

## Supplementary Information

### Chemoenzymatic synthesis of sulfated *O*-glycopeptides from human CD34

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## 1. General materials and methods

Low-resolution mass spectrometry (LRMS) was measured on ESI apparatus using a Shimadzu LC-MS2020. High-resolution mass spectrometry (HRMS) was measured on ESI apparatus using Agilent 1290 G6460A Q-TOF. Compound analysis was recorded on Shimadzu LC-MS2020-ESI with XBrigde® Amide 3.5  $\mu$ m, 2.1 mm x 150 mm column (Waters). Compound purification was performed on a C18 column (Bio-Rad Laboratories, 1.5 x 20 cm, 73711522) packed with C18 silica gel (Waters, WAT035672).

Fmoc-Ser(*t*Bu)-Wang Resin was purchased from GL Biochem (shanghai) Ltd. (GLS240319-41701). Chemical reagents were purchased from *J&K* Scientific Ltd. and TCI Shanghai, China. Cytidine-5'-monophospho-N-acetylneurameric acid (CMP-Neu5Ac), uridine 5'-diphospho-N-acetylglucosamine (UDP-GlcNAc), guanosine 5'-diphospho- $\beta$ -L-fucose (GDP-Fuc), uridine 5'-diphosphogalactose (UDP-Gal) and PAPS were purchased from GLYCOGENE. Calf intestine alkaline phosphatase (CIAP) were purchased from BioLabs® Inc. Biotinylated lectins SNA, MAL-II, AAL was purchased from Vector Labs. Recombinant human L-selectin-Fc chimera was purchased from Abclonal. Recombinant human E-selectin-Fc chimera and recombinant human P-selectin-Fc chimera were purchased from Acro Biosystems. Biotinylated goat anti-Human IgG Fc Antibody and Streptavidin-AlexaFluor® 635 were purchased from Thermo-Fisher Scientific.

## 2. Glycosyltransferases expression and purification

Bacterial *Photobacterium phosphoreum*  $\alpha$ -2,3-sialyltransferase (*Ppa*-2,3SiaT) was expressed in *E. coli* system and purified as described previously.<sup>[1]</sup> The construct was transformed into *E. coli* BL21 (DE3) cells, and protein expression was induced in LB medium containing 100  $\mu$ g/mL kanamycin with agitation at 37 °C with 200 rpm until the OD value reached 0.4-0.6, followed by the addition of isopropyl- $\beta$ -D-thiogalactopyranoside (IPTG) to reach a final concentration of 0.4-0.6 mM. After growth at 20 °C with agitation for 16 h, cells were harvested by

centrifugation (8000 g, 10 min, 4 °C) and resuspended in lysis buffer (50 mM Tris-HCl, 250 mM NaCl, pH 7.5). Next, cells in the lysis buffer was processed using a high-pressure crusher (Union-Biotech (Shanghai) Co., Ltd.) at 10,000 psi, and the lysate was clarified by centrifugation (8000 g, 30 min, 4 °C). The lysate was centrifuged to remove the precipitate, and the resulting crude enzyme solution was purified as described previously.<sup>[1]</sup>

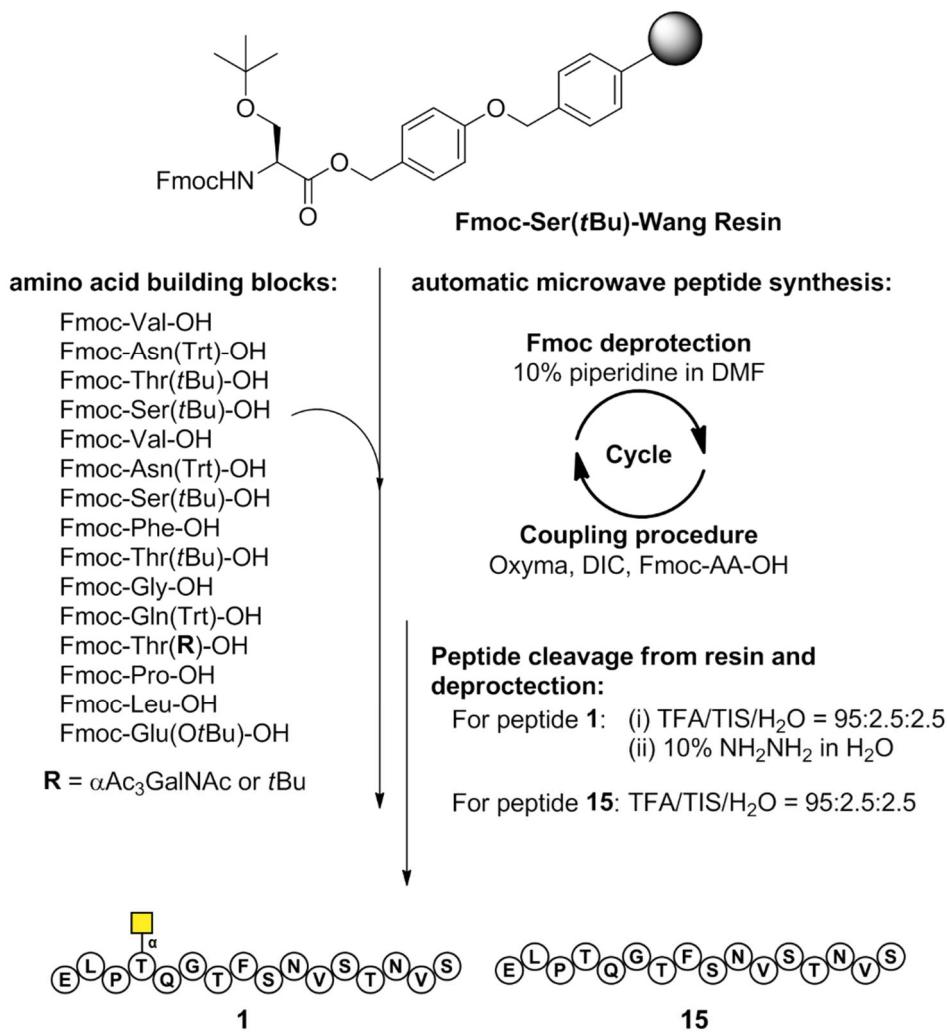
Human glycosyltransferases C1GalT1, GCNT1, B4GalT1, ST6Gal1, ST3Gal4, CHST2, and FUT6 were expressed and purified according to the methods described in the literature.<sup>[2-7]</sup> In this study, the catalytic domains of human glycosyltransferases were expressed as soluble secretory fusion proteins by transient transfection of suspension-cultured HEK293 cells. His-tagged proteins from the supernatant of HEK293 cells and the lysate of *E. coli* BL21 (DE3) cells were purified by Ni<sup>2+</sup>-NTA affinity chromatography. The Ni<sup>2+</sup>-NTA column was pre-equilibrated with five column volumes of binding buffer (50 mM Tris-HCl, 250 mM NaCl, 5 mM imidazole, pH 7.5). The column was washed with washing buffer (50 mM Tris-HCl, 250 mM NaCl, 40 mM imidazole, pH 7.5). The target proteins were eluted with elution buffer (50 mM Tris-HCl, 250 mM NaCl, 200 mM imidazole, pH 7.5). Peak fractions were pooled and concentrated to ~1 mg/mL using an ultrafiltration pressure cell membrane (Millipore, Billerica, MA) with a 10 kDa molecular weight cut off.

### 3. The synthesis of the target peptides 1-15

#### The synthesis of the target peptides 1 and 15

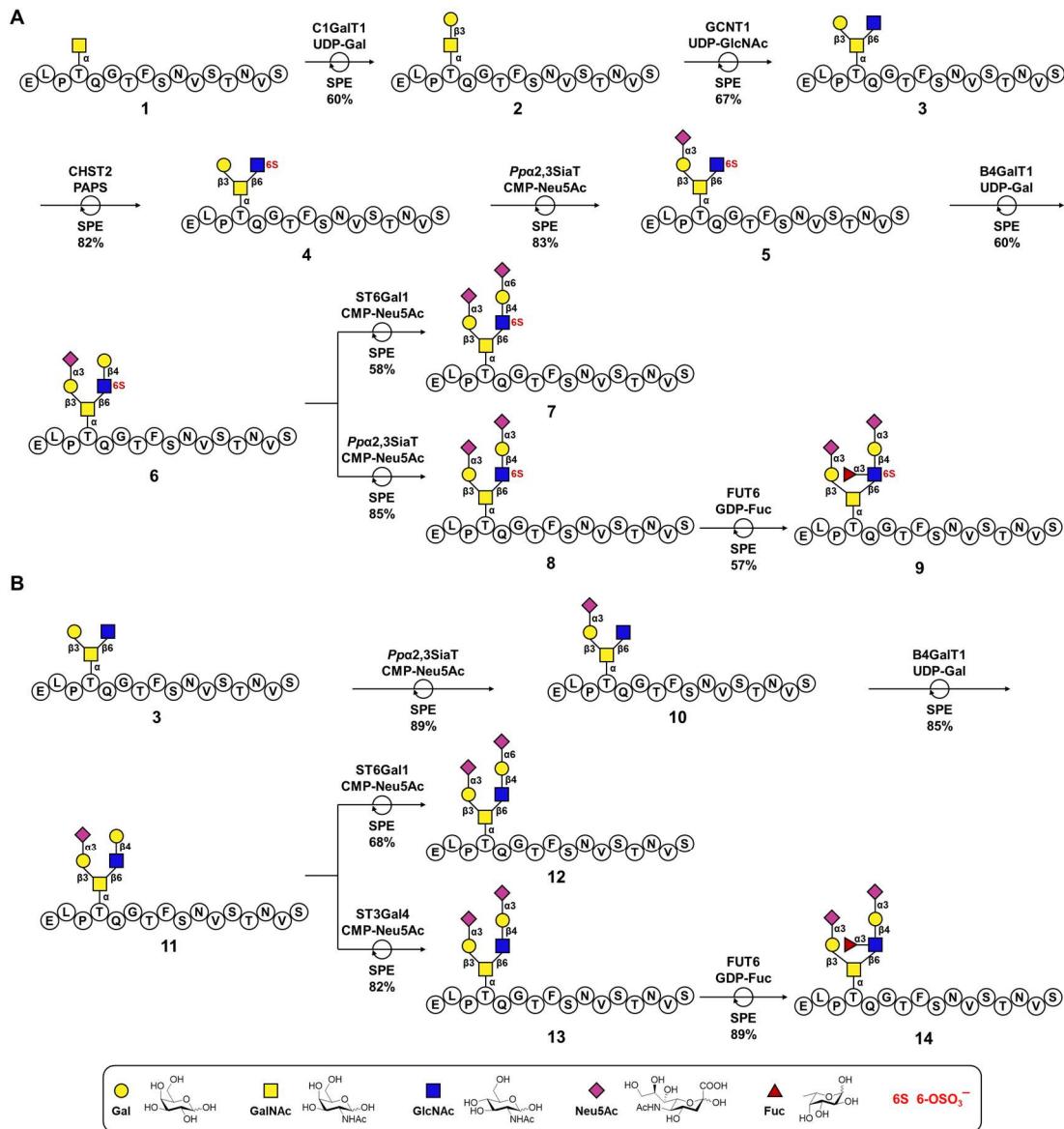
The synthesis of peptide **1** and **15** was carried out using the automatic microwave peptide synthesizer Liberty Blue 2.0 (Scheme S1). The glycosyl amino acid Fmoc-Thr(αAc<sub>3</sub>GalNAc)-OH was synthesized as described in our previous study.<sup>[8]</sup> The procedure includes: 1) deprotection with 10 % piperidine in DMF for 2 min; 2) coupling with Oxyma (1 mmol, 5 equiv) in DMF and DIC (2 mmol, 10 equiv) in DMF with Fmoc-AA-OH (1.2 mmol, 6.0 equiv) for 2 min. For the synthesis of glycopeptide **1**, Fmoc-Thr(αAc<sub>3</sub>GalNAc) building block (2.5 equiv.) was used. The peptide chain was cleaved from the resin with trifluoroacetic acid (TFA) (10 mL, containing 2.5% TIS and 2.5% H<sub>2</sub>O) at room temperature for 3 h, followed by

filtration through a polytetrafluoroethylene (PTFE) filter. Isopropyl ether was added to make the product as precipitate, which was then collected and deacetylated with a 10% hydrazine hydrate solution for 10 min and purified on a C18 column to obtain the pure peptide (eluent: H<sub>2</sub>O to 30% MeCN; 100.0 mg for compound **1** that can serve as a Gal acceptor for subsequent enzymatic elongation, 26% yield, 0.2 mmol scale; 57.3 mg for compound **15**, 34% yield, 0.1 mmol scale).



