  
Peptide ID: GP2.13  
Internal ID: GP2.13  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPA{GalNAca1-T}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1822.9$



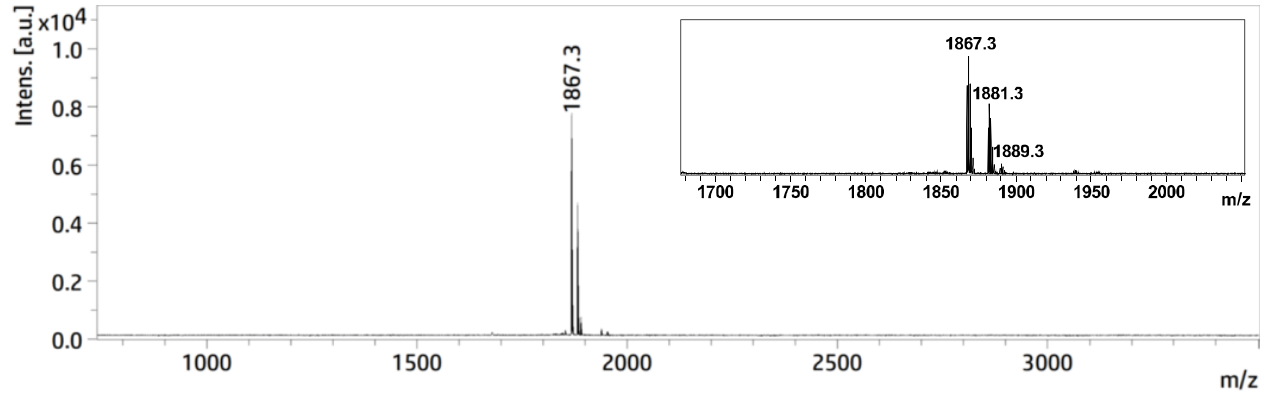
Spectrum: 38  
Peptide ID: GP2.14  
Internal ID: GP2.14  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPP{GalNAca1-T}ASPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1822.9$



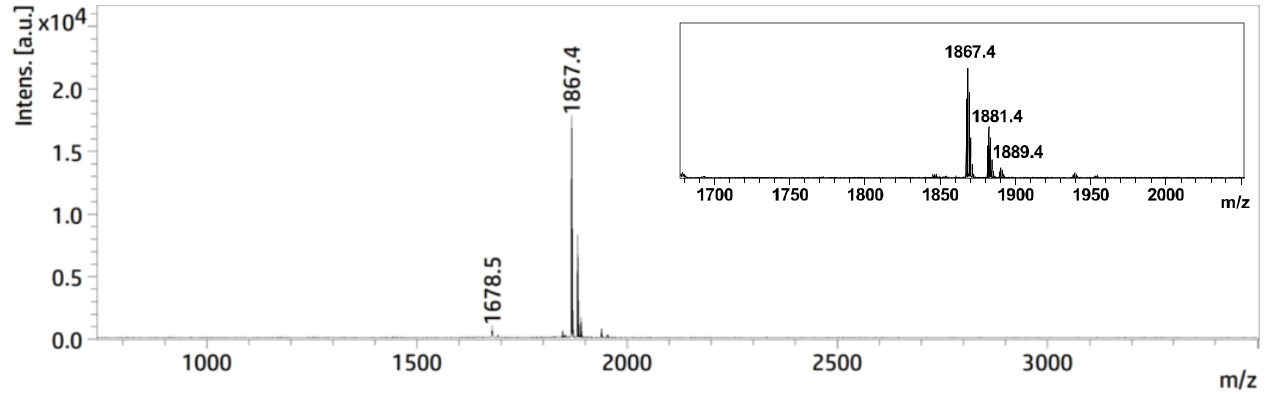
Spectrum: 39  
Peptide ID: GP2.15  
Internal ID: GP2.15  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTXP{GalNAca1-T}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1866.9$



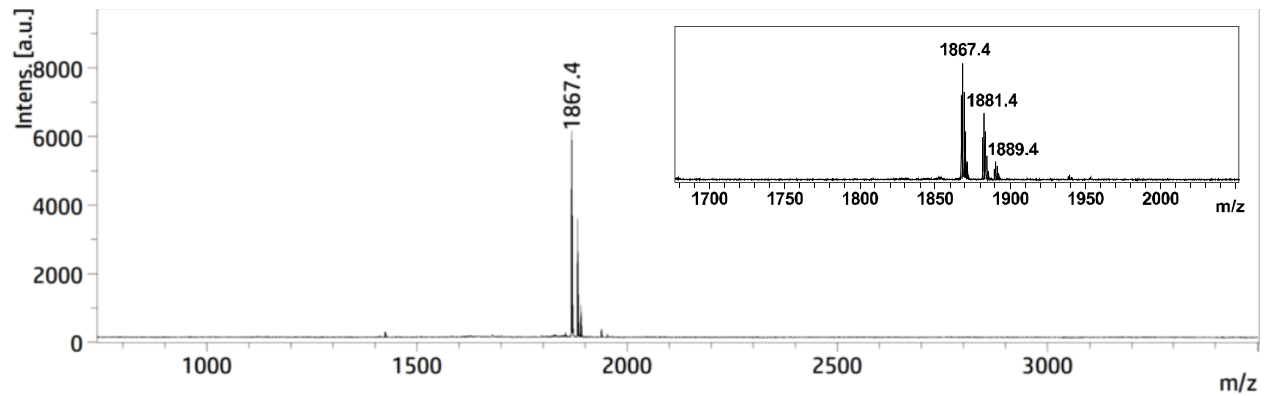
Spectrum: 40  
Peptide ID: GP2.16  
Internal ID: GP2.16  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPX{GalNAca1-T}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1866.9$



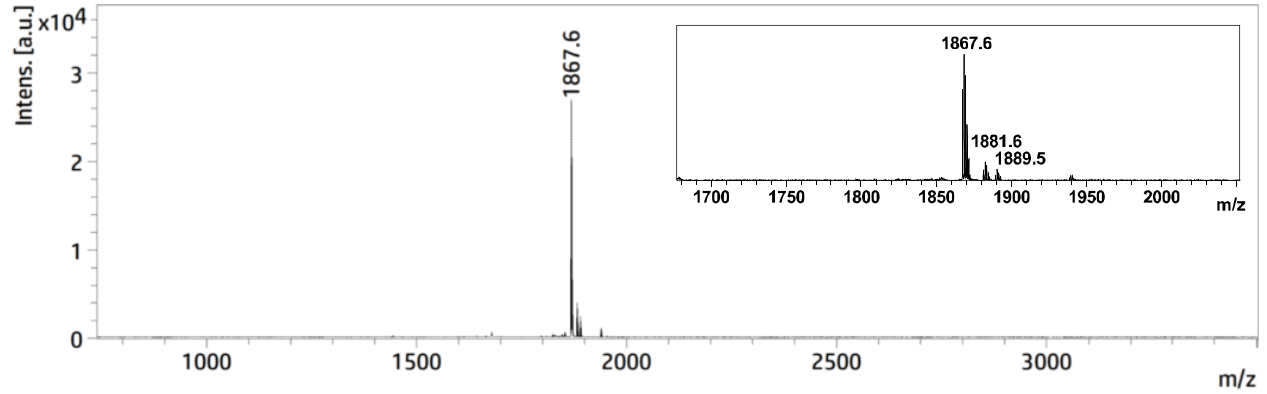
Spectrum: 41  
Peptide ID: GP2.17  
Internal ID: GP2.17  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPP{GalNAca1-T}XSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1866.9$



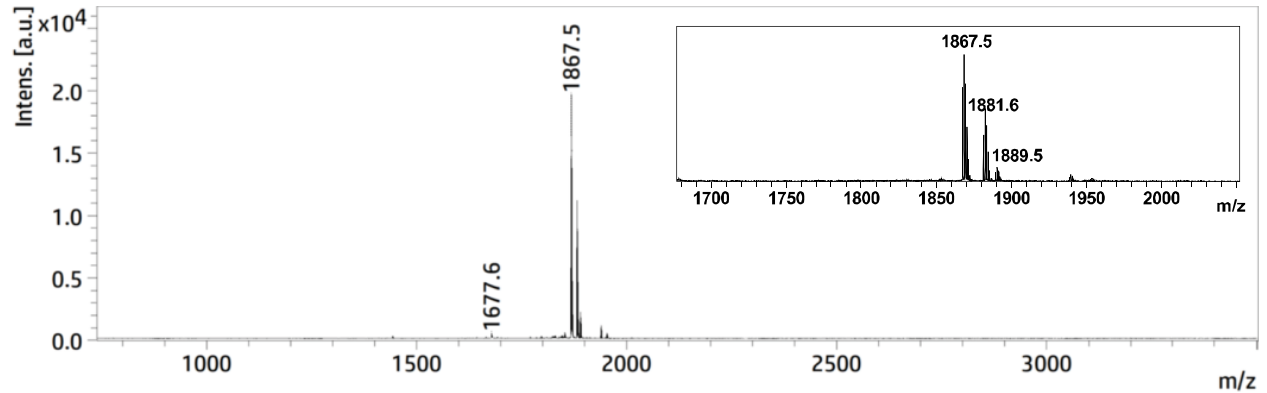
Spectrum: 42  
Peptide ID: GP2.18  
Internal ID: GP2.18  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTxP{GalNAca1-T}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1866.9$



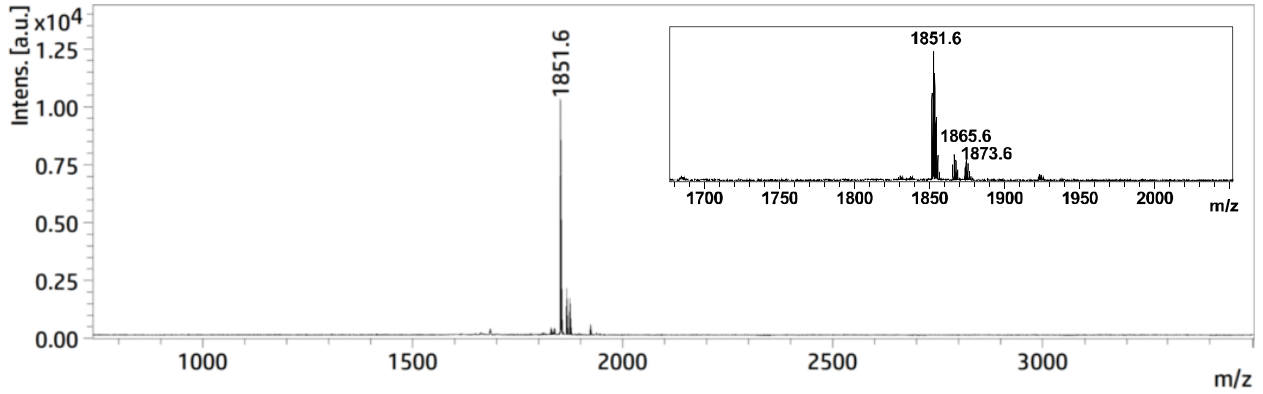
Spectrum: 43  
Peptide ID: GP2.19  
Internal ID: GP2.19  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTP<sub>x</sub>{GalNAca1-T}<sub>x</sub>PSPSA-COOH  
Calculated Mass [M+Na]<sup>+</sup> = 1866.9



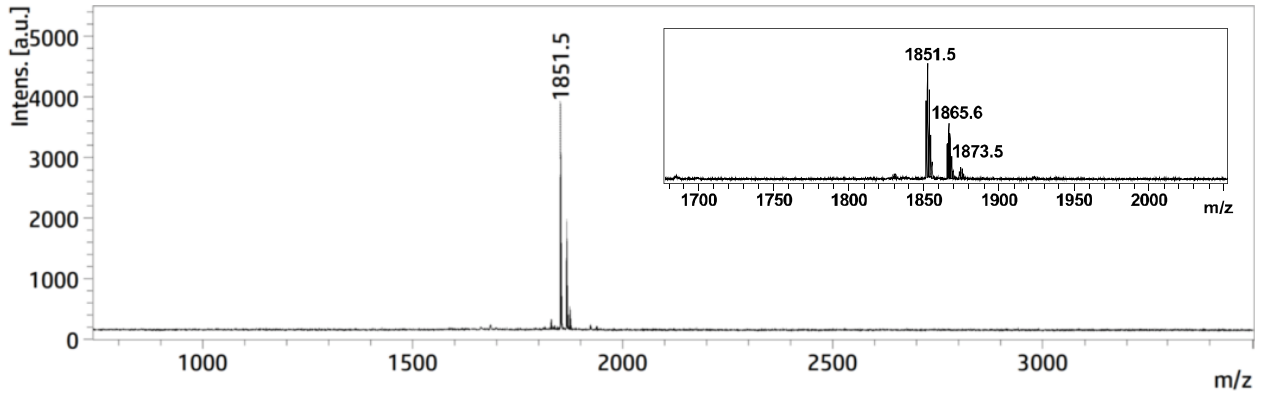
Spectrum: 44  
Peptide ID: GP2.20  
Internal ID: GP2.20  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPP<sub>x</sub>{GalNAca1-T}<sub>x</sub>SPSA-COOH  
Calculated Mass [M+Na]<sup>+</sup> = 1866.9



Spectrum: 45  
Peptide ID: GP2.21  
Internal ID: GP2.21  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPP{GalNAcb1-C}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1851.5$

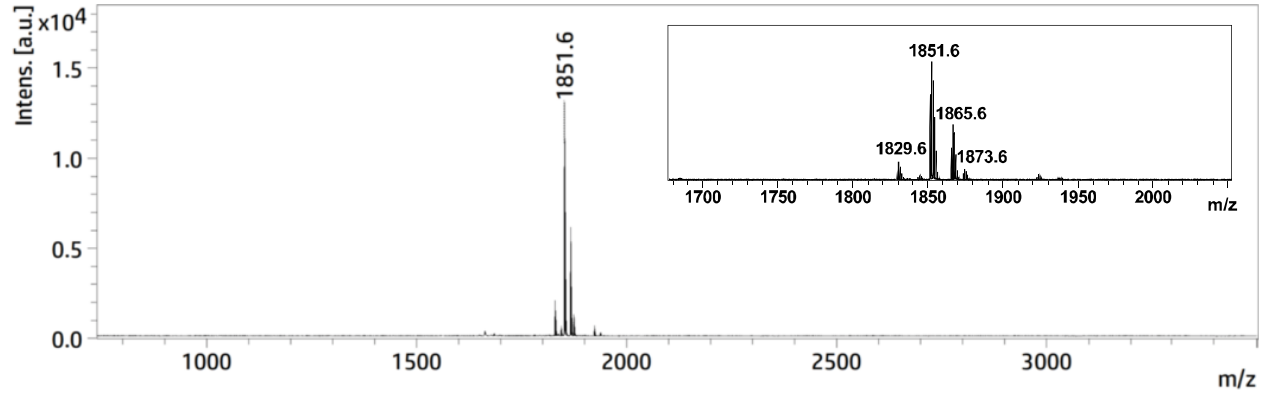


Spectrum: 46  
Peptide ID: GP2.22  
Internal ID: GP2.22  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPP{GlcNAcb1-C}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1851.5$

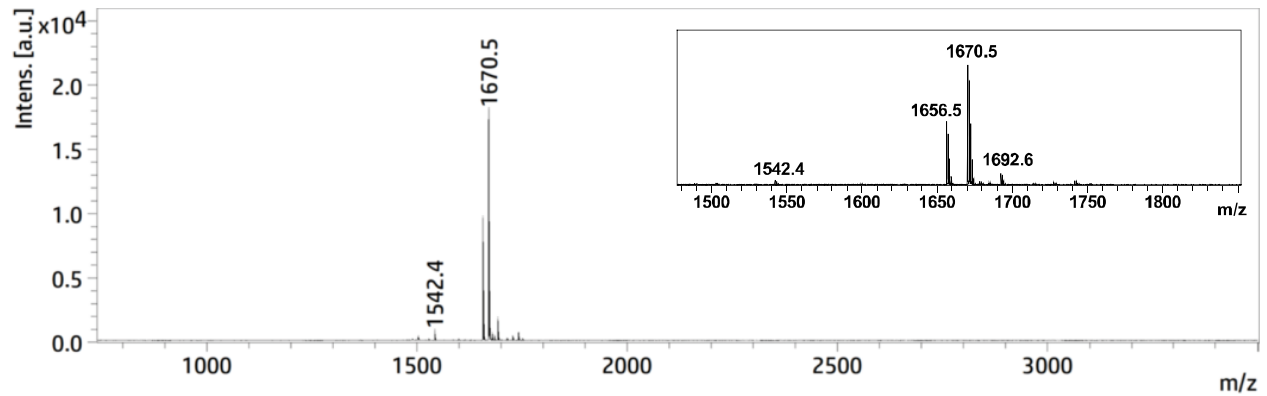




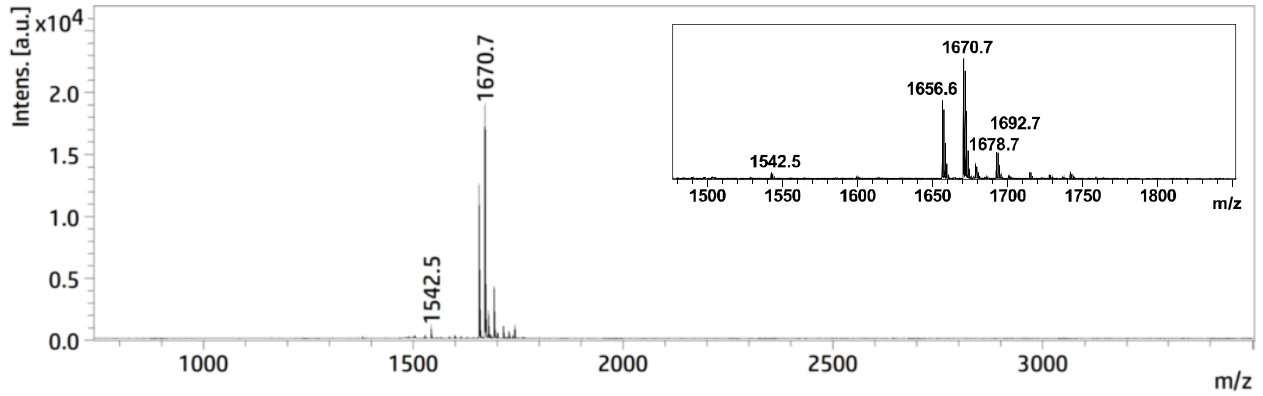
Spectrum: 47  
Peptide ID: GP2.23  
Internal ID: GP2.23  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPP{ManNAc1-C}PSPSA-COOH  
Calculated Mass  $[M+Na]^+$  = 1851.5



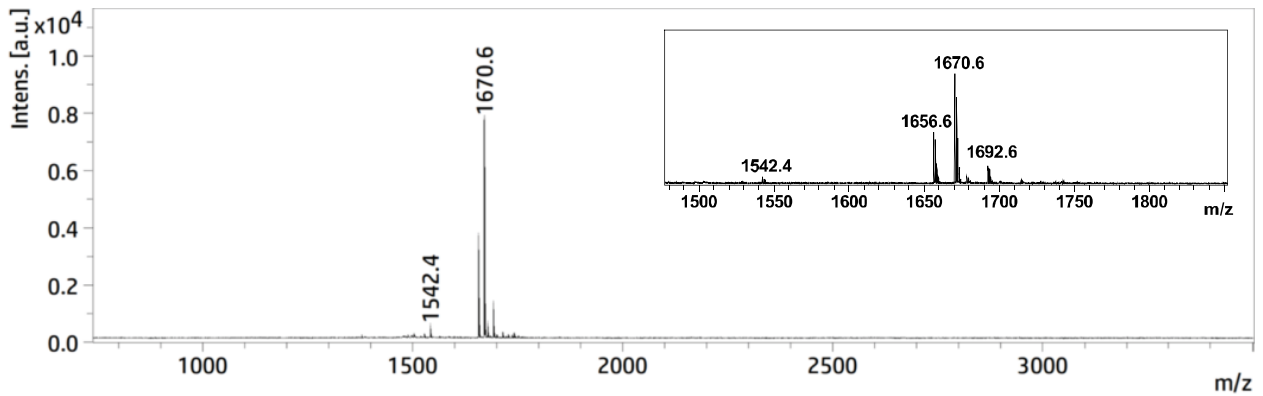
Spectrum: 48  
Peptide ID: GP2.24  
Internal ID: GP2.24  
Purification Level: SepPak C18 purified  
Sequence: AcNH-KYLAEVA{GalNAc1-C}GDDRA-COOMe  
Calculated Mass  $[M+H]^+$  = 1670.8



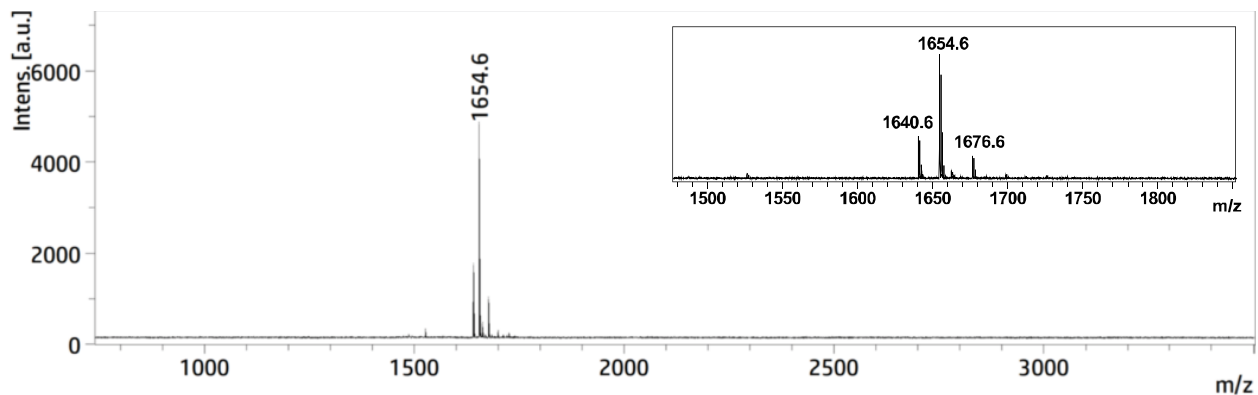
Spectrum: 49  
Peptide ID: GP2.25  
Internal ID: GP2.25  
Purification Level: SepPak C18 purified  
Sequence: AcNH-KYLAEVA{GlcNAc1-C}GDDRA-COOMe  
Calculated Mass  $[M+H]^+ = 1670.8$



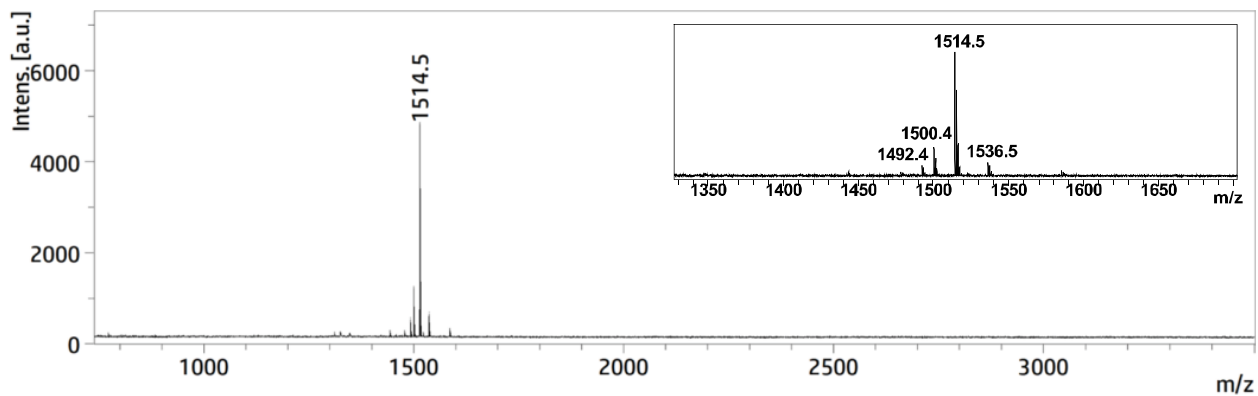
Spectrum: 50  
Peptide ID: GP2.26  
Internal ID: GP2.26  
Purification Level: SepPak C18 purified  
Sequence: AcNH-KYLAEVA{ManNAc1-C}GDDRA-COOMe  
Calculated Mass  $[M+H]^+ = 1670.8$



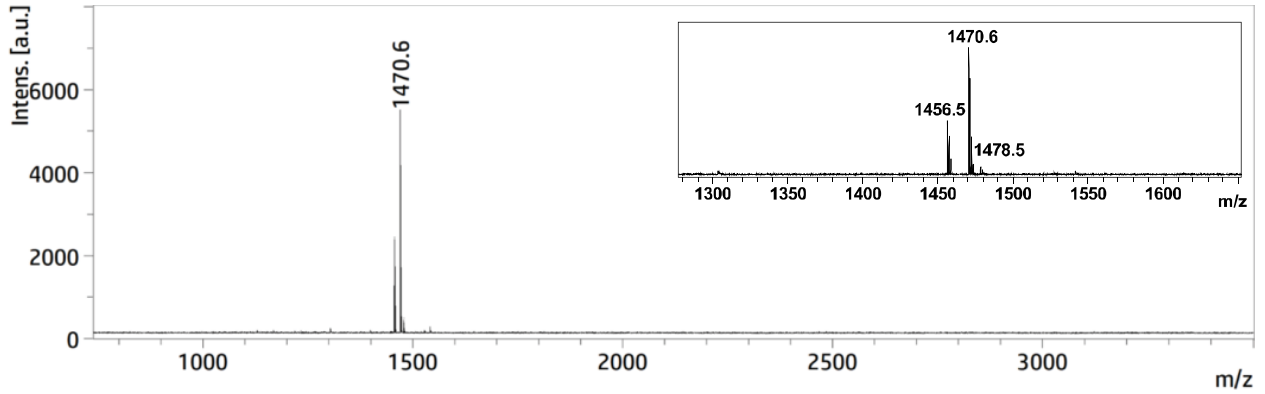
Spectrum: 51  
Peptide ID: GP2.27  
Internal ID: GP2.27  
Purification Level: SepPak C18 purified  
Sequence: AcNH-KYLAEVA{GlcNAc1-S}GDDRA-COOMe  
Calculated Mass  $[M+H]^+ = 1654.7$



