

## Supporting Information

### Photocatalytic Acylation of Lysine Screened by a Microfluidic-Based Chemical Robotic System

Zhanfeng Hou,<sup>a†</sup> Chuan Wan,<sup>c†</sup> Heming Jiang,<sup>d†</sup> Yuena Wang,<sup>d</sup> Yun Xing,<sup>a</sup> Jinpeng Wang,<sup>a</sup> Zhihong Liu,<sup>b</sup> Xiaochun Guo,<sup>a</sup> Yuhao An,<sup>b</sup> Wei Han,<sup>a</sup> Rui Wang,<sup>b\*</sup> Xinhao Zhang,<sup>d\*</sup> Feng Yin,<sup>b,d\*</sup> Zigang Li,<sup>a,d,e\*</sup>

<sup>a</sup>State Key Laboratory of Chemical Oncogenomics, School of Chemical Biology and Biotechnology, Peking University Shenzhen Graduate School, Shenzhen 518055, China;

<sup>b</sup>Pingshan Translational Medicine Center, Shenzhen Bay Laboratory, Shenzhen 518118, China;

<sup>c</sup>College of Health Science and Environmental Engineering, Shenzhen Technology University, Shenzhen 518118, China;

<sup>d</sup>Shenzhen Bay Laboratory, Shenzhen 518132, China;

<sup>e</sup>Frontiers Medical Center, Tianfu Jincheng Laboratory, Chengdu 610212, Sichuan, China;

\*Corresponding author. Email: wangrui@szbl.ac.cn, zhangxh@szbl.ac.cn, yinfeng@pkusz.edu.cn, lizg@pkusz.edu.cn.

†These authors contributed equally to this work.

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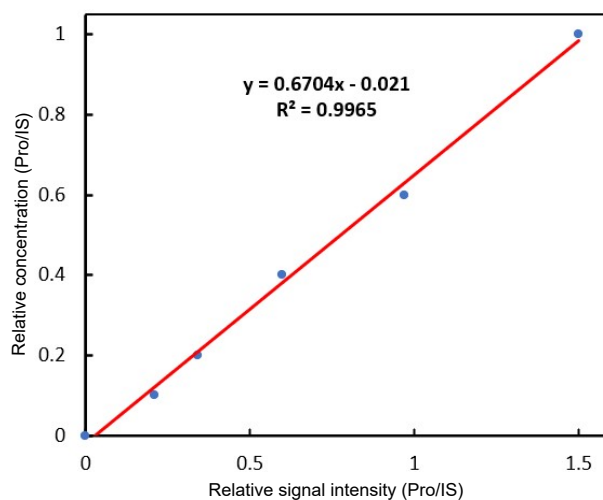
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## 1. Supporting Information for instrument and machine learning

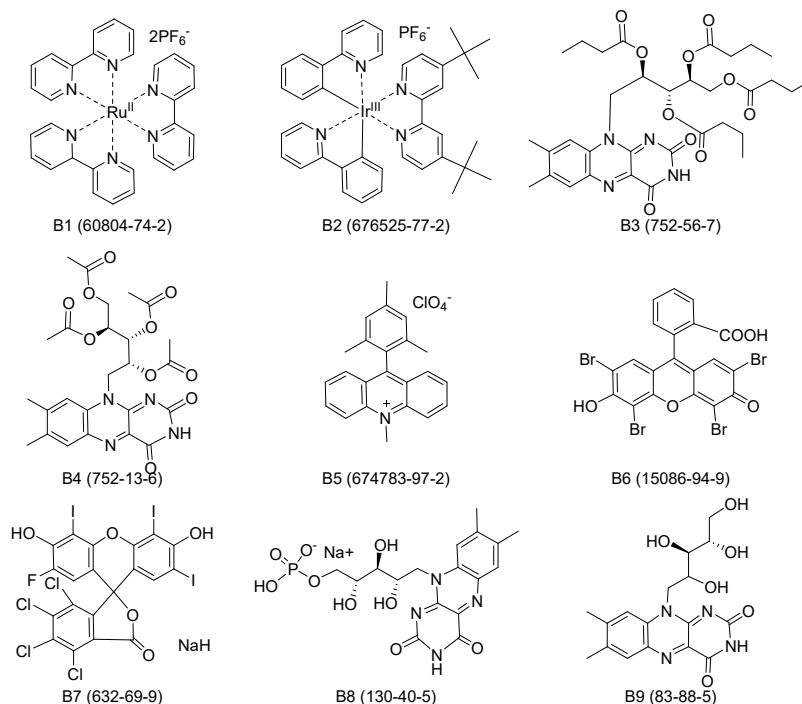


**Figure S1.** The major structure of the high-throughput microfluidic-based chemical robotic system.

The system design, configuration and application method of high-throughput microfluidic-based chemical robotic system are shown in the unpublished manuscript: Heming Jiang, Ying Chen, Meirong Huang, Tingjun Liu, Yun-Dong Wu, Xinhao Zhang. Exploring unknown chemical space with an accessible high throughput screening (OPEN-HTS) chemical robotic system.



**Figure S2.** Correlation between the relative concentration (pro/IS) of reaction mixture and the relative signal intensity detected by LC-MS.



**Figure S3.** Nine different photocatalysts (B1-B9).

**Table S1.** The Screening Results of The Total 18 Conditions.

Entry	Catalyst loading	AcSK equivalent	Time (min)	Temperature (°C)	Yield (%)
1	0.1	4	2	15	18.2
2	0.2	4	2	15	14.0
3	0.4	4	2	15	21.8
4	0.1	6	2	15	16.6
5	0.2	6	2	15	25.1
6	0.4	6	2	15	44.6
7	0.1	8	2	15	11.3
8	0.2	8	2	15	21.2
9	0.4	8	2	15	46.1
10	0.4	6	1	5	39.9
11	0.4	6	2	5	44.6
12	0.4	6	4	5	46.8
13	0.4	6	1	15	39.8
14	0.4	6	2	15	30.3
15	0.4	6	4	15	34.6
16	0.4	6	1	25	19.4
17	0.4	6	2	25	34.1
18	0.4	6	4	25	13.5

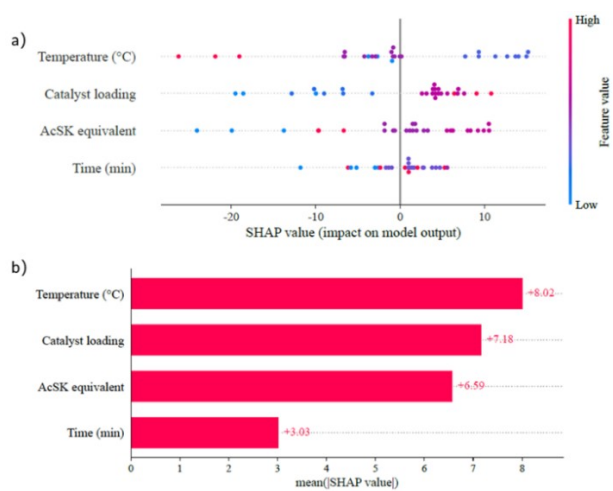
Procedure: the substrate of peptide (0.001 mmol, 1.0 equiv.), substrate AcSK (4.0, 6.0 or 8.0 equiv.) and Dibenzyl sulfoxide (0.0001 mmol, 0.2 equiv.) are added to a 4 ml clear glass vial, and then the co-solvent

of 1.0 mL (MeCN:H<sub>2</sub>O =1:1, PBS buffer, pH 7.4 ) is added. The catalyst B9 (0.1, 0.2 or 0.4 equiv.) is added to a 4 mL clear glass vial, and then the co-solvent of 1.0 mL (MeCN:H<sub>2</sub>O =1:1, PBS buffer, pH 7.4 ) is added. 9 different samples were prepared in this process. Then these 9 samples are transferred to the sample pool of the chemical robot, and reaction screening process started with sample injection and irradiation under blue LED (4.8 W) modules(5, 15 or 25 °C). In this experiments, 18 reactions with 4 variables are conducted, and the results are shown in **Table S1**.

**Table S2.** The Screening Results of The Total 9 Conditions.

Entry	Catalyst loading	AcSK equivalent	Time (min)	Temperature (°C)	Yield (%)
1	0.2	6.5	1	10	49.6
2	0.2	6.5	2	10	41.1
3	0.2	6.5	4	10	59.8
4	0.4	6.5	1	10	44.9
5	0.4	6.5	2	10	69.3
6	0.4	6.5	4	10	68.4
7	0.6	6.5	2	10	77.1
8	0.6	6.5	4	10	74.5
9	0.6	6.5	2.5	10	83.5

Procedure: the substrate of peptide (0.001 mmol, 1.0 equiv.), substrate AcSK (0.0065 mmol, 6.5 equiv.) and Dibenzyl sulfoxide (0.0001 mmol, 0.2 equiv.) are added to a 4 mL clear glass vial, and then the co-solvent of 1.0 mL (MeCN:H<sub>2</sub>O =1:1, PBS buffer, pH 7.4 ) is added. The catalyst B9 (0.2, 0.4 or 0.6 equiv.) is added to a 4 mL clear glass vial, and then the co-solvent of 1.0 mL (MeCN:H<sub>2</sub>O =1:1, PBS buffer, pH 7.4 ) is added. Then these 4 samples are transferred to the sample pool of the chemical robot, and reaction screening process started with sample injection and irradiation under blue LED (4.8 W) modules(10 °C). In this experiments, 8 reactions with 2 variables are conducted, and the results are shown in **Table S2**.



**Figure S4.** Feature importance analyzed by SHAP (with Gaussian Process Regressor model and 26 data sets in Table S1 and Table S2). a) SHAP value of 4 features: Temperature, Catalyst loading, AcSK equivalent and Time. b) mean absolute SHAP value of above 4 features.



## 2. Supporting information for organic chemistry

### 2.1 General information

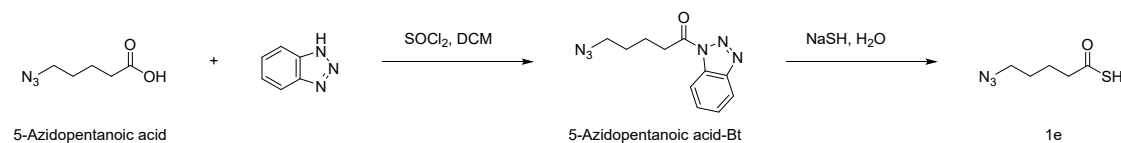
All chemical reagents are commercially available from *Energy Chemical* without purification. The reactions were monitored by TLC (silica gel-G). **Nuclear Magnetic Resonance (NMR)** spectra were recorded on Qone 400 MHz spectrometer using trimethylsilane (TMS) as internal standard under ambient temperature (20 °C). **High-Resolution Mass Spectrometry (HRMS)** were measured on a Q\_Exactive\_Focus. **Mass Spectrometry (MS)** to screen the molecular weight of HPLC fractions were carried out on SHIMAZU LC-MS 8030 in positive ion mode.

#### General method for preparative LC

Preparative LC were performed on a Shimadzu LC-6AD system equipped with Shimadzu Shim-pack GIST C18 column (20 × 250 mm, 5 μm; room temperature). Water (containing 0.1% TFA) and pure CH<sub>3</sub>CN were used as solvents in linear gradient mixtures at a flow rate of 8 mL·min<sup>-1</sup>.