**Scheme S1.** Chemical synthesis of compounds **1** and **15**

## Enzymatic synthesis of diverse *O*-glycopeptides 2-14



**Figure S1.** Synthesis of *O*-glycopeptides 2-14

## General procedure for the installation of $\beta$ 1,3-Gal by C1GalT1

To a solution of glycopeptides (2-20 mM), UDP-Gal (3-30 mM, 1.5 equiv), and MnCl<sub>2</sub> (10 mM) in Tris HCl buffer (100 mM, pH ≈ 7.0) was added C1GalT1 (350 µg/mL) and calf intestine alkaline phosphatase (CIAP, 10 U/mL), and the mixture was incubated at 37 °C for 16 h. Subsequently, ESI-MS analysis was performed to monitor the reaction every 8 h, and the additional enzymes and sugar nucleotide were added until no starting material was detected. The reaction mixture was centrifuged, and the resulting supernatant was loaded on a C18 cartridge (eluent: H<sub>2</sub>O to 30% MeCN).

Product containing fractions were combined and lyophilized to give the  $\beta$ 1,3-galactosylated glycopeptides as a white amorphous solid.

#### **General procedure for the installation of $\beta$ 1,6-GlcNAc by GCNT1**

To a solution of glycopeptides (2-20 mM), UDP-GlcNAc (3-30 mM, 1.5 equiv), and MnCl<sub>2</sub> (10 mM) in Tris-HCl buffer (50 mM, pH  $\approx$  7.5) was added GCNT1 (110  $\mu$ g/mL) and calf intestine alkaline phosphatase (CIAP, 10U/mL), and the mixture was incubated at 37 °C for 12 h. Subsequently, ESI-MS analysis was performed to monitor the reaction every 4 h, and the additional enzymes and sugar nucleotide were added until no starting material was detected. The reaction mixture was centrifuged, and the resulting supernatant was loaded on a C18 cartridge (eluent: H<sub>2</sub>O to 30% MeCN). Product containing fractions were combined and lyophilized to give the  $\beta$ 1,6-GlcNAc branched glycopeptides as a white amorphous solid.

#### **General procedure for the installation of $\beta$ 1,4-Gal by B4GalT1**

To a solution of glycopeptides (2-20 mM), UDP-Gal (3-30 mM, 1.5 equiv), and MnCl<sub>2</sub> (10 mM) in Tris-HCl buffer (50 mM, pH  $\approx$  7.5) was added B4GalT1 (150  $\mu$ g/mL) and calf intestine alkaline phosphatase (CIAP, 10U/mL), and the mixture was incubated at 37 °C for 12 h. Subsequently, ESI-MS analysis was performed to monitor the reaction every 6 h, and the additional enzymes and sugar nucleotide were added until no starting material was detected. The reaction mixture was centrifuged, and the resulting supernatant was loaded on a C18 cartridge (eluent: H<sub>2</sub>O to 30% MeCN). Product containing fractions were combined and lyophilized to give the  $\beta$ 1,4-galactosylated glycopeptides as a white amorphous solid.

#### **General procedure for the installation of $\alpha$ 2,6-Neu5Ac by ST6Gal1**

To a solution of glycopeptides (2-20 mM) and CMP-Neu5Ac (3-30 mM, 1.5 equiv) in Tris-HCl buffer (100 mM, pH  $\approx$  7.2) was added ST6Gal1 (300  $\mu$ g/mL) and calf intestine alkaline phosphatase (CIAP, 10 U/mL), and the mixture was incubated for 16 h at 37 °C. Subsequently, ESI-MS analysis was performed to monitor the reaction every 6 h, and the additional enzymes and sugar nucleotide were added until no

starting material was detected. The reaction mixture was centrifuged, and the resulting supernatant was loaded on a C18 cartridge (eluent: H<sub>2</sub>O to 30% MeCN). Product containing fractions were combined and lyophilized to give the  $\alpha$ 2,6-sialylated glycopeptides as a white amorphous solid.

#### **General procedure for the installation of $\alpha$ 2,3-Neu5Ac by ST3Gal4**

To a solution of glycopeptides (2-20 mM) and CMP-Neu5Ac (3-30 mM, 1.5 equiv) in Tris-HCl buffer (100 mM, pH  $\approx$  7.2) was added ST3Gal4 (300  $\mu$ g/mL) and calf intestine alkaline phosphatase (CIAP, 10 U/mL), and the mixture was incubated for 18 h at 37 °C. Subsequently, ESI-MS analysis was performed to monitor the reaction every 8 h, and the additional enzymes and sugar nucleotide were added until no starting material was detected. The reaction mixture was centrifuged, and the resulting supernatant was loaded on a C18 cartridge (eluent: H<sub>2</sub>O to 30% MeCN). Product containing fractions were combined and lyophilized to give the  $\alpha$ 2,3-sialylated glycopeptides as a white amorphous solid.

#### **General procedure for the installation of GDP-Fuc by FUT6**

To a solution of glycopeptides (2-20 mM) and GDP-Fuc (3-30 mM, 1.5 equiv) and MnCl<sub>2</sub> (10 mM) in Tris-HCl buffer (50 mM, pH  $\approx$  7.5) was added FUT6 (200  $\mu$ g/mL) and calf intestine alkaline phosphatase (CIAP, 10 U/mL), and the mixture was incubated for 18 h at 37 °C. Subsequently, ESI-MS analysis was performed to monitor the reaction every 8 h, and the additional enzymes and sugar nucleotide were added until no starting material was detected. The reaction mixture was centrifuged, and the resulting supernatant was loaded on a C18 cartridge (eluent: H<sub>2</sub>O to 30% MeCN). Product containing fractions were combined and lyophilized to give the fucosylated glycopeptides as a white amorphous solid.

#### **General procedure for the installation of PAPS by CHST2**

To a solution of glycopeptides (2-20 mM) and PAPS (3-30 mM, 1.5 equiv) in Tris-HCl buffer (50 mM, pH  $\approx$  7.5) was added CHST2 (1000  $\mu$ g/mL) and the mixture was incubated for 12 h at 37 °C. Subsequently, ESI-MS analysis was performed to

monitor the reaction every 4 h, and the additional enzymes and PAPS were added until no starting material was detected. The reaction mixture was centrifuged, and the resulting supernatant was loaded on a C18 cartridge (eluent: H<sub>2</sub>O to 30% MeCN). Product containing fractions were combined and lyophilized to give the sulfated glycopeptides as a white amorphous solid.

**General procedure for the installation of  $\alpha$ 2,3-Neu5Ac by *Ppa*-2,3SiaT**

To a solution of glycopeptides (2-20 mM) and CMP-Neu5Ac (3-30 mM, 1.5 equiv) in Tris-HCl buffer (100 mM, pH ≈ 8.0) was added *Ppa*-2,3SiaT (300  $\mu$ g/mL) and the mixture was incubated for 6 h at 37 °C. Subsequently, ESI-MS analysis was performed to monitor the reaction every 3 h and the additional enzymes and sugar nucleotide were added until no starting material was detected. The reaction mixture was centrifuged, and the resulting supernatant was loaded on a C18 cartridge (eluent: H<sub>2</sub>O to 30% MeCN). Product containing fractions were combined and lyophilized to give the  $\alpha$ 2,3-sialylated glycopeptides as a white amorphous solid.

#### 4. LC-MS characterizations of compounds 1-15

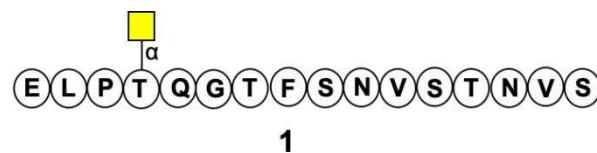
##### 4.1 The procedure for analysis of compounds 1-15

**Table S1.** The procedure for analysis of compounds 1-15

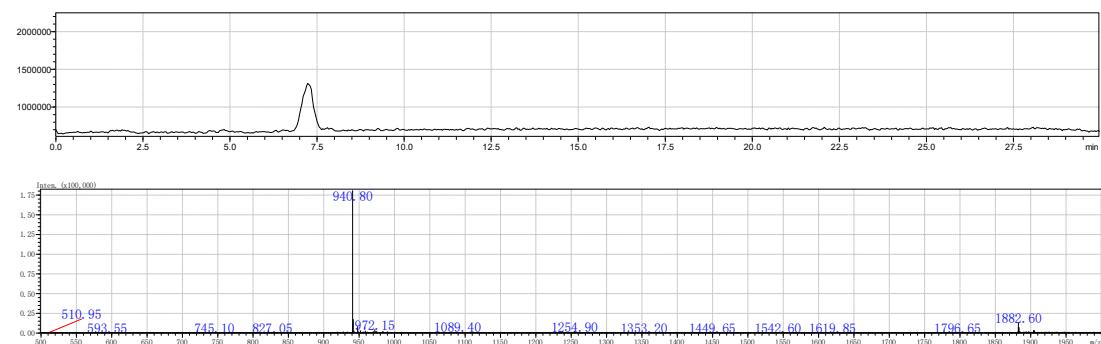
Time(min)	A%
0	30
20	50
23	60
26	30
30	30

Analysis was performed on Shimadzu LC-MS2020 with XBridge® Amide 3.5  $\mu$ m, 2.1 mm x 150 mm column (Waters) at a flow rate of 0.20 mL/min using ESI-MS for compound detection. Mobile phase A consisted of 10 mM ammonium formate adjusted to pH  $\approx$  3.5 using formic acid; mobile phase B consisted of 100% acetonitrile.

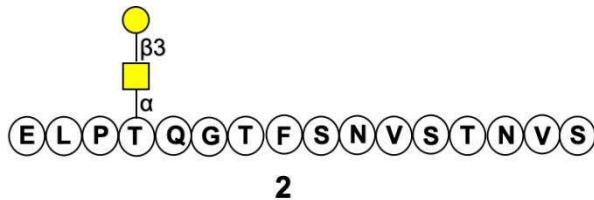
##### 4.2 LC-MS data for compounds 1-15



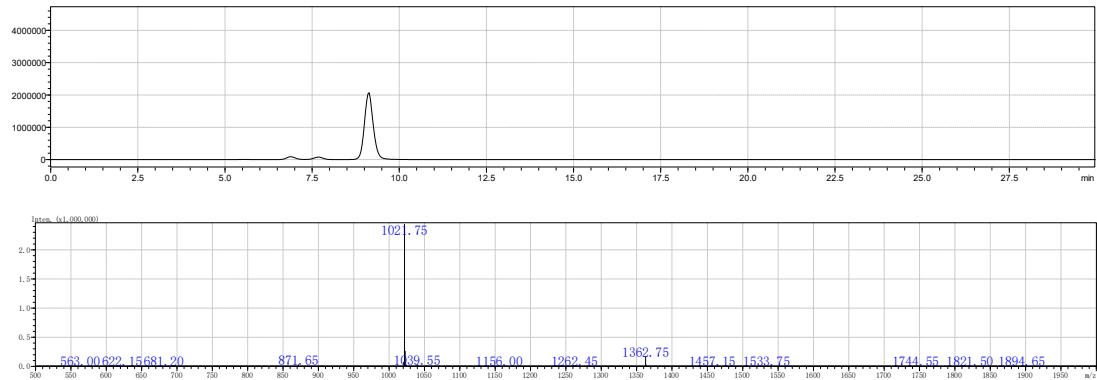
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{79}H_{124}N_{20}O_{33}^{2-}$ , 940.44; found 940.80, (100.0 mg, 26% overall yield).