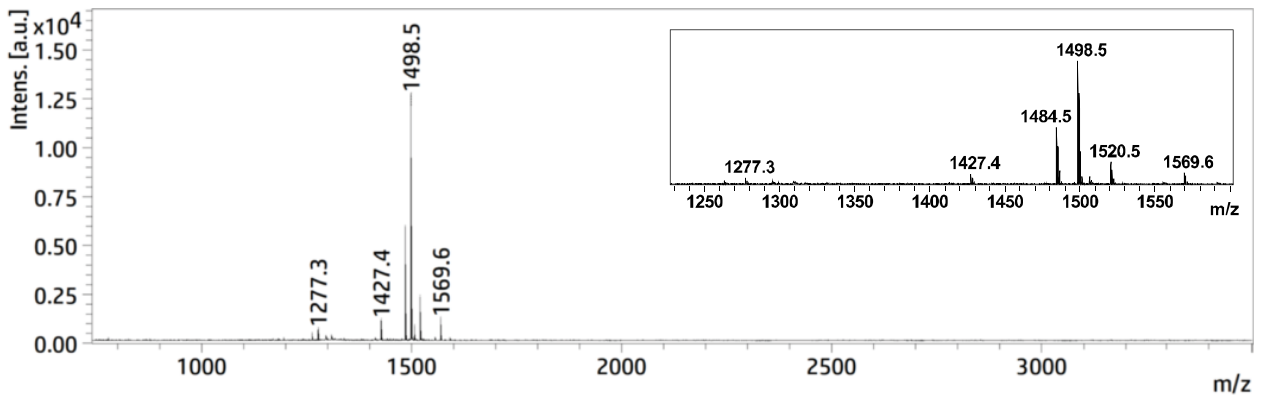
Spectrum: 52  
Peptide ID: GP2.28  
Internal ID:  
Purification Level: SepPak C18 purified  
Sequence: AcNH-KSSPVI{GlcNAc1-C}AGGQDA-COOMe  
Calculated Mass  $[M+Na]^+ = 1514.6$



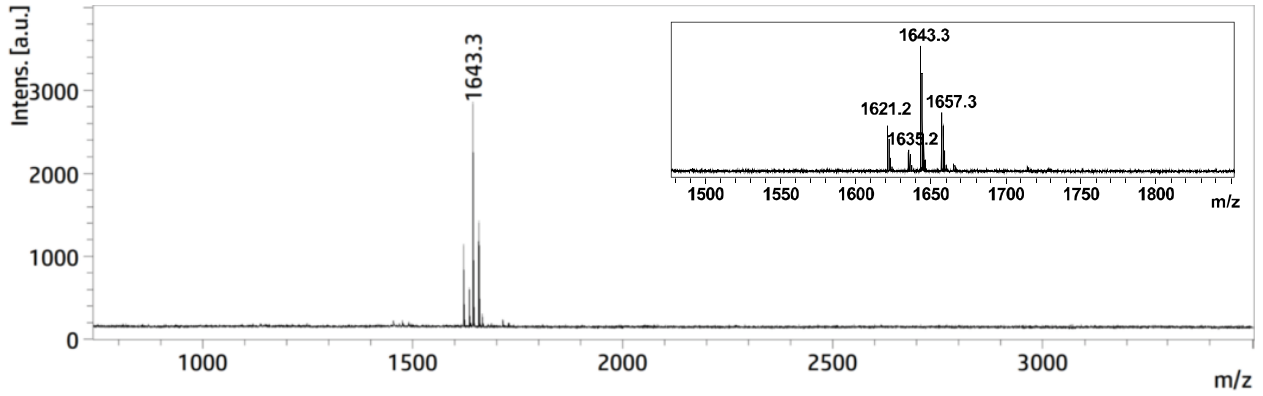
Spectrum: 53  
Peptide ID: GP2.29  
Internal ID: GP2.29  
Purification Level: SepPak C18 purified  
Sequence: AcNH-KSSPVI{GlcNAc1-C}AGGQAA-COOMe  
Calculated Mass  $[M+Na]^+ = 1470.6$



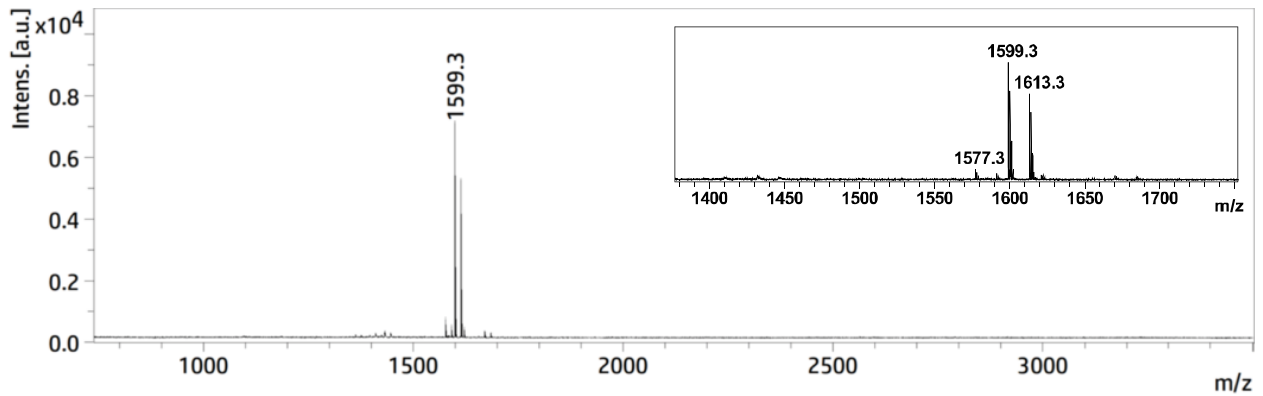
Spectrum: 54  
Peptide ID: GP2.30  
Internal ID: GP2.30  
Purification Level: SepPak C18 purified  
Sequence: AcNH-KSSPVI{GlcNAc1-S}AGGQDA-COOMe  
Calculated Mass  $[M+Na]^+ = 1498.6$



Spectrum: 55  
Peptide ID: GP2.31  
Internal ID: GP2.31  
Purification Level: SepPak C18 purified  
Sequence: AcNH-KTTKIP{GlcNAc1-C}DSPQSA-COOH  
Calculated Mass  $[M+Na]^+ = 1643.3$



Spectrum: 56  
Peptide ID: GP2.32  
Internal ID: GP2.32  
Purification Level: SepPak C18 purified  
Sequence: AcNH-KTTKIP{GlcNAc1-C}ASPQSA-COOH  
Calculated Mass  $[M+Na]^+ = 1599.3$



Spectrum: 57

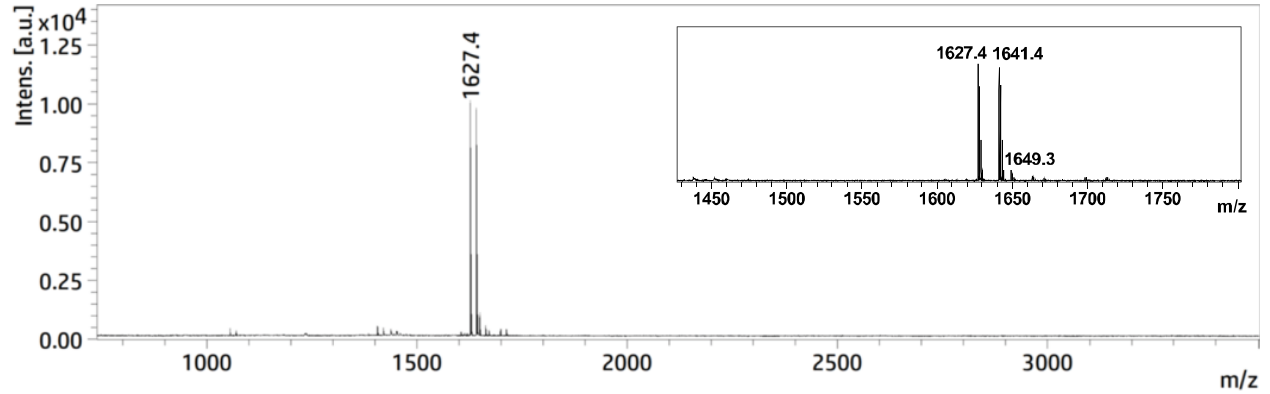
Peptide ID: GP2.33

Internal ID: GP2.33

Purification Level: SepPak C18 purified

Sequence: AcNH-KTTKIP{GlcNAc1-S}DSPQSA-COOH

Calculated Mass  $[M+Na]^+ = 1627.2$



Spectrum: 58

Peptide ID: GP2.34

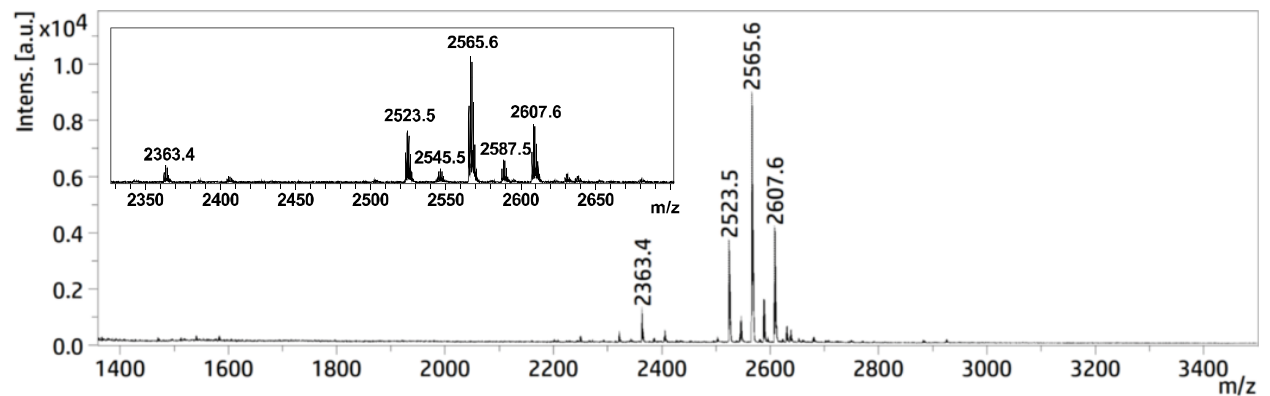
Internal ID: GP2.34

Purification Level: SepPak C18 purified

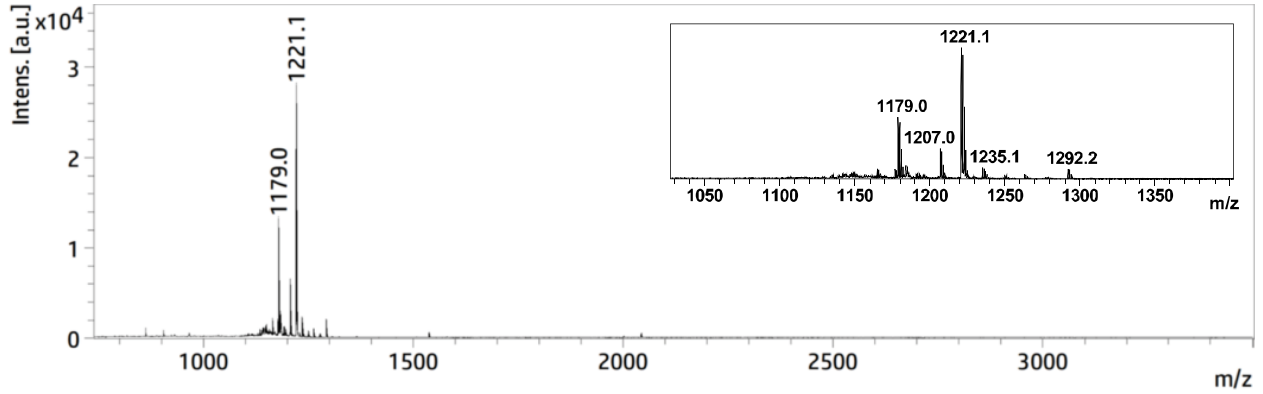
Sequence: FINH-KVAL{GlcNAc1-2Man1-6(GlcNAc1-2Man1-3)Man1-4GlcNAc1-4GlcNAc1-N}KTA-COOH

Calculated Mass  $[M+Na]^+ = 2523.5$  |  $[M+Ac+Na]^+ = 2565.5$  |  $[M+2Ac+Na]^+ = 2607.5$

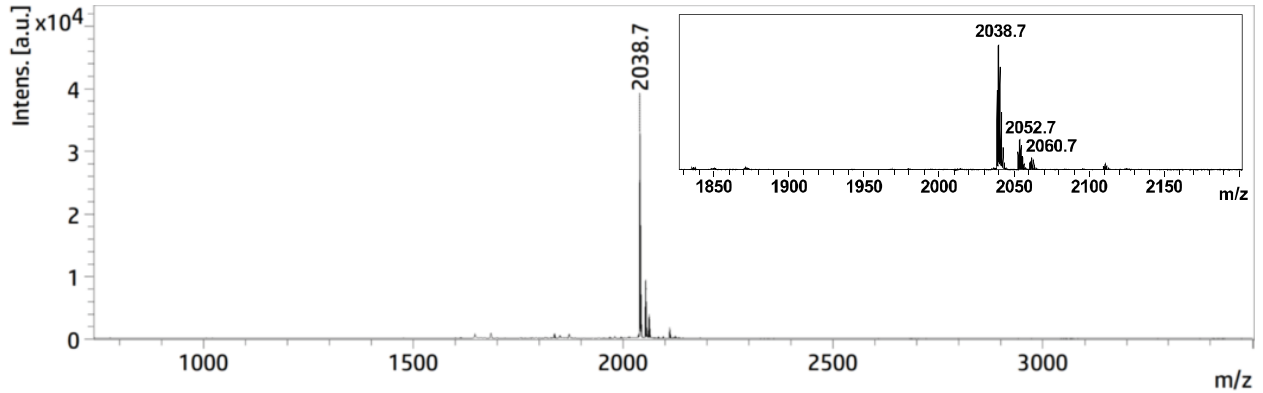
Notes: The extra acetylation was caused as a result of N-capping step performed on the membrane while this spot was still on it. As a result the acetyls attached onto the fluorescein hydroxyl groups.



Spectrum: 59  
Peptide ID: GP2.35  
Internal ID: GP2.35  
Purification Level: SepPak C18 purified  
Sequence: FINH-KTPSPSA-COOMe  
Calculated Mass  $[M+Na]^+ = 1178.7$  |  $[M+Ac+Na]^+ = 1220.7$



Spectrum: 60  
Peptide ID: GP2.36  
Internal ID: GP2.36  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPS{GalNAca1-T}PP{GalNAca1-S}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 2038.6$



Spectrum: 61

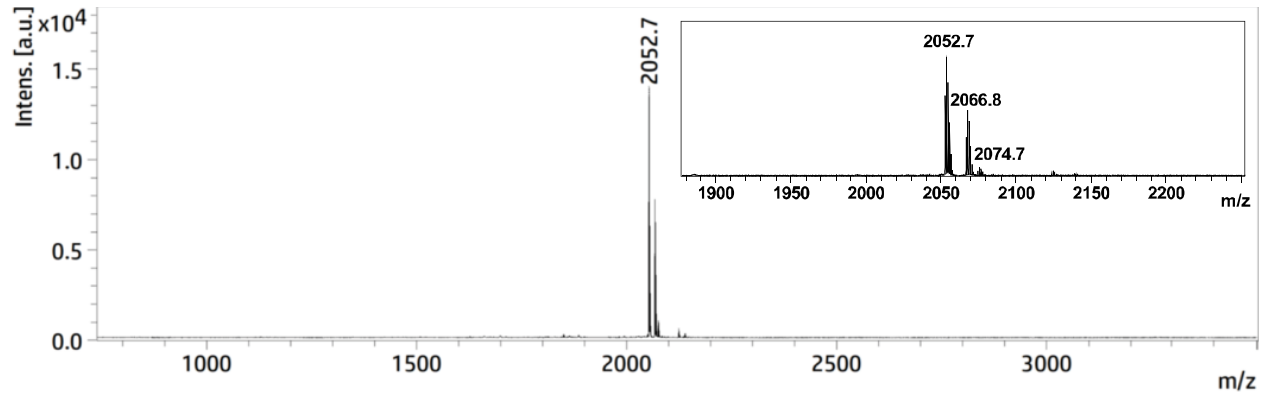
Peptide ID: GP2.37

Internal ID: GP2.37

Purification Level: SepPak C18 purified

Sequence: FINH-KVPS{GalNAca1-T}PP{GalNAca1-T}PSPSA-COOH

Calculated Mass  $[M+Na]^+ = 2052.6$



Spectrum: 62

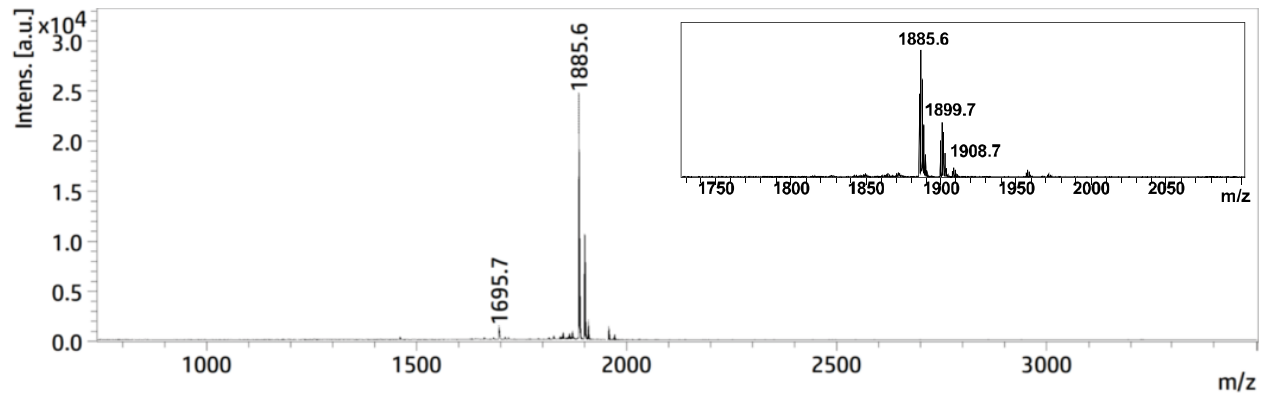
Peptide ID: GP2.38

Internal ID: GP2.38

Purification Level: SepPak C18 purified

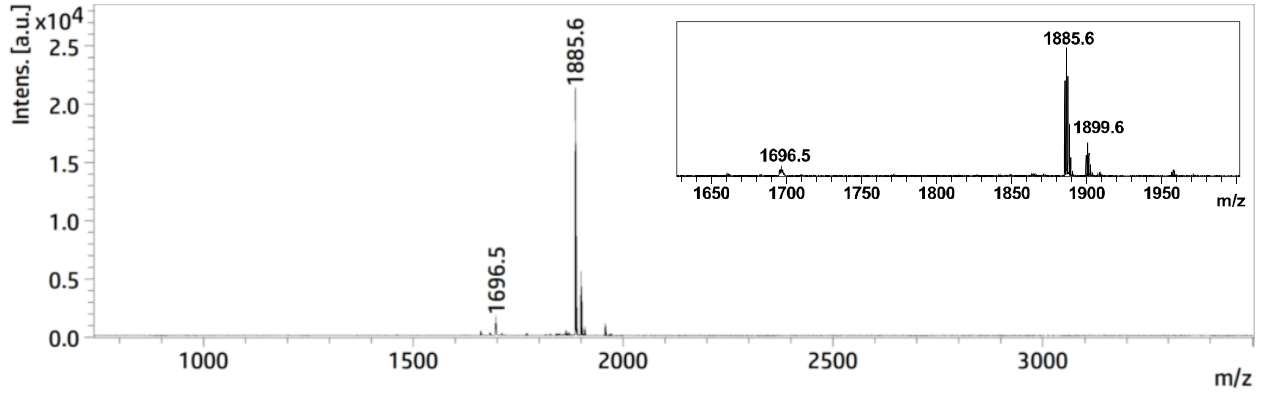
Sequence: FINH-KVPSTXX{GalNAca1-T}PSPSA-COOH

Calculated Mass  $[M+Na]^+ = 1885.6$

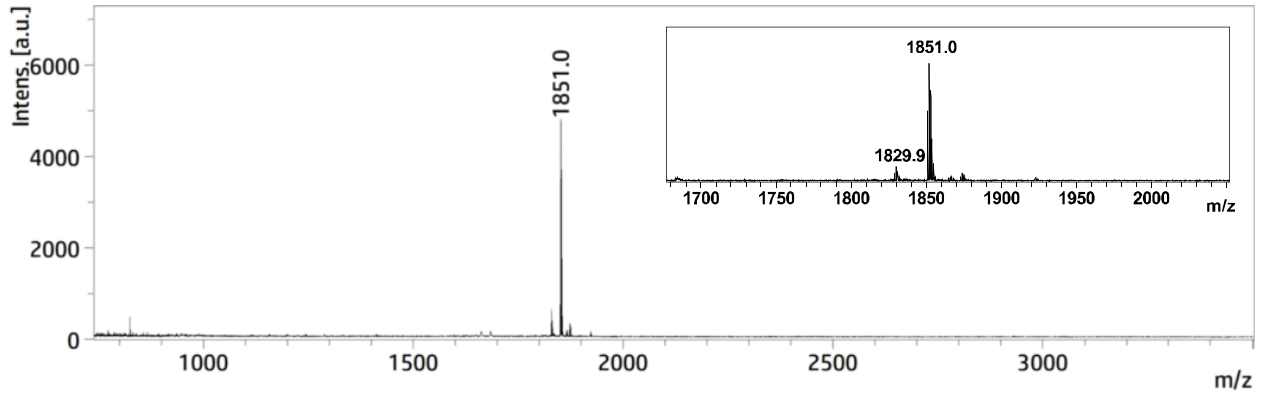




Spectrum: 63  
Peptide ID: GP2.39  
Internal ID: GP2.39  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTxx{GalNAca1-T}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1885.6$



Spectrum: 64  
Peptide ID: GP2.40 (repeat of GP2.21)  
Internal ID: GP2.40  
Purification Level: SepPak C18 purified  
Sequence: FINH-KVPSTPP{GalNAcb1-C}PSPSA-COOH  
Calculated Mass  $[M+Na]^+ = 1851.5$



## HPLC Chromatography For Glycopeptides

### GP1 Library HPLC Chromatography

#### Method 1: Semi-prep

Note- For this library semi-prep HPLC was performed on the crude material and hence there are a few minor peaks observed in the chromatograms. However, the major peak was found to be the product peak, which was isolated and confirmed to be >90% purity before use in other assays. The aim of showing these chromatograms is to let the reader judge the efficacy of synthesis straight out of the method.

Instrument: Shimadzu Prominence HPLC with SPD-20AV UV-Vis detector (Detector B) and RF-20A Fluorescence detector (Detector A)

Solvent A: 0.1% trifluoroacetic acid with 95:5 water:acetonitrile.

Solvent B: 0.1% trifluoroacetic acid with 95:5 acetonitrile:water.

Column: Phenomenex Luna® Omega 5µm PS C18 100Å 250 x 4.6 mm

Column Temperature: 40 °C

Flow rate: 1.25 ml/min

Total run time: 60 min

UV-Vis Detector: 220 nm

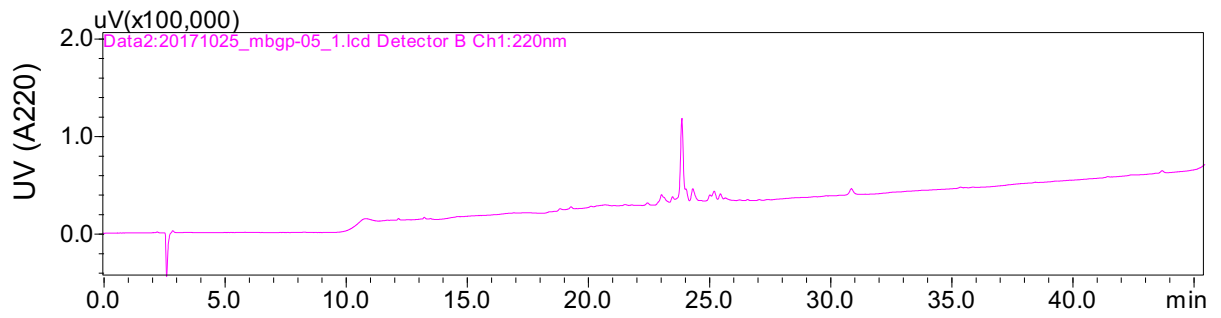
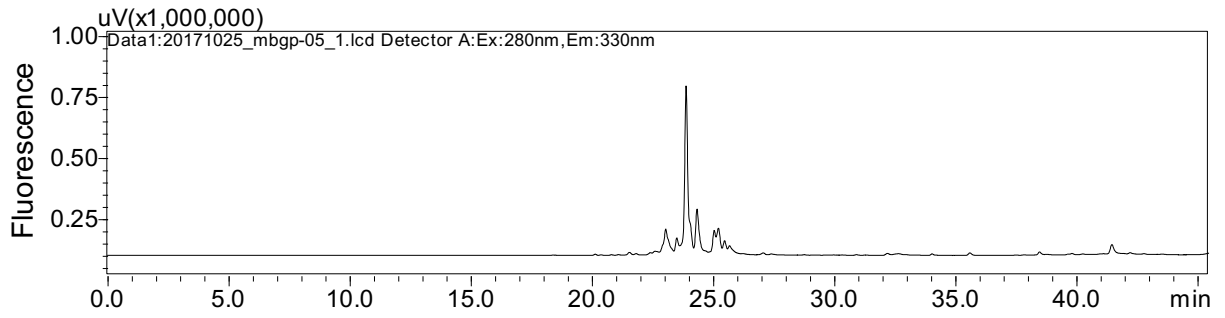
Fluorescence: Ex: 280 nm Em: 330 nm

Method: A sample of the glycopeptide was dissolved in 0.15 ml of solvent A. The sample was split into 3 injections of 50 µl each and injected onto the column. A 60 minute gradient was, in which the gradient gradually went from 0%-50% B over the first 40 minutes, followed by a wash cycle consisting of a sharp increase to 95% and back down (See details below). Fractions were collected with a vial volume set at 1.25 ml based on a slope of 100 µV/sec and level of 200000 µV. Fractions were analyzed by MALDI-MS for target mass. The fractions which contained the target mass were pooled and dried as final compounds.