### 2.2 Synthesis of thioacids

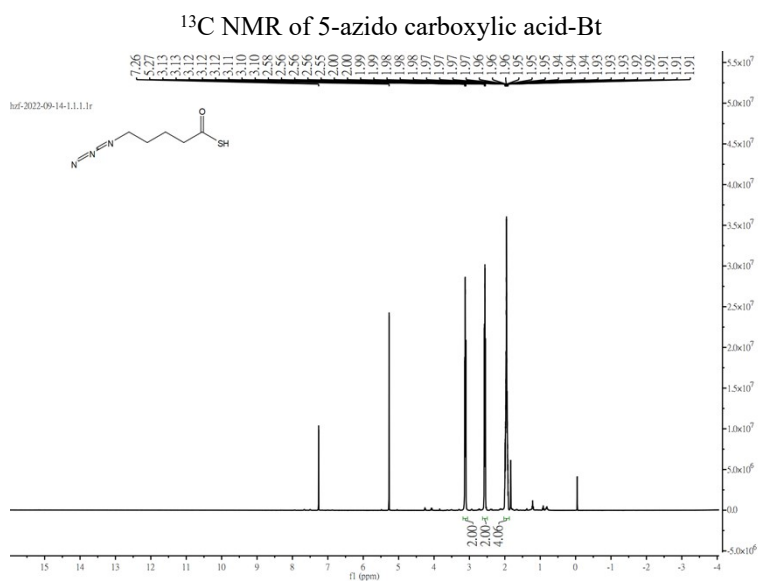
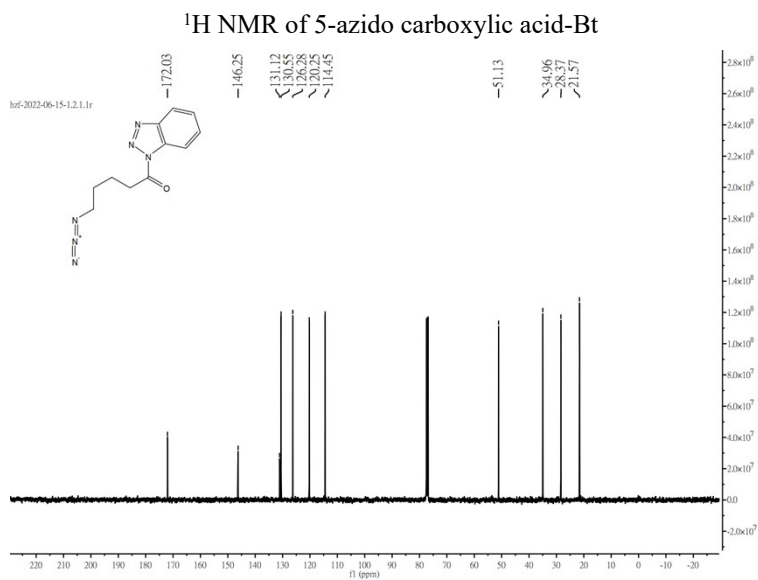
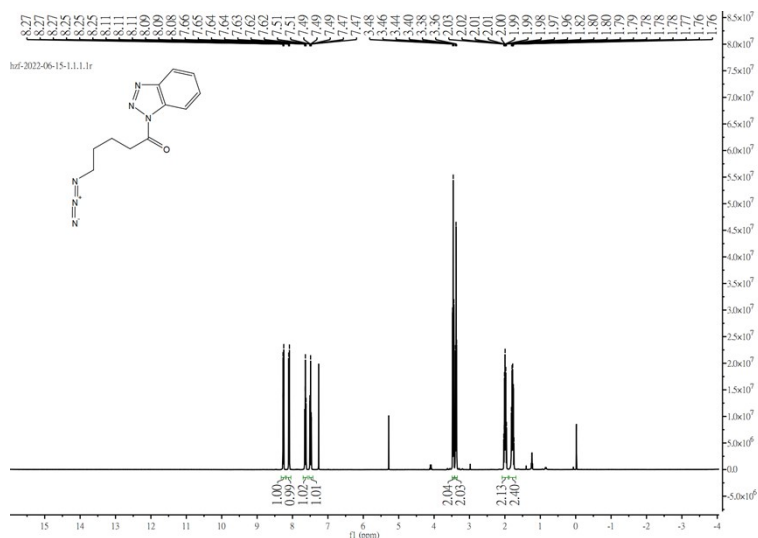
The synthesis of thioacid **1e** was followed the similar procedure of the previous reports.



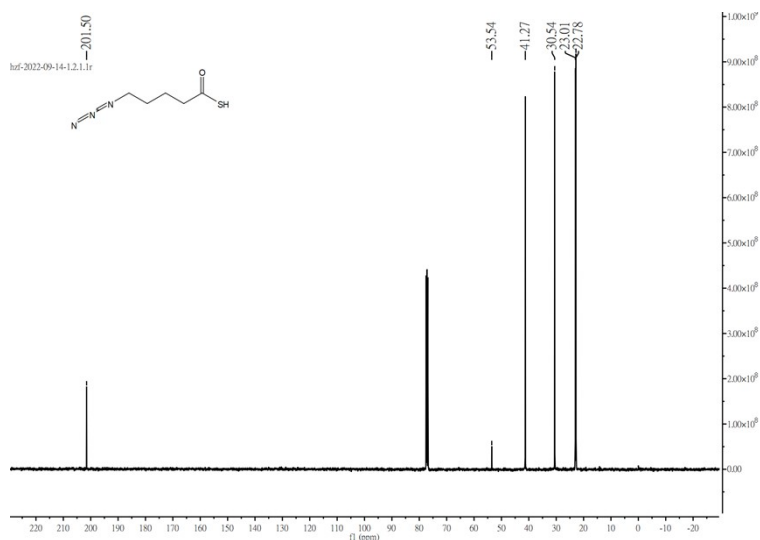
To a stirred solution of benzotriazole (1.5 g, 4.0 equiv., 12.6 mmol) in DCM (15 mL) was added SOCl<sub>2</sub> (328 mg, 1.1 equiv., 2.75 mmol) at room temperature, and the mixture was kept for 30 min. A solution of 5-azido carboxylic acid (358 mg, 1.0 equiv., 2.5 mmol) in DCM (2.5 mL) was added, and precipitation of white solid was observed from the reaction mixture after 1h. The mixture was filtered and washed with DCM, and the combined filtrate was washed with 10% NaOH aqueous solution and brine, then dried over Na<sub>2</sub>SO<sub>4</sub> and concentrated. The residue was purified by flash chromatography (eluent: EtOAc/PE = 1/20) to give the 5-azidopentanoic acid-Bt as a colorless oil (513 mg, 84% yield). <sup>1</sup>H NMR (500 MHz, Chloroform-*d*) δ 8.26 (dt, *J* = 8.2, 1.0 Hz, 1H), 8.10 (dt, *J* = 8.2, 1.0 Hz, 1H), 7.64 (ddd, *J* = 8.3, 7.1, 1.0 Hz, 1H), 7.49 (ddd, *J* = 8.2, 7.1, 1.0 Hz, 1H), 3.46 (t, *J* = 7.3 Hz, 2H), 3.38 (t, *J* = 6.7 Hz, 2H), 2.11 – 1.90 (m, 2H), 1.87 – 1.69 (m, 2H). <sup>13</sup>C NMR (101 MHz, Chloroform-*d*) δ 172.0, 146.2, 131.1, 130.6, 126.3, 120.3, 114.5, 51.1, 35.0, 28.4, 21.6.

To a stirred solution of 5-azidopentanoic acid-Bt (100 mg, 1.0 equiv., 0.4 mmol) in H<sub>2</sub>O (1 mL) was added NaSH (67 mg, 3 equiv., 1.2 mmol) at room temperature. The mixture was stirred at room temperature overnight. The mixture was added to a mixture of ethyl acetate and an aqueous solution of 1 M HCl. The organic layer was separated and the aqueous layer was extracted with ethyl acetate. The organic layers were washed with brine, dried Na<sub>2</sub>SO<sub>4</sub> and concentrated in vacuo to give the crude product **1e**. The residue was purified by flash chromatography (eluent: DCM/MeOH = 50/1) to give the **1e** as a colorless oil (32 mg, 51% yield). <sup>1</sup>H NMR (400 MHz, Chloroform-*d*) δ 3.12 (ddd, *J* = 6.4, 5.0, 1.0 Hz, 1H), 2.75 – 2.45 (m, 1H), 2.11 – 1.87 (m, 2H). <sup>13</sup>C NMR (101 MHz, Chloroform-*d*) δ 201.5, 53.5, 41.3,

30.5, 23.0, 22.8. **HRMS (ESI-TOF)** Calc. for C<sub>5</sub>H<sub>8</sub>N<sub>3</sub>OS [M-H]<sup>+</sup>, 158.0383, found, 158.0385.

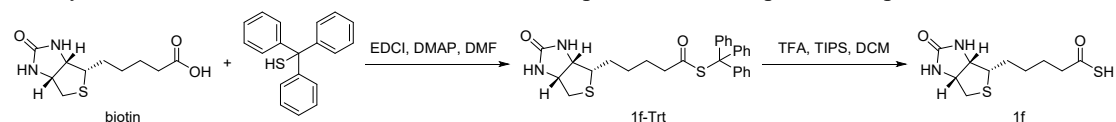






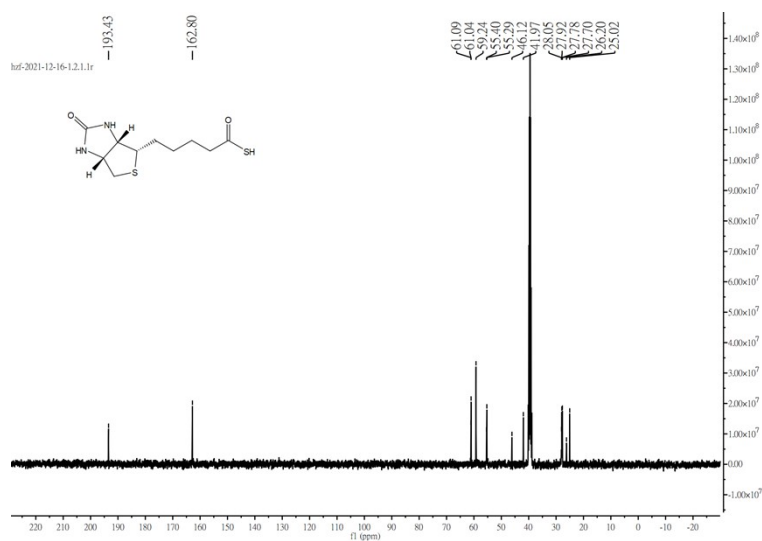
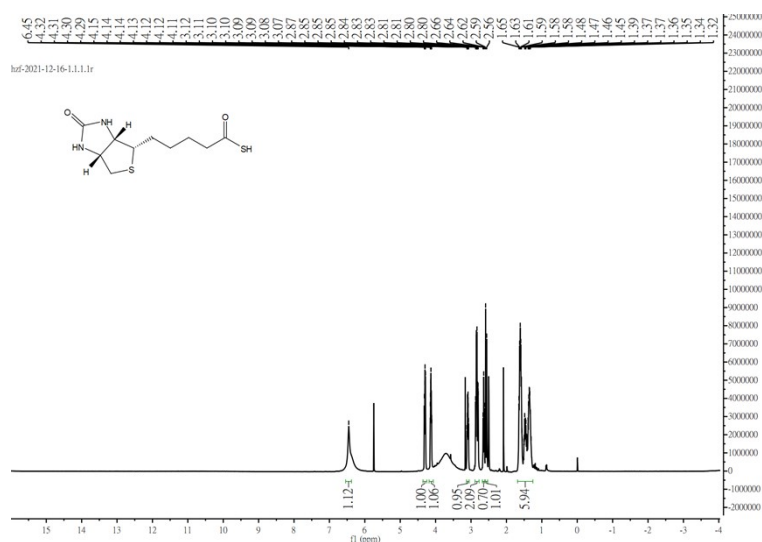
$^{13}\text{C}$  NMR of **1e**

The synthesis of thioacid **1f** was followed the similar procedure of the previous reports.



To a glass flask was added biotin (2.44 g, 1.0 equiv., 10 mmol), triphenylmethanethiol (3.04 g, 1.1 equiv., 11 mmol), EDCI (2.11 g, 1.1 equiv., 11 mmol), DMAP (122 mg, 0.1 equiv., 1 mmol) and 25 mL DMF. The mixture was stirred at room temperature overnight. After completion of the reaction, water was added and the desired product was filtered. The product biotin-Trt (4.37 g, 87%) as a white solid, was used without further purification.

To a stirred solution of biotin-Trt (503 mg, 1.0 equiv., 1 mmol) in  $\text{CH}_2\text{Cl}_2$  (3.0 mL/mmol) in a 25 mL round-bottomed flask was added TFA (1 mL), followed immediately by the addition of TIPS (317 mg, 2.0 equiv., 2 mmol). The reaction was stirred for 15 min, and the stirring bar, solvent, TFA and TIPS were removed in vacuo, maintaining the temperature below 30 °C. After completion of the reaction, ether was added and the desired product was filtered. The product **1f** (237 mg, 91%) as a white solid.  $^1\text{H}$  NMR (400 MHz,  $\text{DMSO}-d_6$ )  $\delta$  6.45 (s, 1H), 4.30 (dd,  $J = 7.7, 4.9$  Hz, 1H), 4.13 (ddd,  $J = 7.6, 4.4, 2.8$  Hz, 1H), 3.09 (ddd,  $J = 8.4, 6.2, 4.3$  Hz, 1H), 2.95 – 2.76 (m, 2H), 2.74 – 2.53 (m, 2H), 1.73 – 1.18 (m, 6H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{DMSO}-d_6$ )  $\delta$  193.4, 162.8, 61.1, 61.0, 59.2, 55.4, 55.3, 46.1, 42.0, 28.0, 27.9, 27.8, 27.7, 26.2, 25.0. HRMS (ESI-TOF) Calc. for  $\text{C}_{10}\text{H}_{15}\text{N}_2\text{O}_2\text{S}_2$   $[\text{M}-\text{H}]^+$ , 259.0569, found, 259.0578.