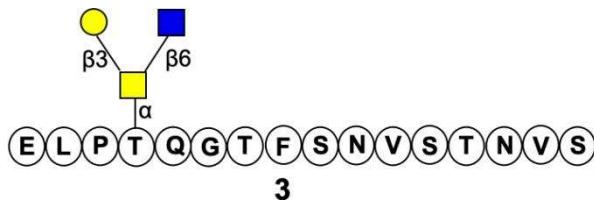
**Figure S2.** LC-MS profile and focused ESI-MS of compound 1, eluting at 7.23 min



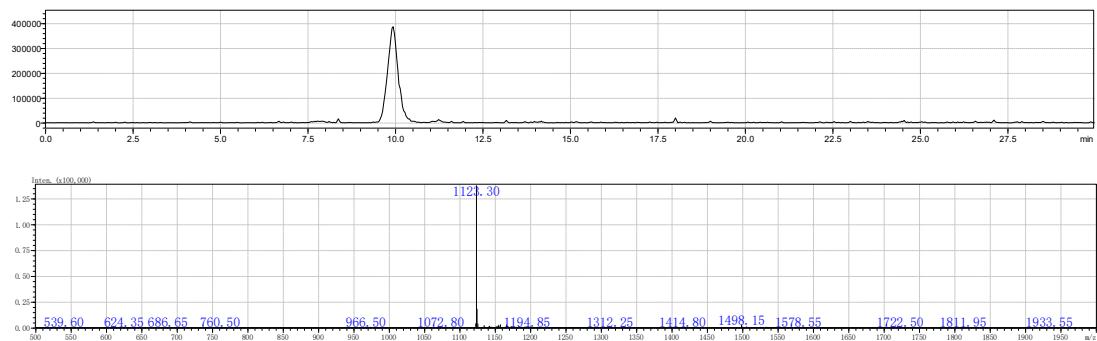
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{85}H_{134}N_{20}O_{38}^{2-}$ , 1021.47; found 1021.75, (13.0 mg, 60% yield).



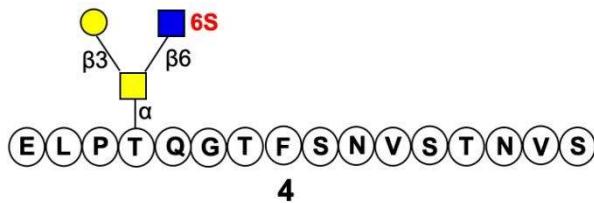
**Figure S3.** LC-MS profile and focused ESI-MS of compound 2, eluting at 9.13 min



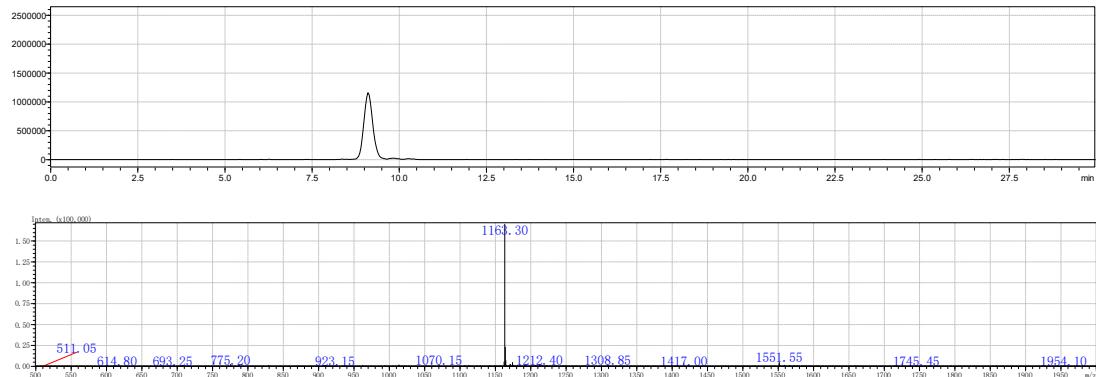
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{93}H_{147}N_{21}O_{43}^{2-}$ , 1123.01; found 1123.30, (9.0 mg, 67% yield).



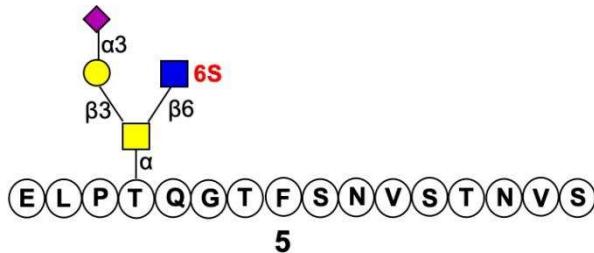
**Figure S4.** LC-MS profile and focused ESI-MS of compound 3, eluting at 9.93 min



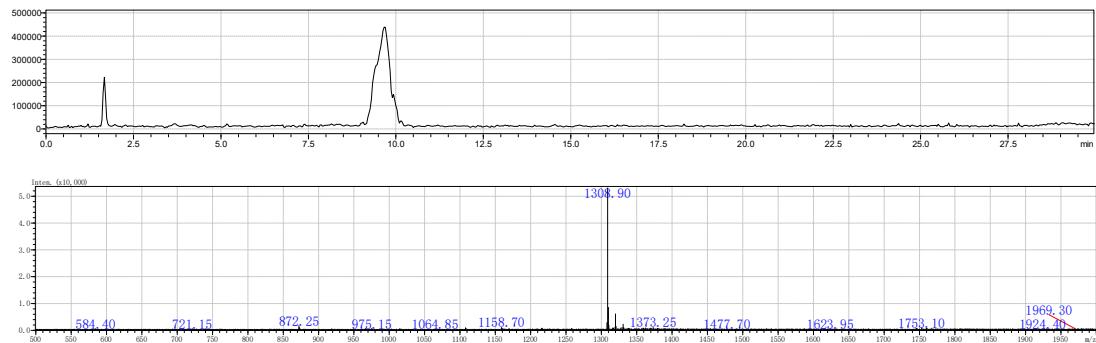
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{93}H_{147}N_{21}O_{46}S^{2-}$ , 1162.98; found 1163.30, (8.4 mg, 82% yield).



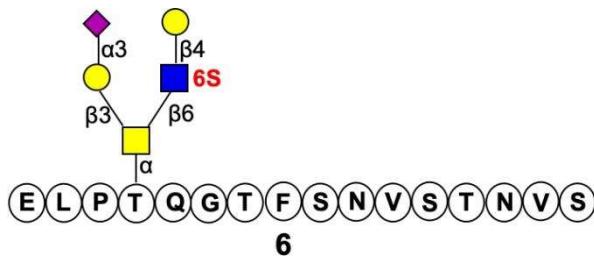
**Figure S5.** LC-MS profile and focused ESI-MS of compound 4, eluting at 9.10 min



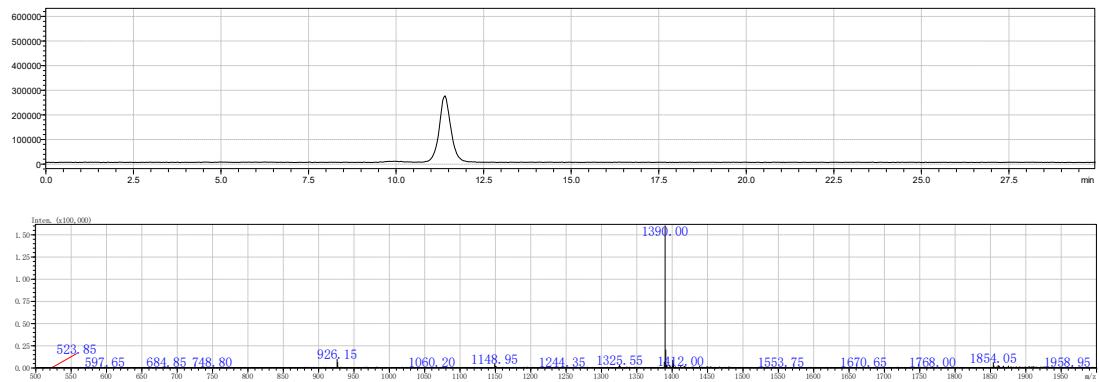
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{104}H_{164}N_{22}O_{54}S^{2-}$ , 1308.53; found 1308.90, (5.2 mg, 83% yield).



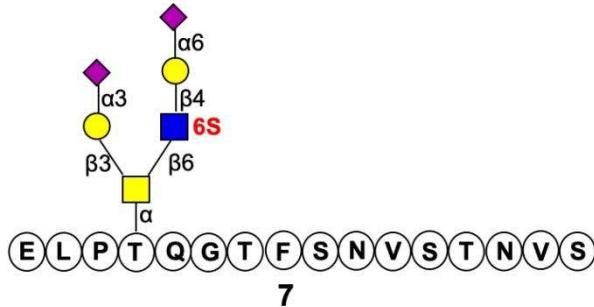
**Figure S6.** LC-MS profile and focused ESI-MS of compound 5, eluting at 9.66 min



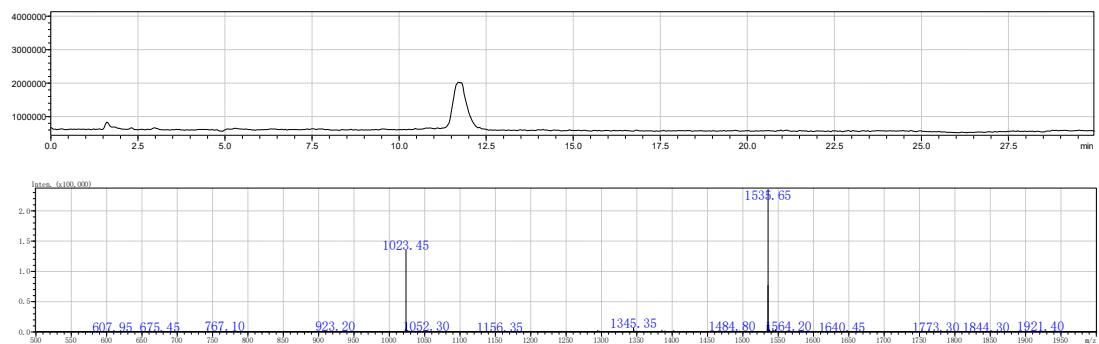
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{110}H_{174}N_{22}O_{59}S^{2-}$ , 1389.56; found 1390.00, (4.4 mg, 60% yield).



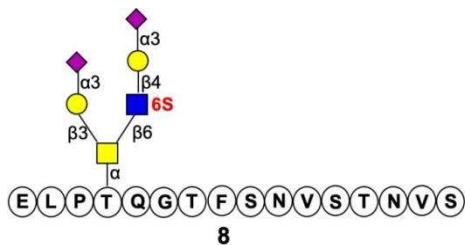
**Figure S7.** LC-MS profile and focused ESI-MS of compound **6**, eluting at 11.40 min



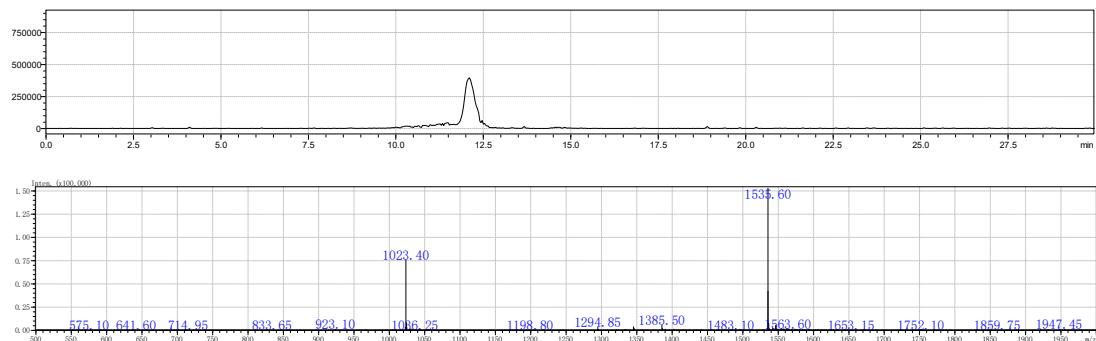
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{121}H_{191}N_{23}O_{67}S^{2-}$ , 1535.11; found 1535.65;  $[M-3H]^{3-}$  calcd for  $C_{121}H_{190}N_{23}O_{67}S^{3-}$ , 1023.07; found 1023.45, (1.2 mg, 58% yield).