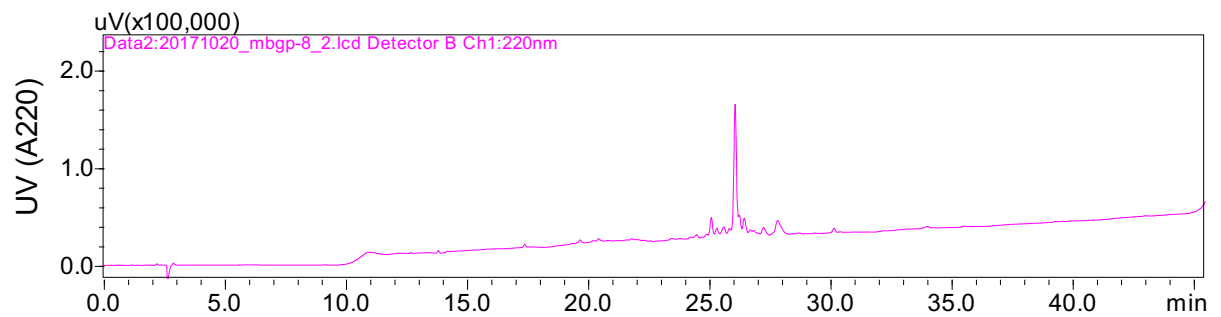
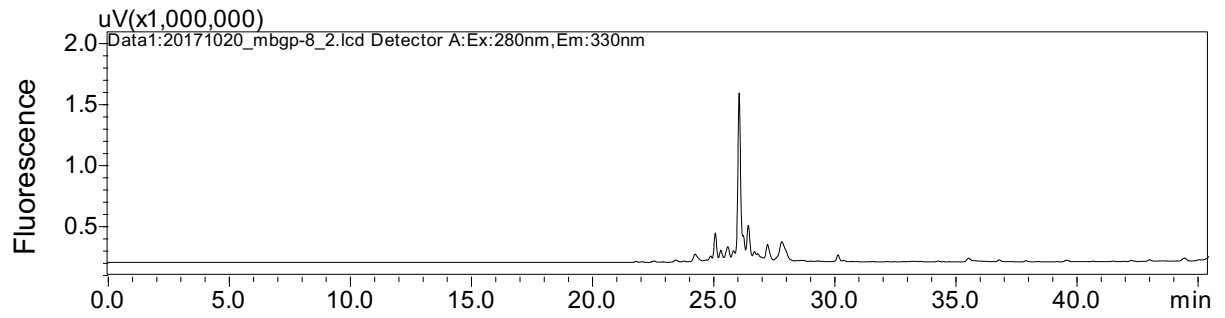
#### Gradient Details:

	Time	Module	Command	Value
1	0.01	Pumps	Total Pump A Flow	1.25
2	0.02	RF-20A(DET.A)	Zero	
3	0.02	SPD-20AV(DET.B)	Zero	
4	0.03	Pumps	Solvent B Conc.	0
5	3.00	Pumps	Solvent B Conc.	0
6	40.00	Pumps	Solvent B Conc.	50
7	42.00	Pumps	Solvent B Conc.	95
8	50.00	Pumps	Solvent B Conc.	95
9	51.00	Pumps	Solvent B Conc.	0
10	60.00	Controller	Stop	

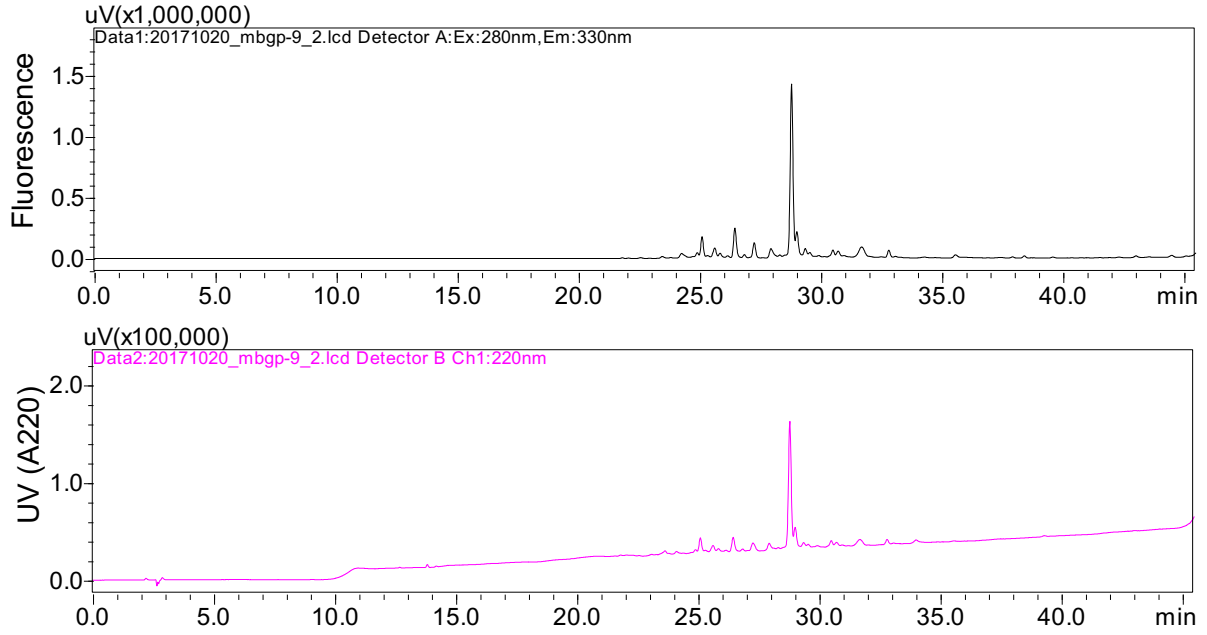
### GP1.1



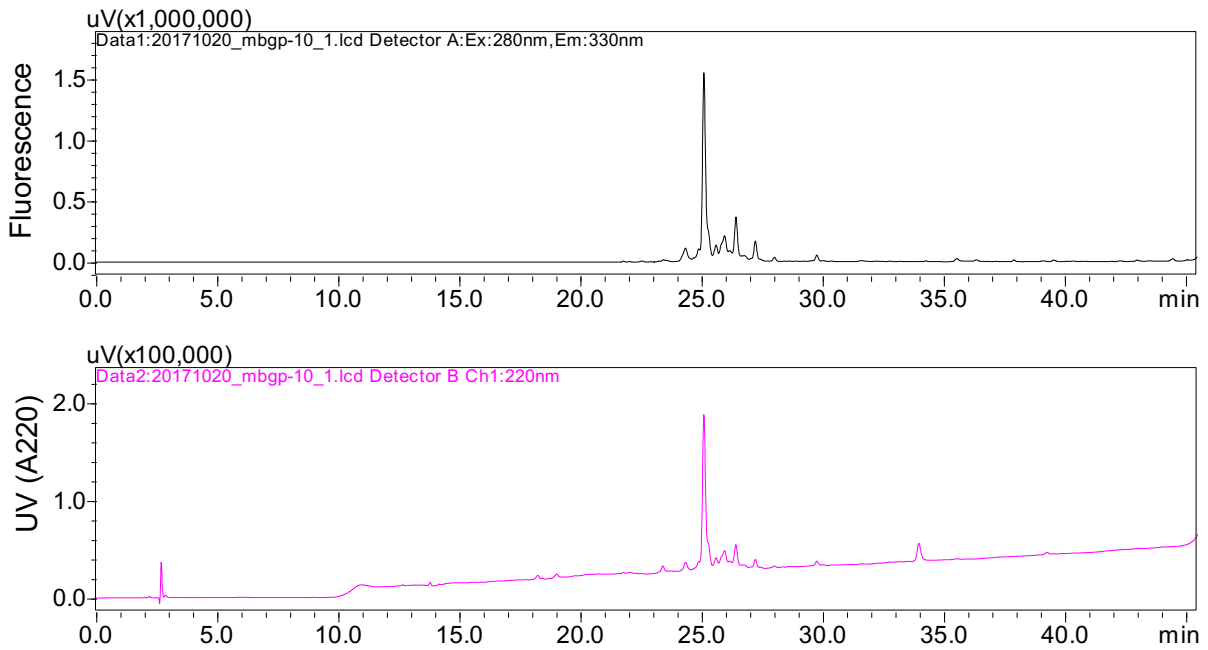
### GP1.2



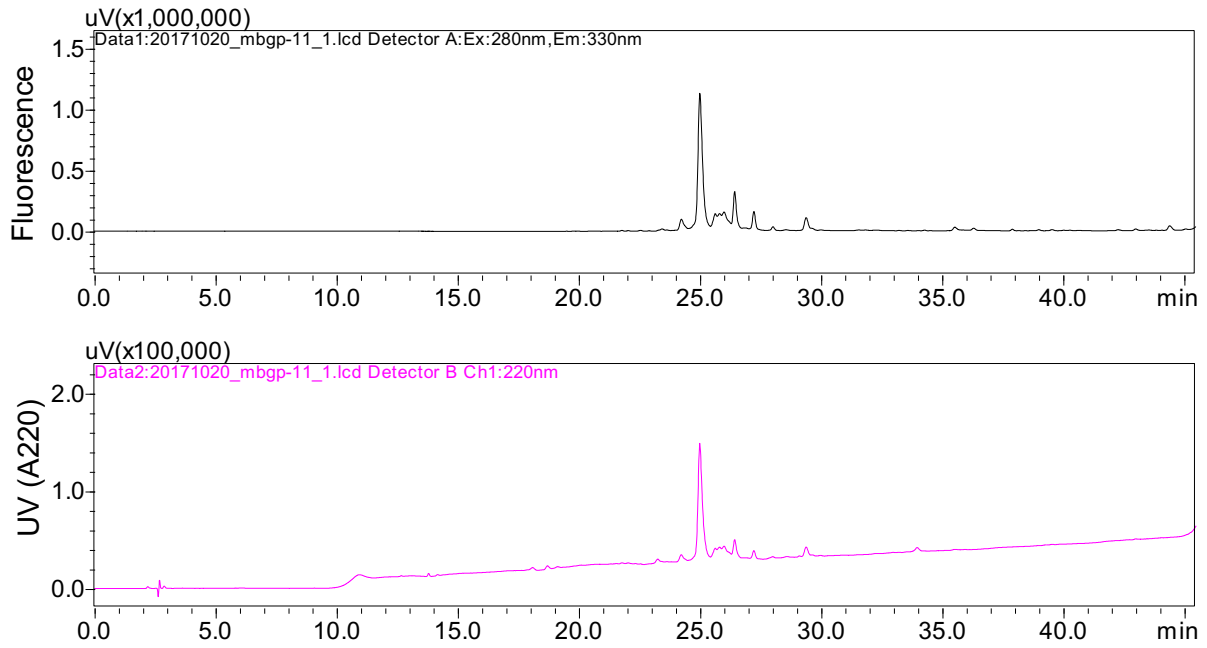
### GP1.3



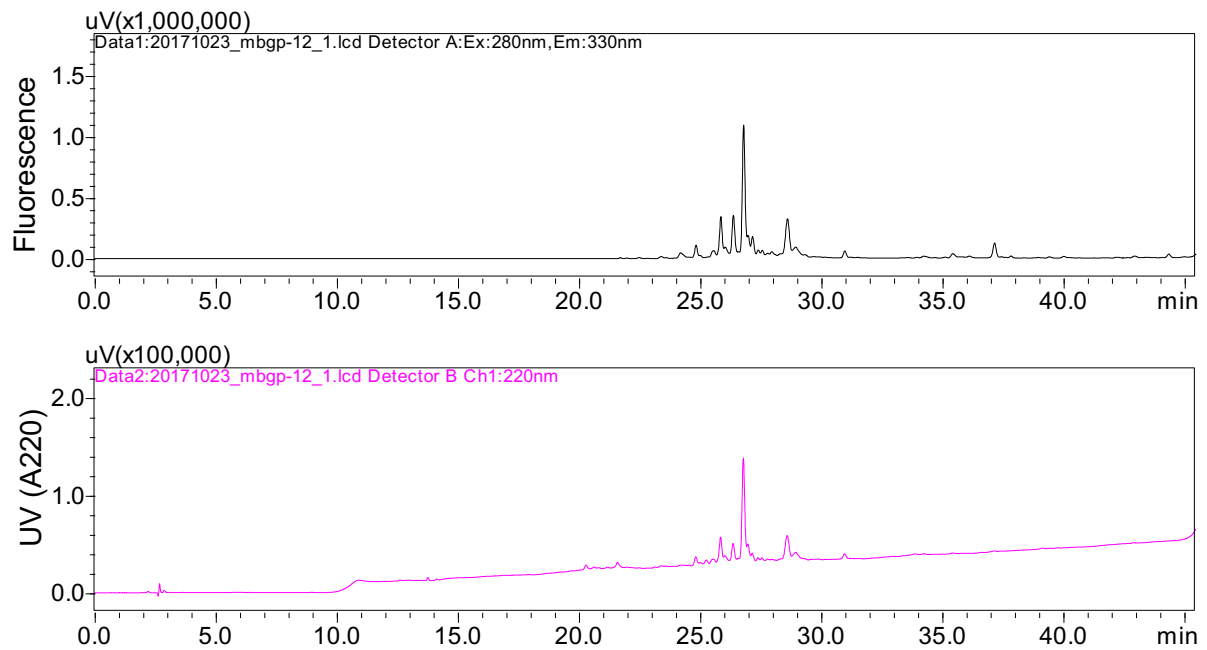
### GP1.4



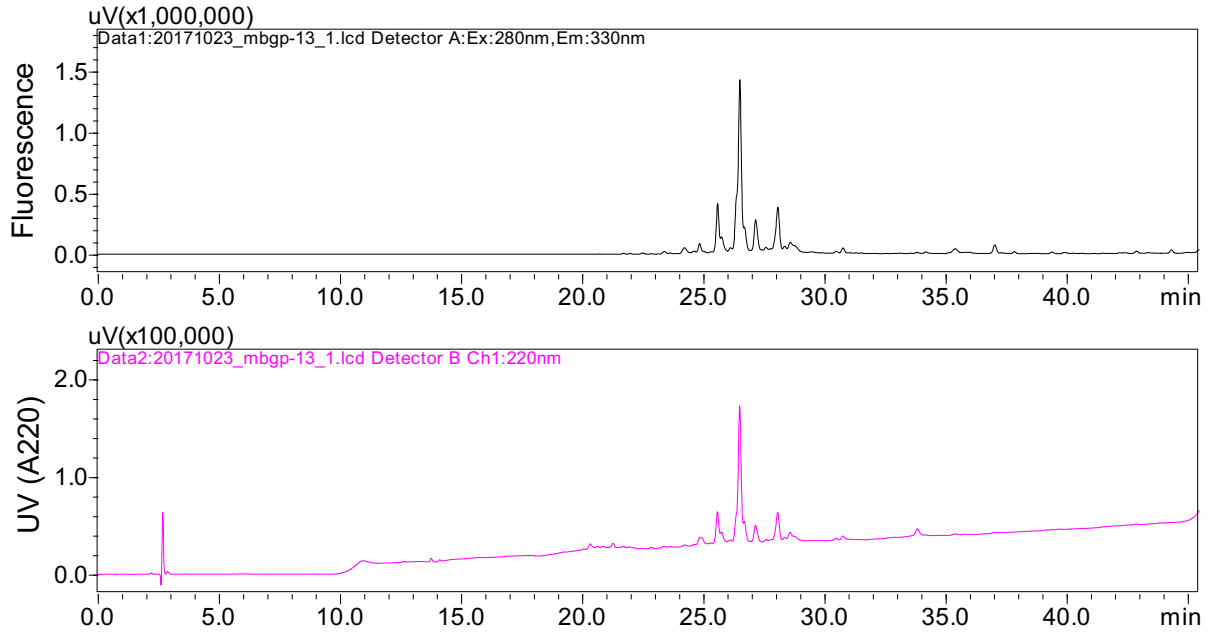
### GP1.5



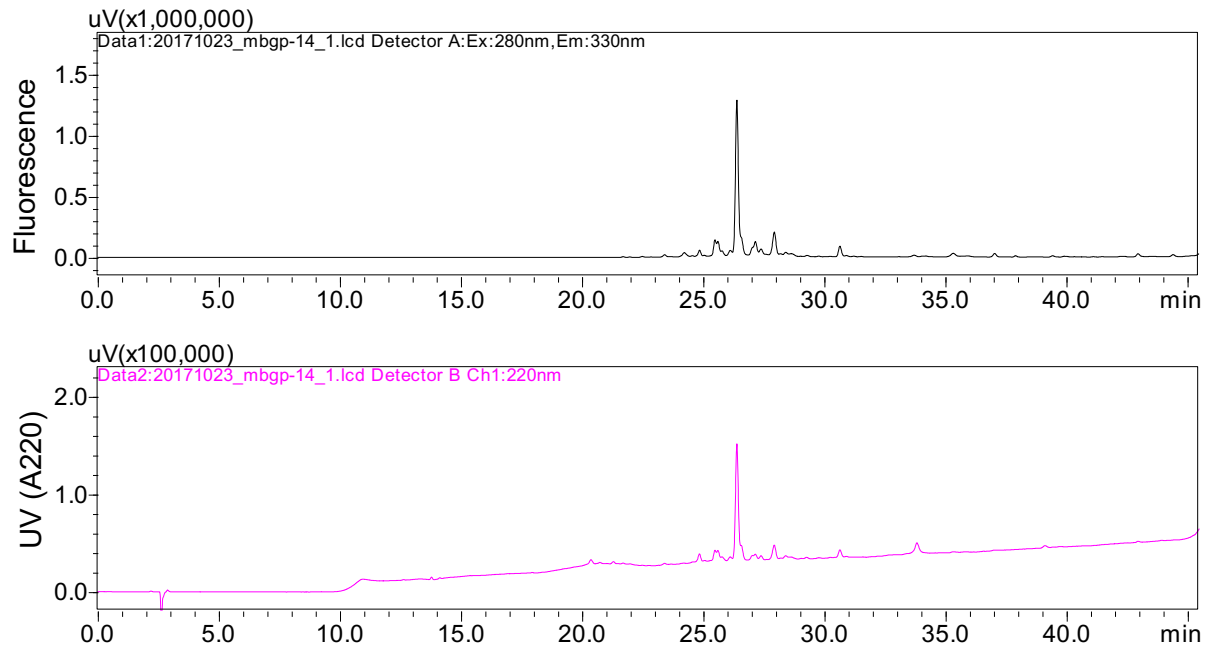
### GP1.6



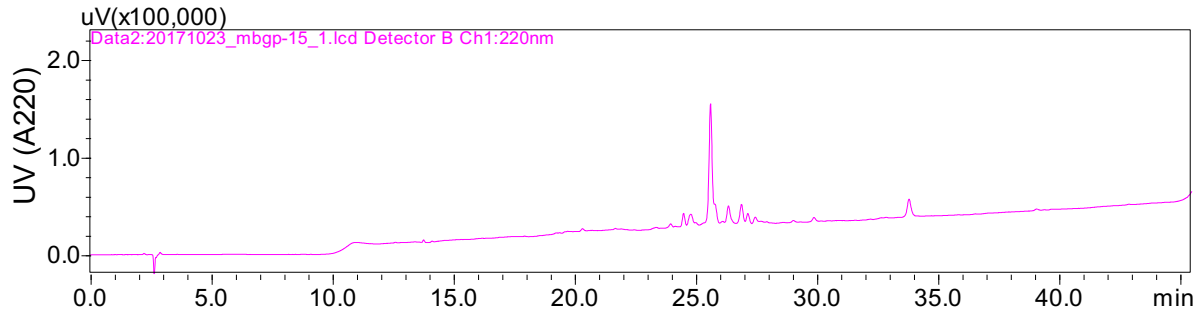
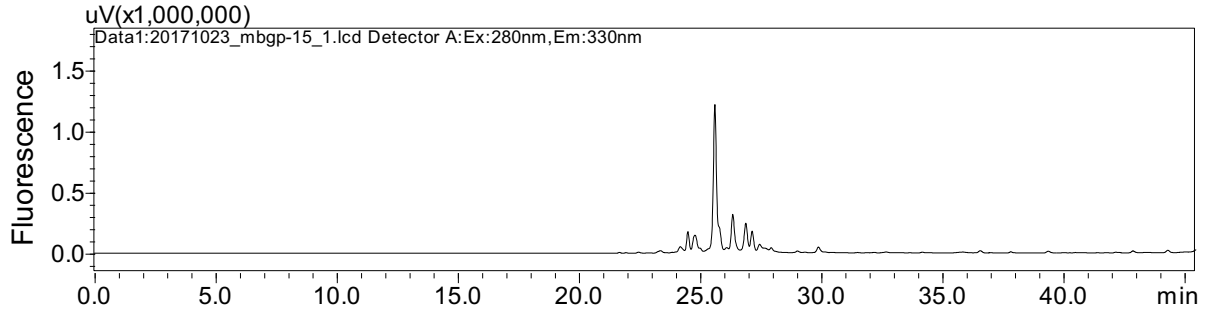
**GP1.7**



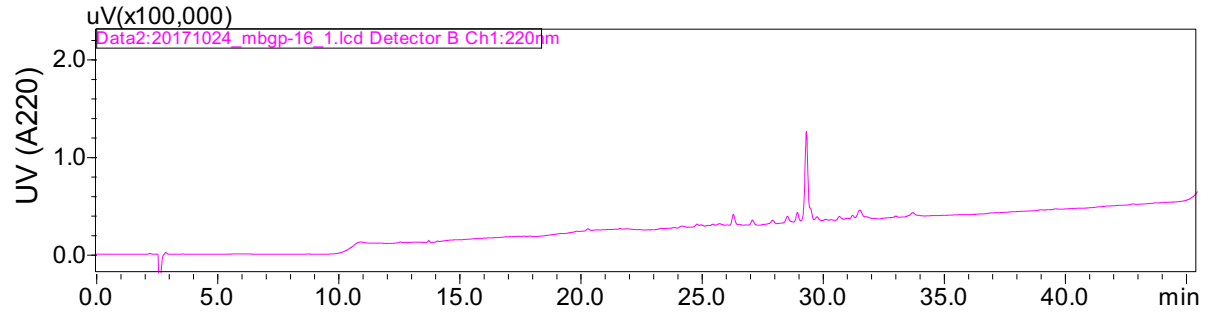
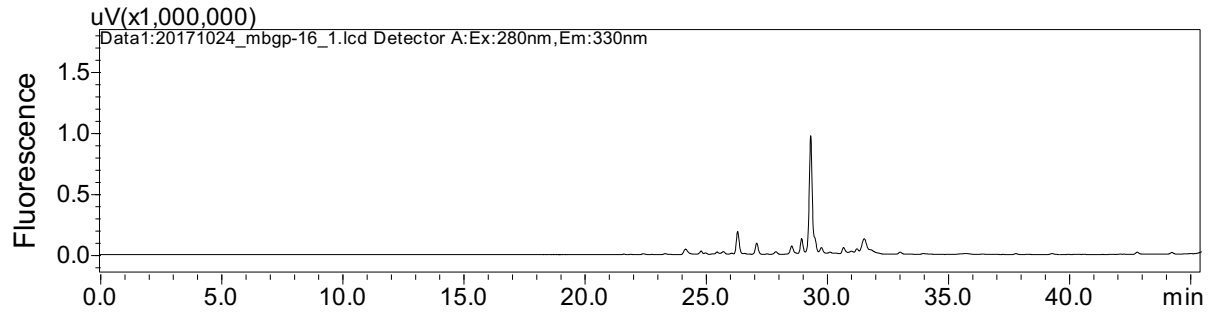
**GP1.8**