### 2.3 General procedure A for the light promoted amidation by thioacids

To a glass flask was added thioacid **1** (1 mmol), amine compound **2** (0.5 mmol), RFTA (5% mol),  $\text{Na}_3\text{PO}_4$  (1 mmol) and 8 mL water. The flask was then sealed and equipped with magnetic bar. The reaction was stirred and irradiated with 450 nm blue LED light (16 W) for 30 min. For the substrate **2a-2d**, the resulting aqueous solution was extracted by EtOAc ( $3 \times 10$  mL). The organic phase was collected, and dried by  $\text{Na}_2\text{SO}_4$ . After concentration under vacuum, the crude product was purified by flash column chromatography using eluent solution Hexane/EtOAc (10:1). For the substrate **2e-2j**, the resulting solution was purified directly via preparative HPLC after filtration. Desired distillates were identified by MS and lyophilized to obtain target products **3**.

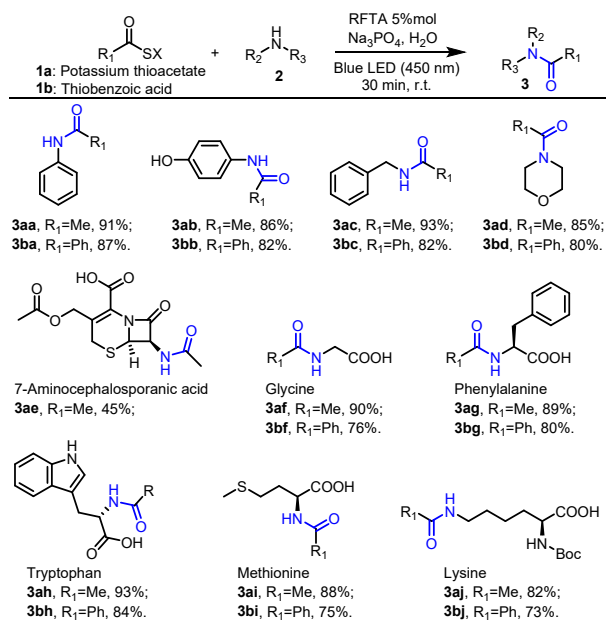
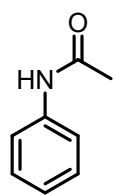
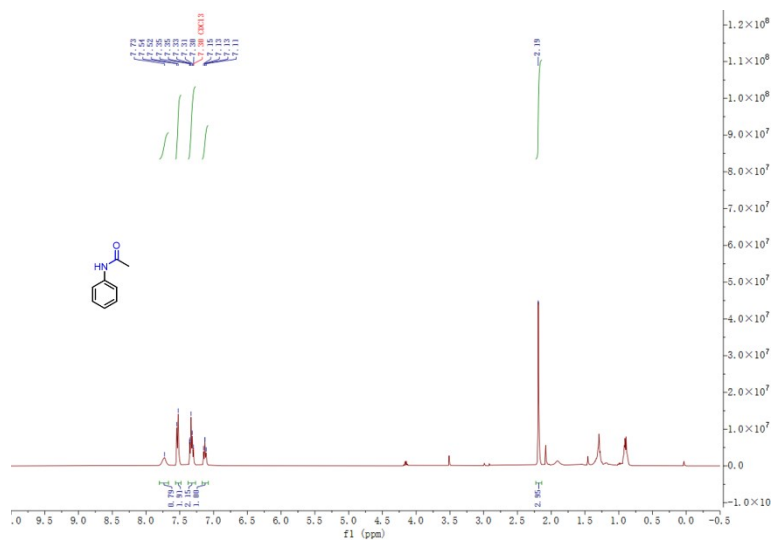


Figure S5 Scope of the acylation between thioacids and micromolecules.

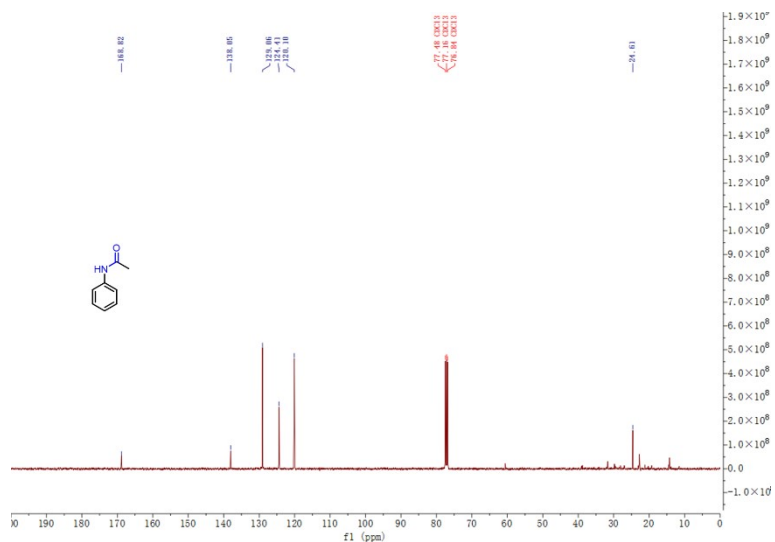
### 2.3.1 NMR spectra of acylation of amino compounds



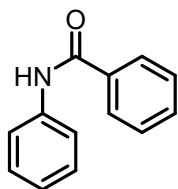
**3aa,** yellow oil, 91%. <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ 7.73 (s, 1H), 7.53 (d, *J* = 8.0 Hz, 2H), 7.38 – 7.27 (m, 2H), 7.17 – 7.08 (m, 1H), 2.19 (s, 3H). <sup>13</sup>C NMR (101 MHz, CDCl<sub>3</sub>) δ 168.8, 138.1, 129.1, 124.4, 120.1, 24.6.



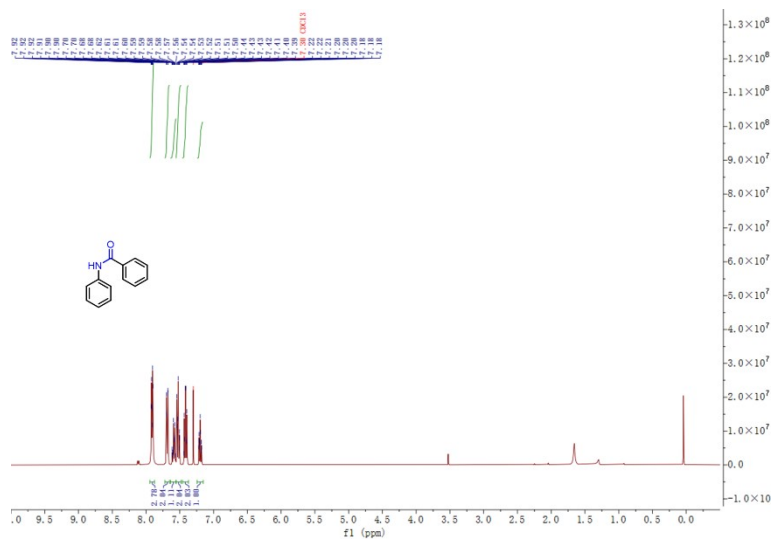
<sup>1</sup>H NMR spectrum of **3aa**



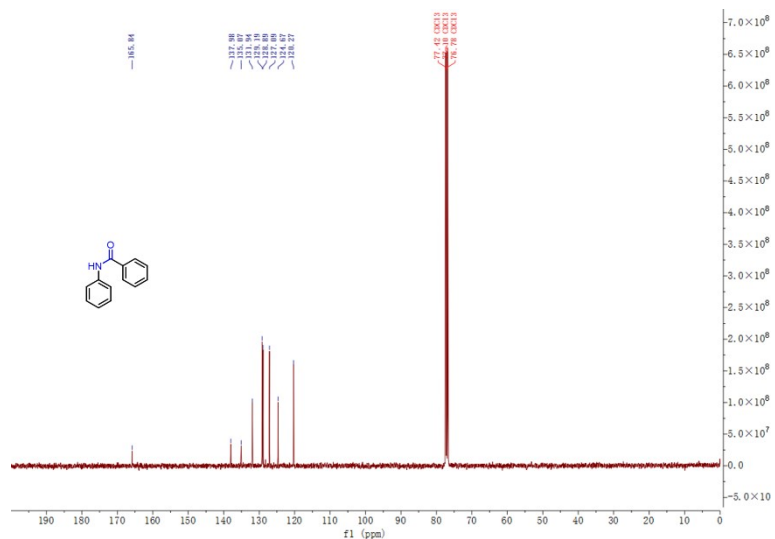
$^{13}\text{C}$  NMR spectrum of 3aa



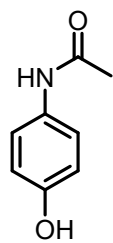
**3ba**, yellow solid, 87%.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.91 (dd,  $J = 7.0, 1.7$  Hz, 3H), 7.72 – 7.65 (m, 2H), 7.64 – 7.56 (m, 1H), 7.56 – 7.48 (m, 2H), 7.46 – 7.37 (m, 2H), 7.20 (td,  $J = 7.4, 1.2$  Hz, 1H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  165.8, 138.0, 135.1, 131.9, 129.2, 128.9, 127.1, 124.7, 120.3.



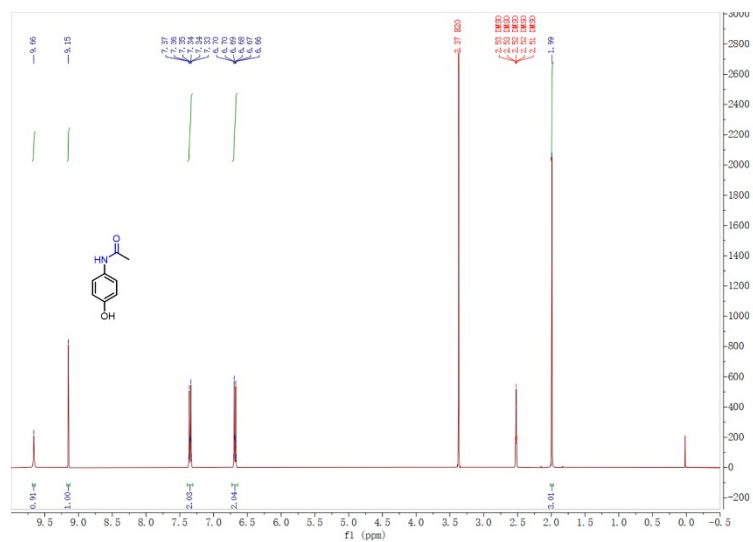
$^1\text{H}$  NMR spectrum of 3ba



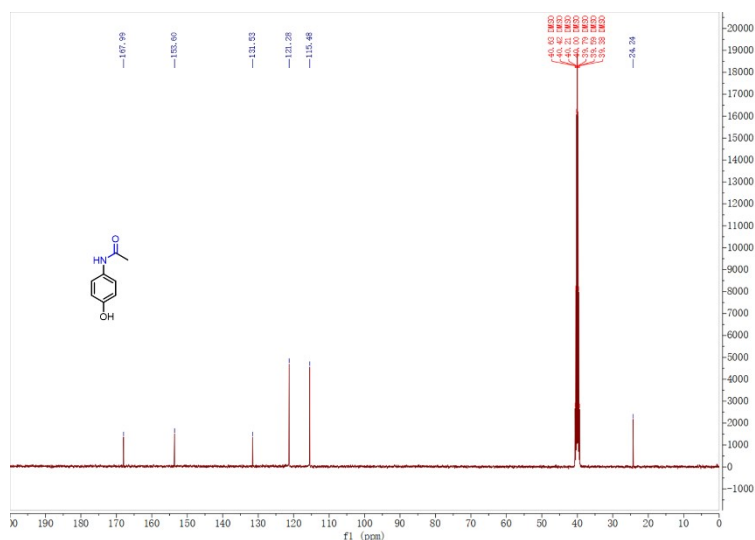
$^{13}\text{C}$  NMR spectrum of **3ba**



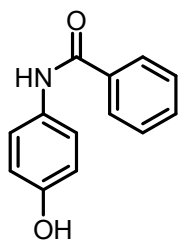
**3ab**, white solid, 86%.  $^1\text{H}$  NMR (400 MHz,  $\text{DMSO-}d_6$ )  $\delta$  9.66 (s, 1H), 9.15 (s, 1H), 7.39 – 7.31 (m, 2H), 6.73 – 6.64 (m, 2H), 1.99 (s, 3H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{DMSO-}d_6$ )  $\delta$  168.0, 153.6, 131.5, 121.3, 115.5, 24.2.