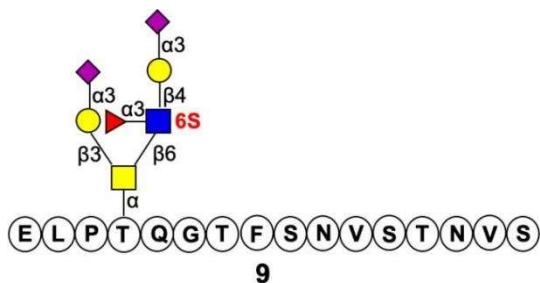
**Figure S8.** LC-MS profile and focused ESI-MS of compound **7**, eluting at 12.10 min



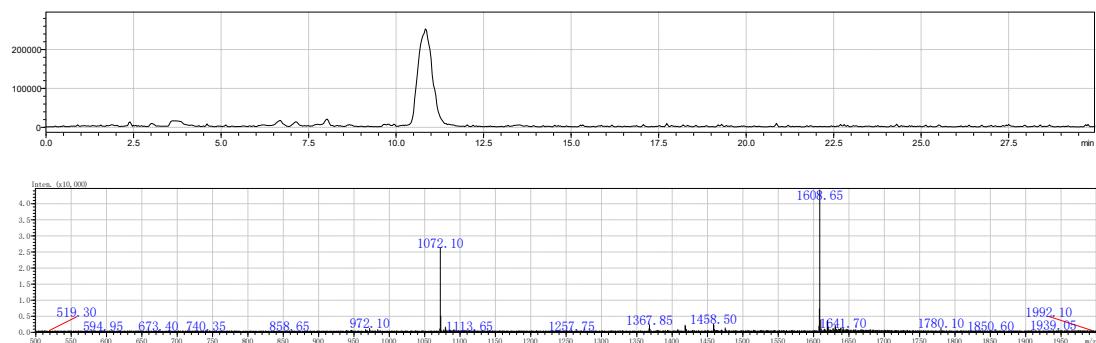
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{121}H_{191}N_{23}O_{67}S^{2-}$ , 1535.11; found 1535.60;  $[M-3H]^{3-}$  calcd for  $C_{121}H_{190}N_{23}O_{67}S^{3-}$ , 1023.07; found 1023.40, (1.7 mg, 85% yield).



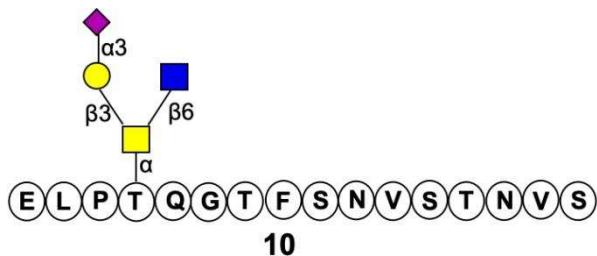
**Figure S9.** LC-MS profile and focused ESI-MS of compound **8**, eluting at 11.73 min



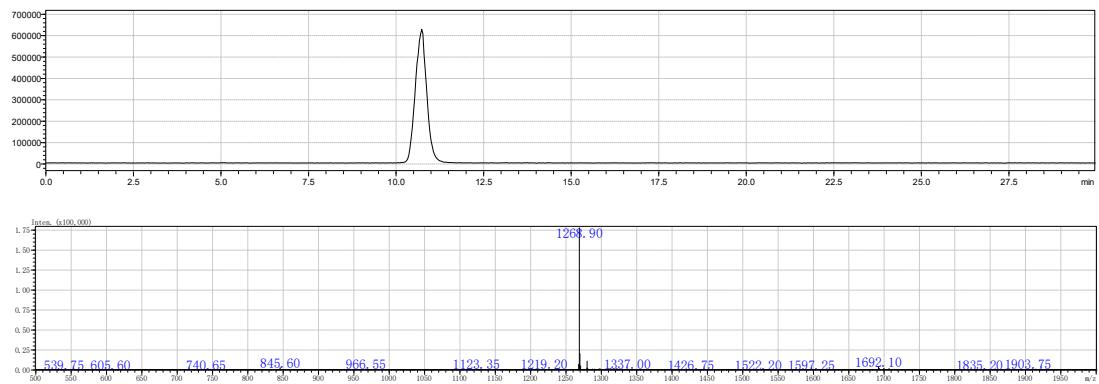
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{127}H_{201}N_{23}O_{71}S^{2-}$ , 1608.13; found 1608.65;  $[M-3H]^{3-}$  calcd for  $C_{127}H_{200}N_{23}O_{71}S^{3-}$ , 1071.76; found 1072.10, (0.9 mg, 57% yield).



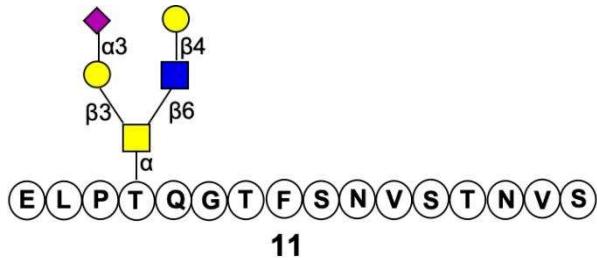
**Figure S10.** LC-MS profile and focused ESI-MS of compound **9**, eluting at 10.83 min



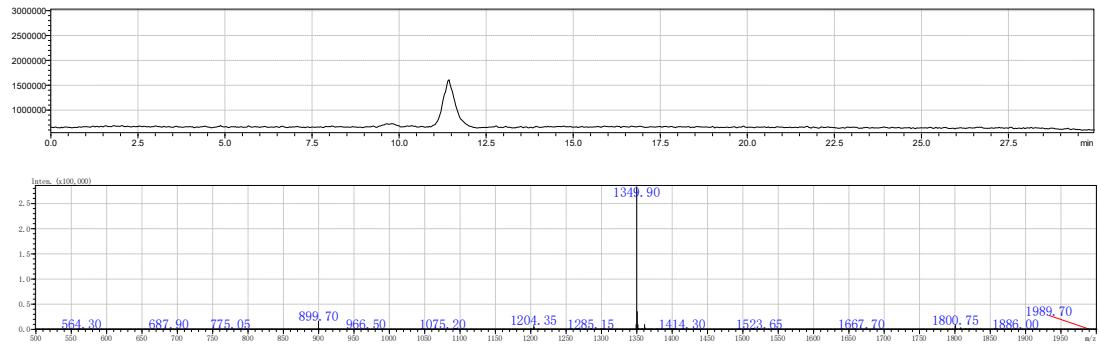
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{104}H_{164}N_{22}O_{51}^{2-}$ , 1268.55; found 1268.90, (6.3 mg, 89% yield).



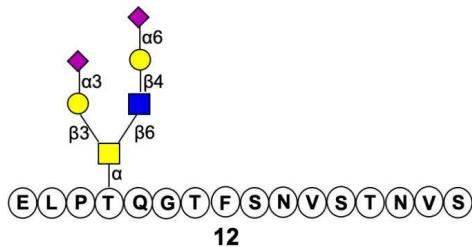
**Figure S11.** LC-MS profile and focused ESI-MS of compound **10**, eluting at 10.73 min



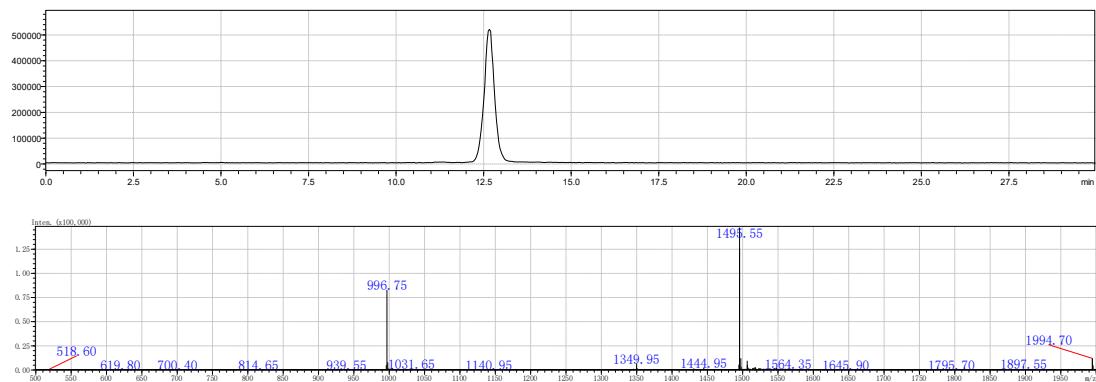
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{110}H_{174}N_{22}O_{56}^{2-}$ , 1349.58; found 1349.90, (5.8 mg, 85% yield).



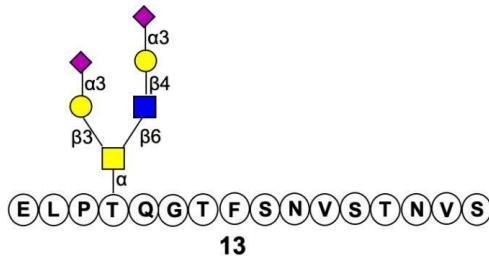
**Figure S12.** LC-MS profile and focused ESI-MS of compound **11**, eluting at 11.43 min



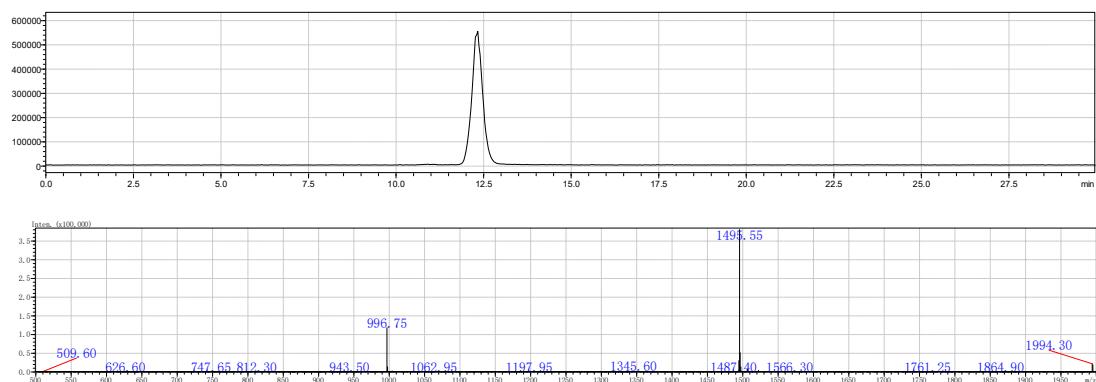
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{121}H_{191}N_{23}O_{64}^{2-}$ , 1495.13; found 1495.55;  $[M-3H]^{3-}$  calcd for  $C_{121}H_{190}N_{23}O_{64}^{3-}$ , 996.42; found 996.75, (1.0 mg, 68% yield).