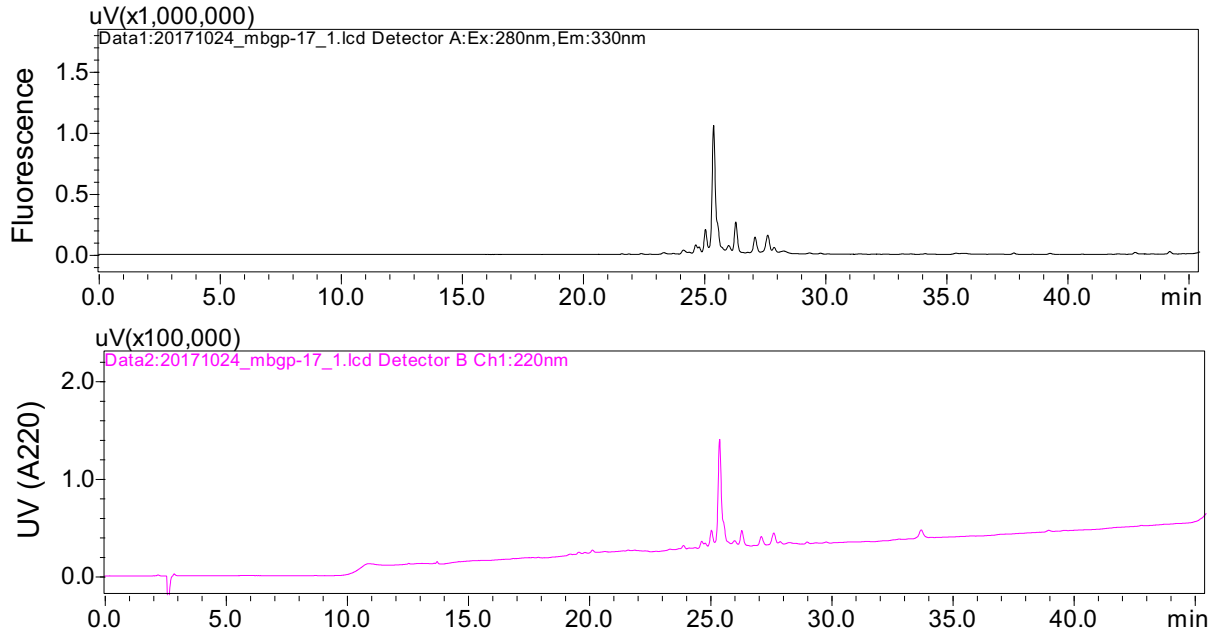
### GP1.9



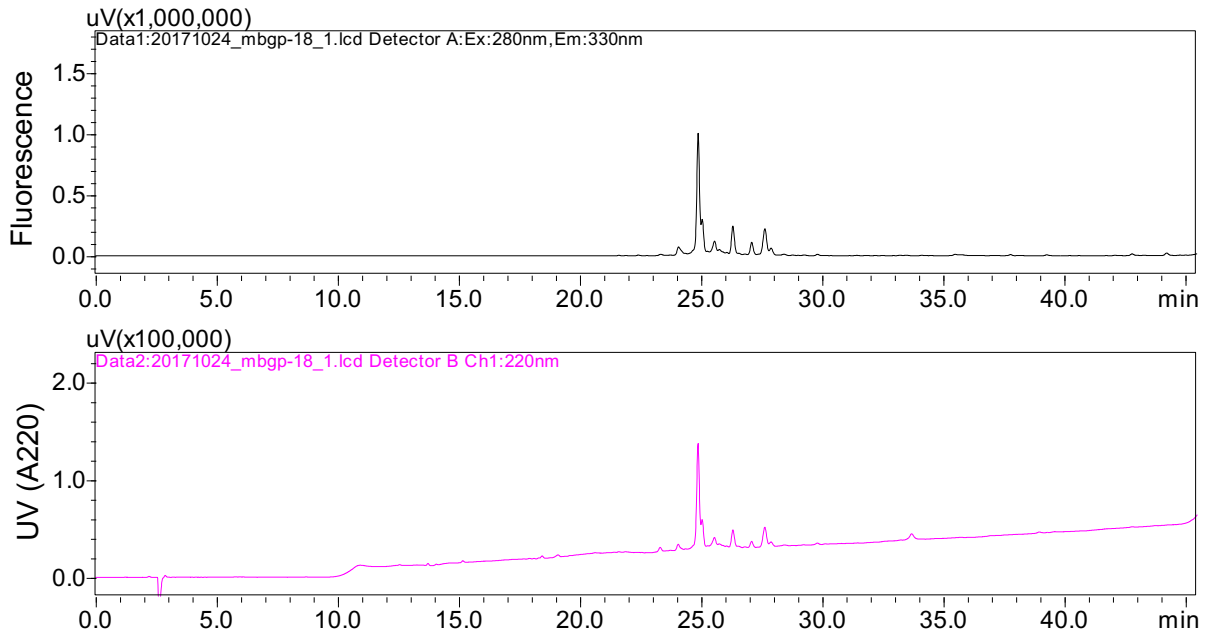
### GP1.10



### GP1.11

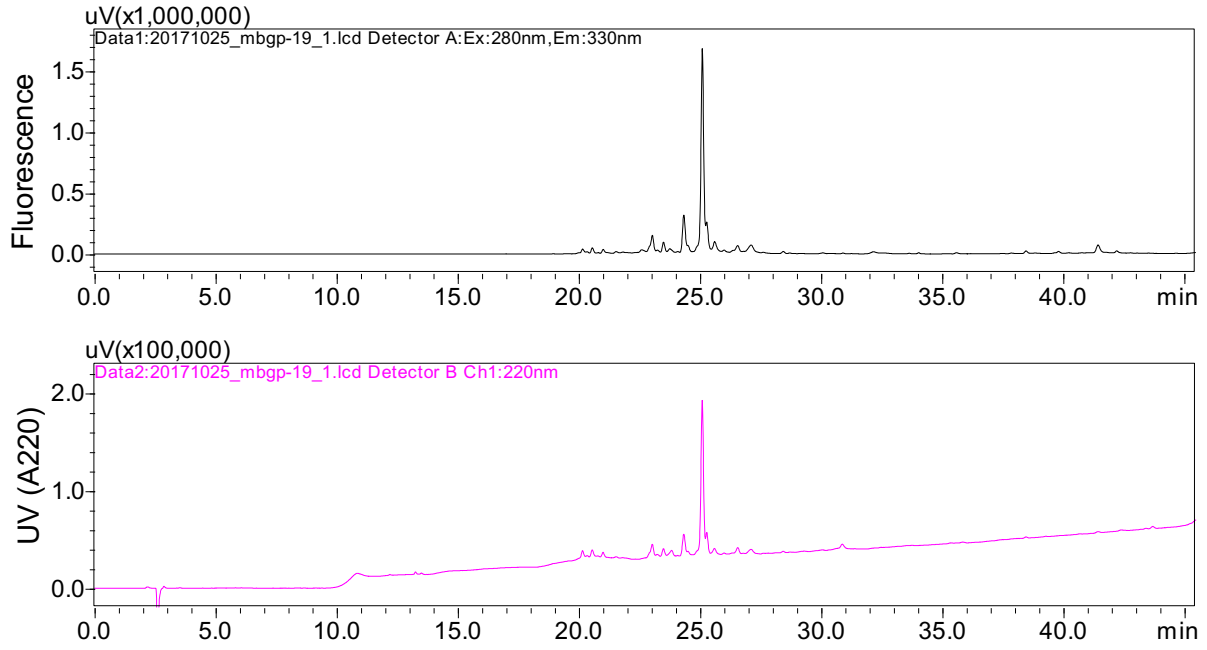


### GP1.12

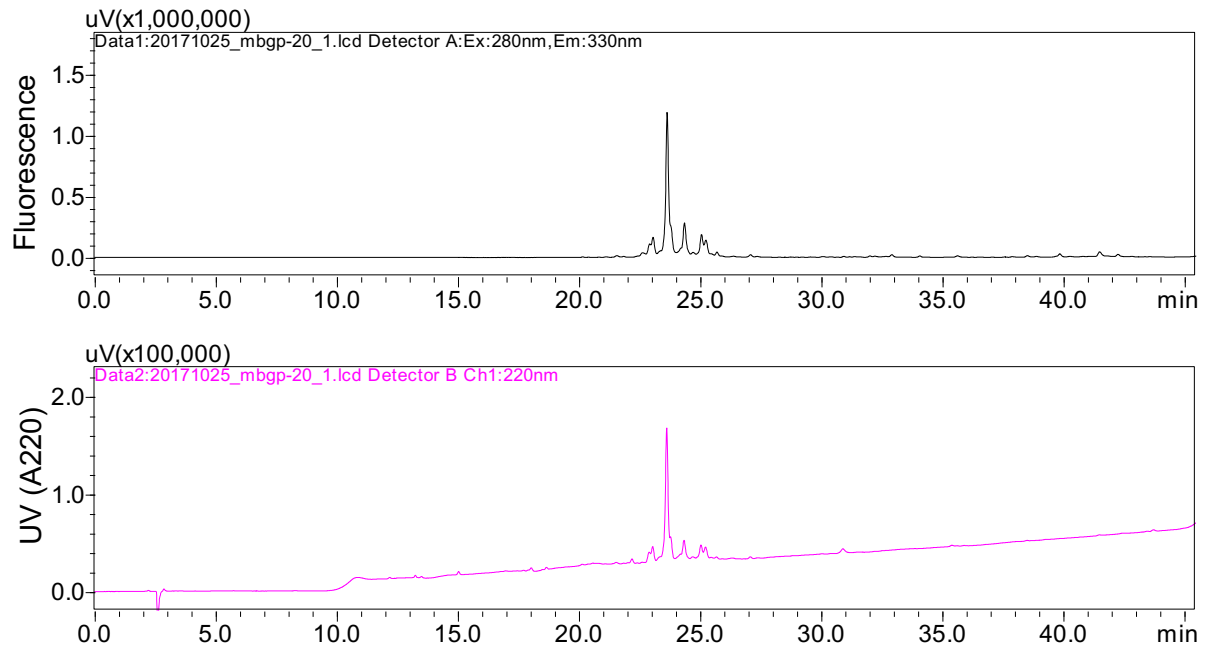




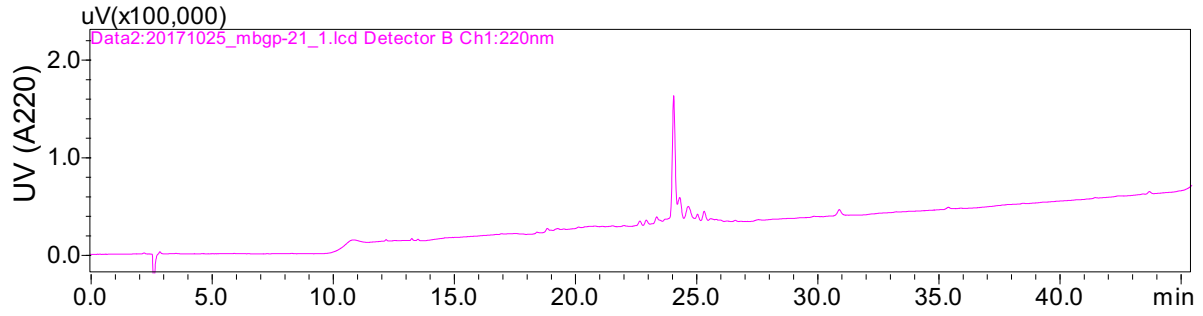
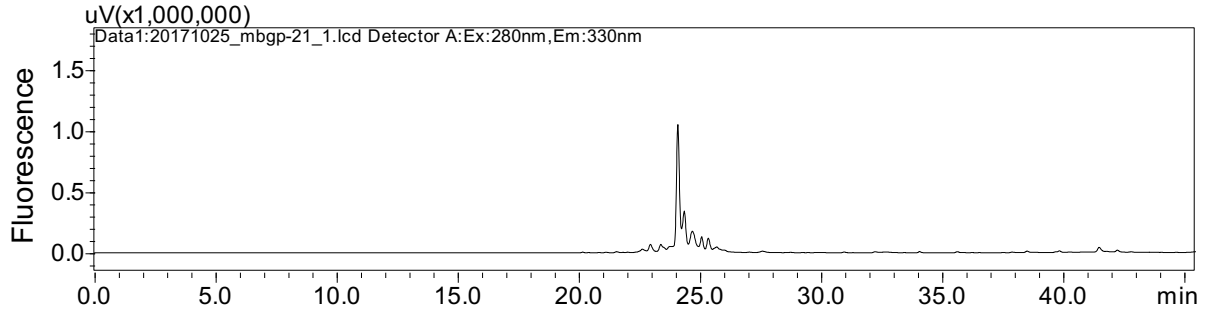
### GP1.13



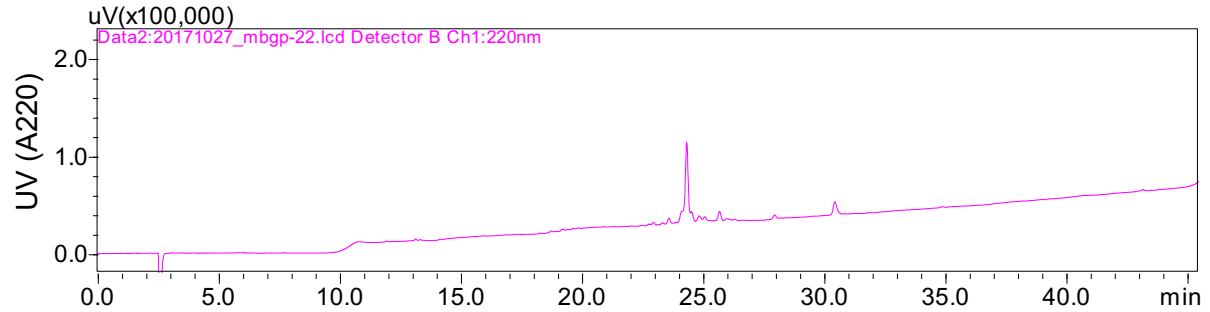
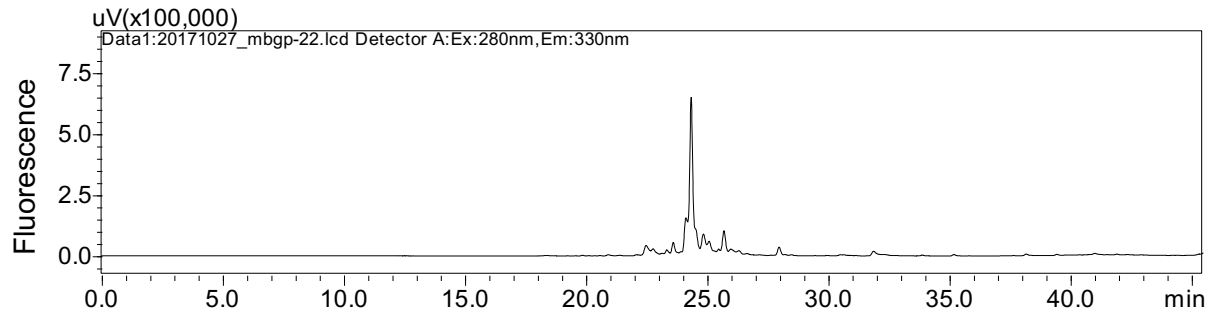
### GP1.14



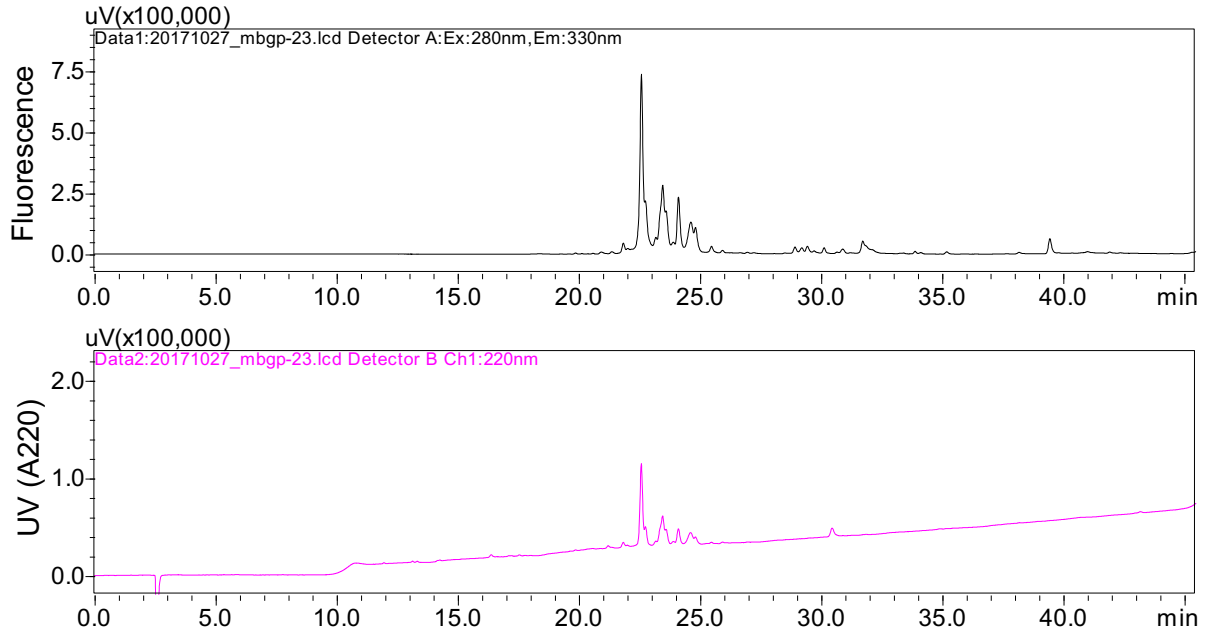
### GP1.15



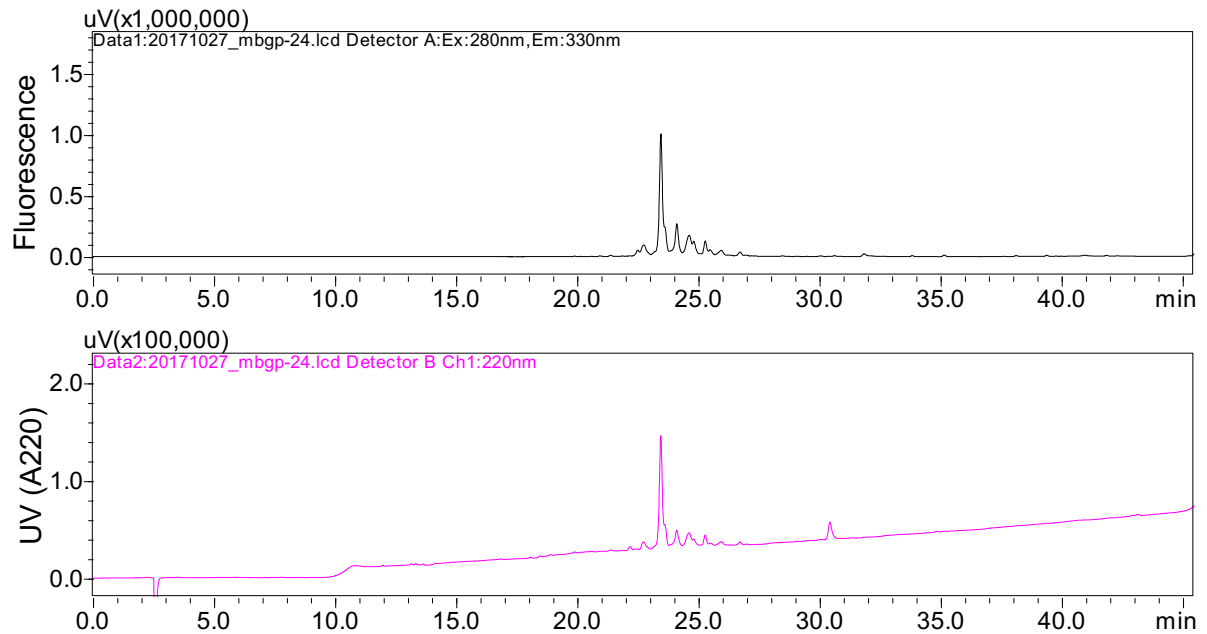
### GP1.16



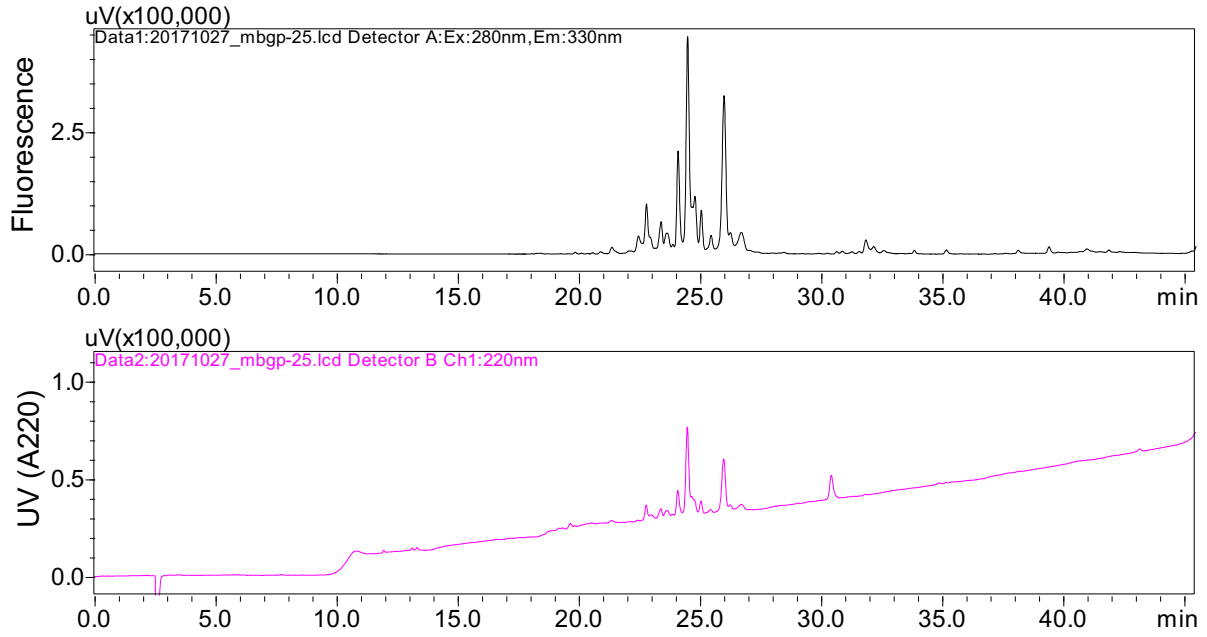
**GP1.17**



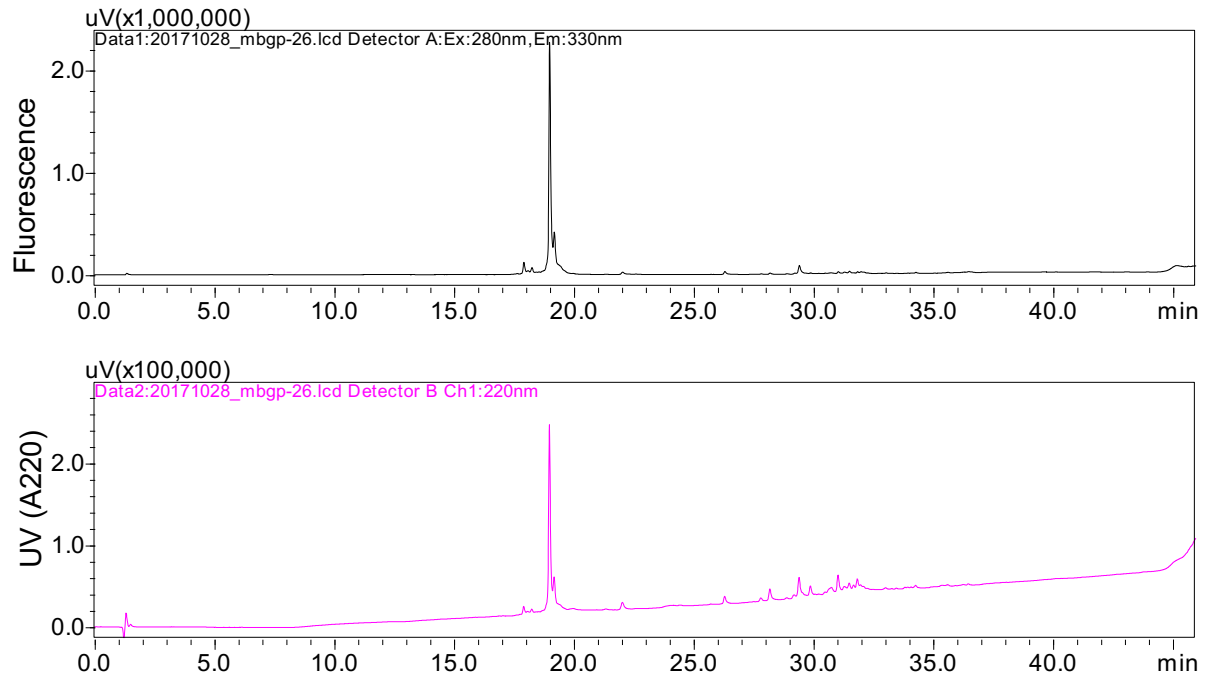
**GP1.18**



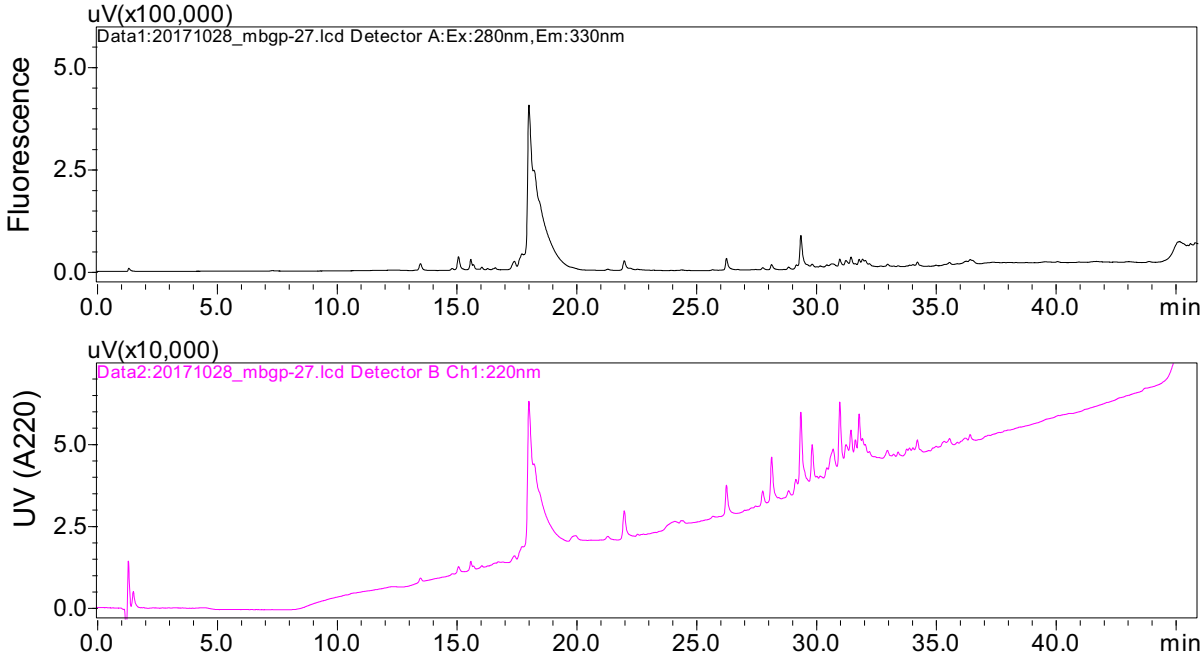
### GP1.19



### GP1.20



GP1.21



## GP2 Library HPLC Chromatography

### Method 2: Analytical

Note- For this series the peptides were first purified over SepPak C18 and then checked on analytical HPLC. The shoulder peak is for C-terminus -OMe/-OH transesterification due to the use of methanol (See Figure 3). The shoulder peak was isolated for most cases and checked using MALDI to confirm this observation. For our purposes, the difference in C-terminus group does not have dramatic effect and hence we consider the two species together for the purity. All compounds were confirmed to be >90% pure after isolation before use in other assays.

Instrument: Shimadzu Prominence HPLC with SPD-20AV UV-Vis detector (Detector B) and RF-20A Fluorescence detector (Detector A)

Solvent A: 0.1% trifluoroacetic acid with 95:5 water:acetonitrile.

Solvent B: 0.1% trifluoroacetic acid with 95:5 acetonitrile:water.

Column: Phenomenex Kinetex® 2.6 µm Polar C18 100Å 150 x 4.6 mm

Column Temperature: 40 °C

Flow rate: 1 ml/min

Total run time: 35 min

UV-Vis Detector: 220 nm

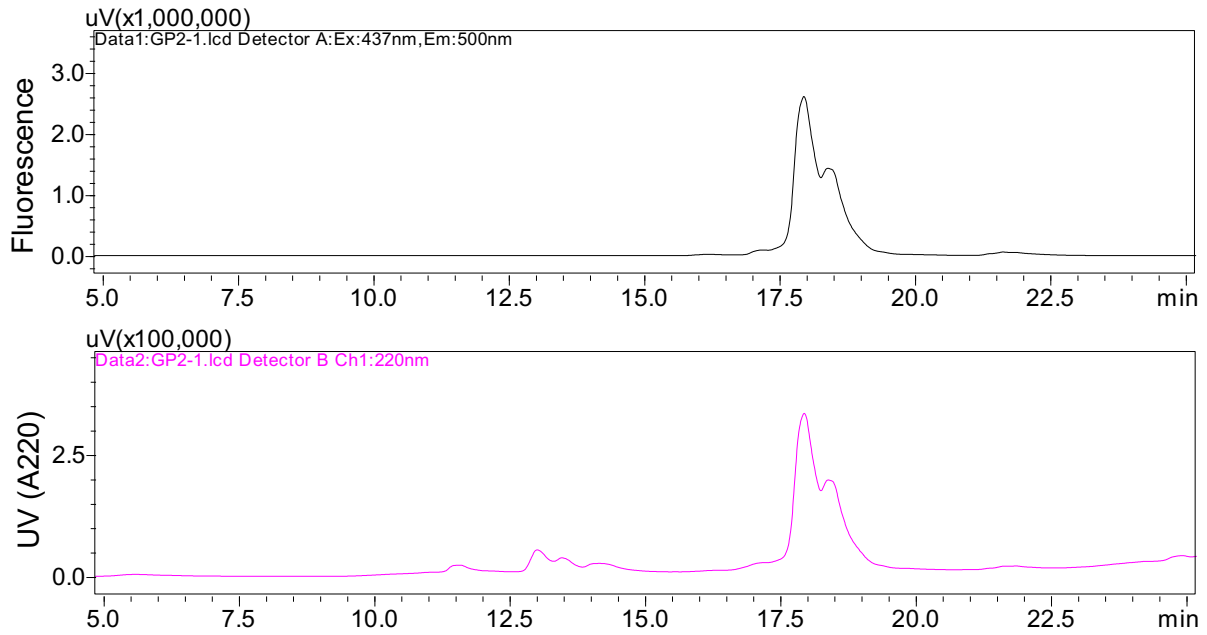
Fluorescence: Ex: 437 nm Em: 500 nm (Fluorescein at low pH)

Method: A 5µL sample of the stock glycopeptide (100 – 440 µM) obtained after SepPak C18, was dissolved in 45 µl of solvent A. 40 µl of this was injected onto the column. A 35 minute gradient was, in which the gradient gradually went from 0%-50% B over the first 20 minutes, followed by a wash cycle consisting of a sharp increase to 95% and back down (See details below). Fractions were collected with a vial volume set at 1 ml based on a slope of 1000 µV/sec and level of 20000 µV. Fractions were analyzed by MALDI-MS for target mass.