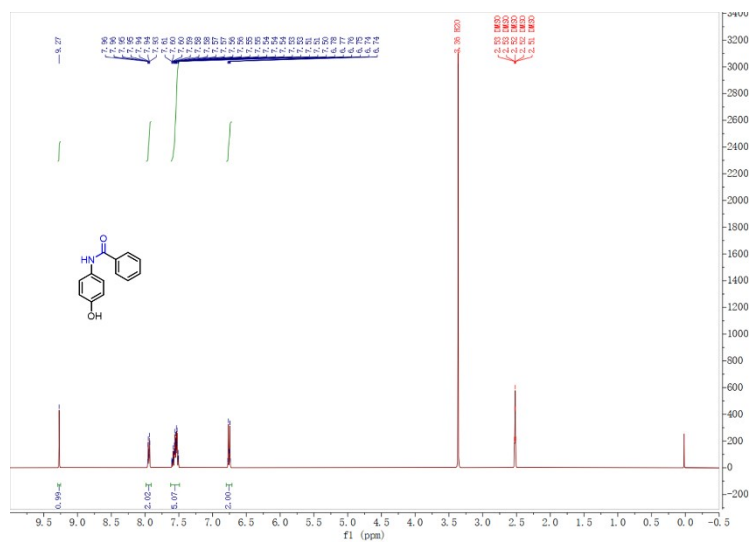
$^1\text{H}$  NMR spectrum of **3ab**



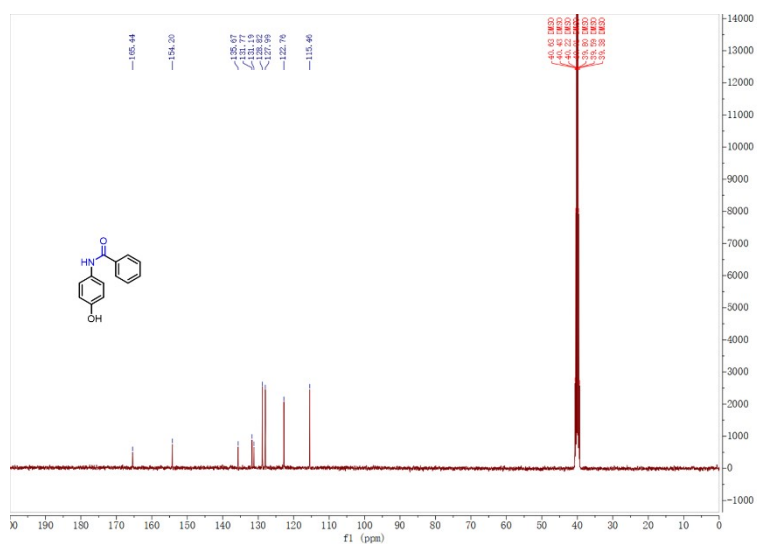
$^{13}\text{C}$  NMR spectrum of **3ab**



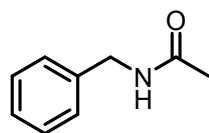
**3bb**, gray solid, 82%.  $^1\text{H}$  NMR (400 MHz,  $\text{DMSO-}d_6$ )  $\delta$  10.04 (s, 1H), 9.27 (s, 1H), 7.98 – 7.91 (m, 2H), 7.62 – 7.49 (m, 5H), 6.80 – 6.71 (m, 2H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{DMSO-}d_6$ )  $\delta$  165.4, 154.2, 135.7, 131.8, 131.2, 128.8, 128.0, 122.8, 115.5.



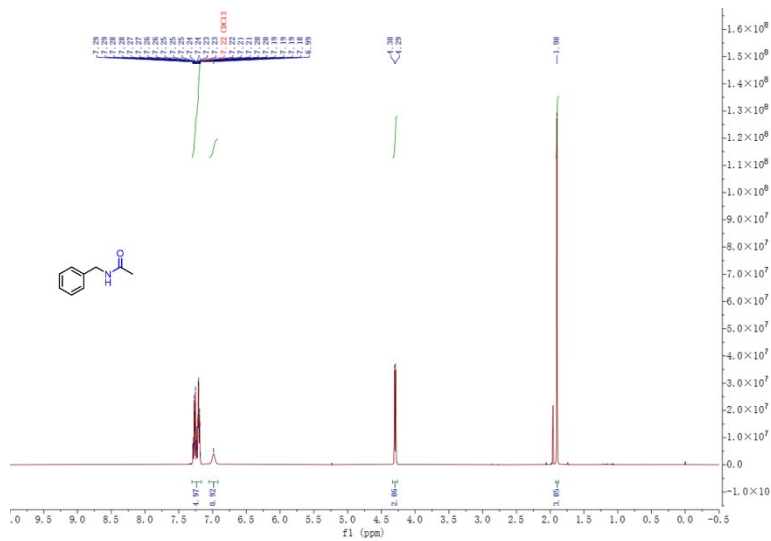
$^1\text{H}$  NMR spectrum of **3bb**



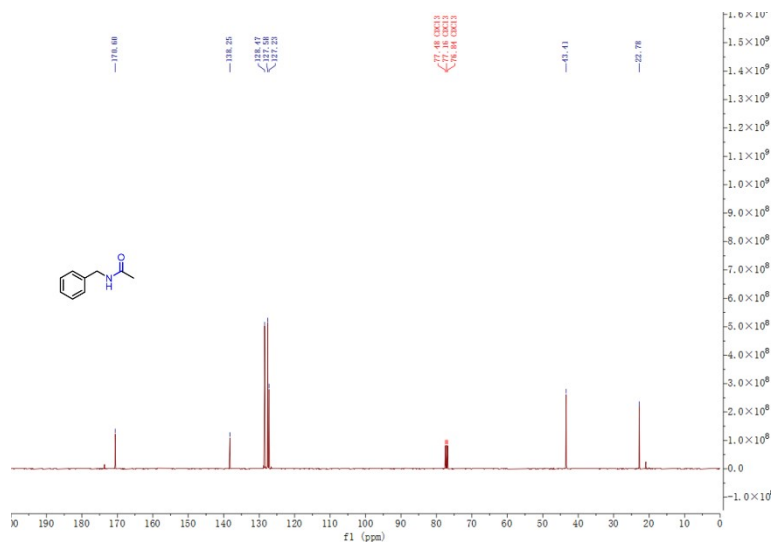
<sup>13</sup>C NMR spectrum of **3bb**



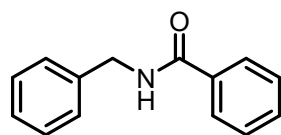
**3ac**, yellow oil, 93%. <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ 7.31 – 7.17 (m, 5H), 6.99 (s, 1H), 4.30 (d, *J* = 5.8 Hz, 2H), 1.90 (s, 3H). <sup>13</sup>C NMR (101 MHz, CDCl<sub>3</sub>) δ 170.6, 138.3, 128.5, 127.6, 127.2, 43.4, 22.8.



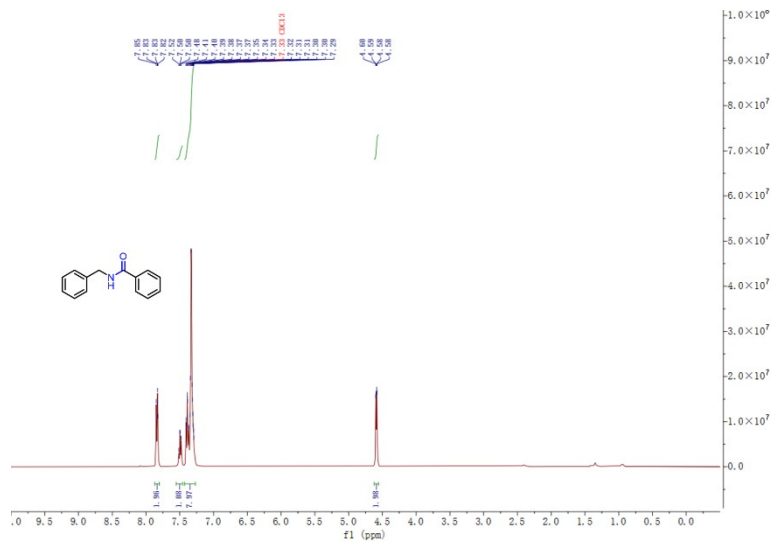
<sup>1</sup>H NMR spectrum of **3ac**



$^{13}\text{C}$  NMR spectrum of **3ac**

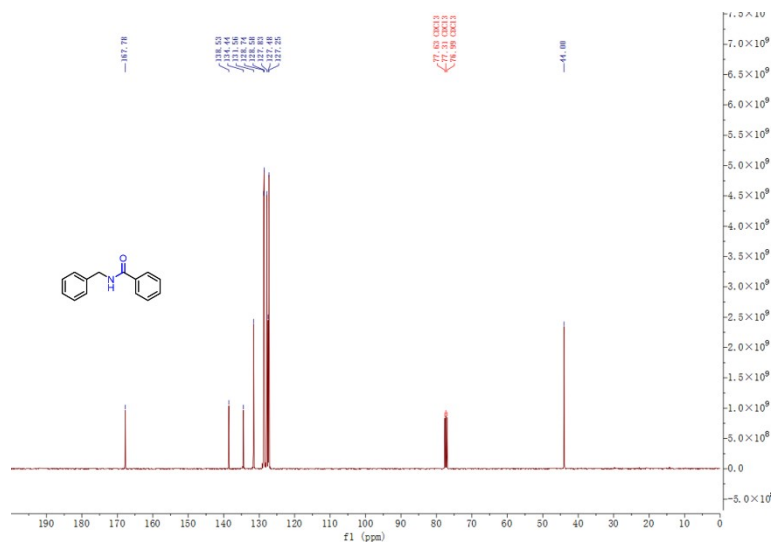


**3bc**, yellow solid, 82%.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.87 – 7.80 (m, 2H), 7.55 – 7.46 (m, 1H), 7.43 – 7.27 (m, 8H), 4.59 (dd,  $J = 5.9, 1.7$  Hz, 2H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  167.8, 138.5, 134.4, 131.6, 128.7, 128.6, 127.8, 127.5, 127.3, 44.0.

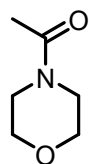


$^1\text{H}$  NMR spectrum of **3bc**

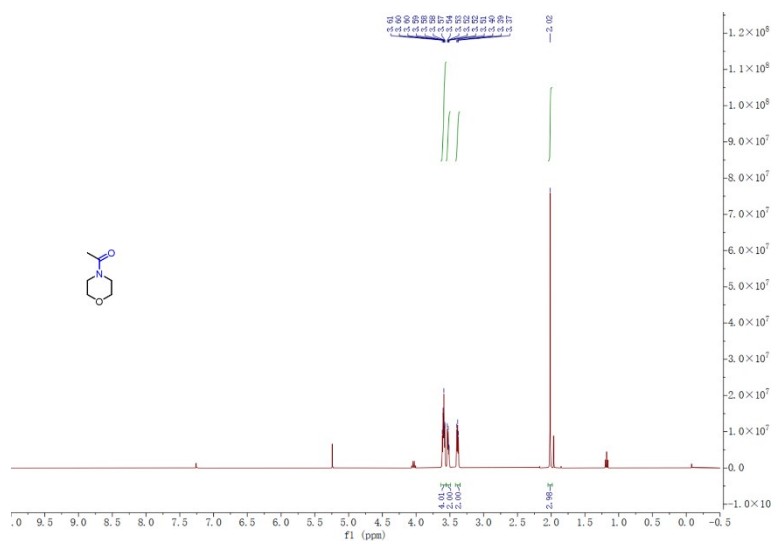




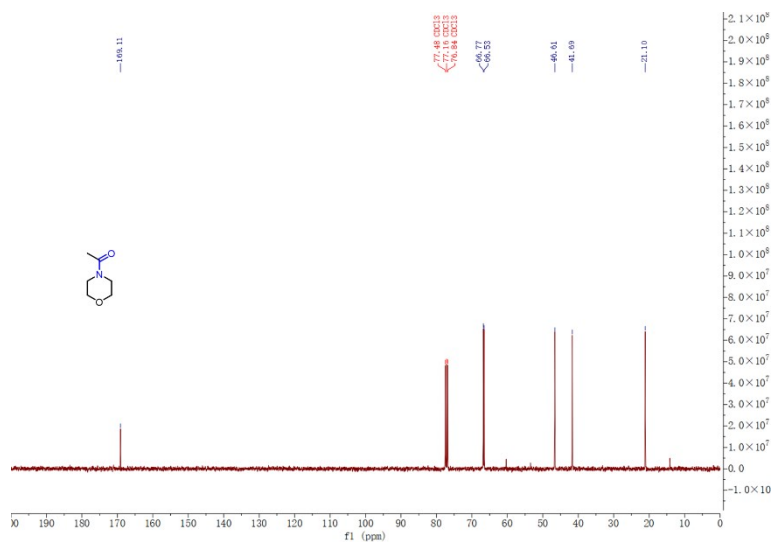
$^{13}\text{C}$  NMR spectrum of **3bc**



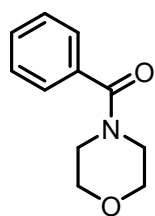
**3ad**, yellow oil, 85%.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  3.63 – 3.55 (m, 4H), 3.53 (dd,  $J = 6.3, 4.2$  Hz, 2H), 3.42 – 3.35 (m, 2H), 2.02 (s, 3H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  169.1, 66.8, 66.5, 46.6, 41.7, 21.1.