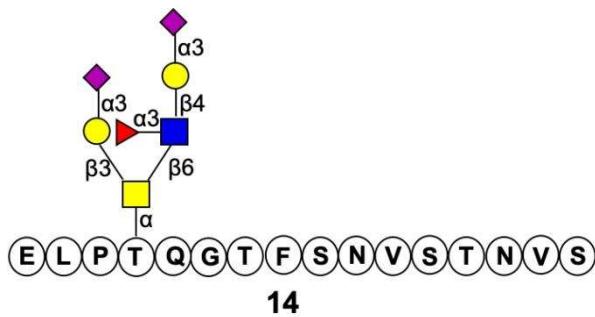
**Figure S13.** LC-MS profile and focused ESI-MS of compound **12**, eluting at 12.66 min



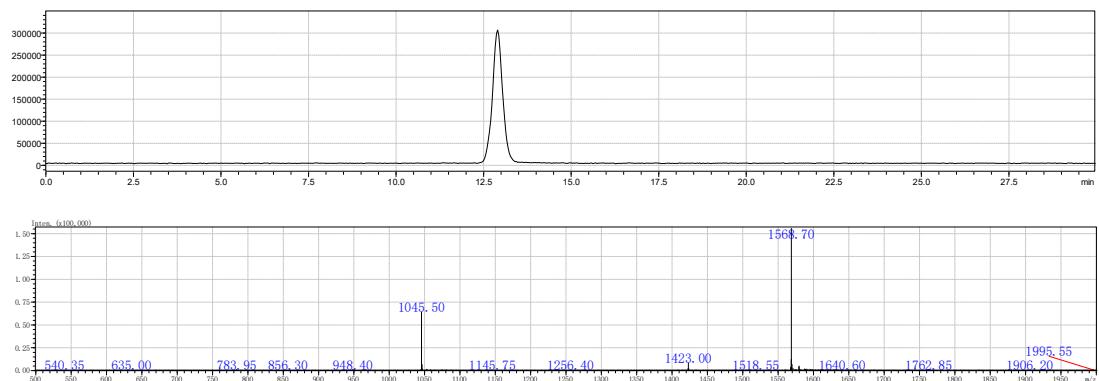
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{121}H_{191}N_{23}O_{64}^{2-}$ , 1495.13; found 1495.55;  $[M-3H]^{3-}$  calcd for  $C_{121}H_{190}N_{23}O_{64}^{3-}$ , 996.42; found 996.75, (2.0 mg, 82% yield)



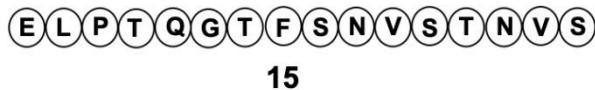
**Figure S14.** LC-MS profile and focused ESI-MS of compound **13**, eluting at 12.33 min



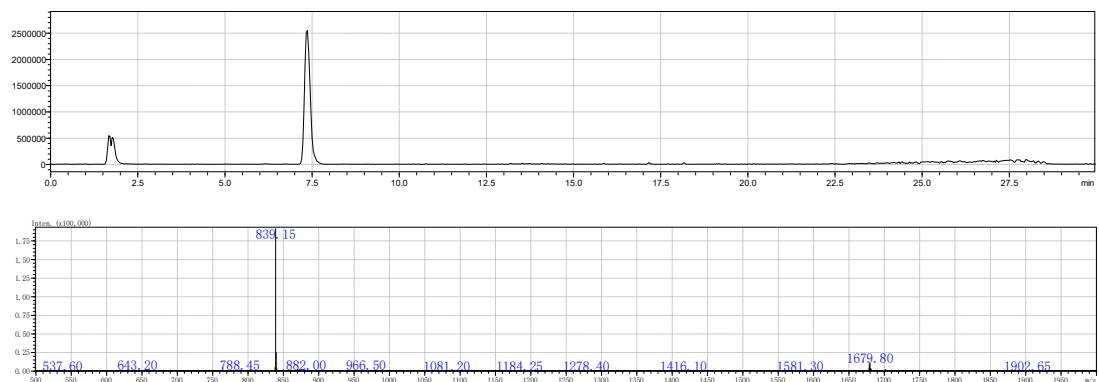
ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{127}H_{201}N_{23}O_{68}^{2-}$ , 1568.16; found 1568.70;  $[M-3H]^{3-}$  calcd for  $C_{127}H_{200}N_{23}O_{68}^{3-}$ , 1045.10; found 1045.50, (1.4 mg, 89% yield)



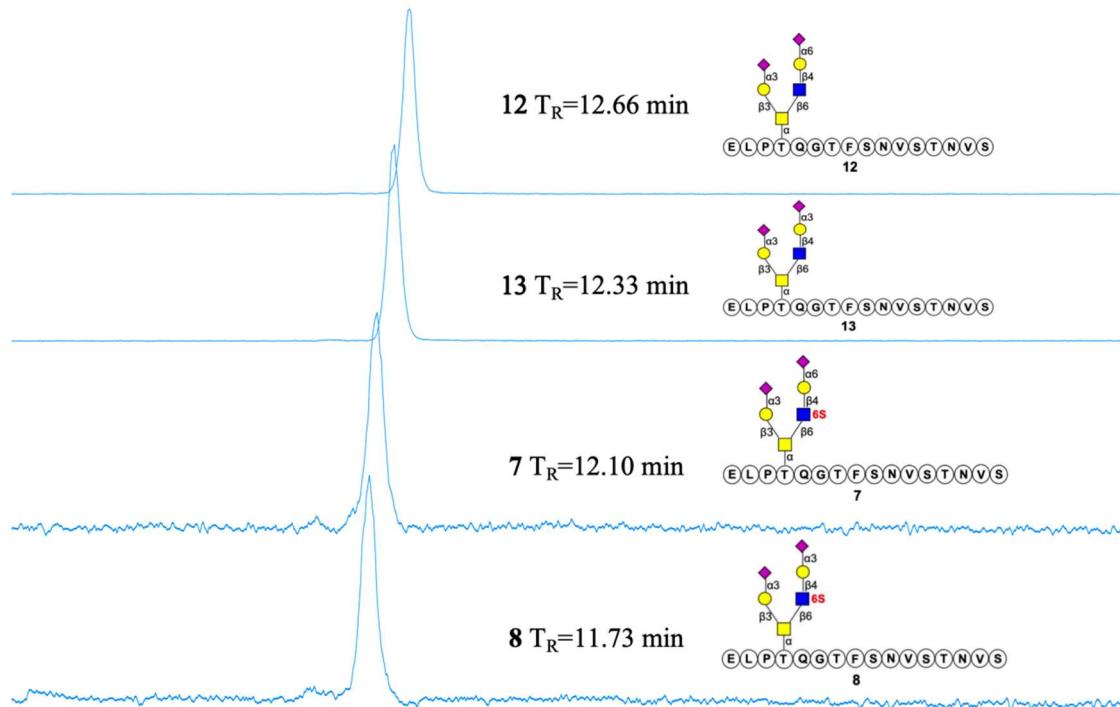
**Figure S15.** LC-MS profile and focused ESI-MS of compound **14**, eluting at 12.90 min



ESI-MS:  $[M-2H]^{2-}$  calcd for  $C_{71}H_{111}N_{19}O_{28}^{2-}$ , 839.90; found 839.15. (57.3 mg, 34% yield)



**Figure S16.** LC-MS profile and focused ESI-MS of compound **15**, eluting at 7.36 min



**Figure S17.** LC-MS profiles of different sialylated glycopeptides **12**, **13**, **7** and **8** exhibit distinct retention times to clear differentiation of each compound

## 5. Glycan microarray experiment

### Glycan microarray printing

The synthesized glycopeptides (100  $\mu$ M) were dissolved in sodium phosphate buffer solution (pH 8.5, 250 mM) and printed on NHS-activated glass slides (Nexterion Slide H, Schott Inc.) using a Scienion sciCLEAN 8 non-contact microarray printer at a relative humidity of 55% in replicates of six with spot volume  $\sim$ 400 pL. The slides were incubated overnight in a saturated NaCl chamber (providing enough humidity environment), after which were quenched with 50 mM ethanolamine in a Tris buffer (pH 9.0, 100 mM). The blocked slides were then rinsed with DI water, dried by centrifugation, and kept in a desiccator at room temperature for future use.

### Screening procedure

**Plant lectins:** Subarrays were incubated with 100  $\mu$ L biotinylated proteins at specific concentrations (AAL: 10  $\mu$ g/mL; SNA: 10  $\mu$ g/mL; MALII: 10  $\mu$ g/mL) in TSM binding buffer (20 mM Tris-HCl, pH 7.4, 150 mM NaCl, 2 mM CaCl<sub>2</sub>, 2 mM MgCl<sub>2</sub>, 0.05% Tween, 1% BSA) for 1 h at room temperature. Then the solution was removed

from each chamber, followed by four repeating washes with 200  $\mu$ L TSM washing buffer (20 mM Tris-HCl, 150 mM NaCl, 2 mM CaCl<sub>2</sub>, 2 mM MgCl<sub>2</sub>, 0.05% Tween), four repeating washes with 200  $\mu$ L TSM buffer (20 mM Tris-HCl, pH 7.4, 150 mM NaCl, 2 mM CaCl<sub>2</sub> and 2 mM MgCl<sub>2</sub>), and two repeating washes with 200  $\mu$ L DI water. Subarrays were then incubated with 100  $\mu$ L Streptavidin-AlexaFluor® 635 (5  $\mu$ g/mL) in TSM binding buffer for 1 h at room temperature, followed by the washing procedure as described above.

**Selectins:** Subarrays were incubated with 100  $\mu$ L recombinant human E-, P-, L-Selectin (Fc tag) protein (50  $\mu$ g/mL) in TSM binding buffer (100  $\mu$ L) for 1 h at room temperature, followed by a washing procedure as described above. Next, the subarray was incubated with biotinylated goat anti-Human IgG Fc Antibody (5  $\mu$ g/mL, 100  $\mu$ L) for 1 h at room temperature and washed as previous procedure. Finally, Streptavidin-AlexaFluor® 635 (5  $\mu$ g/mL, 100  $\mu$ L) was added for 1 h incubation, followed by washing procedure as described above.

### Data analysis

The pre-prepared slides were scanned for fluorescence on an InnoScan 710 Microarray Scanner. The data were processed with Mapix software and further analyzed using IBM SPSS. Relative fluorescence values (RFU) were calculated by averaging four independent replicates (corrected for mean background) on the glycan array after removal of the highest and lowest signals. The error bars indicate the standard deviation (SD) of RFU. Data were graphed using OriginPro2024. Bar graphs represent the mean  $\pm$  SD for each compound.

## 6. HR-MS data and spectra

**Table S2.** Analysis of glycopeptides by HR-MS

Entry	Glycopeptide	Formula	Theoretical mass	Charge	Observed m/z	Diff(ppm)
1	<b>1</b>	C <sub>79</sub> H <sub>126</sub> N <sub>20</sub> O <sub>33</sub>	1882.8796	2	942.4472	-0.11
2	<b>2</b>	C <sub>85</sub> H <sub>136</sub> N <sub>20</sub> O <sub>38</sub>	2044.9324	2	1023.4742	-0.66
3	<b>3</b>	C <sub>93</sub> H <sub>149</sub> N <sub>21</sub> O <sub>43</sub>	2248.0118	2	1125.013	0.19
4	<b>4</b>	C <sub>93</sub> H <sub>149</sub> N <sub>21</sub> O <sub>46</sub> S	2327.9686	2	1164.9919	-0.28
5	<b>5</b>	C <sub>104</sub> H <sub>166</sub> N <sub>22</sub> O <sub>54</sub> S	2619.0640	2	1310.5394	-0.11
6	<b>6</b>	C <sub>110</sub> H <sub>176</sub> N <sub>22</sub> O <sub>59</sub> S	2781.1169	2	1391.5648	0.63
7	<b>7</b>	C <sub>121</sub> H <sub>193</sub> N <sub>23</sub> O <sub>67</sub> S	3072.2123	2	1537.1142	-0.53
8	<b>8</b>	C <sub>121</sub> H <sub>193</sub> N <sub>23</sub> O <sub>67</sub> S	3072.2123	2	1537.1129	0.31
9	<b>9</b>	C <sub>127</sub> H <sub>203</sub> N <sub>23</sub> O <sub>71</sub> S	3218.2702	2	1610.1425	-0.06
10	<b>10</b>	C <sub>104</sub> H <sub>166</sub> N <sub>22</sub> O <sub>51</sub>	2539.1072	2	1270.5608	0.04
11	<b>11</b>	C <sub>110</sub> H <sub>176</sub> N <sub>22</sub> O <sub>56</sub>	2701.1601	2	1351.5878	-0.39
12	<b>12</b>	C <sub>121</sub> H <sub>193</sub> N <sub>23</sub> O <sub>64</sub>	2992.2555	2	1497.1345	0.35
13	<b>13</b>	C <sub>121</sub> H <sub>193</sub> N <sub>23</sub> O <sub>64</sub>	2992.2555	2	1497.1343	0.5
14	<b>14</b>	C <sub>127</sub> H <sub>203</sub> N <sub>23</sub> O <sub>68</sub>	3138.3134	2	1570.1646	-0.42
15	<b>15</b>	C <sub>71</sub> H <sub>113</sub> N <sub>19</sub> O <sub>28</sub>	1679.8002	2	840.9079	-0.58