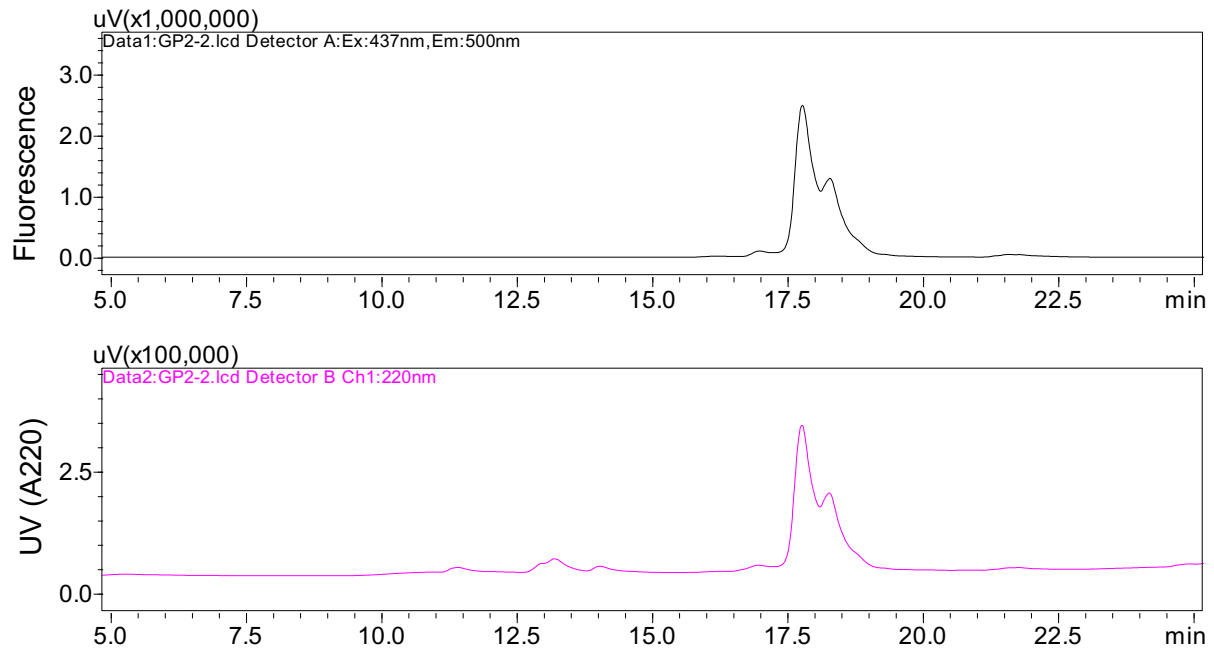
#### Gradient Details:

	Time	Module	Command	Value
1	0.01	Pumps	Total Pump A Flow	1
2	0.02	RF-20A(DET.A)	Zero	
3	0.02	SPD-20AV(DET.B)	Zero	
4	0.03	Pumps	Solvent B Conc.	0
5	3.00	Pumps	Solvent B Conc.	0
6	20.00	Pumps	Solvent B Conc.	50
7	22.00	Pumps	Solvent B Conc.	95
8	28.00	Pumps	Solvent B Conc.	95
9	29.00	Pumps	Solvent B Conc.	0
10	35.00	Controller	Stop	

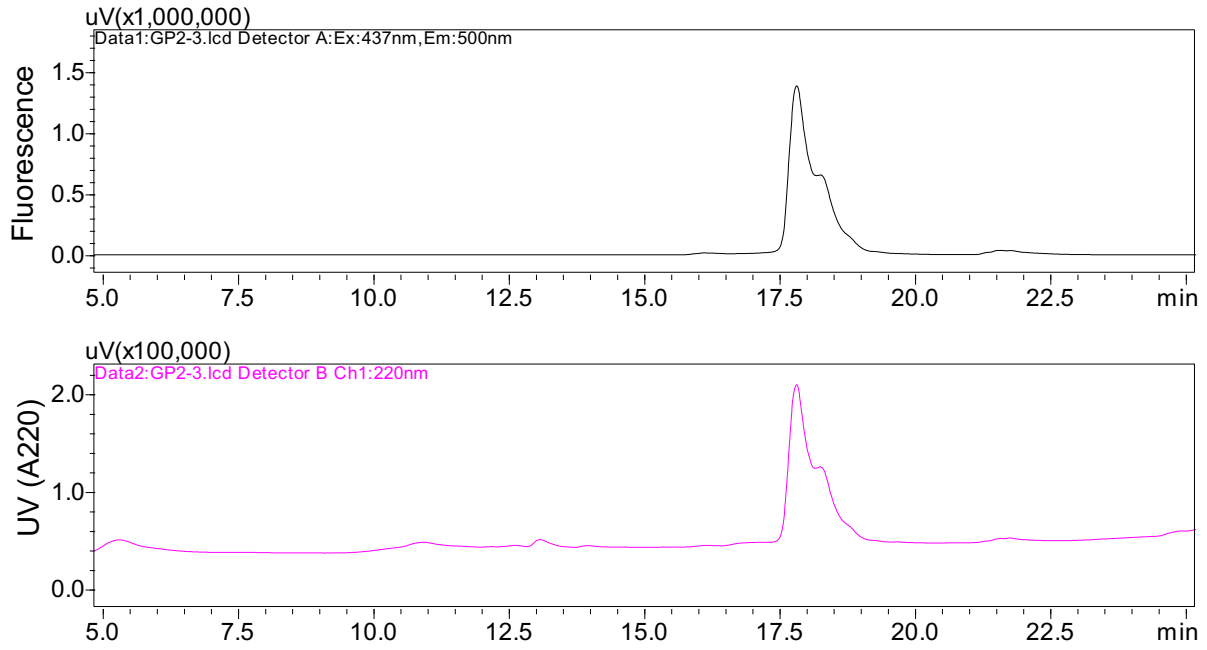
## GP2.1



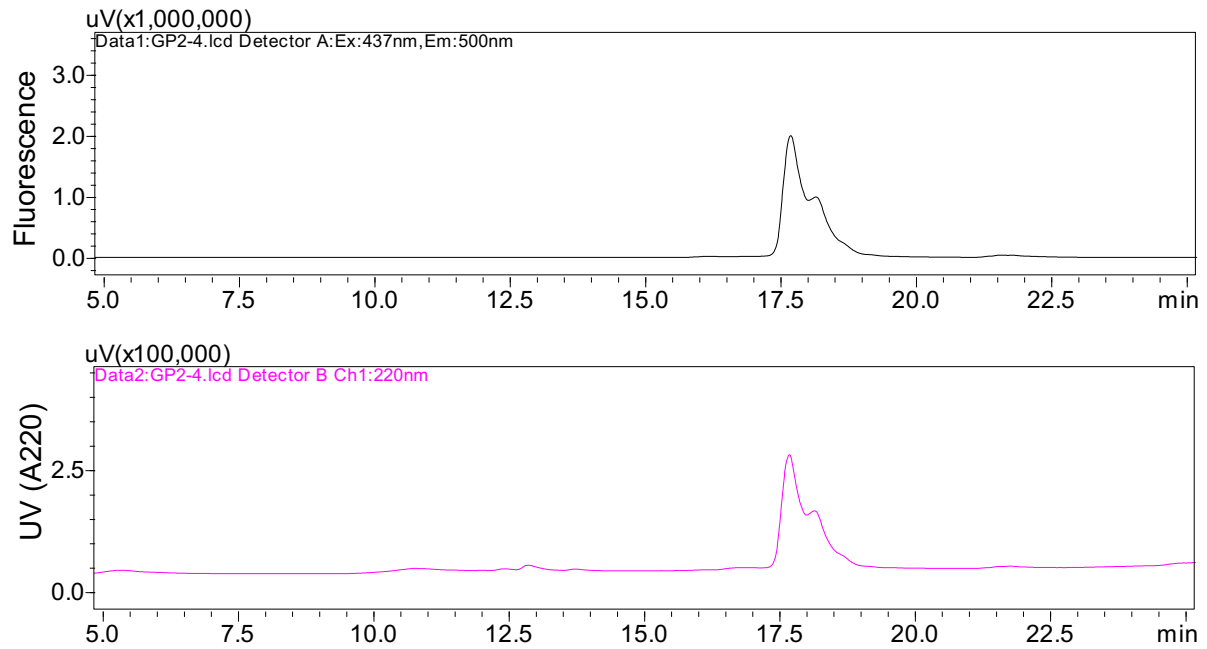
## GP2.2



### GP2.3

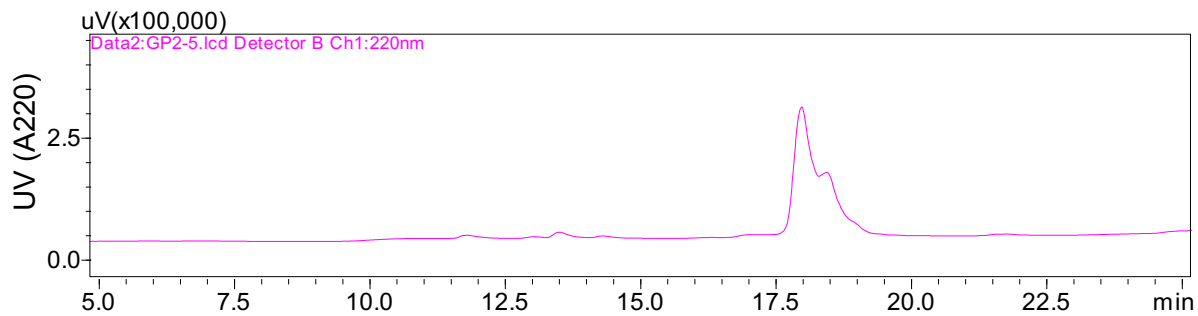
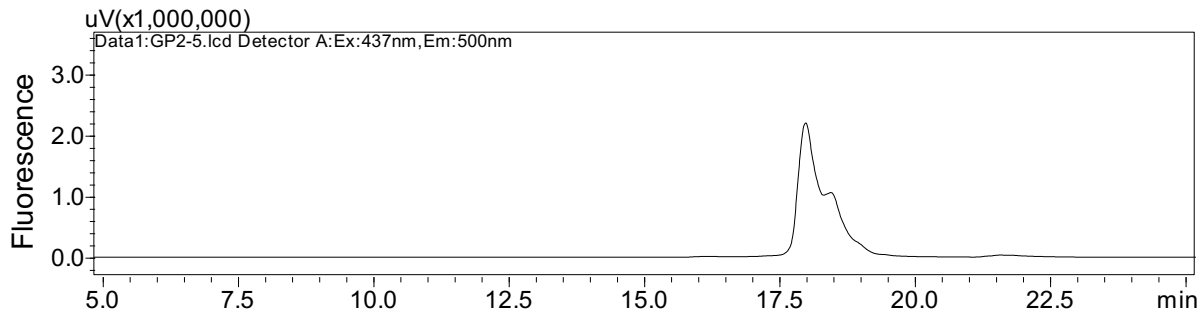


### GP2.4

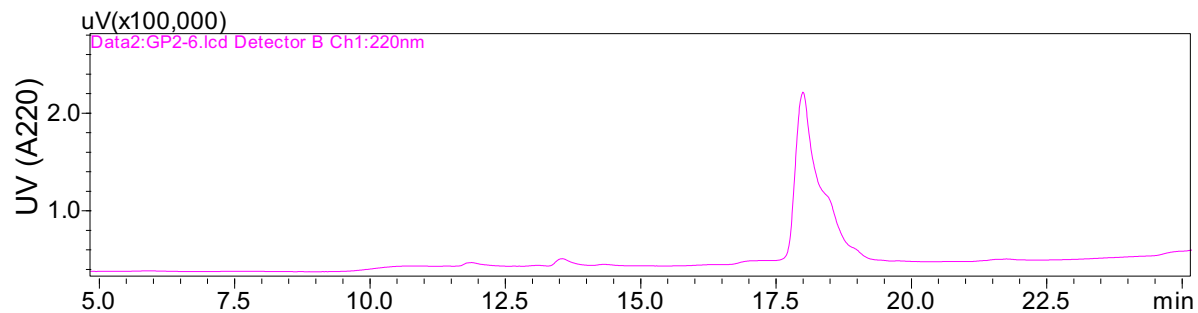
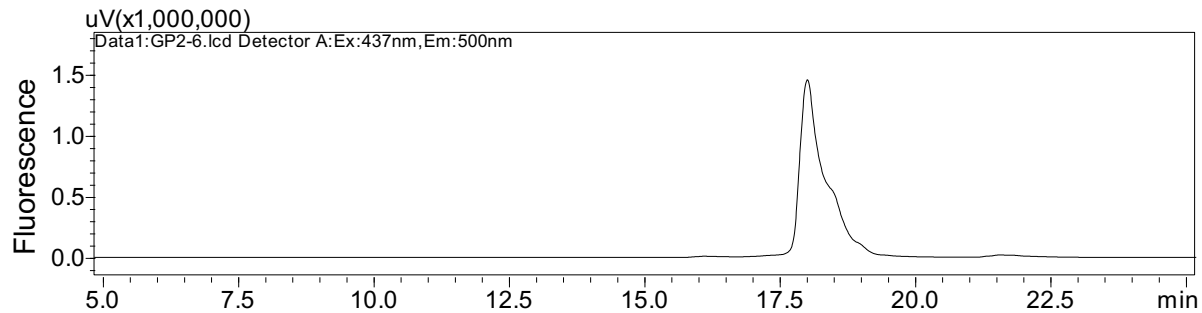




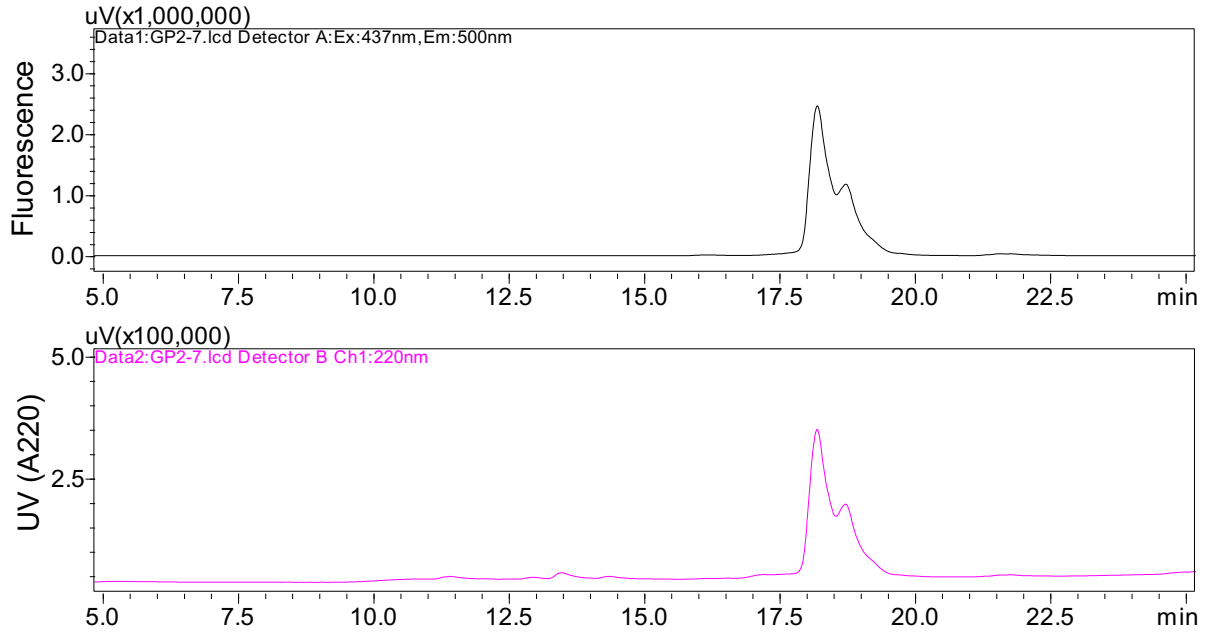
## GP2.5



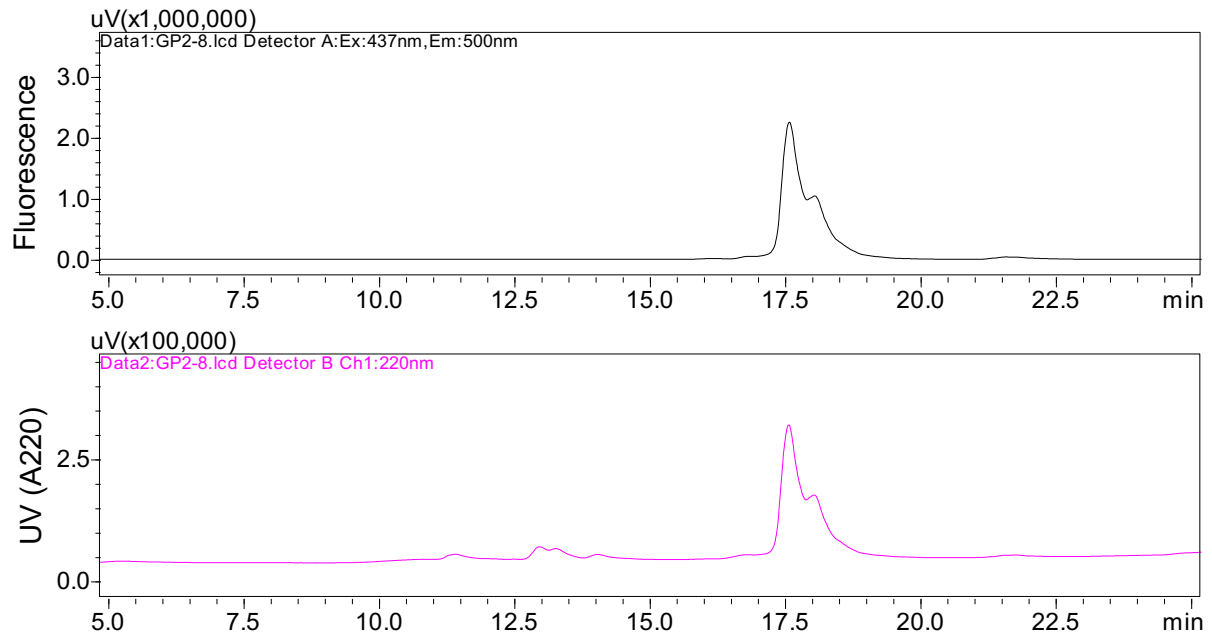
## GP2.6



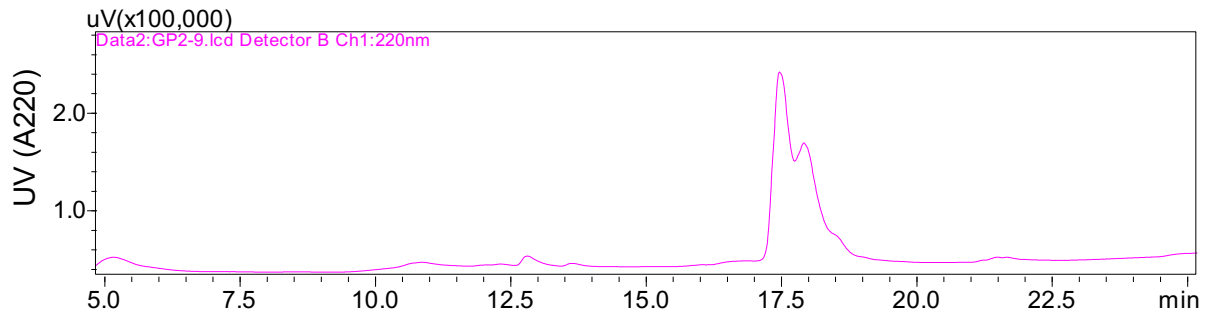
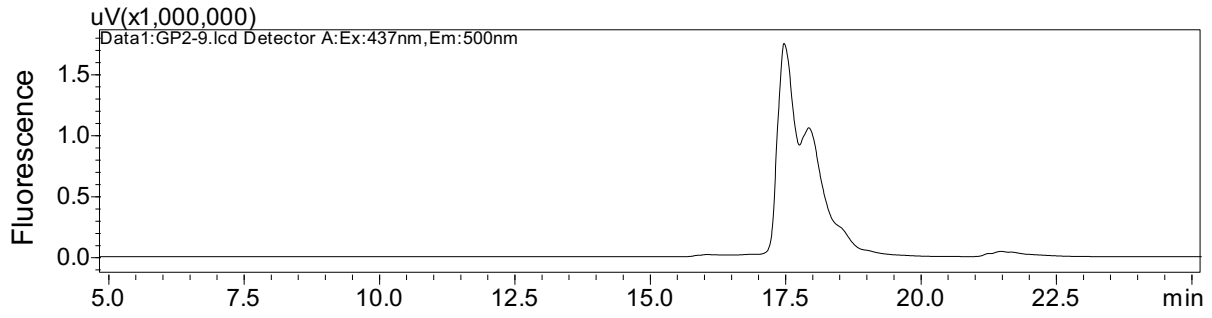
### GP2.7



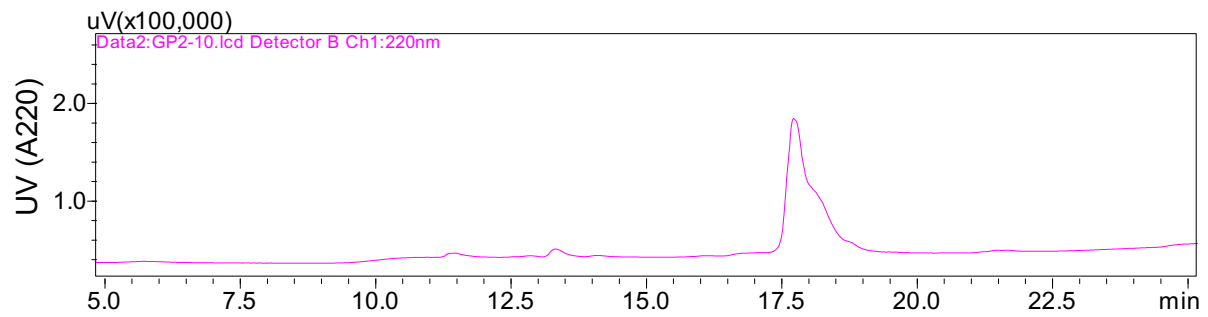
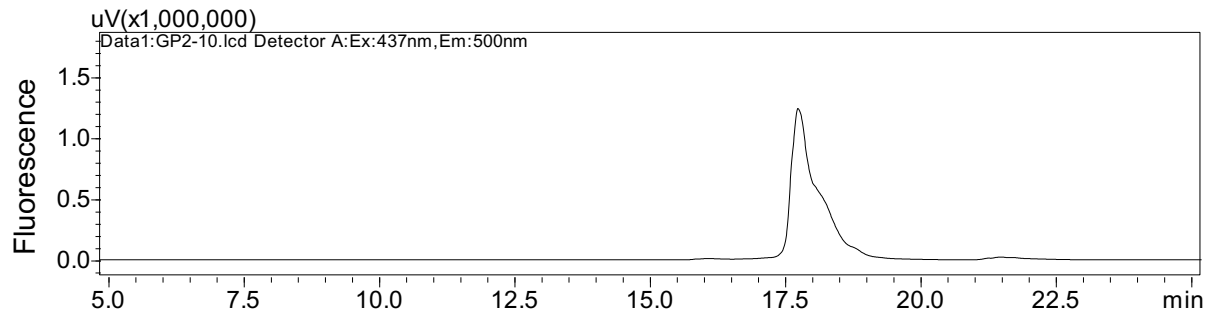
### GP2.8



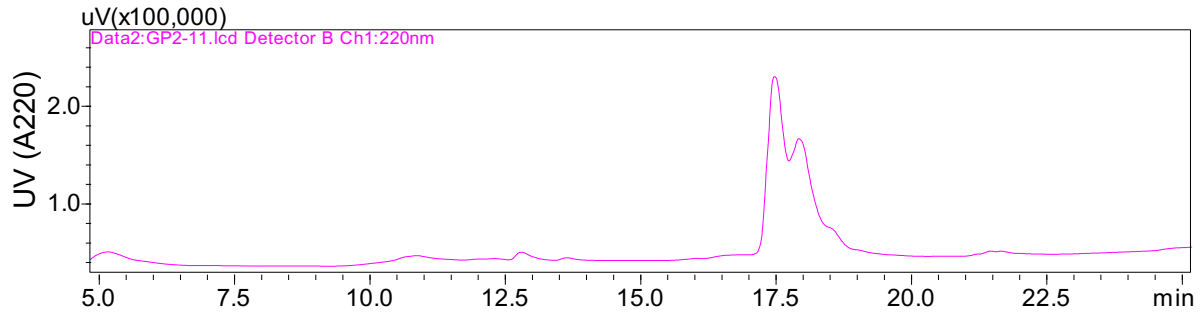
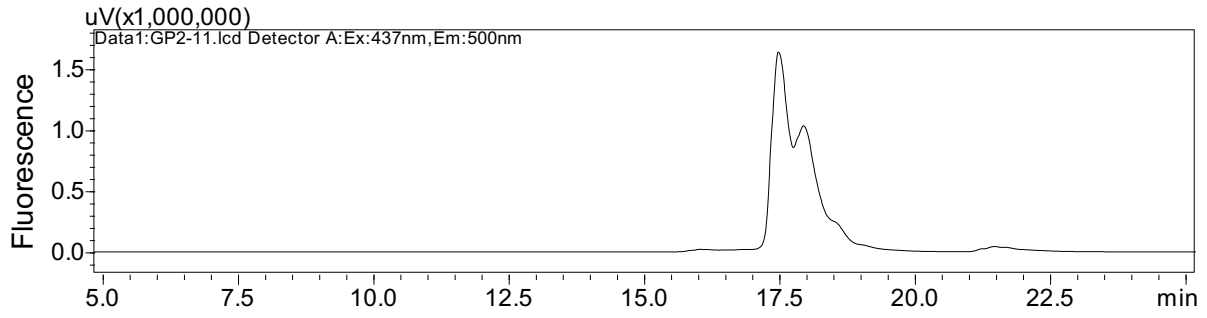
### GP2.9