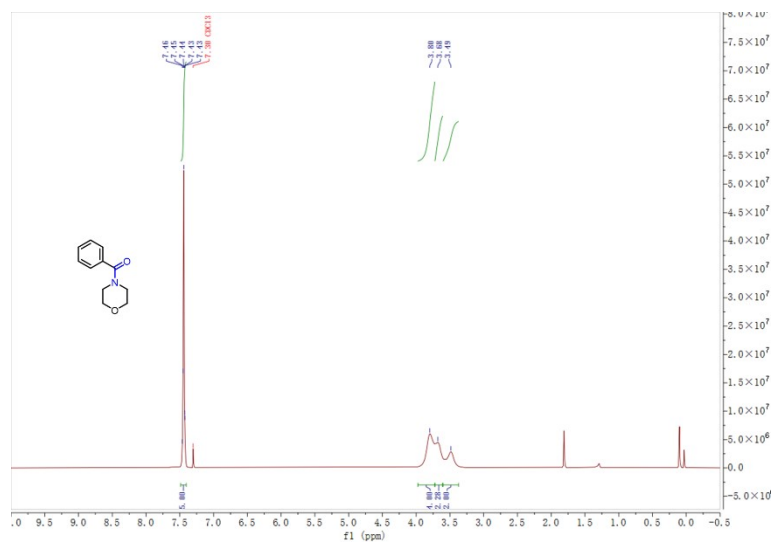
$^1\text{H}$  NMR spectrum of **3ad**



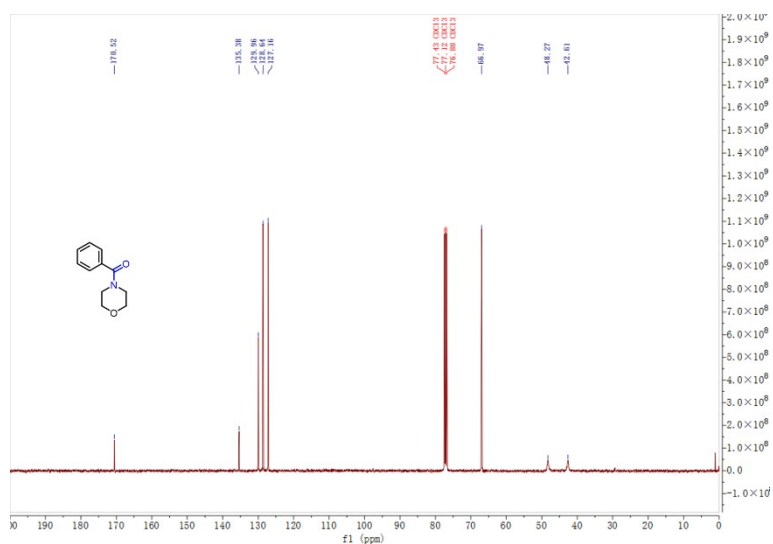
$^{13}\text{C}$  NMR spectrum of **3ad**



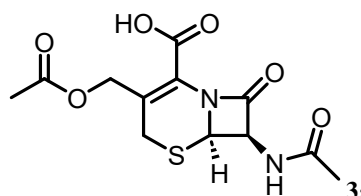
**3bd**, yellow solid, 80%.  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.45 (d,  $J = 3.9$  Hz, 5H), 3.80 (s, 4H), 3.68 (s, 2H), 3.49 (s, 2H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{CDCl}_3$ )  $\delta$  170.5, 135.4, 130.0, 128.6, 127.2, 67.0, 48.3, 42.6.



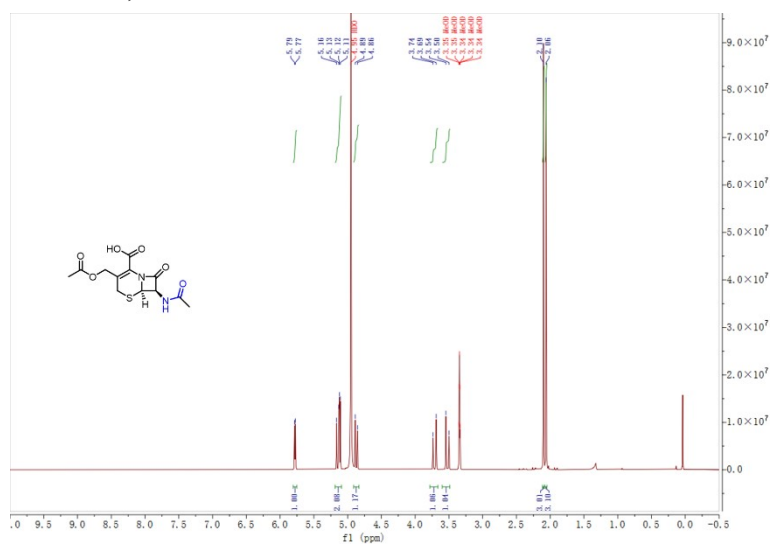
$^1\text{H}$  NMR spectrum of **3bd**



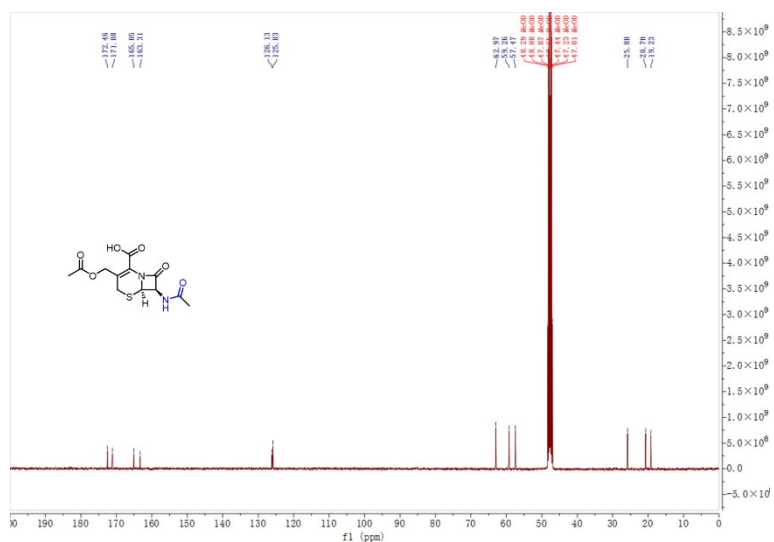
$^{13}\text{C}$  NMR spectrum of **3bd**



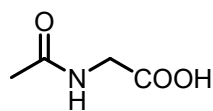
**3ae**, white powder, 45%.  $^1\text{H}$  NMR (400 MHz, Methanol- $d_4$ )  $\delta$  5.78 (d,  $J$  = 4.8 Hz, 1H), 5.19 – 5.09 (m, 2H), 4.87 (d,  $J$  = 13.1 Hz, 1H), 3.71 (d,  $J$  = 18.3 Hz, 1H), 3.52 (d,  $J$  = 18.3 Hz, 1H), 2.10 (s, 3H), 2.06 (s, 3H).  $^{13}\text{C}$  NMR (101 MHz, Methanol- $d_4$ )  $\delta$  172.5, 171.1, 165.1, 163.3, 126.1, 125.8, 63.0, 59.3, 57.5, 25.8, 20.7, 19.2. HRMS  $m/z$  (ESI-TOF):  $[\text{M}+\text{H}]^+$  calcd for  $\text{C}_{12}\text{H}_{14}\text{O}_6\text{N}_2\text{SNa}^+$  337.0465, found 337.0466.



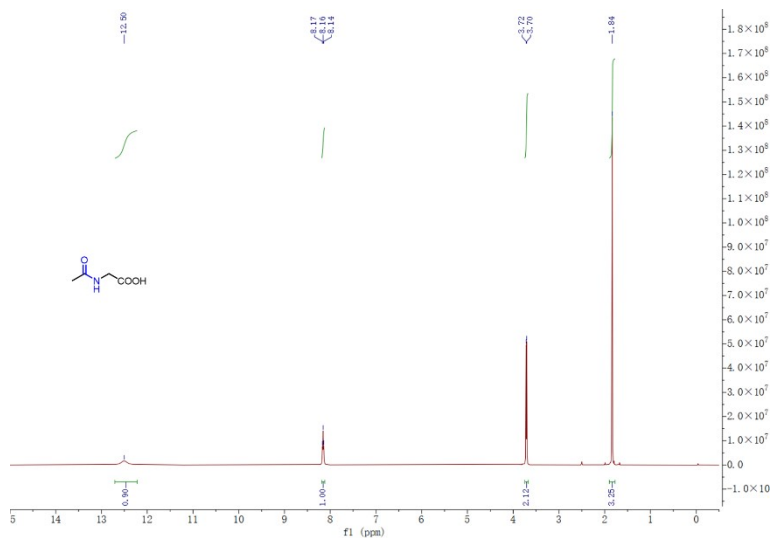
$^1\text{H}$  NMR spectrum of **3ae**



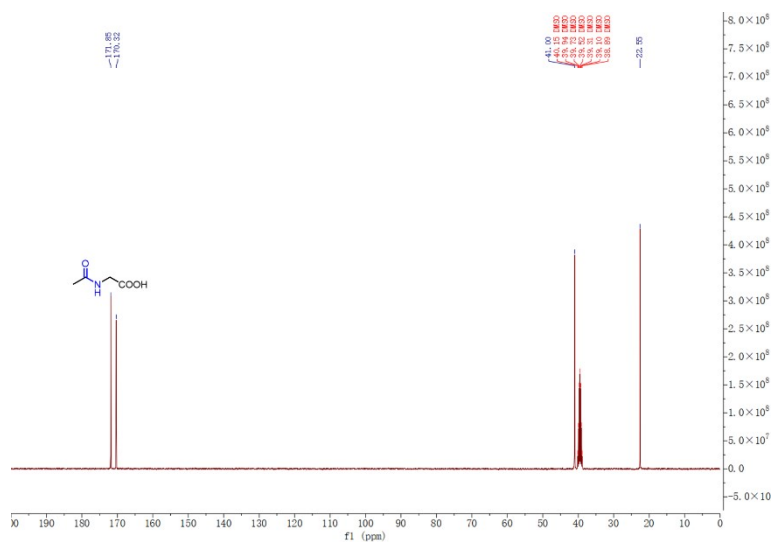
$^{13}\text{C}$  NMR spectrum of **3ae**



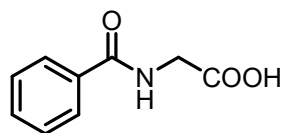
**3af**, white powder, 90%.  $^1\text{H}$  NMR (400 MHz,  $\text{DMSO-}d_6$ )  $\delta$  12.50 (s, 1H), 8.16 (t,  $J$  = 5.9 Hz, 1H), 3.71 (d,  $J$  = 6.0 Hz, 2H), 1.84 (s, 3H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{DMSO-}d_6$ )  $\delta$  171.9, 170.3, 41.0, 22.6.



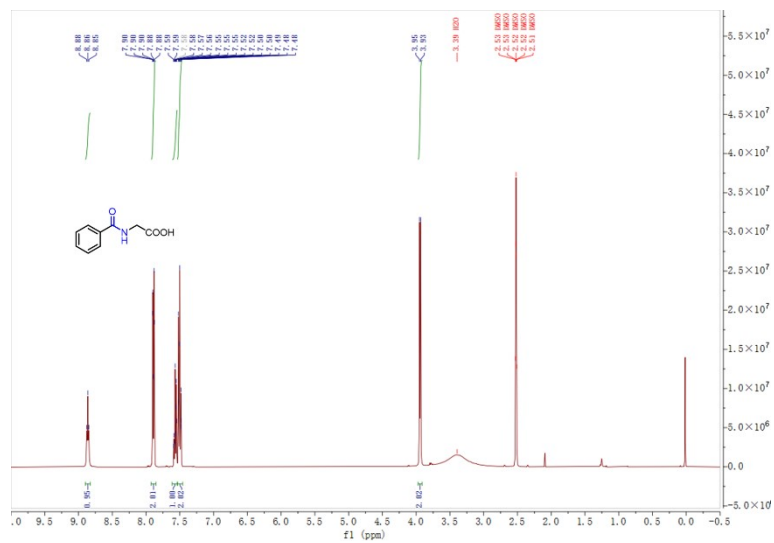
$^1\text{H}$  NMR spectrum of **3af**



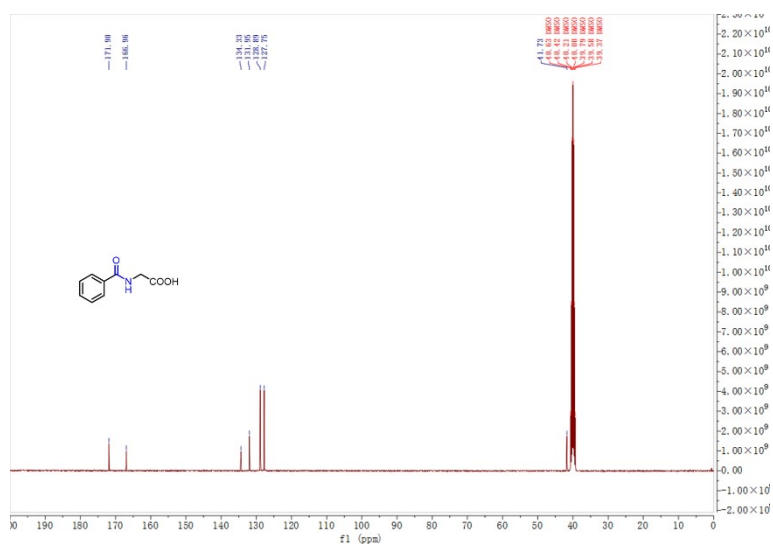
$^{13}\text{C}$  NMR spectrum of **3af**



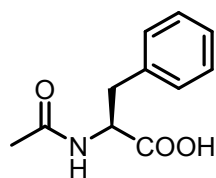
**3bf**, white powder, 76%.  $^1\text{H}$  NMR (400 MHz,  $\text{DMSO}-d_6$ )  $\delta$  8.86 (t,  $J = 5.9$  Hz, 1H), 7.92 – 7.85 (m, 2H), 7.61 – 7.54 (m, 1H), 7.50 (dd,  $J = 8.2, 6.6$  Hz, 2H), 3.94 (d,  $J = 5.9$  Hz, 2H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{DMSO}-d_6$ )  $\delta$  171.9, 167.0, 134.3, 132.0, 128.9, 127.8, 41.7.