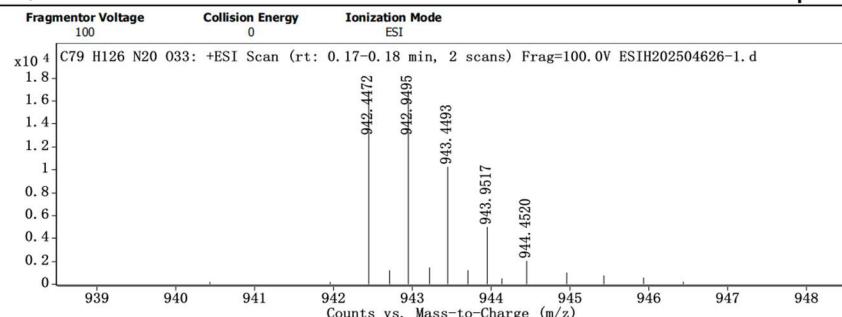
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**Comment** ESIH by huangqiongping

**Sample Name** G0-O-1  
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**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-20231114.m

  
**ELPTQGTFSNVS**

### User Spectra



### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula	Ion
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--- End Of Report ---

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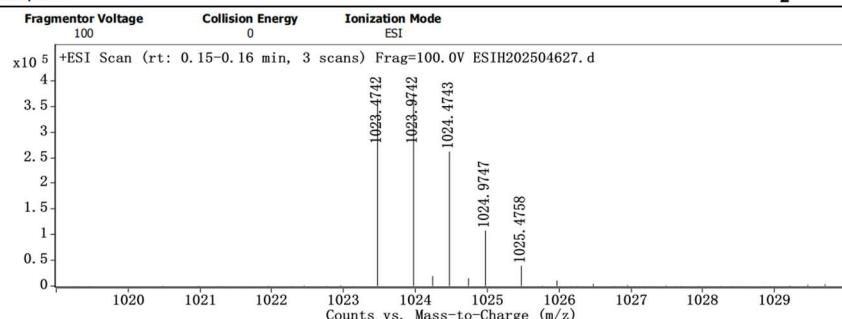
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**Sample Name** G0-O-2  
**Position** P1-A3  
**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-20231114.m

  
**ELPTQGTFSNVS**

### User Spectra



### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula	Ion
1023.4742	1023.4735	-0.68	-0.66	C85 H138 N20 O38	(M+2H)+2

--- End Of Report ---

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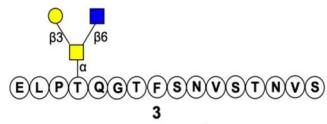
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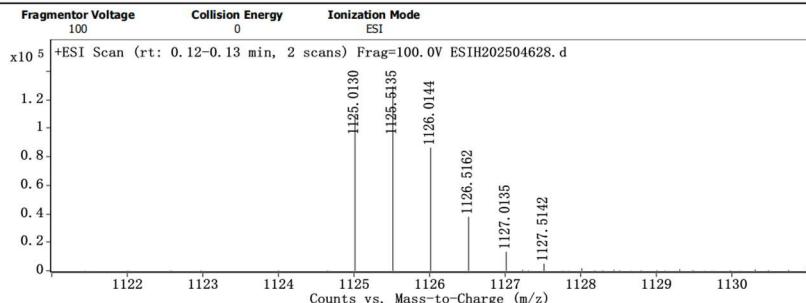
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**Comment** ESIH by huangqiongping

**Sample Name** G0-O-3  
**Position** P1-A4  
**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-2023114.m



### User Spectra



### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula	Ion
1125.013	1125.0132	0.21	0.19	C <sub>93</sub> H <sub>151</sub> N <sub>21</sub> O <sub>43</sub>	(M+2H)+2

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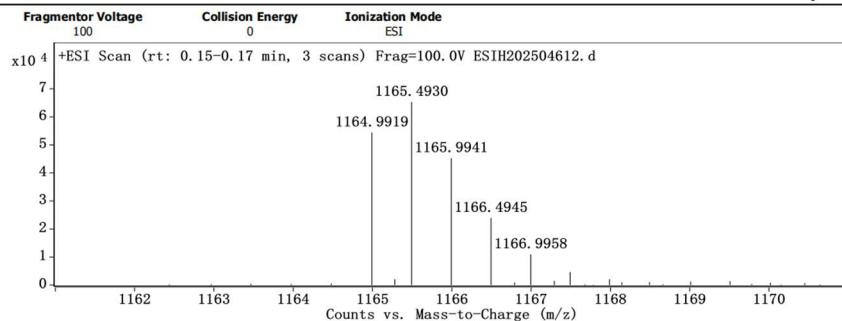
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**Sample Name** G0-S1  
**Position** P1-A6  
**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-2023114.m



### User Spectra



### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula	Ion
1164.9919	1164.9916	-0.33	-0.28	C <sub>93</sub> H <sub>151</sub> N <sub>21</sub> O <sub>46</sub> S	(M+2H)+2

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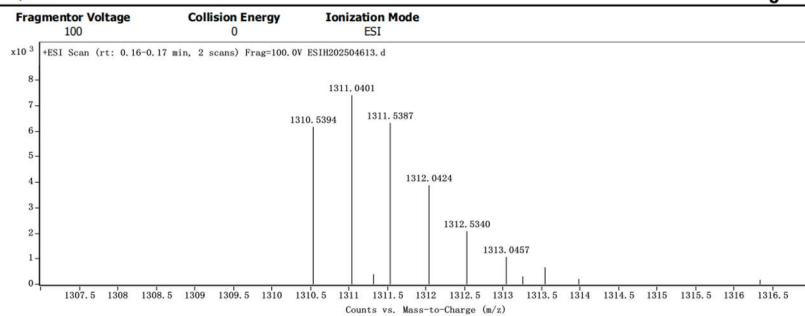
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**Sample Name** G0-S2  
**Position** P1-A7  
**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-20231114.m



### User Spectra



### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula	Ion
1310.5394	1310.5393	-0.14	-0.11	C104 H168 N22 O54 S	(M+2H)+2

--- End Of Report ---

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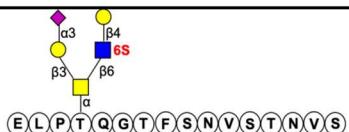
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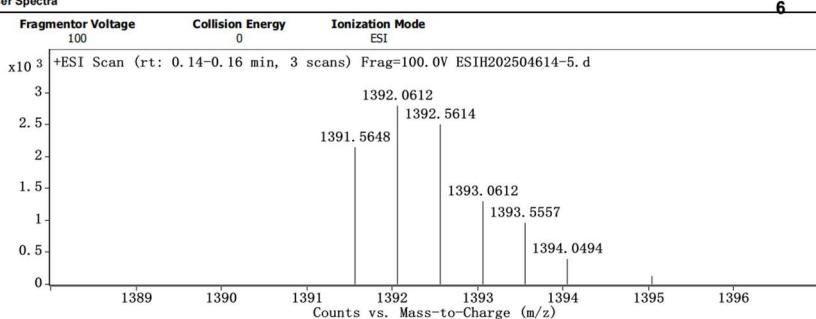
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**Comment** ESIH by huangqiongping

**Sample Name** G0-S3  
**Position** P1-A8  
**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-20231114.m



### User Spectra



### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula	Ion
1391.5648	1391.5657	0.87	0.63	C110 H178 N22 O59 S	(M+2H)+2

--- End Of Report ---

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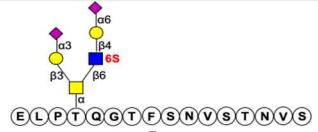
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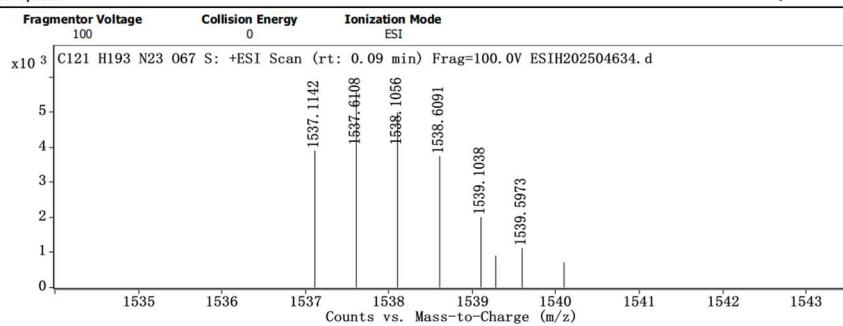
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**Comment** ESIH by huangqiongping

**Sample Name** G0-S6  
**Position** P1-B1  
**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-20231114.m



### User Spectra



### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula	Ion
1537.1142	1537.1134	-0.82	-0.53	C121 H195 N23 O67 S	(M+2H)+2

--- End Of Report ---

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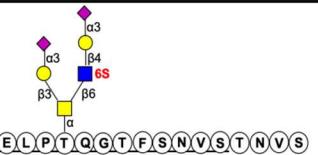
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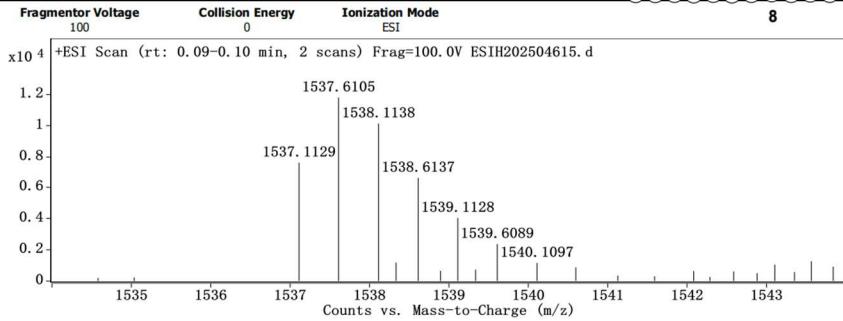
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**Comment** ESIH by huangqiongping

**Sample Name** G0-S4  
**Position** P1-A9  
**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-20231114.m



### User Spectra



### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula	Ion
1537.1129	1537.1134	0.47	0.31	C121 H195 N23 O67 S	(M+2H)+2

--- End Of Report ---

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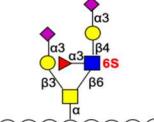
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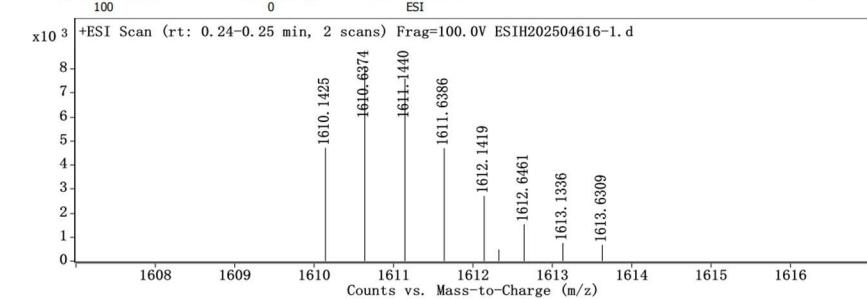
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**Position** P1-B1  
**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-20231114.m



### User Spectr

Fragmentor Voltage	Collision Energy	Ionization Mode
100	0	ESI

1



### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula		Ion	
1610.1425	1610.1424	-0.09	-0.06	C127	H205	N23	O71 S

--- End Of Report ---

 Agilent Technologies

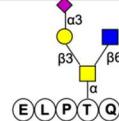
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**Comment** ESIH by huangqiongping

**Sample Name** G0-O-4  
**Position** P1-A5  
**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-2023114.m

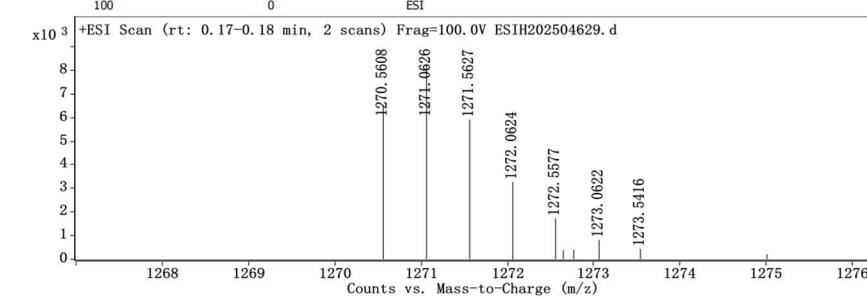


10

### User Spectr

Fragmentor Voltage	Collision Energy	Ionization Mode
100	0	ESI

10



### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula		Ion		
1270.5608	1270.5609	0.05	0.04	C104	H168	N22	O51	(M+2H)+2