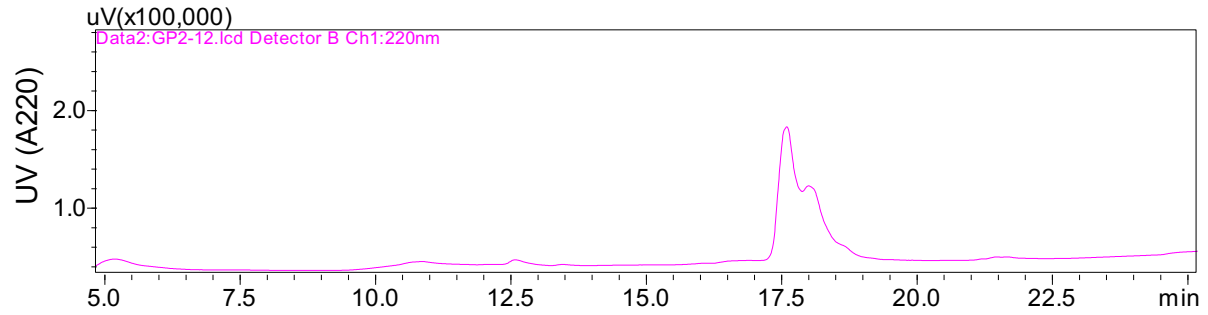
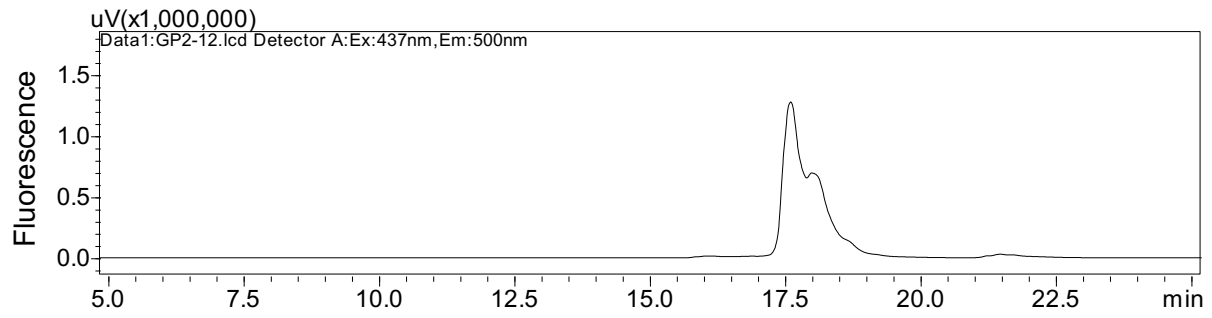
### GP2.10



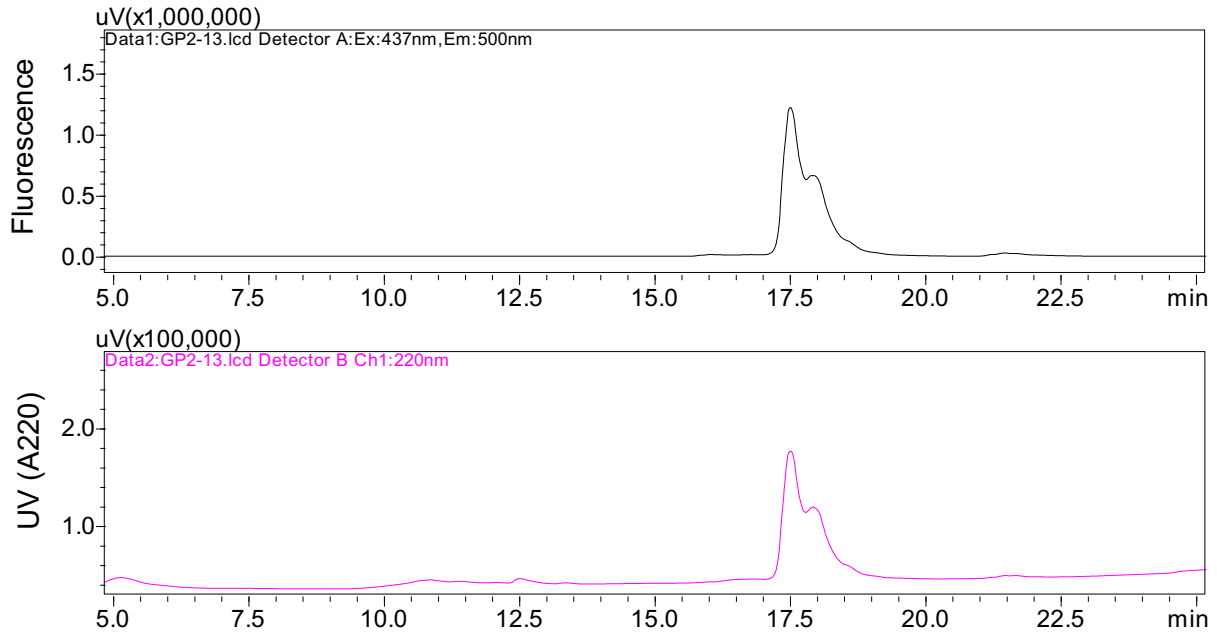
### GP2.11



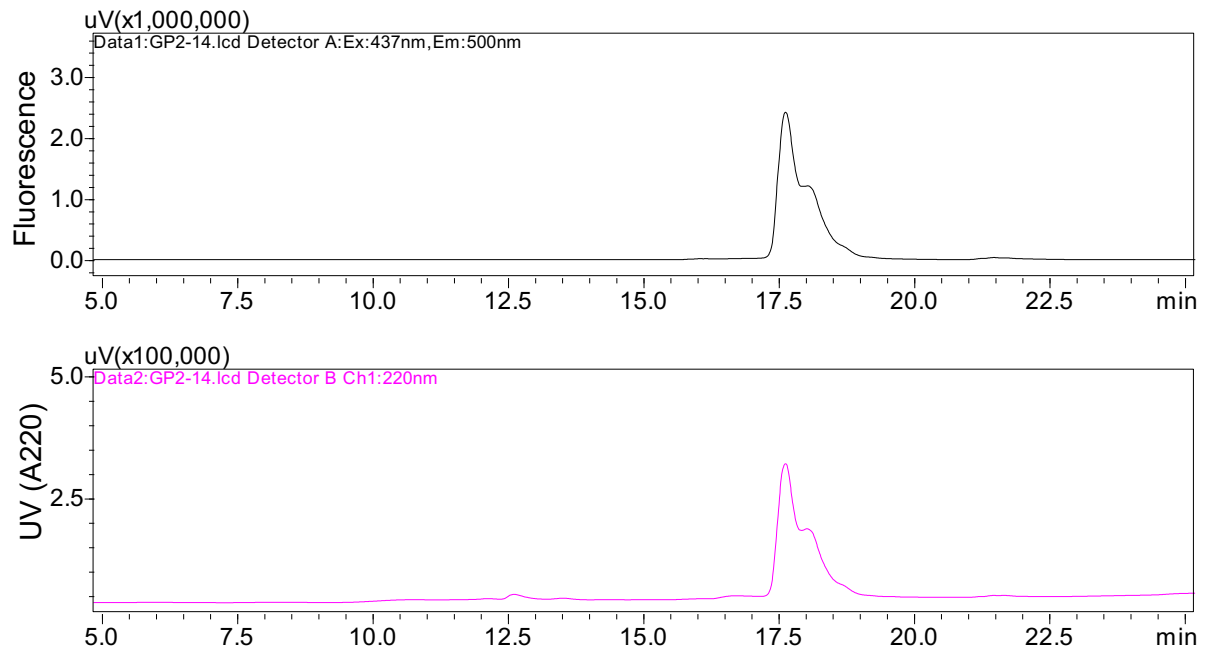
### GP2.12



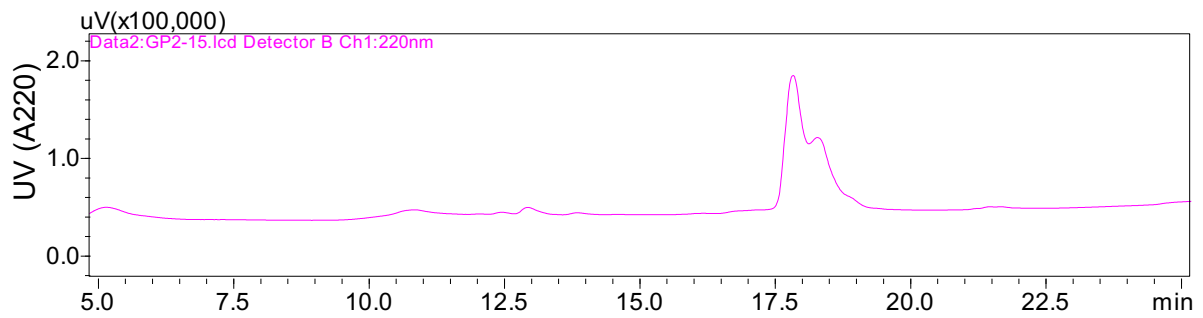
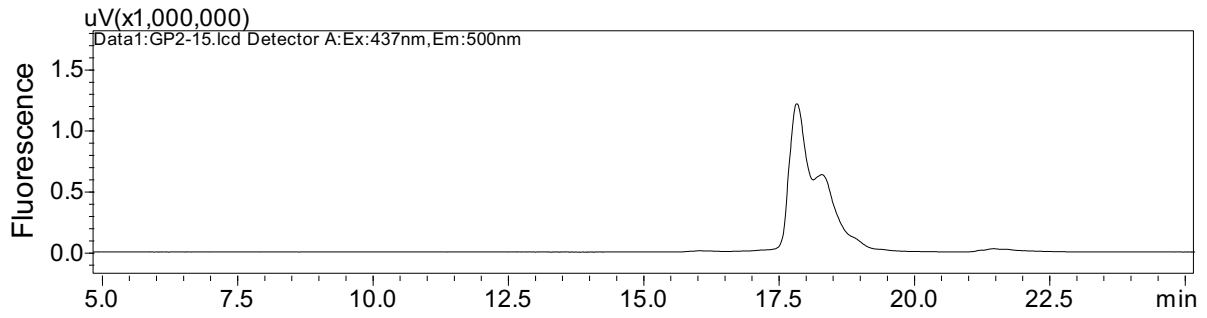
### GP2.13



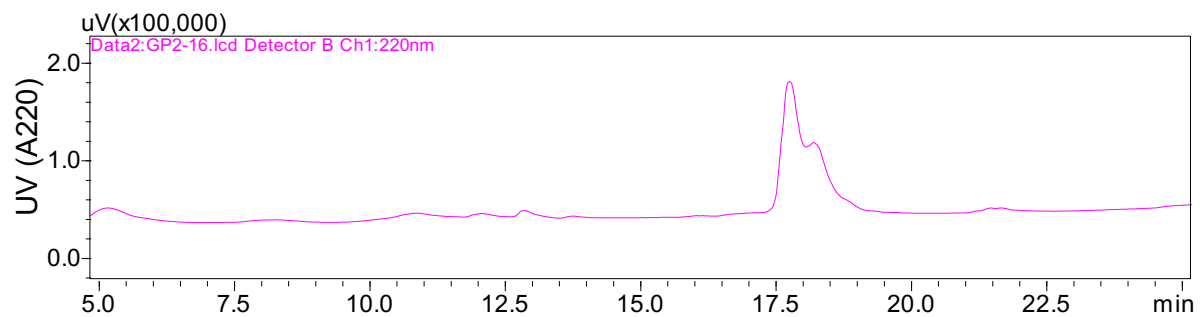
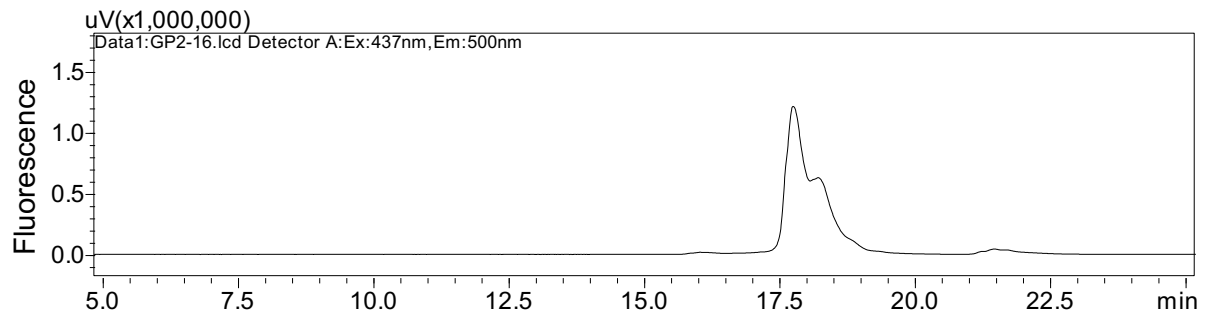
### GP2.14



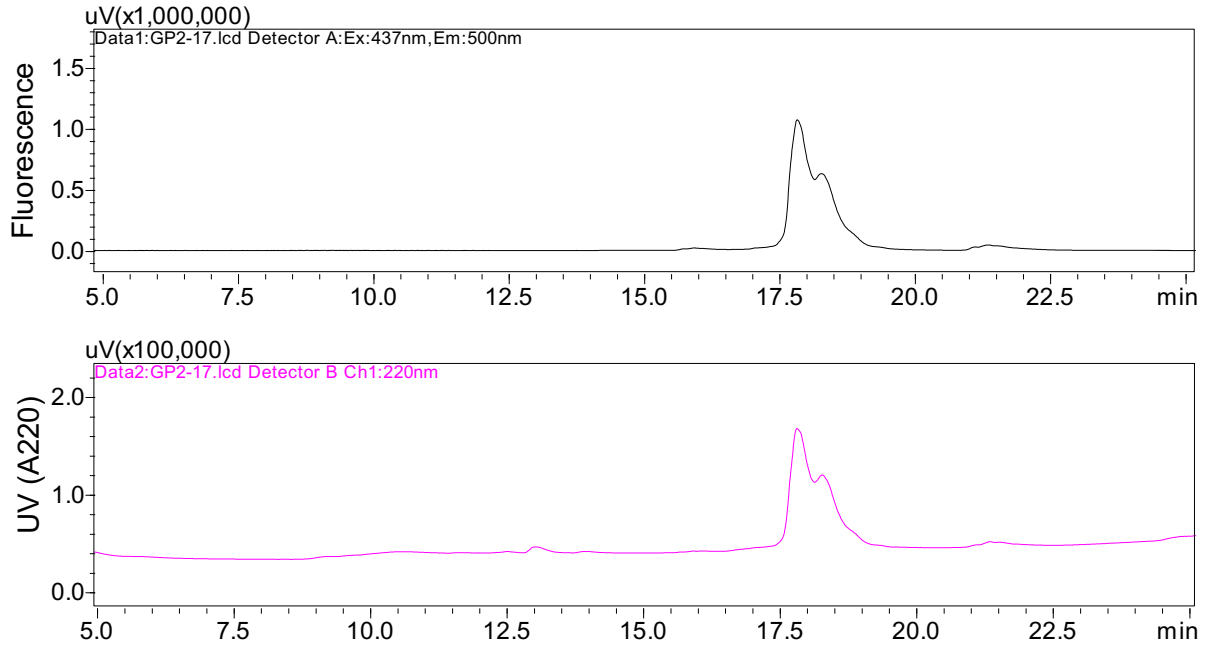
### GP2.15



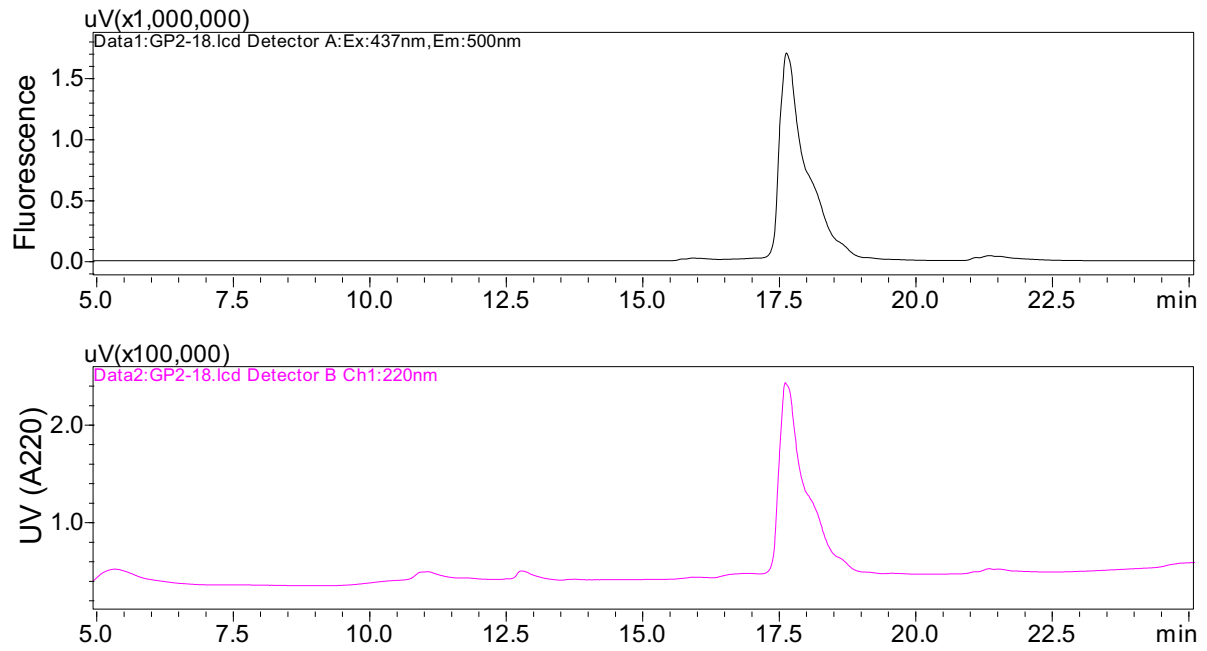
### GP2.16



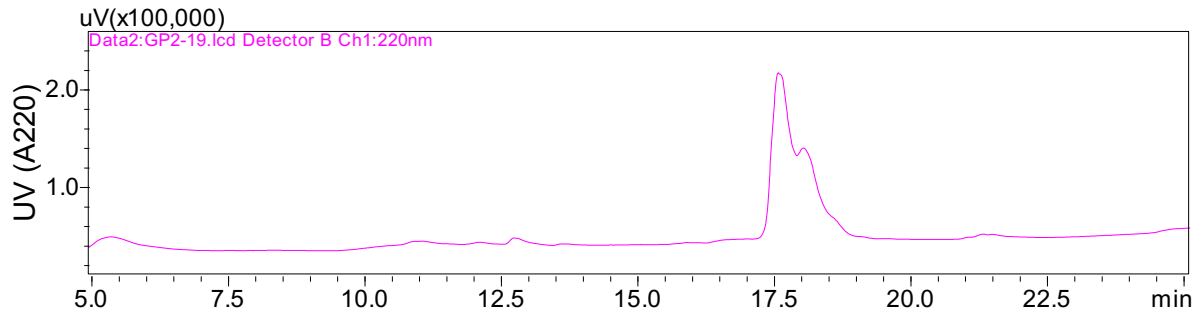
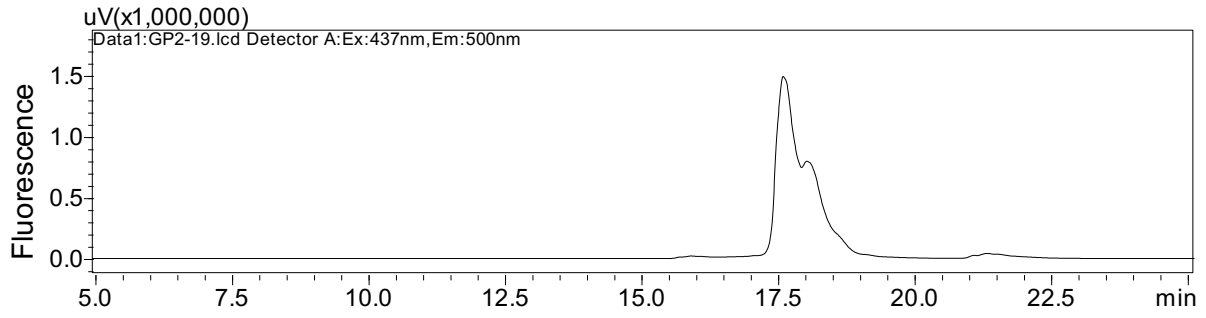
### GP2.17



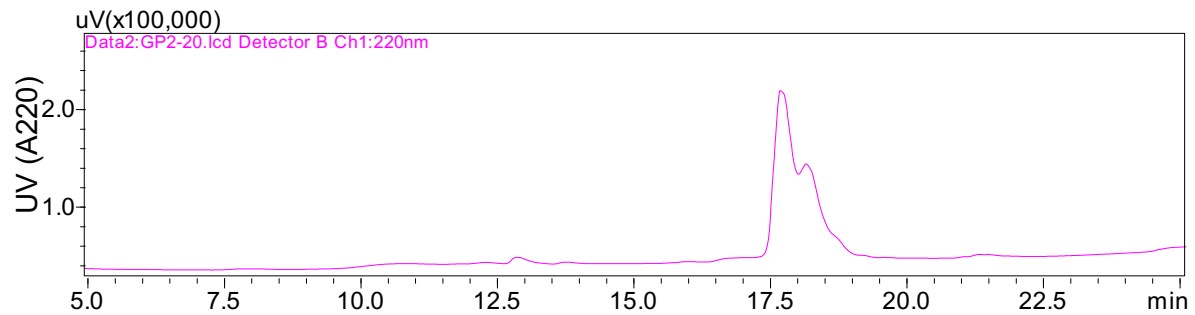
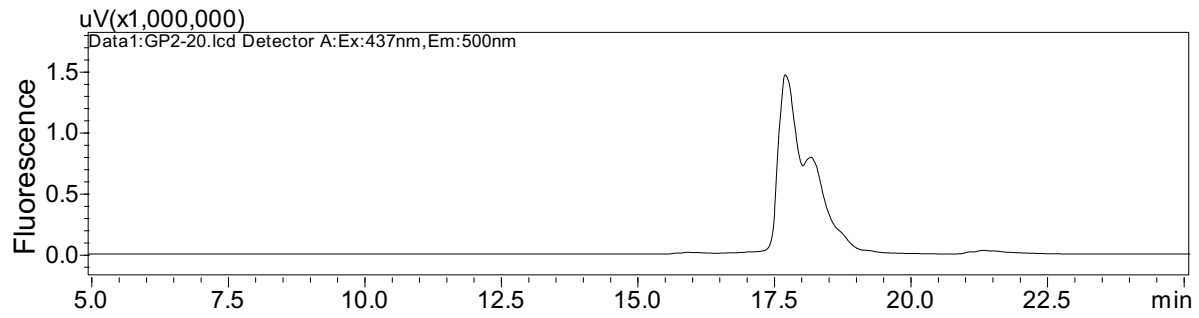
### GP2.18



### GP2.19

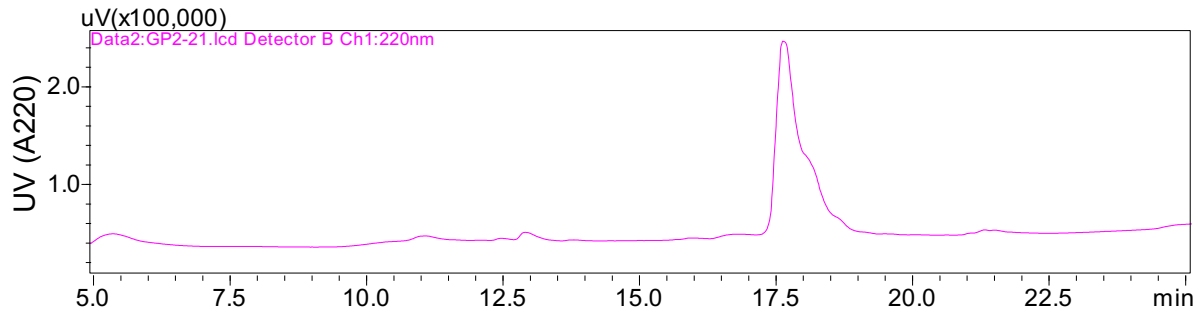
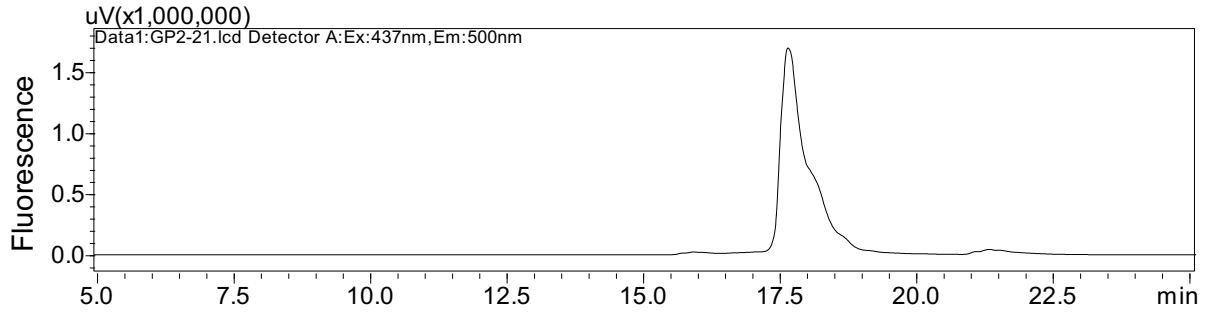


### GP2.20

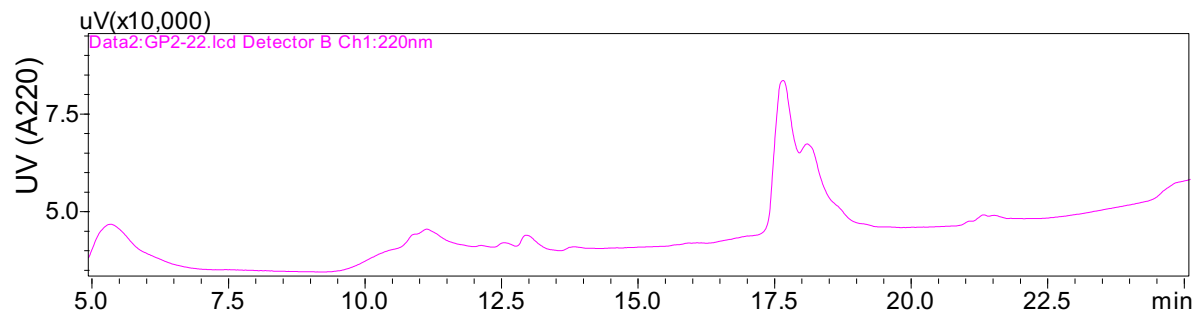
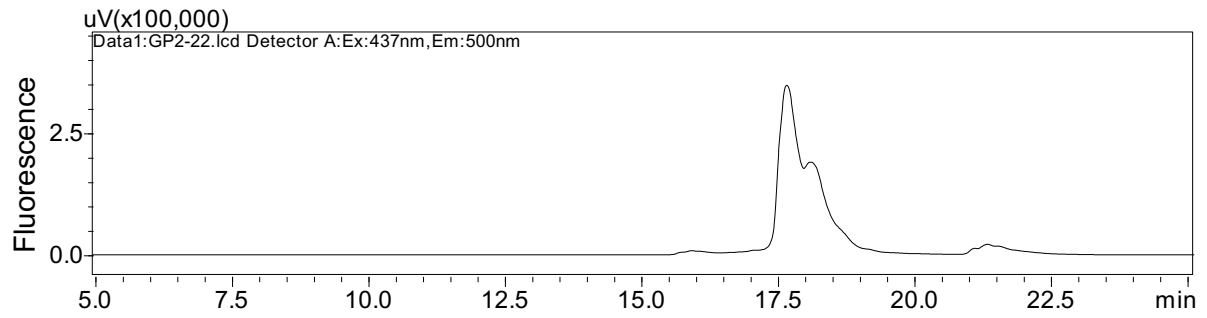