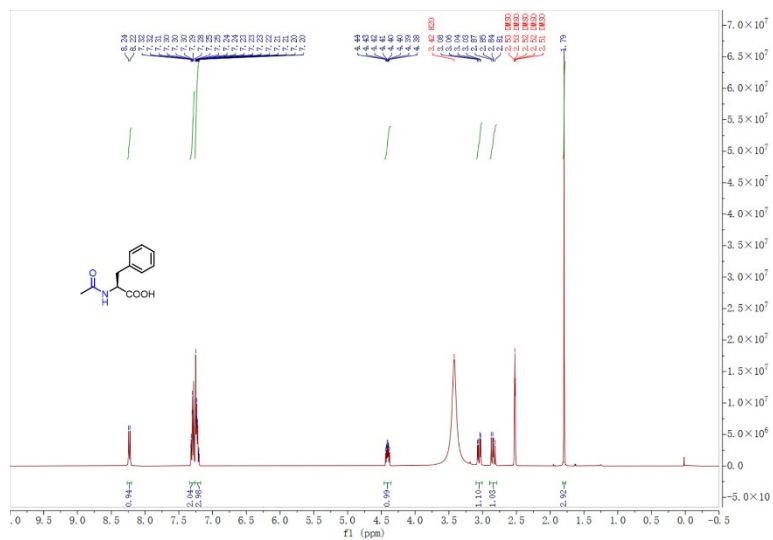
$^1\text{H}$  NMR spectrum of **3bf**



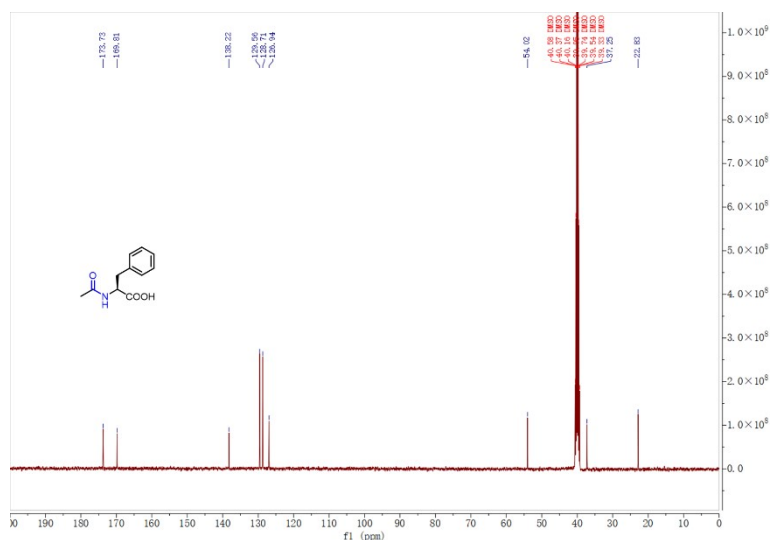
$^{13}\text{C}$  NMR spectrum of **3bf**



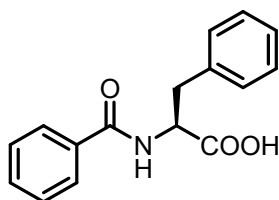
**3ag**, white powder, 89%.  $^1\text{H}$  NMR (400 MHz,  $\text{DMSO}-d_6$ )  $\delta$  8.23 (d,  $J = 8.1$  Hz, 1H), 7.34 – 7.26 (m, 2H), 7.26 – 7.18 (m, 3H), 4.41 (ddd,  $J = 9.5, 8.0, 4.9$  Hz, 1H), 3.05 (dd,  $J = 13.8, 4.9$  Hz, 1H), 2.84 (dd,  $J = 13.8, 9.6$  Hz, 1H), 1.79 (s, 3H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{DMSO}-d_6$ )  $\delta$  173.7, 169.8, 138.2, 129.6, 128.7, 126.9, 54.0, 37.3, 22.8.



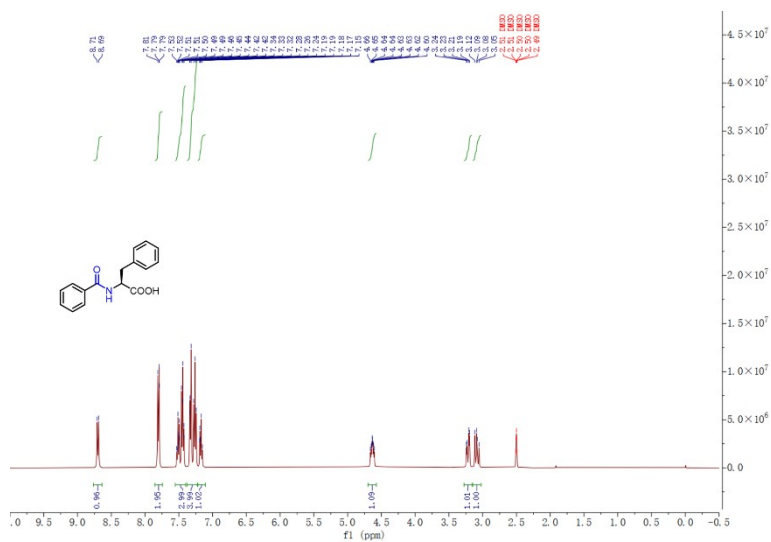
$^1\text{H}$  NMR spectrum of **3ag**



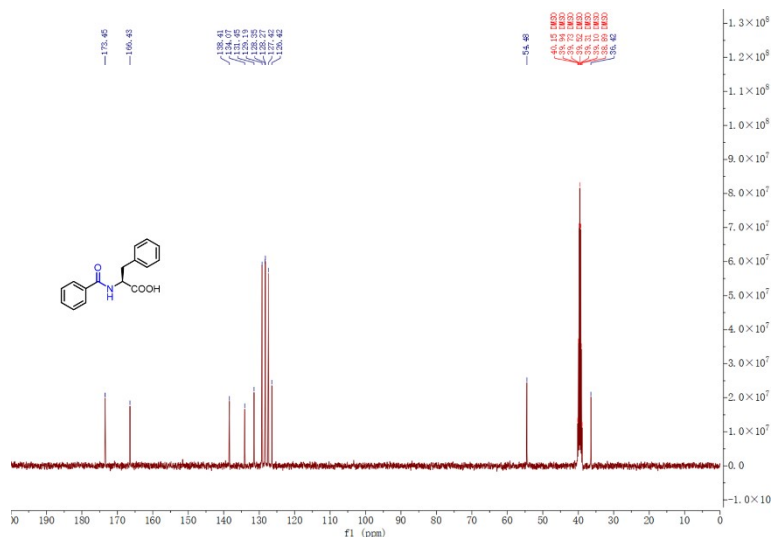
$^{13}\text{C}$  NMR spectrum of **3ag**



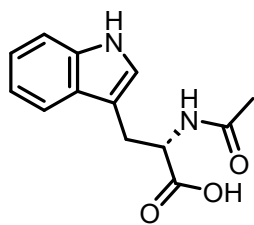
**3bg**, white powder, 80%.  $^1\text{H}$  NMR (400 MHz,  $\text{DMSO-}d_6$ )  $\delta$  8.70 (d,  $J = 8.2$  Hz, 1H), 7.86 – 7.74 (m, 2H), 7.55 – 7.40 (m, 3H), 7.38 – 7.22 (m, 4H), 7.17 (t,  $J = 7.2$  Hz, 1H), 4.63 (ddd,  $J = 10.4, 8.0, 4.3$  Hz, 1H), 3.22 (dd,  $J = 13.8, 4.4$  Hz, 1H), 3.09 (dd,  $J = 13.8, 10.6$  Hz, 1H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{DMSO-}d_6$ )  $\delta$  173.5, 166.4, 138.4, 134.1, 131.5, 129.2, 128.4, 128.3, 127.4, 126.4, 54.5, 36.4.



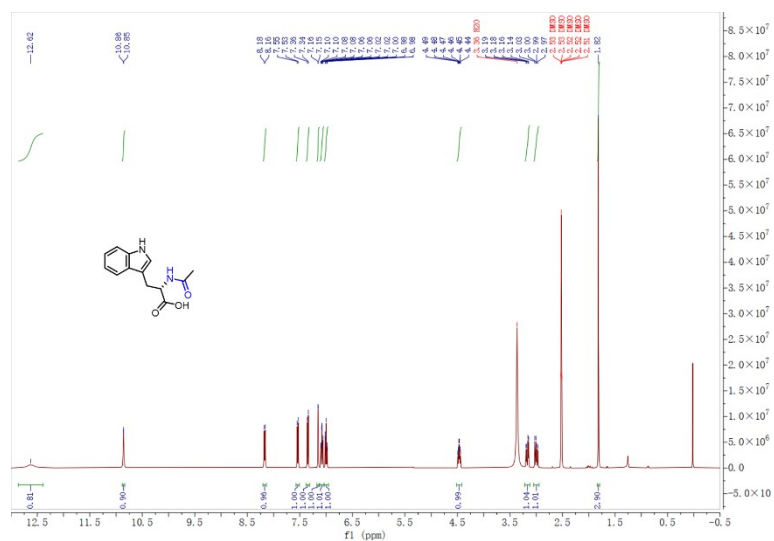
$^1\text{H}$  NMR spectrum of **3bg**



$^{13}\text{C}$  NMR spectrum of **3bg**

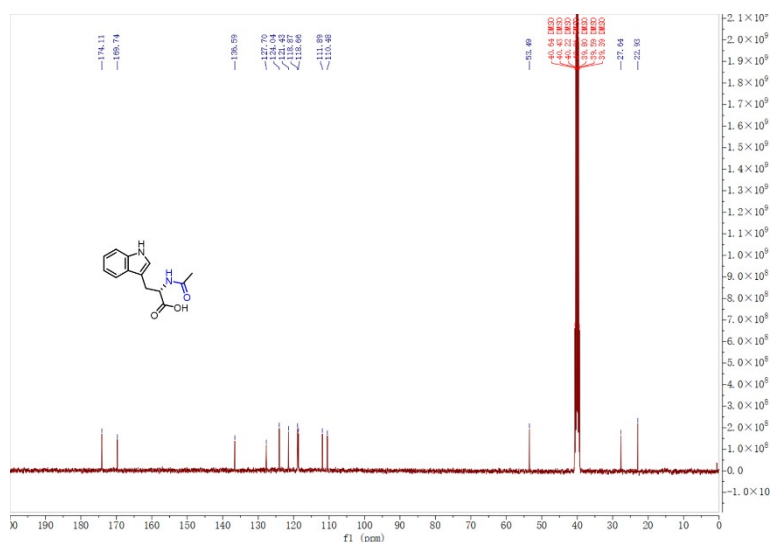


**3ah**, white powder, 93%.  $^1\text{H}$  NMR (400 MHz,  $\text{DMSO}-d_6$ )  $\delta$  12.62 (s, 1H), 10.88 – 10.83 (m, 1H), 8.17 (d,  $J = 7.8$  Hz, 1H), 7.54 (d,  $J = 7.8$  Hz, 1H), 7.35 (d,  $J = 8.0$  Hz, 1H), 7.15 (d,  $J = 2.3$  Hz, 1H), 7.12 – 7.04 (m, 1H), 7.04 – 6.96 (m, 1H), 4.47 (td,  $J = 8.3, 5.1$  Hz, 1H), 3.17 (dd,  $J = 14.6, 5.1$  Hz, 1H), 3.00 (dd,  $J = 14.6, 8.8$  Hz, 1H), 1.82 (s, 3H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{DMSO}-d_6$ )  $\delta$  174.1, 169.7, 136.6, 127.7, 124.0, 121.4, 118.9, 118.7, 111.9, 110.5, 53.5, 27.6, 22.9.