--- End Of Report ---

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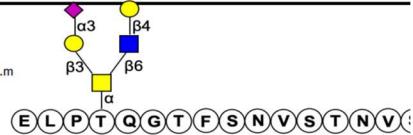
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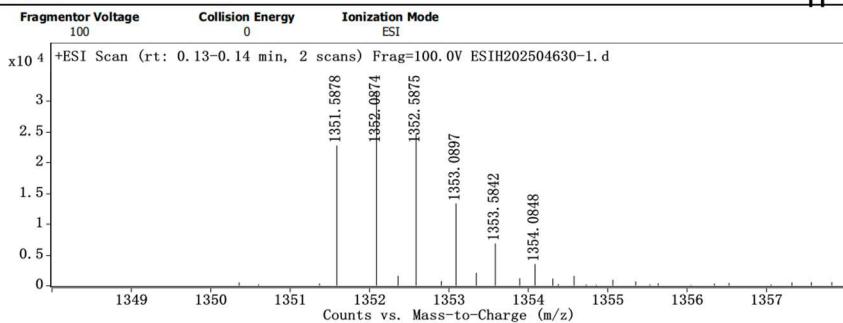
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**Comment** ESIH by huangqiongping

**Sample Name** G0-O-5  
**Position** P1-A6  
**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-20231114.m



### User Spectra



11

### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula	Ion
1351.5878	1351.5873	-0.53	-0.39	C110 H178 N22 O56	(M+2H)+2

--- End Of Report ---

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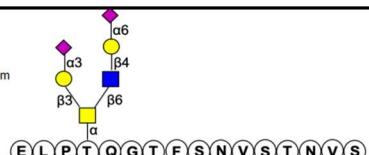
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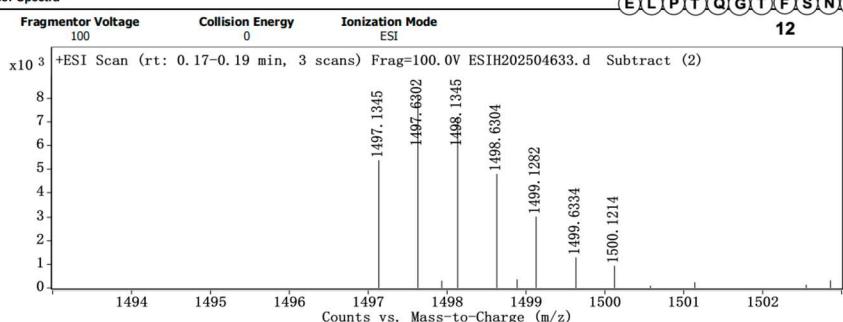
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**Comment** ESIH by huangqiongping

**Sample Name** G0-O-8  
**Position** P1-A9  
**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-20231114.m



### User Spectra



12

### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula	Ion
1497.1345	1497.135	0.52	0.35	C121 H195 N23 O64	(M+2H)+2

--- End Of Report ---

Agilent Technologies

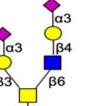
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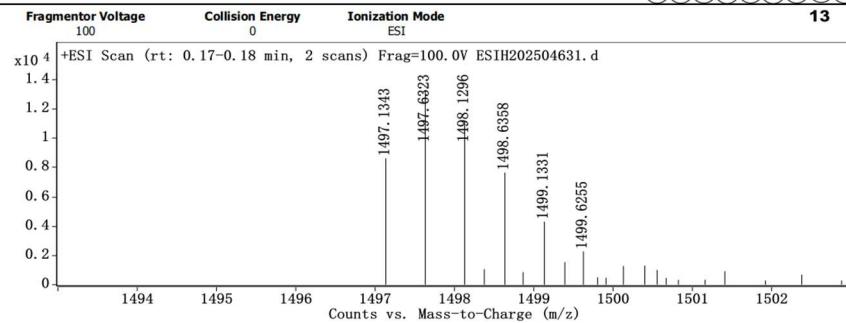
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**Position** P1-A7  
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**DA Method** ESI-HR-20231114.m



(E) (L) (P) (T) (Q) (G) (T) (F) (S) (N) (V) (S) (T) (N) (V) (S)

13

### User Spectra



### Formula Calculator Results

m/z	Calc m/z	Diff (mDa)	Diff (ppm)	Ion Formula	Ion
1497.1343	1497.135	0.75	0.5	C121 H195 N23 O64	(M+2H)+2

-- End Of Report --

Agilent Technologies

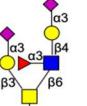
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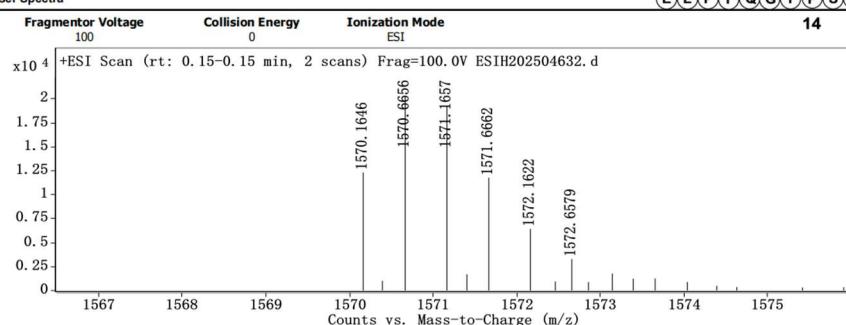
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**Position** P1-A8  
**Acq Method** 20160322\_MS\_ESIH\_POS\_1min.m  
**DA Method** ESI-HR-20231114.m



(E) (L) (P) (T) (Q) (G) (T) (F) (S) (N) (V) (S) (T) (N) (V) (S)

14

### User Spectra



### Formula Calculator Results

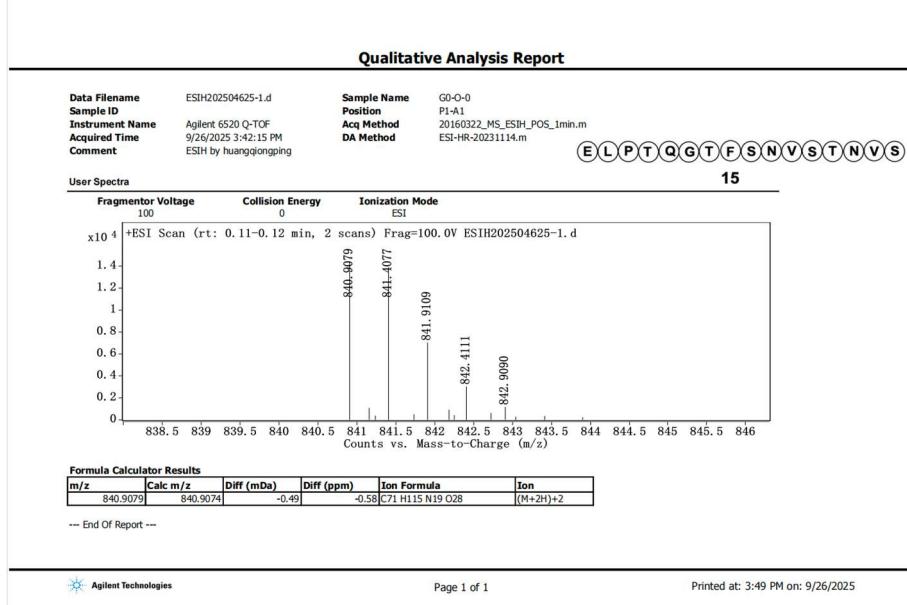
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-- End Of Report --

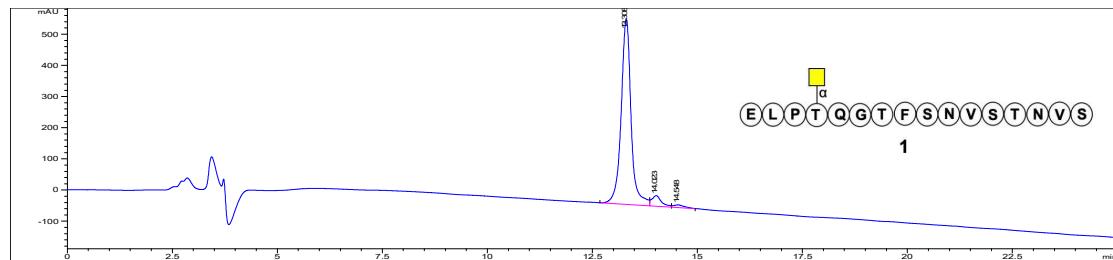
Agilent Technologies

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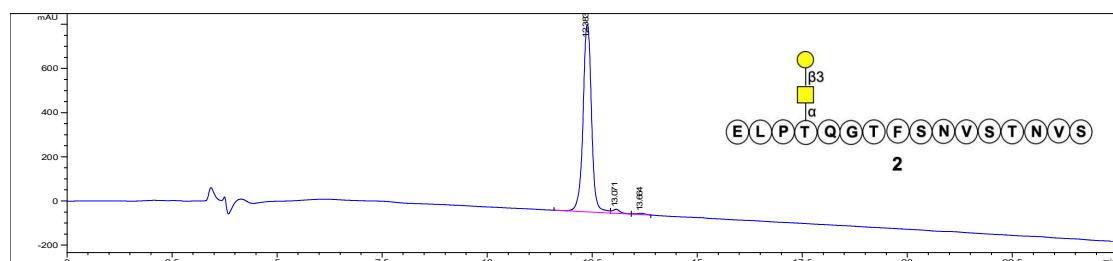
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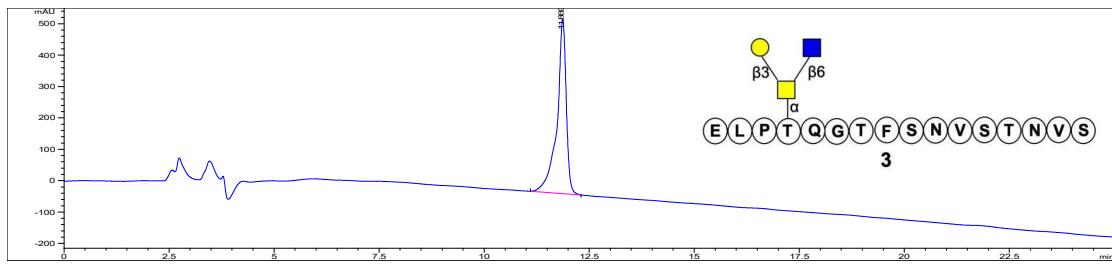
## 7. HPLC spectra of compounds 1-15



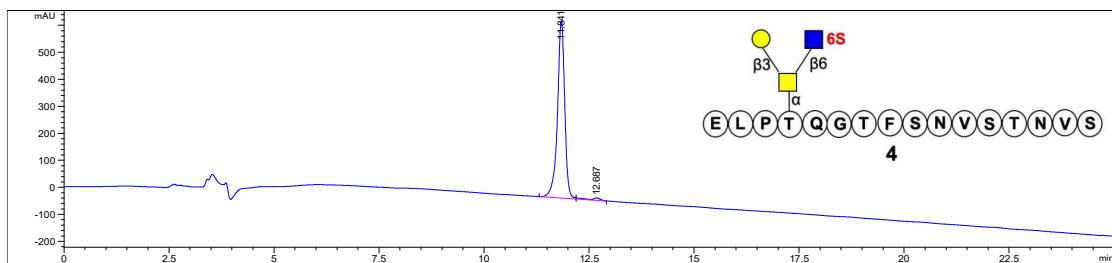
**Figure S18.** HPLC spectra of glycopeptide 1. Purity: 93.2%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