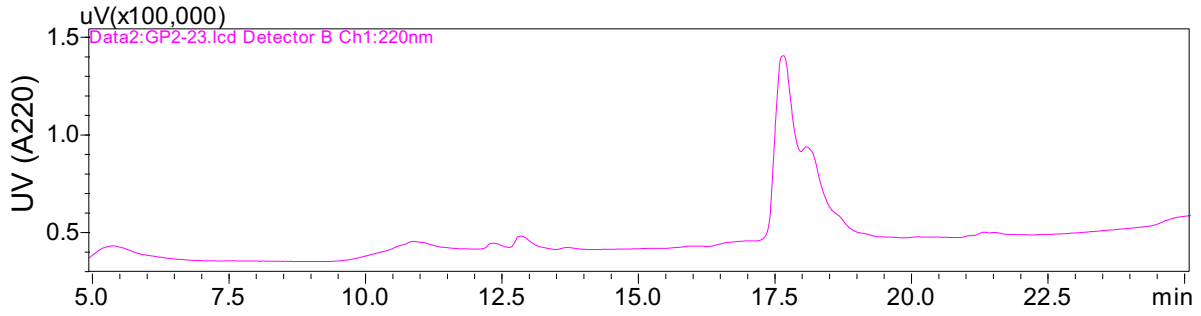
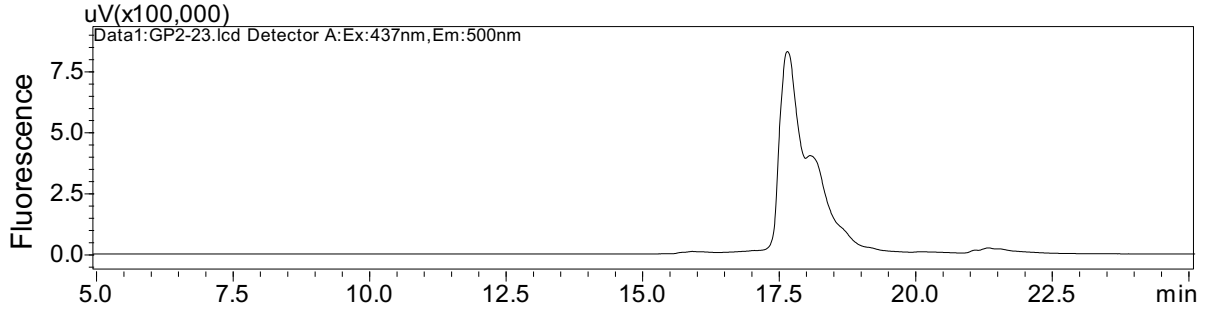
### GP2.21



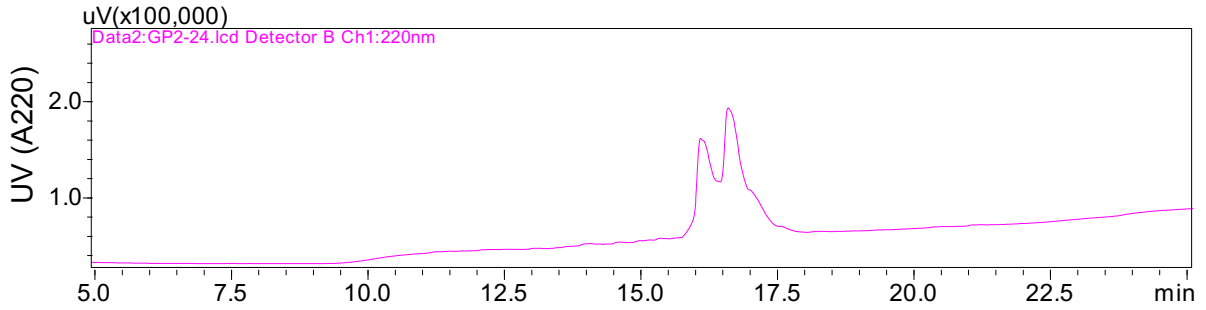
### GP2.22



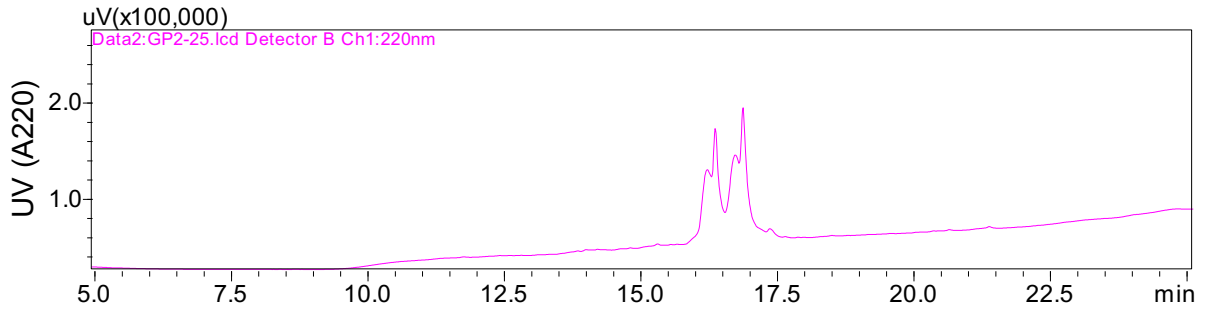
**GP2.23**



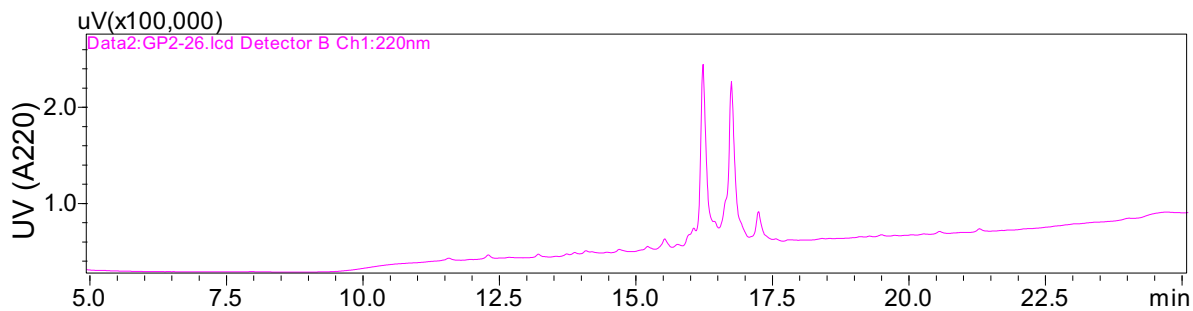
**GP2.24 (no fluorophore)**



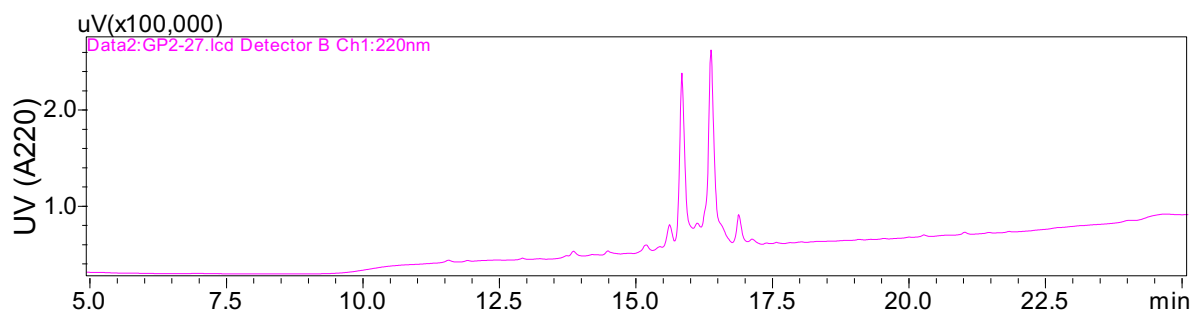
**GP2.25 (no fluorophore)**



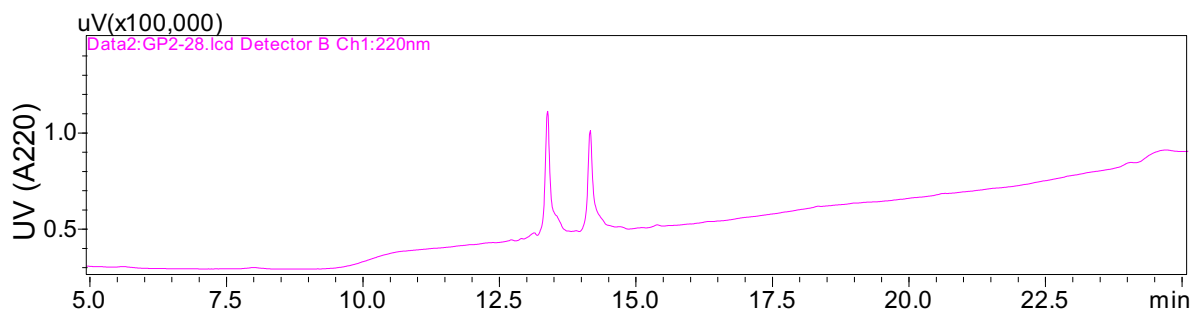
**GP2.26 (no fluorophore)**



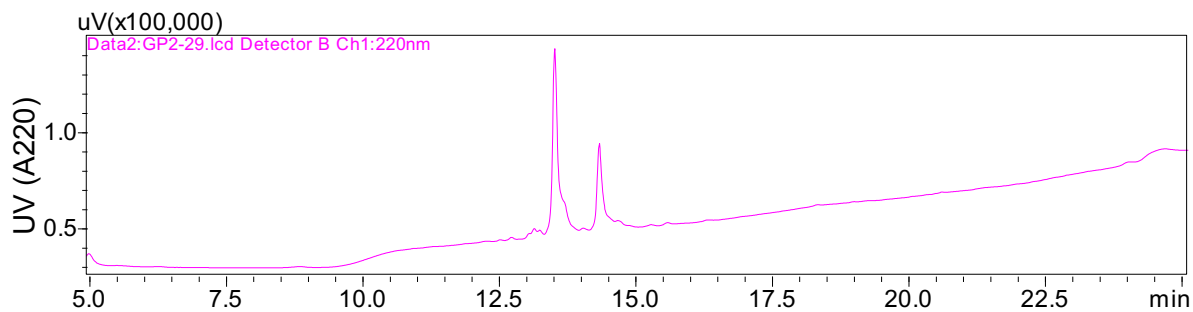
**GP2.27 (no fluorophore)**



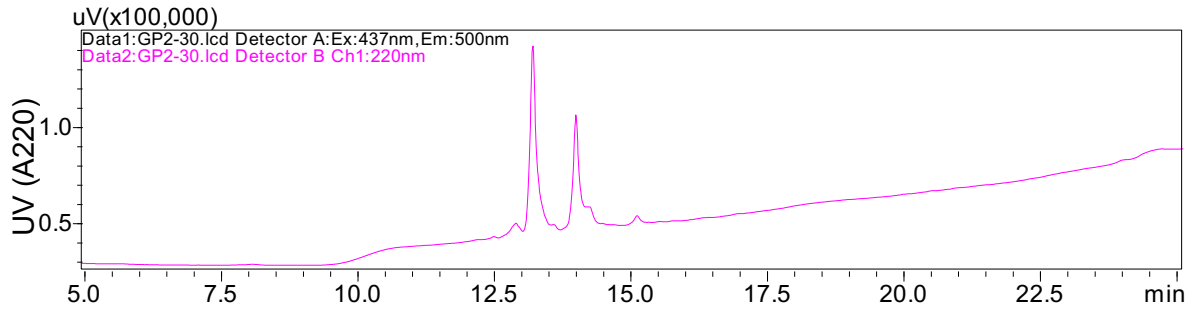
**GP2.28 (no fluorophore)**



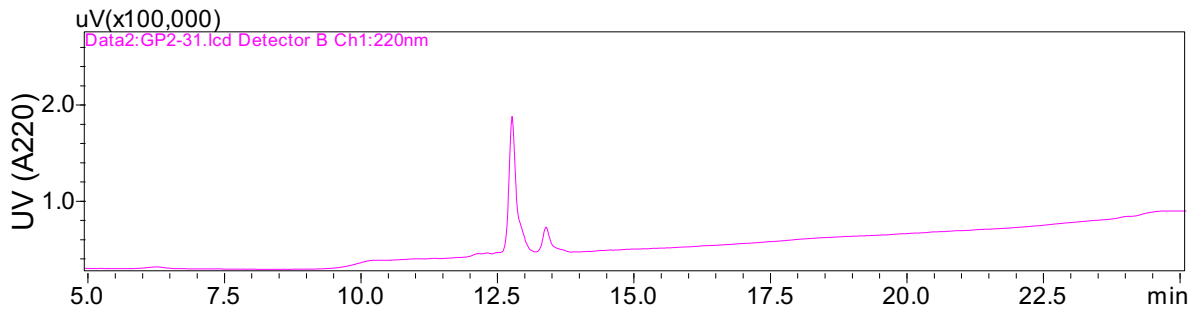
**GP2.29 (no fluorophore)**



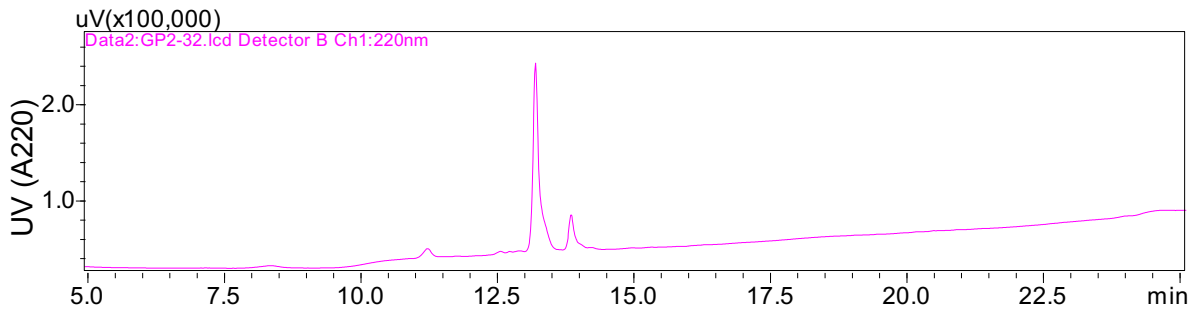
**GP2.30 (no fluorophore)**



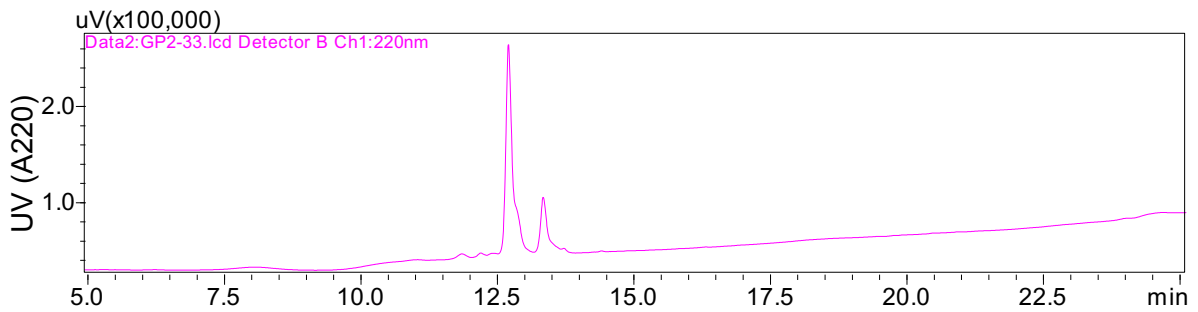
**GP2.31 (no fluorophore)**



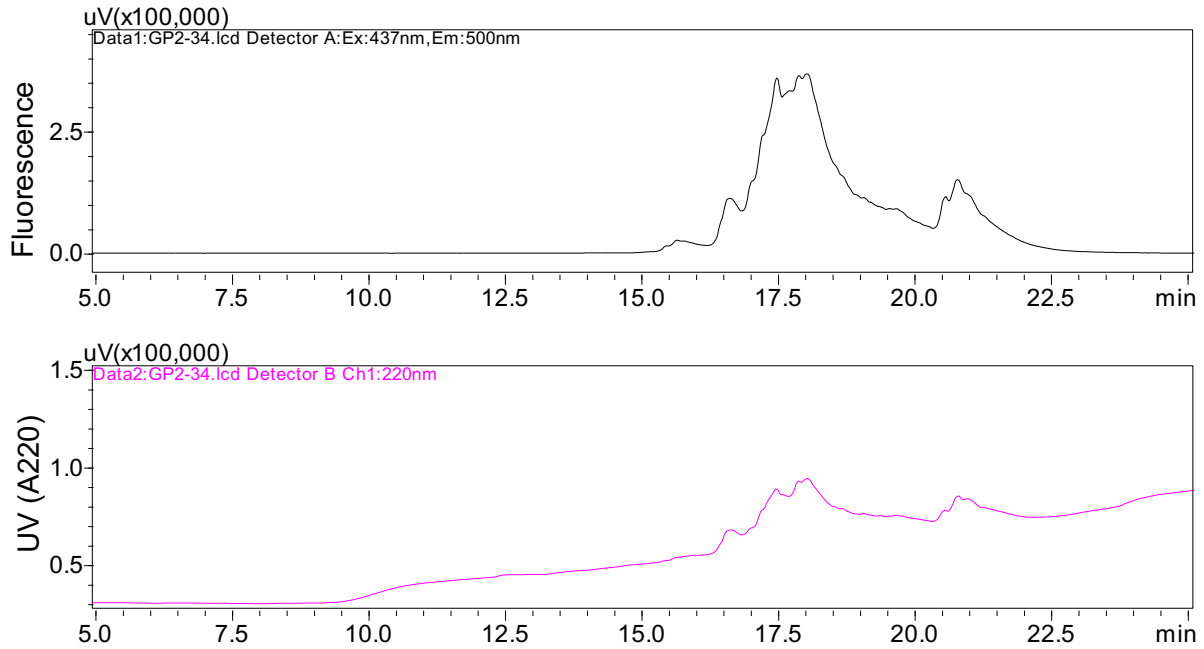
**GP2.32 (no fluorophore)**



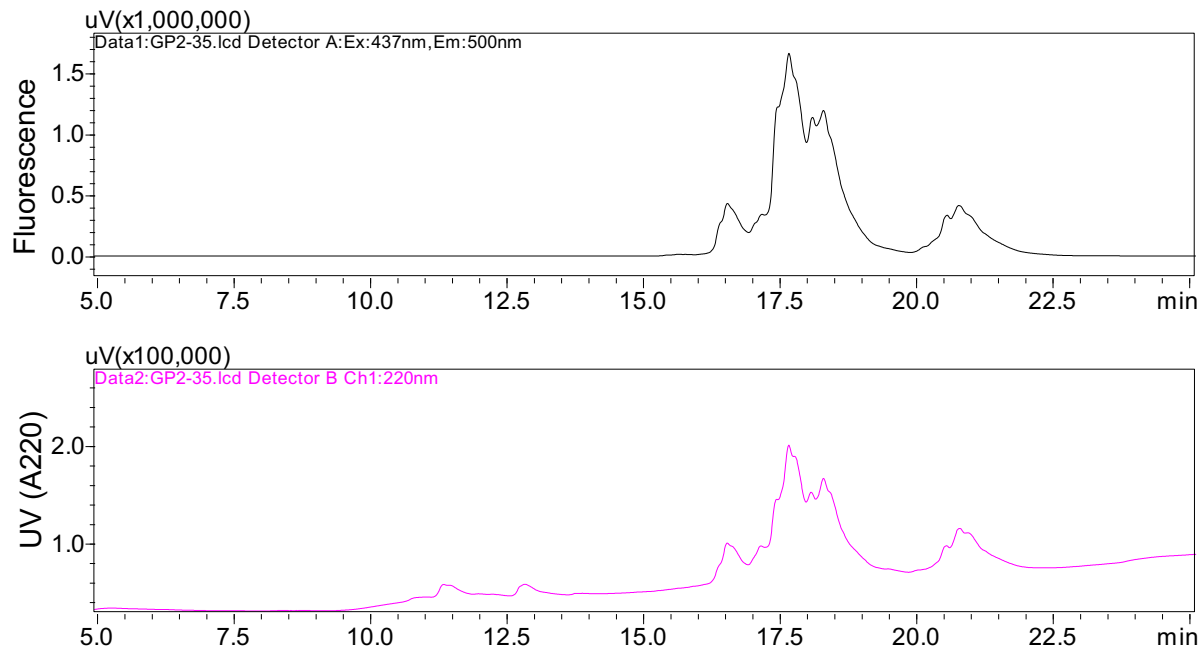
**GP2.33 (no fluorophore)**



### GP2.34\*

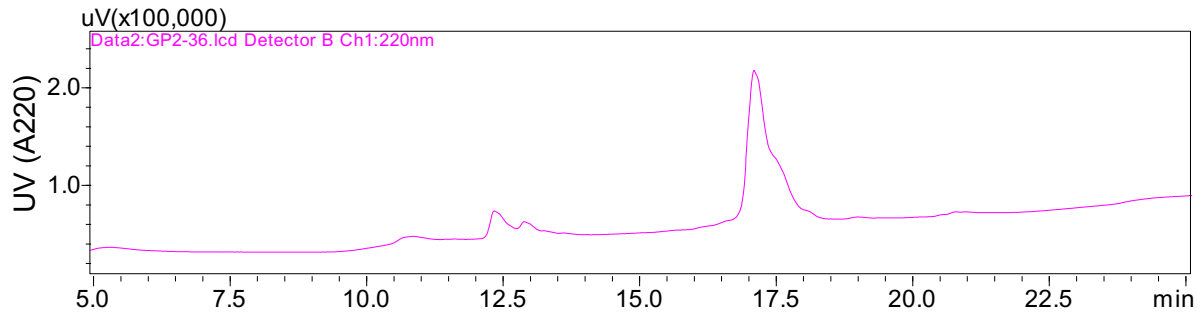
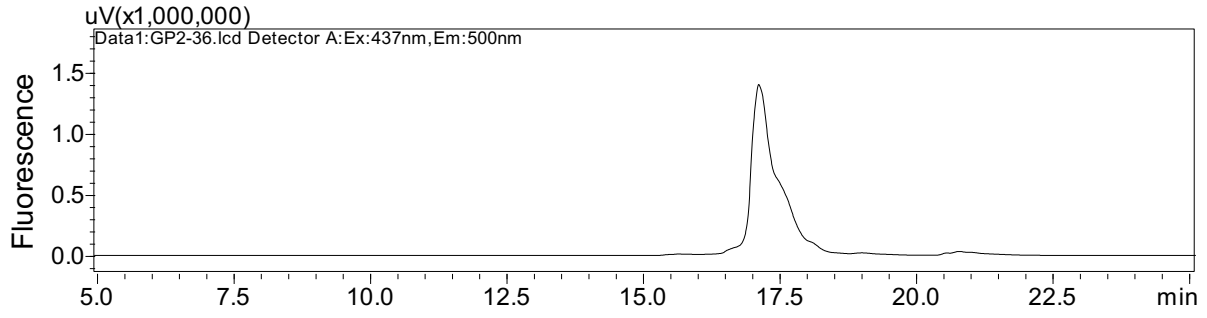


### GP2.35\*

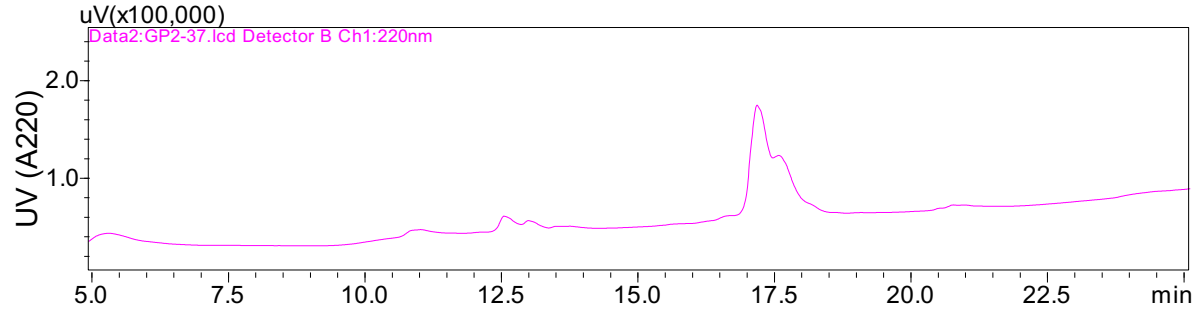
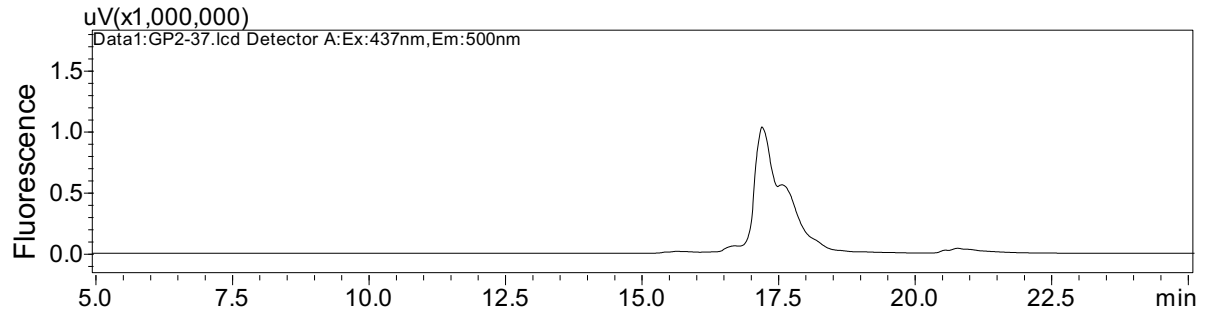


\* **Note-** For GP2.34 and GP2.35 we noticed some acetylation side reaction as the spots were still on the membrane during the N-capping step. Since the side-chains are protected during this stage, the acetylation most-likely occurs on the hydroxyl groups of the fluorescein. As a result, the mixture is a bit more complex with acetylated, -COOH and -COOMe terminal peptides causing broader peaks.