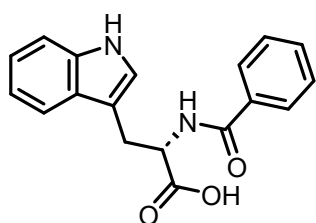


$^1\text{H}$  NMR spectrum of **3ah**

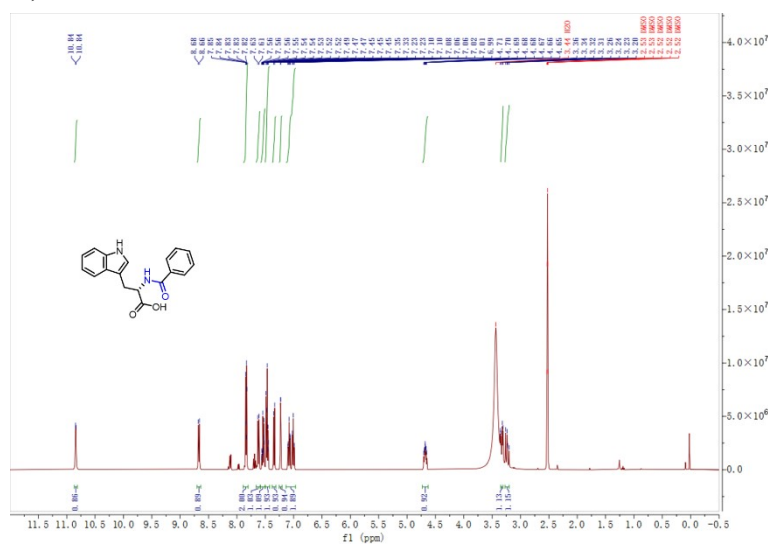




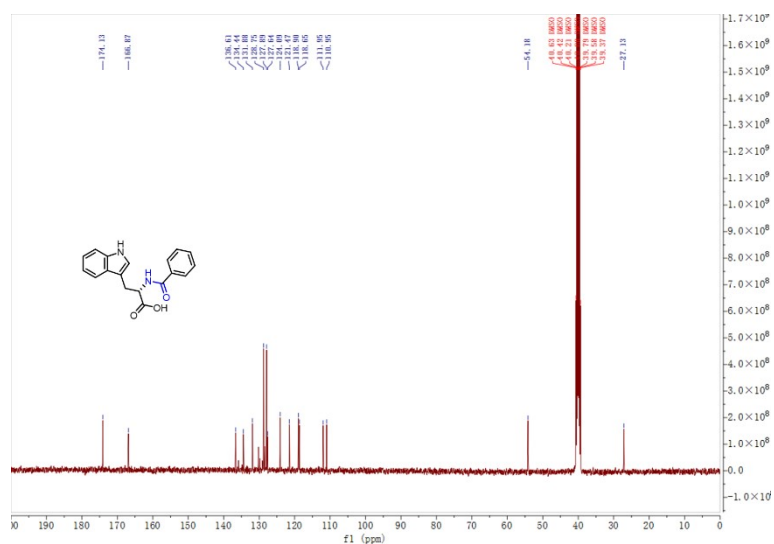
$^{13}\text{C}$  NMR spectrum of **3ah**



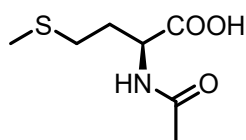
**3bh**, white powder, 84%.  $^1\text{H}$  NMR (400 MHz, DMSO- $d_6$ )  $\delta$  10.84 (d,  $J$  = 2.6 Hz, 1H), 8.67 (d,  $J$  = 7.9 Hz, 1H), 7.89 – 7.80 (m, 2H), 7.62 (d,  $J$  = 7.9 Hz, 1H), 7.58 – 7.50 (m, 1H), 7.47 (dd,  $J$  = 8.2, 6.6 Hz, 2H), 7.34 (d,  $J$  = 8.0 Hz, 1H), 7.23 (d,  $J$  = 2.3 Hz, 1H), 7.13 – 6.97 (m, 2H), 4.68 (ddd,  $J$  = 9.9, 7.8, 4.5 Hz, 1H), 3.35 – 3.31 (m, 1H), 3.23 (dd,  $J$  = 14.7, 9.9 Hz, 1H).  $^{13}\text{C}$  NMR (101 MHz, DMSO- $d_6$ )  $\delta$  174.1, 166.9, 136.6, 134.4, 131.9, 128.8, 127.9, 127.6, 124.1, 121.5, 118.9, 118.7, 112.0, 111.0, 54.2, 27.1.



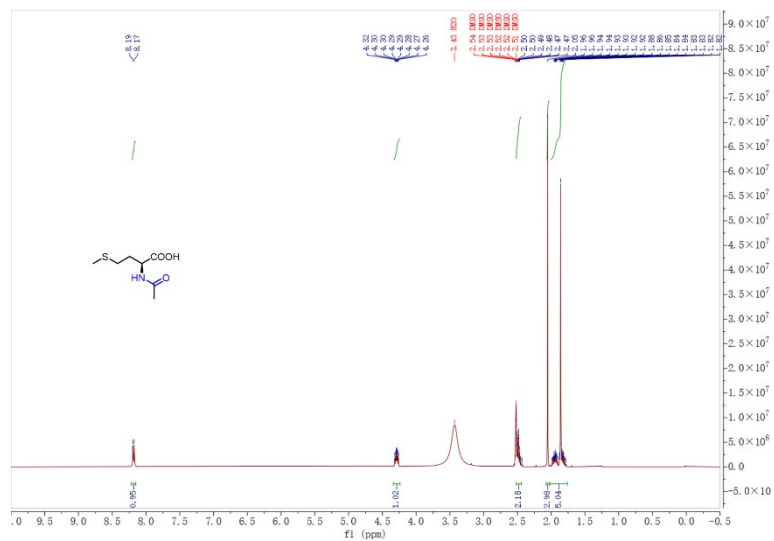
$^1\text{H}$  NMR spectrum of **3bh**



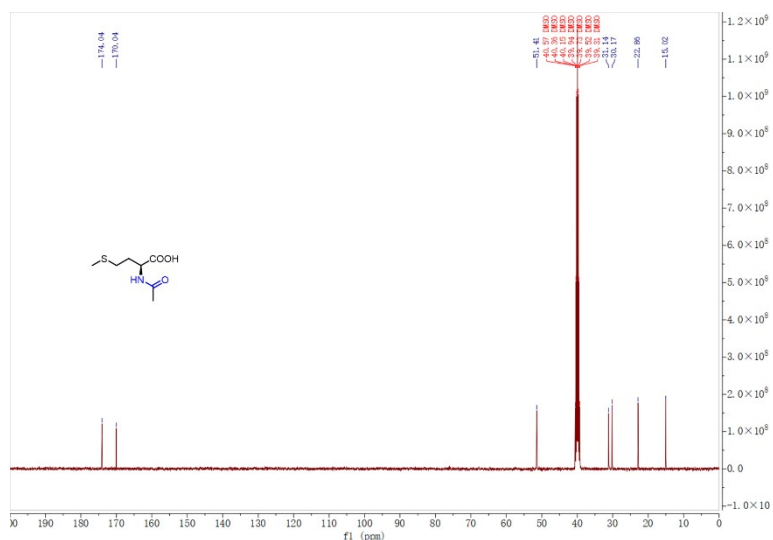
<sup>13</sup>C NMR spectrum of **3bh**



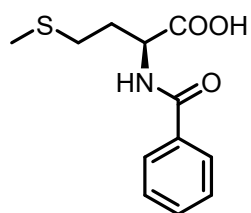
**3ai**, yellow powder, 88%. <sup>1</sup>H NMR (400 MHz, DMSO-*d*<sub>6</sub>) δ 8.18 (d, *J* = 7.8 Hz, 1H), 4.29 (ddd, *J* = 9.3, 7.8, 4.6 Hz, 1H), 2.52 – 2.44 (m, 2H), 2.05 (s, 3H), 2.01 – 1.76 (m, 5H). <sup>13</sup>C NMR (101 MHz, DMSO-*d*<sub>6</sub>) δ 174.0, 170.0, 51.4, 31.1, 30.2, 22.9, 15.0.



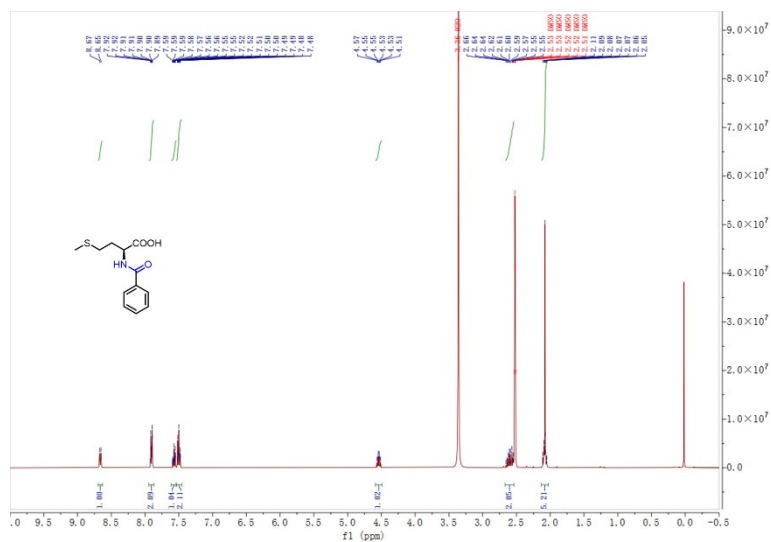
<sup>1</sup>H NMR spectrum of **3ai**



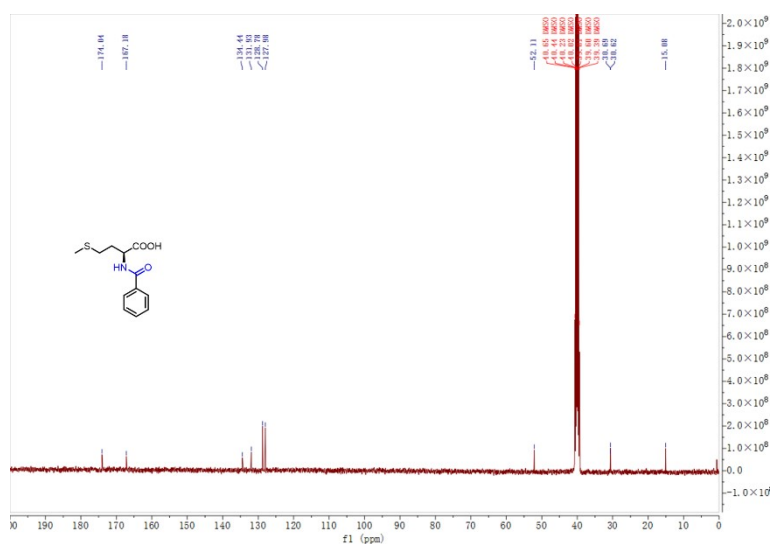
$^{13}\text{C}$  NMR spectrum of **3ai**



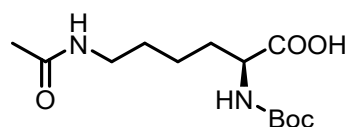
**3bi**, yellow powder, 75%.  $^1\text{H}$  NMR (400 MHz,  $\text{DMSO-}d_6$ )  $\delta$  8.66 (d,  $J = 7.8$  Hz, 1H), 7.94 – 7.87 (m, 2H), 7.61 – 7.54 (m, 1H), 7.54 – 7.46 (m, 2H), 4.54 (td,  $J = 7.8, 6.2$  Hz, 1H), 2.67 – 2.54 (m, 2H), 2.13 – 2.03 (m, 5H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{DMSO-}d_6$ )  $\delta$  174.0, 167.2, 134.4, 131.9, 128.8, 128.0, 52.1, 30.7, 30.6, 15.1.