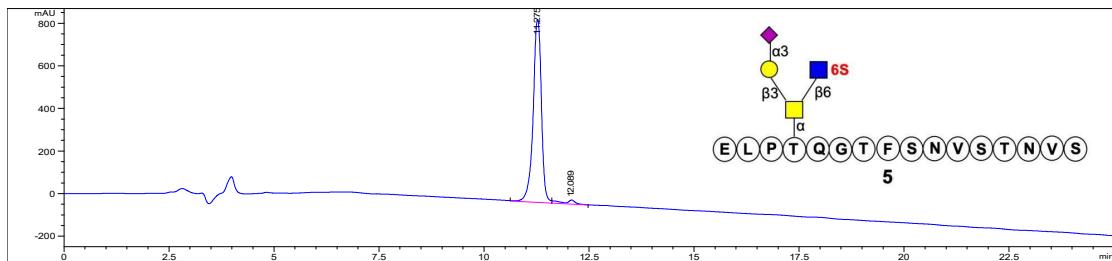
**Figure S19.** HPLC spectra of glycopeptide 2. Purity: 97.4%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



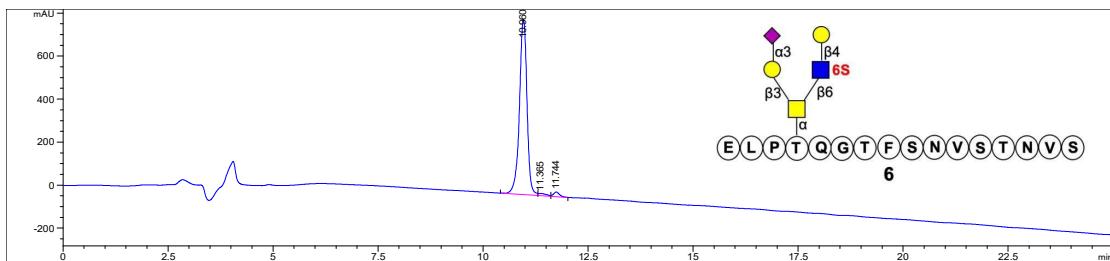
**Figure S20.** HPLC spectra of glycopeptide **3**. Purity: 99.2%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



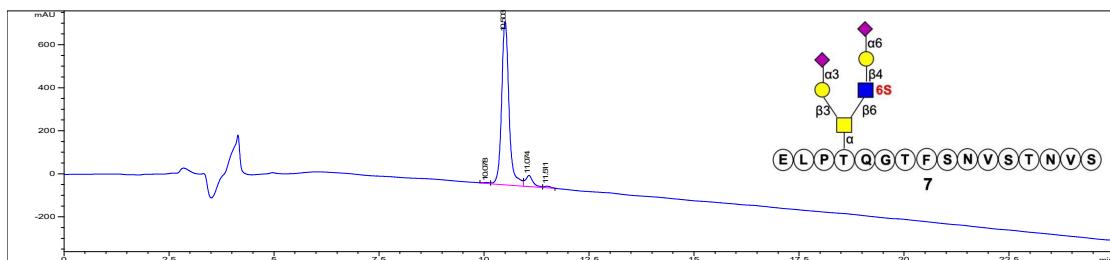
**Figure S21.** HPLC spectra of glycopeptide **4**. Purity: 97.9%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



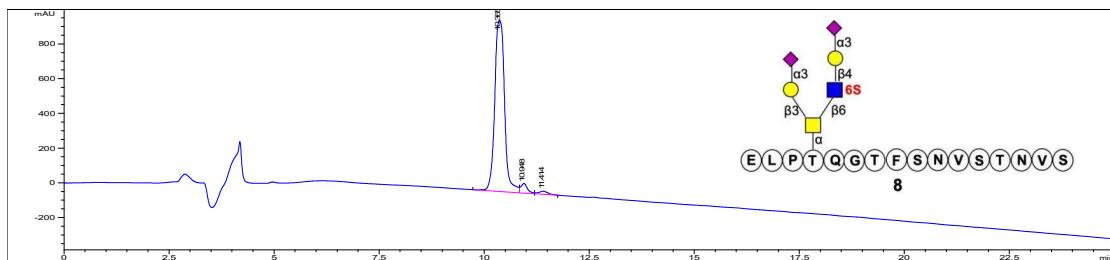
**Figure S22.** HPLC spectra of glycopeptide **5**. Purity: 97.0%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



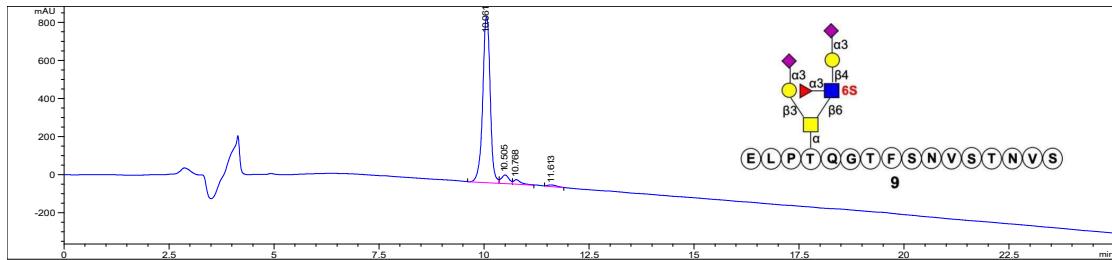
**Figure S23.** HPLC spectra of glycopeptide **6**. Purity: 96.5%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



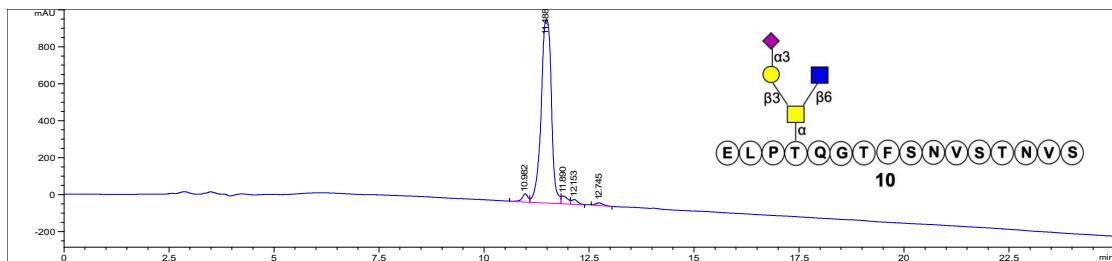
**Figure S24.** HPLC spectra of glycopeptide 7. Purity: 92.4%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



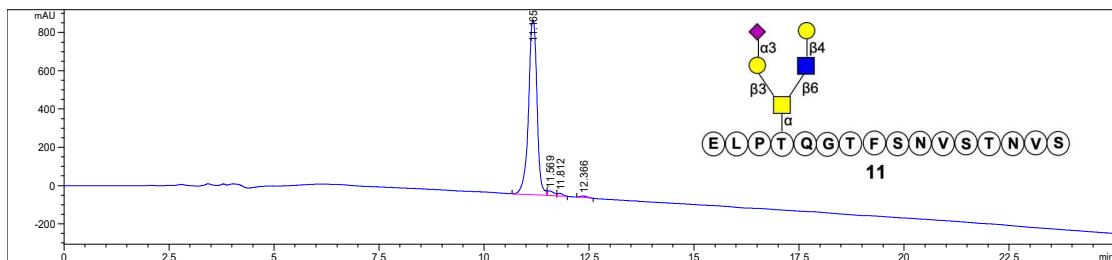
**Figure S25.** HPLC spectra of glycopeptide **8**. Purity: 94.8%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



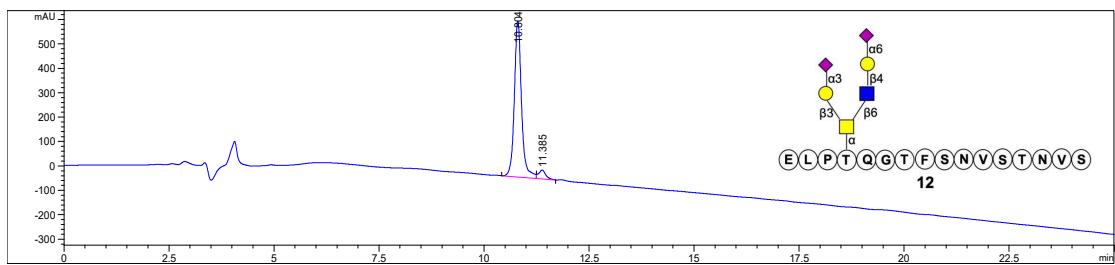
**Figure S26.** HPLC spectra of glycopeptide **9**. Purity: 91.5%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



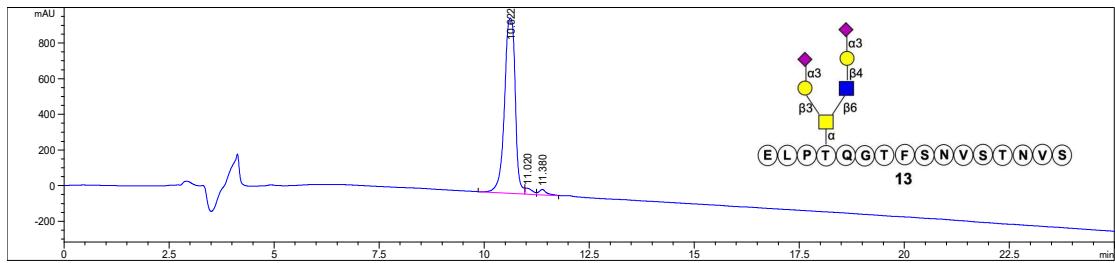
**Figure S27.** HPLC spectra of glycopeptide **10**. Purity: 92.5%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



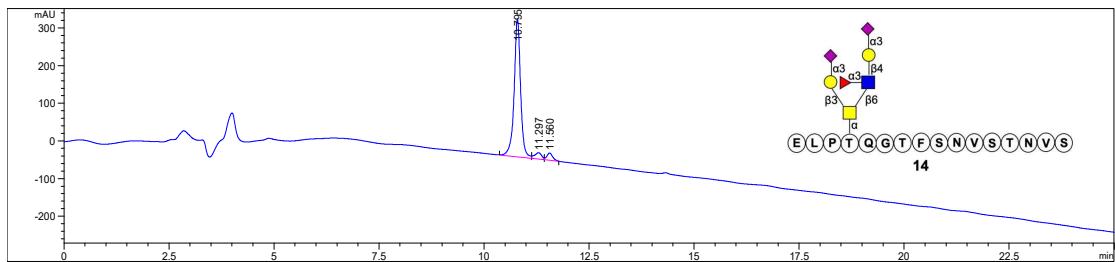
**Figure S28.** HPLC spectra of glycopeptide **11**. Purity: 96.3%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



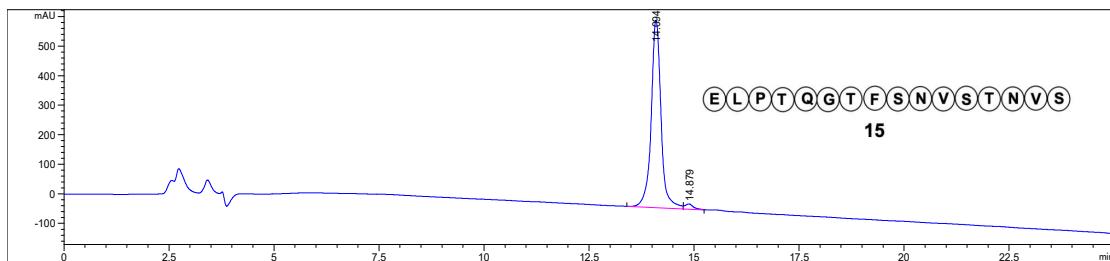
**Figure S29.** HPLC spectra of glycopeptide **12**. Purity: 94.5%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



**Figure S30.** HPLC spectra of glycopeptide **13**. Purity: 95.6%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



**Figure S31.** HPLC spectra of glycopeptide **14**. Purity: 91.2%; HPLC instrument: Agilent Technologies 1260 Infinity equipped with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.



**Figure S32.** HPLC spectra of glycopeptide **15**. Purity: 97.7% HPLC instrument: Agilent Technologies 1260 Infinity coupled with UV detector; Detection: UV absorption at 210 nm; Column: SB-C18, 5  $\mu$ m, 4.6 x 150 mm. Mobile Phase: A, 10 mM ammonium formate (pH 3.5); B, Acetonitrile. Gradient elution: B from 10% to 45% in 25 min. Flow rate: 0.5 mL/min.

## 8. Reference

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