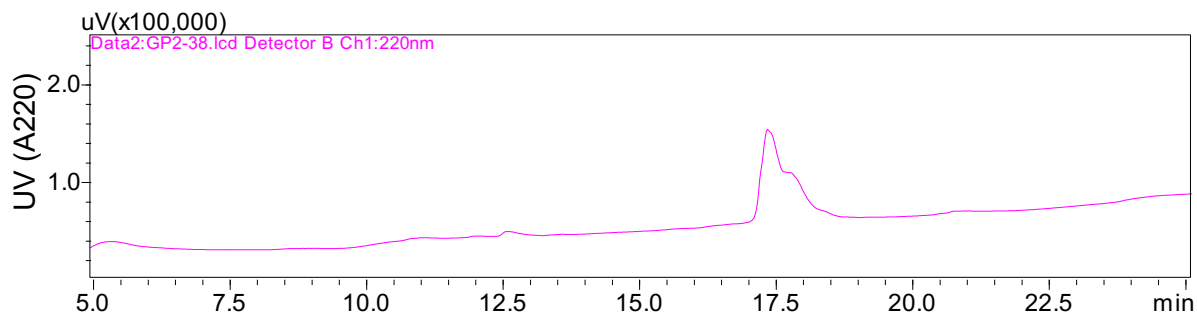
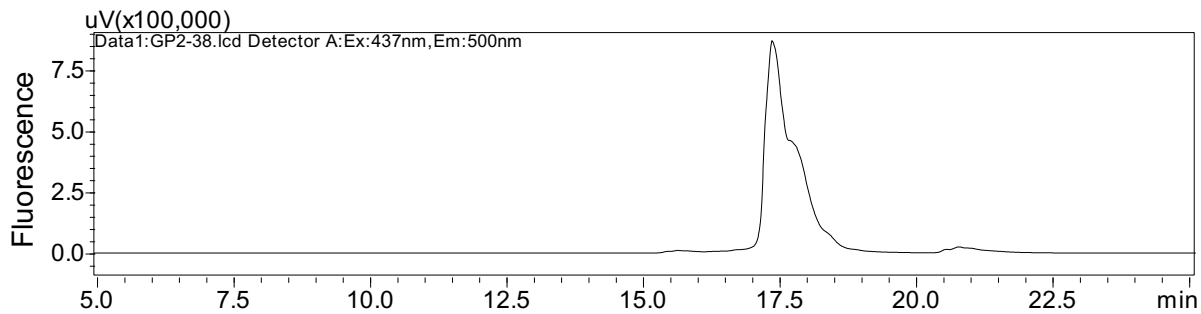
### GP2.36



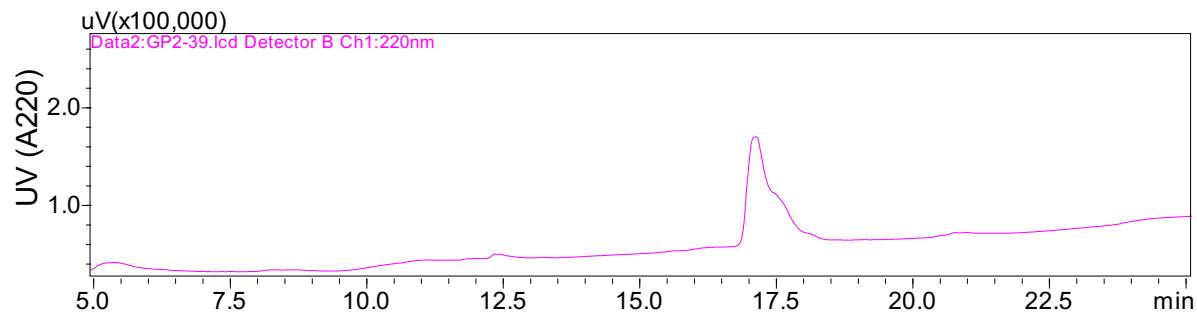
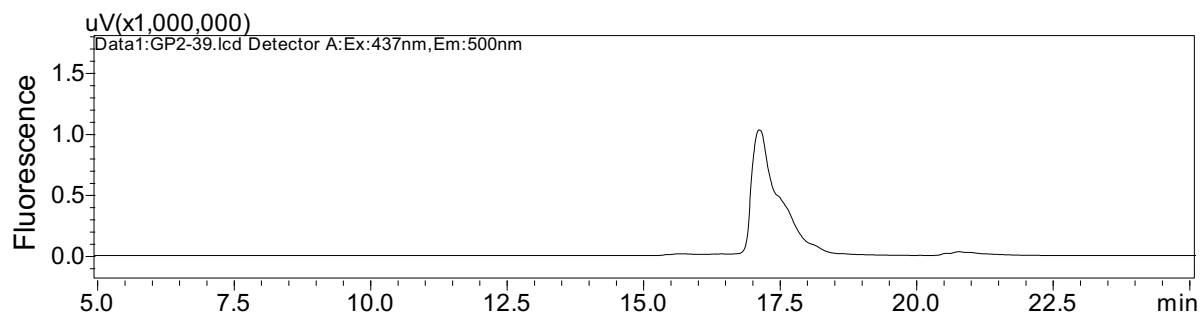
### GP2.37



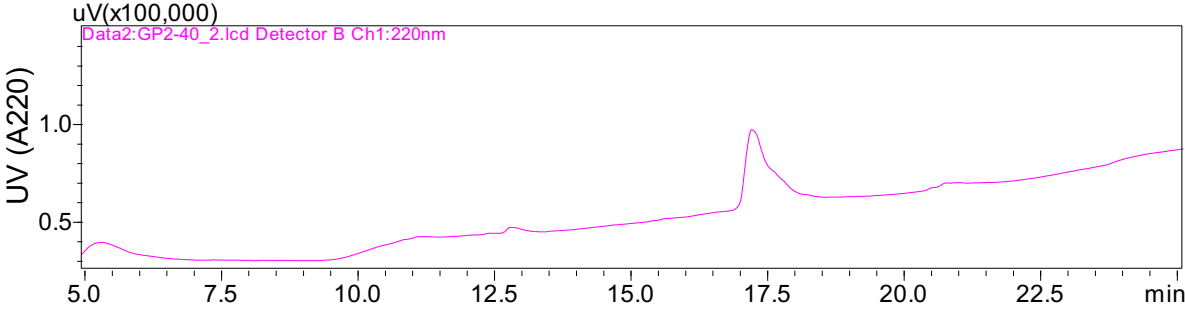
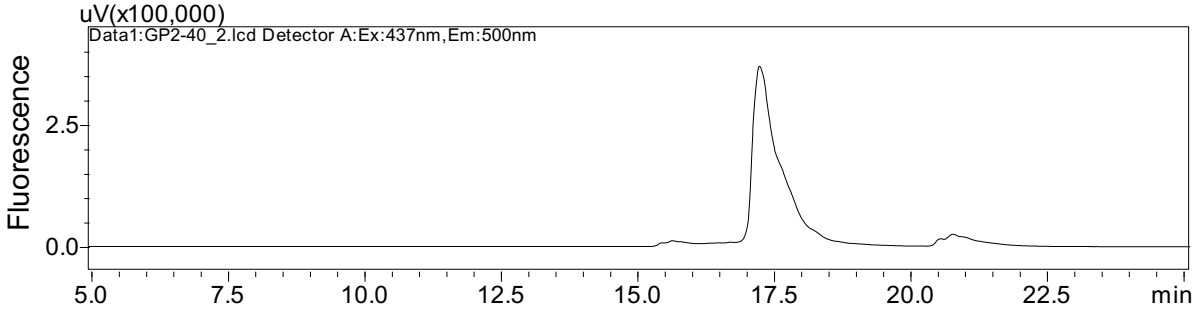
### GP2.38



### GP2.39



**GP2.40**



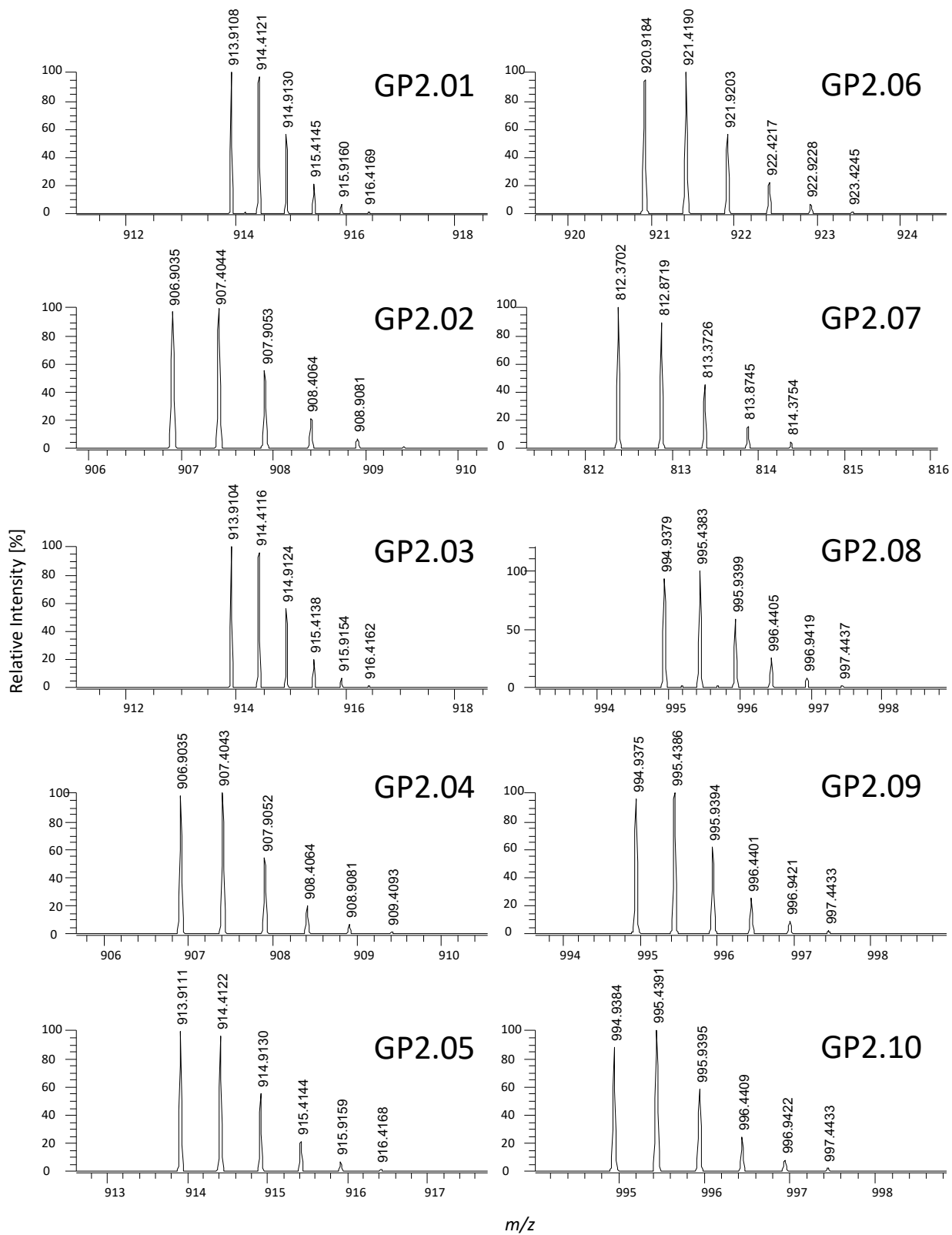


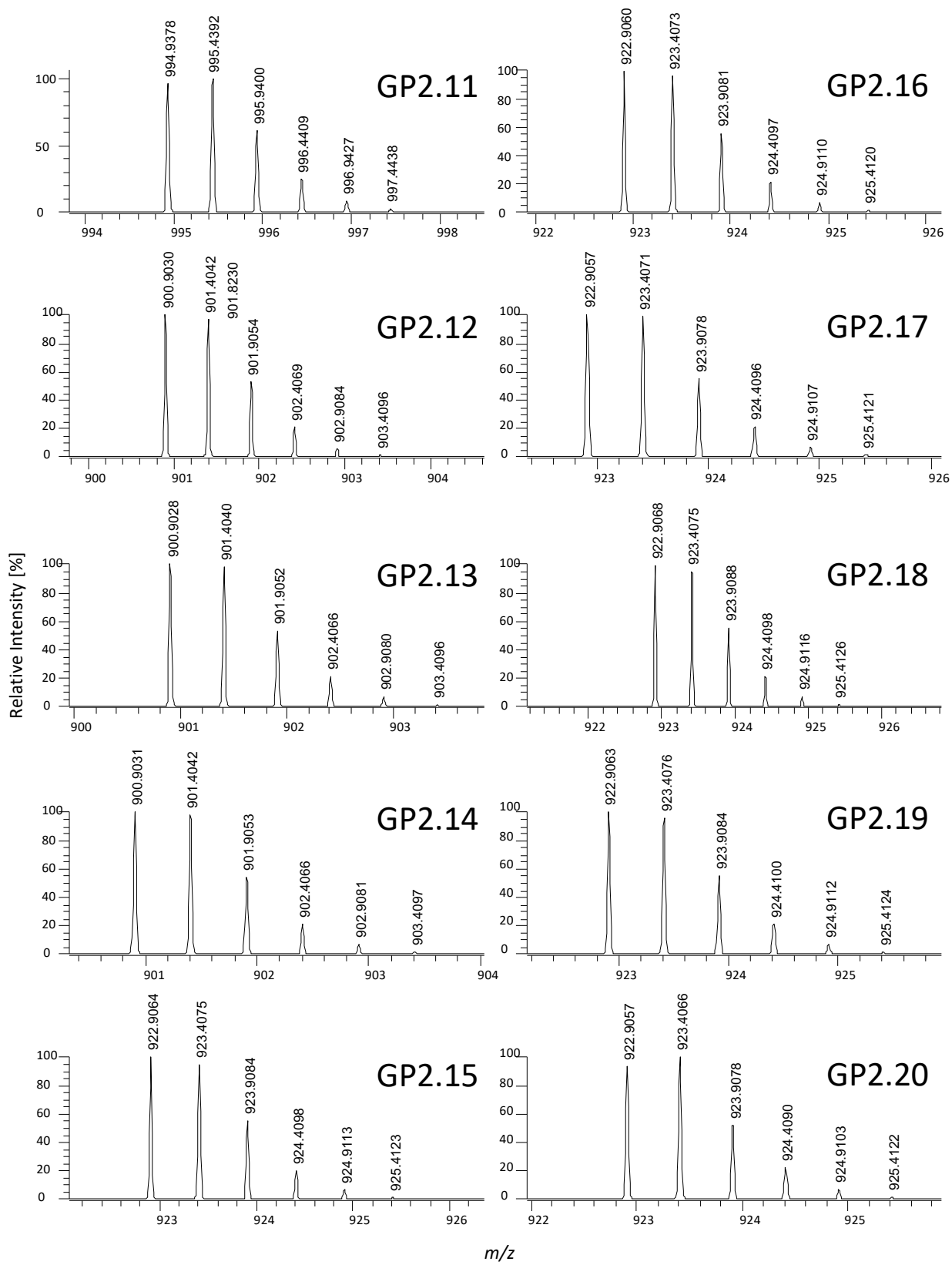
## Orbitrap Characterization of GP2 Library

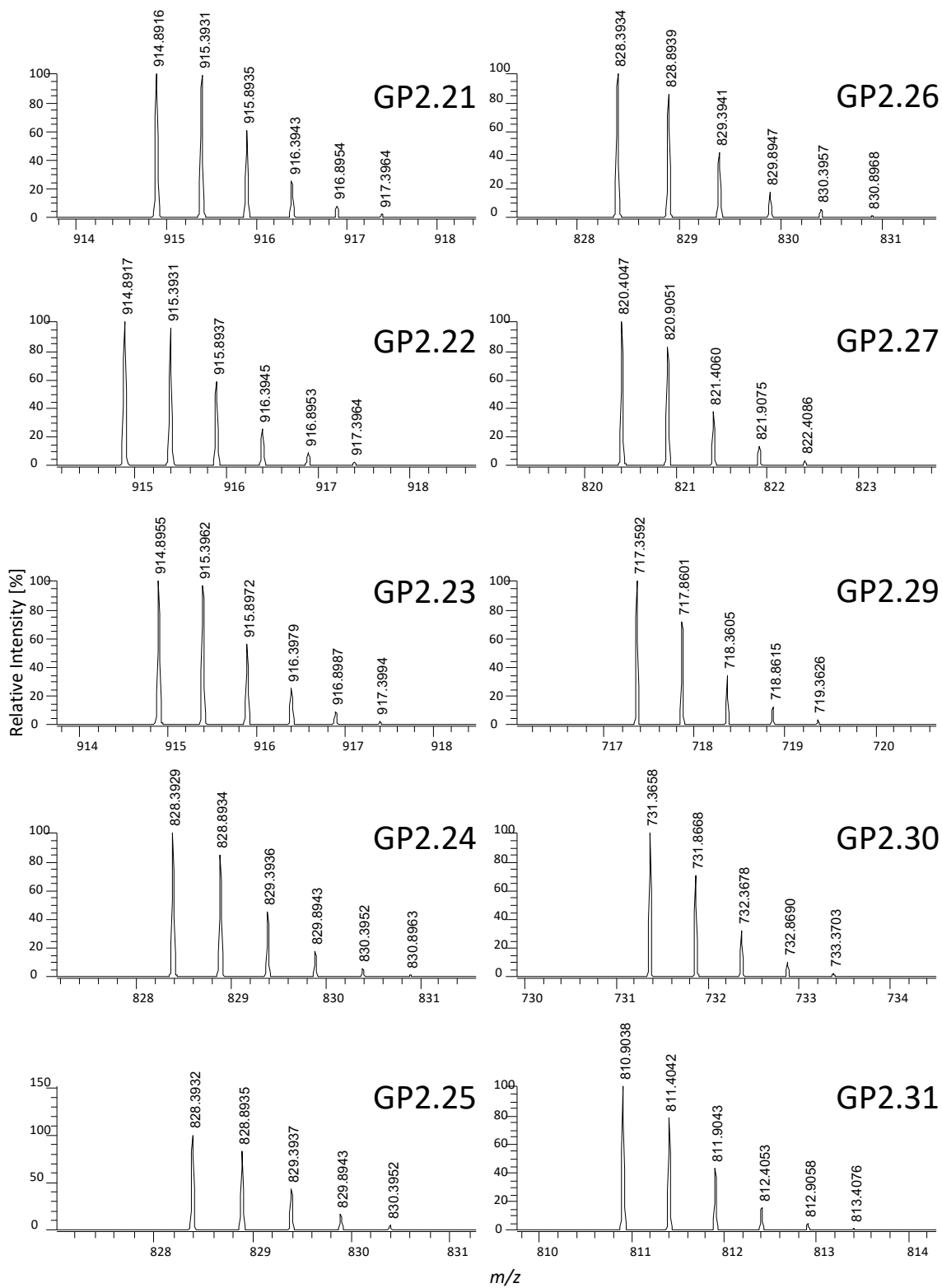
MS spectra of GP2.01-GP.40 by high-resolution C18-RP-LC-MS

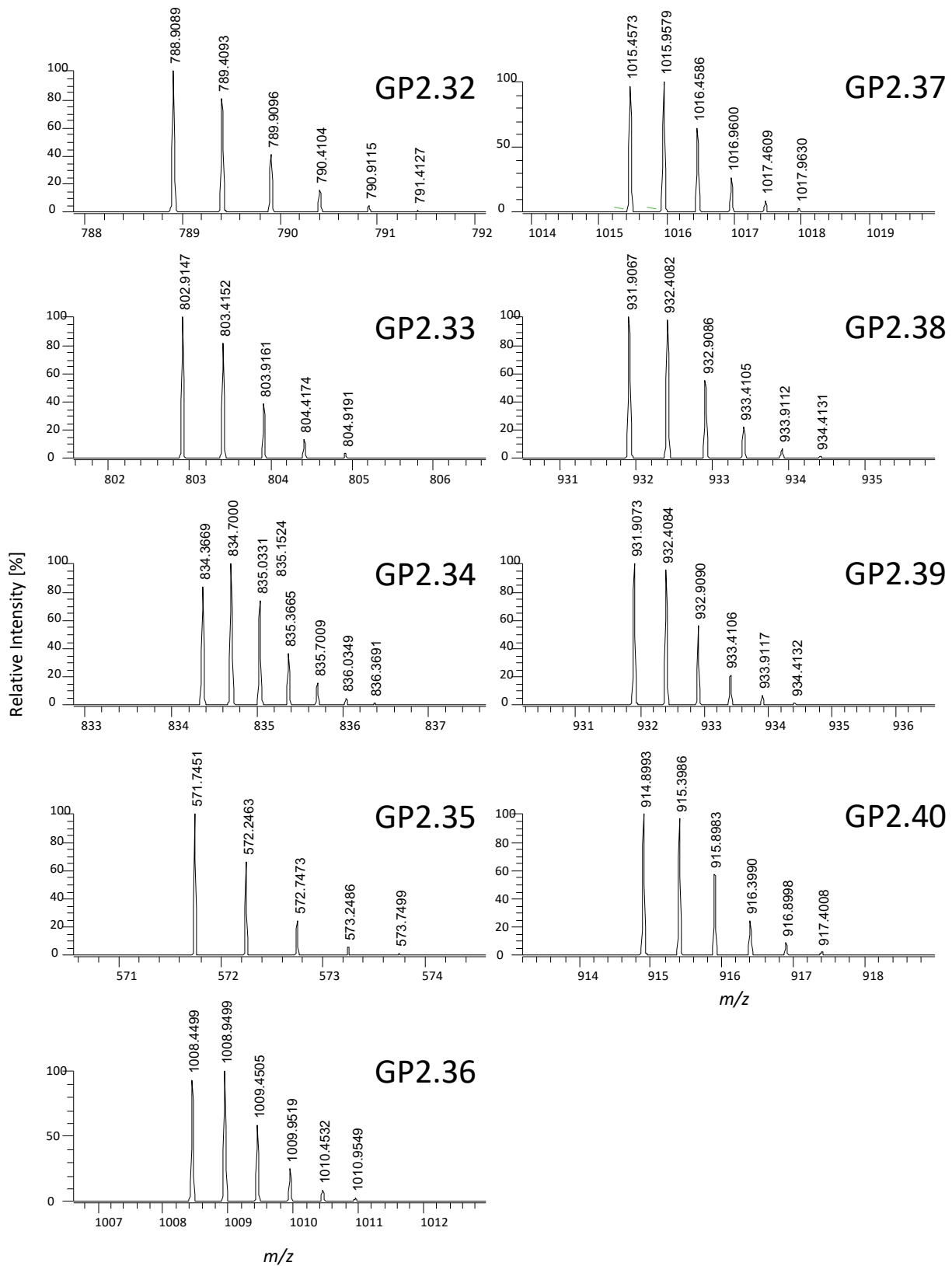
Summary of calculated and observed masses

	[M]	[M+2H] <sup>2+</sup> theor	[M+2H] <sup>2+</sup> observed	ppm error	[M+3H] <sup>3+</sup> theor	[M+3H] <sup>3+</sup> observed	ppm error
GP2.01	1825.7935	913.9040	913.9108	7.4	609.6051	609.6094	7.0
GP2.02	1811.7779	906.8962	906.9035	8.1	604.9332	604.9373	6.7
GP2.03	1825.7935	913.9040	913.9104	7.0	609.6051	609.6090	6.4
GP2.04	1811.7779	906.8962	906.9035	8.1	604.9332	604.9372	6.6
GP2.05	1825.7935	913.9040	913.9111	7.7	609.6051	609.6093	6.9
GP2.06	1839.8092	920.9118	920.9184	7.1	614.2770	614.2812	6.9
GP2.07	1622.7141	812.3643	812.3702	7.2	541.9120	541.9155	6.5
GP2.08	1987.8463	994.9304	994.9379	7.5	663.6227	663.6280	8.0
GP2.09	1987.8463	994.9304	994.9375	7.1	663.6227	663.6276	7.4
GP2.10	1987.8463	994.9304	994.9384	8.0	663.6227	663.6280	8.0
GP2.11	1987.8463	994.9304	994.9378	7.4	663.6227	663.6282	8.3
GP2.12	1799.7779	900.8962	900.9030	7.6	600.9332	600.9375	7.1
GP2.13	1799.7779	900.8962	900.9028	7.3	600.9332	600.9375	7.1
GP2.14	1799.7779	900.8962	900.9031	7.7	600.9332	600.9374	7.0
GP2.15	1843.7841	922.8993	922.9064	7.7	615.6020	615.6065	7.4
GP2.16	1843.7841	922.8993	922.9060	7.2	615.6020	615.6062	6.9
GP2.17	1843.7841	922.8993	922.9057	6.9	615.6020	615.6063	7.0
GP2.18	1843.7841	922.8993	922.9068	8.1	615.6020	615.6064	7.2
GP2.19	1843.7841	922.8993	922.9063	7.6	615.6020	615.6066	7.5
GP2.20	1843.7841	922.8993	922.9057	6.9	615.6020	615.6059	6.4
GP2.21	1827.7550	914.8848	914.8916	7.5	610.2589	610.2632	7.0
GP2.22	1827.7550	914.8848	914.8917	7.6	610.2589	610.2633	7.1
GP2.23	1827.7550	914.8848	914.8955	11.7	610.2589	610.2657	11.1
GP2.24	1654.7509	828.3827	828.3929	12.3	552.5909	N/A	N/A
GP2.25	1654.7509	828.3827	828.3932	12.6	552.5909	N/A	N/A
GP2.26	1654.7509	828.3827	828.3934	12.9	552.5909	N/A	N/A
GP2.27	1638.7738	820.3942	820.4047	12.9	547.2652	N/A	N/A
GP2.28	1476.6767	739.3456	N/A	N/A	493.2328	N/A	N/A
GP2.29	1432.6869	717.3507	717.3592	11.8	478.5696	N/A	N/A
GP2.30	1460.6995	731.3570	731.3658	12.0	487.9071	N/A	N/A
GP2.31	1619.7713	810.8929	810.9038	13.4	540.9310	N/A	N/A
GP2.32	1575.7815	788.8980	788.9089	13.8	526.2678	N/A	N/A
GP2.33	1603.7942	802.9044	802.9147	12.9	535.6053	N/A	N/A
GP2.34	2500.0416	1251.0281	1251.0440	12.7	834.3545	834.3669	14.9
GP2.35	1141.4605	571.7375	571.7451	13.3	381.4941	N/A	N/A
GP2.36	2014.8573	1008.4359	1008.4499	13.9	672.6264	672.6359	14.2
GP2.37	2028.8729	1015.4437	1015.4573	13.4	677.2982	677.3074	13.5
GP2.38	1861.7747	931.8946	931.9067	13.0	621.5988	621.6066	12.5
GP2.39	1861.7747	931.8946	931.9073	13.6	621.5988	621.6070	13.1
GP2.40	1827.7550	914.8848	914.8993	15.9	610.2589	610.2680	14.8









## References

Huberty, M.C., Vath, J.E., Yu, W., and Martin, S.A. (1993). Site-specific carbohydrate identification in recombinant proteins using MALD-TOF MS. *Anal Chem* 65, 2791-2800.