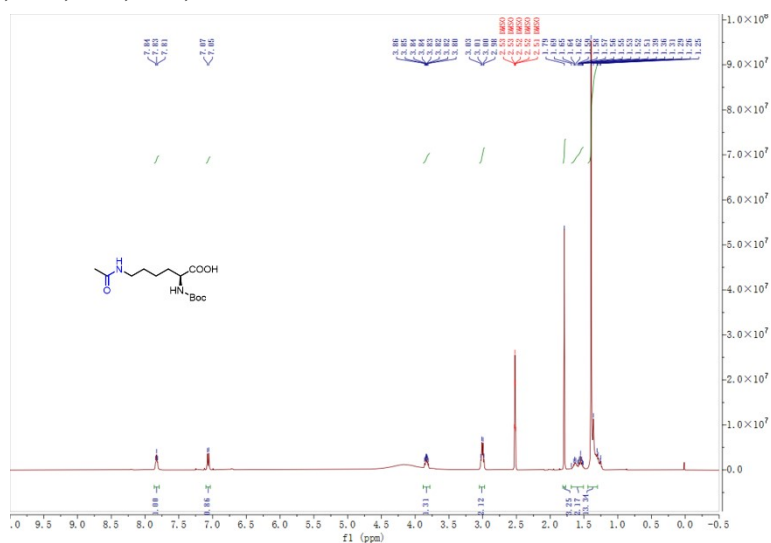
$^1\text{H}$  NMR spectrum of **3bi**



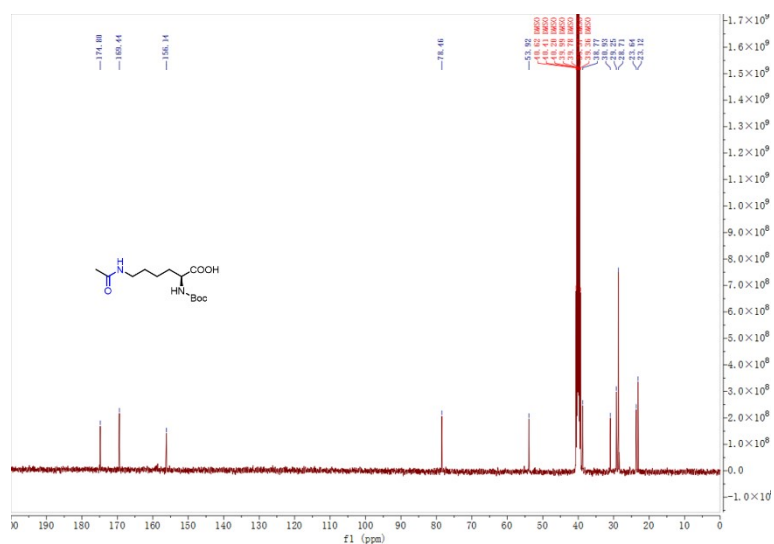
$^{13}\text{C}$  NMR spectrum of **3bi**



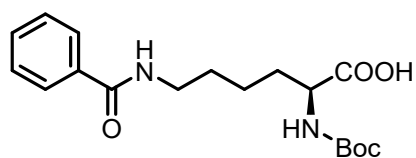
**3aj**, white powder, 82%.  $^1\text{H}$  NMR (400 MHz,  $\text{DMSO}-d_6$ )  $\delta$  7.83 (t,  $J = 5.6$  Hz, 1H), 7.06 (d,  $J = 8.0$  Hz, 1H), 3.83 (ddd,  $J = 9.4, 7.9, 4.7$  Hz, 1H), 3.00 (q,  $J = 6.4$  Hz, 2H), 1.79 (s, 3H), 1.69 – 1.51 (m, 2H), 1.39 (s, 13H).  $^{13}\text{C}$  NMR (101 MHz,  $\text{DMSO}-d_6$ )  $\delta$  174.8, 169.4, 156.1, 78.5, 53.9, 38.8, 30.9, 29.3, 28.7, 23.6, 23.1.



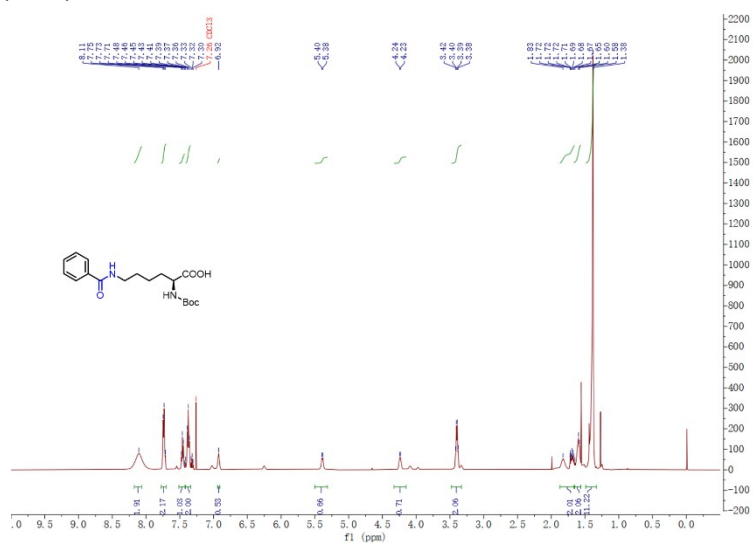
$^1\text{H}$  NMR spectrum of **3aj**



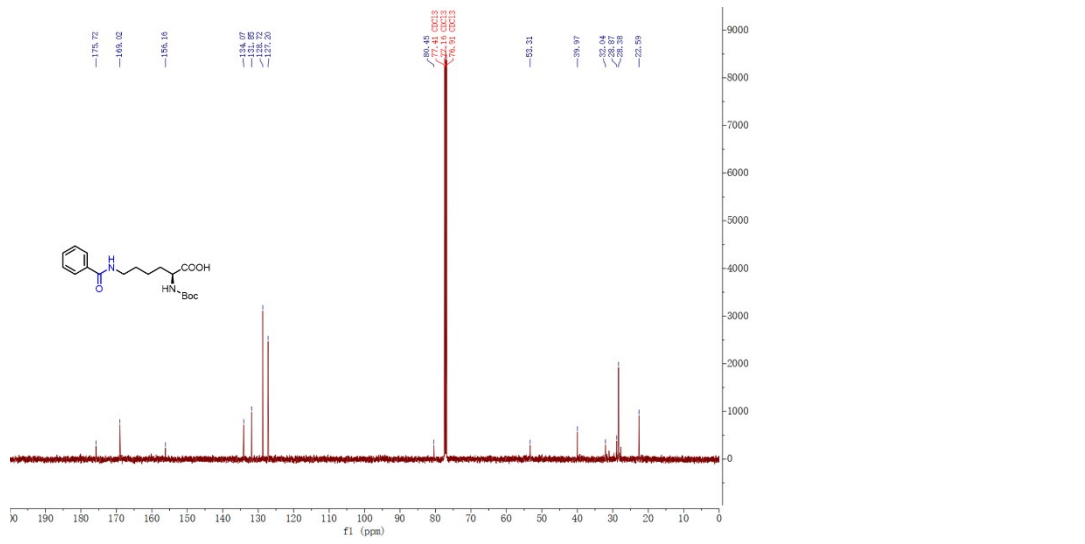
$^{13}\text{C}$  NMR spectrum of **3aj**



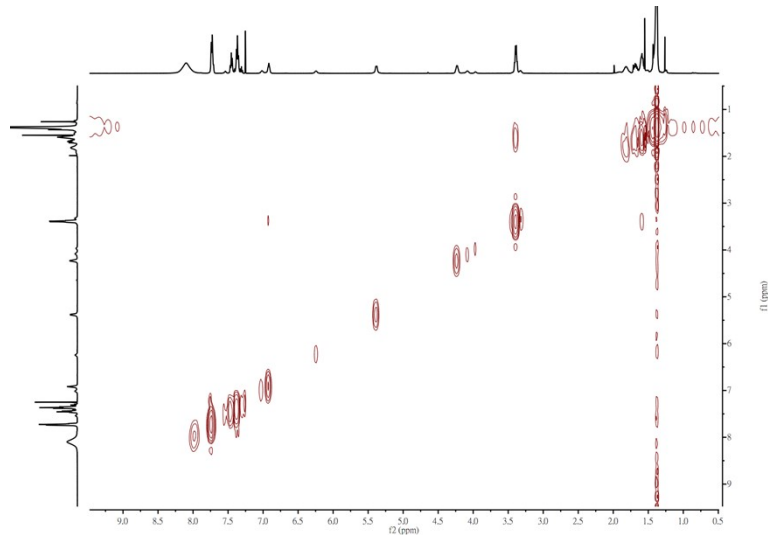
**3bj**, white powder, 73%.  $^1\text{H}$  NMR (500 MHz,  $\text{CDCl}_3$ )  $\delta$  8.11 (s, 2H), 7.73 (t,  $J = 8.5$  Hz, 2H), 7.45 (q,  $J = 9.0, 8.1$  Hz, 1H), 7.37 (t,  $J = 7.5$  Hz, 2H), 6.92 (s, 1H), 5.39 (d,  $J = 6.9$  Hz, 1H), 4.33 – 4.15 (m, 1H), 3.40 (q,  $J = 6.5$  Hz, 2H), 1.87 – 1.66 (m, 2H), 1.66 – 1.56 (m, 2H), 1.38 (s, 11H).  $^{13}\text{C}$  NMR (126 MHz,  $\text{CDCl}_3$ )  $\delta$  175.7, 169.0, 156.2, 134.1, 131.9, 128.7, 127.2, 80.5, 53.3, 40.0, 32.0, 28.9, 28.4, 22.6.



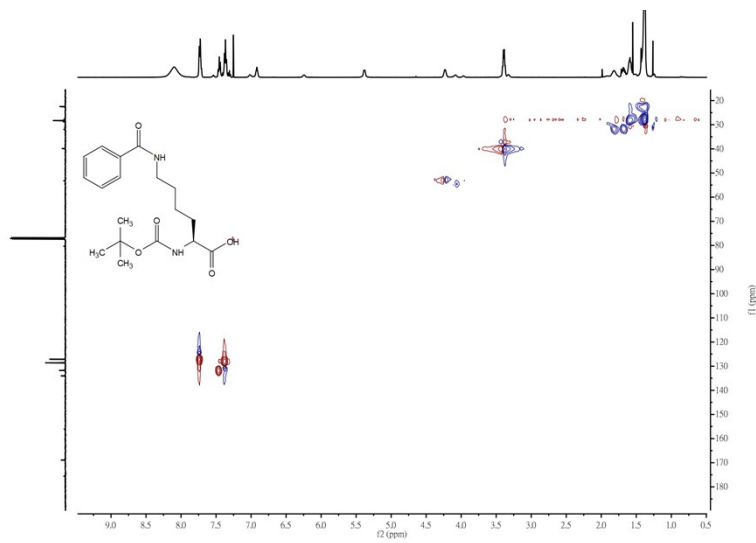
$^1\text{H}$  NMR spectrum of **3bj**



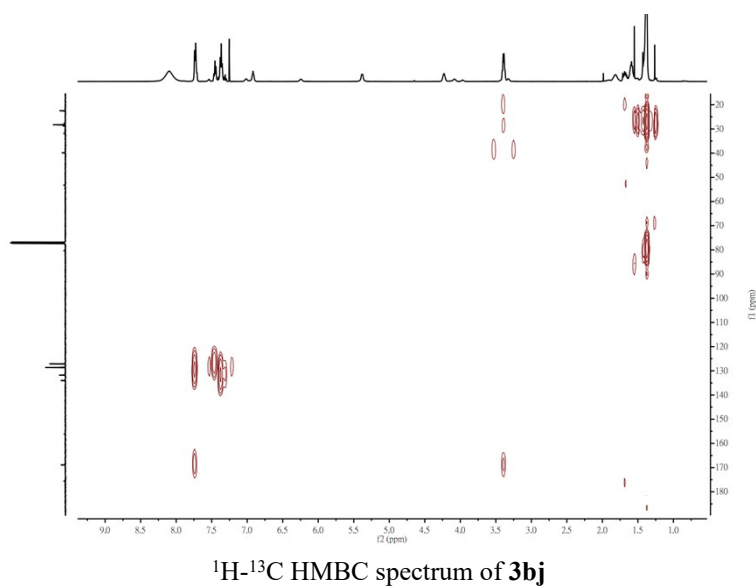
$^{13}\text{C}$  NMR spectrum of **3bj**



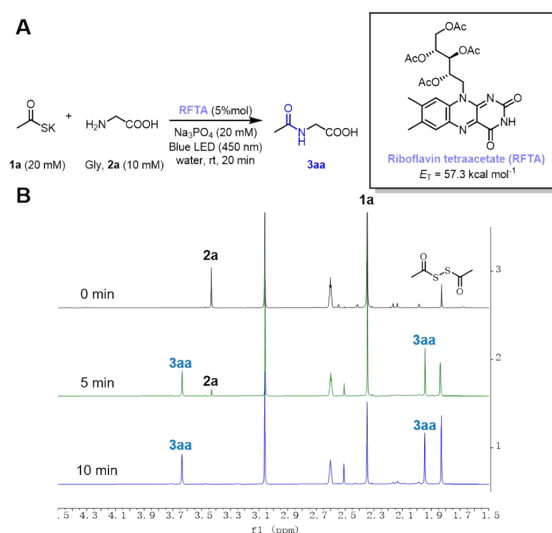
$^1\text{H}$ - $^1\text{H}$  COSY spectrum of **3bj**



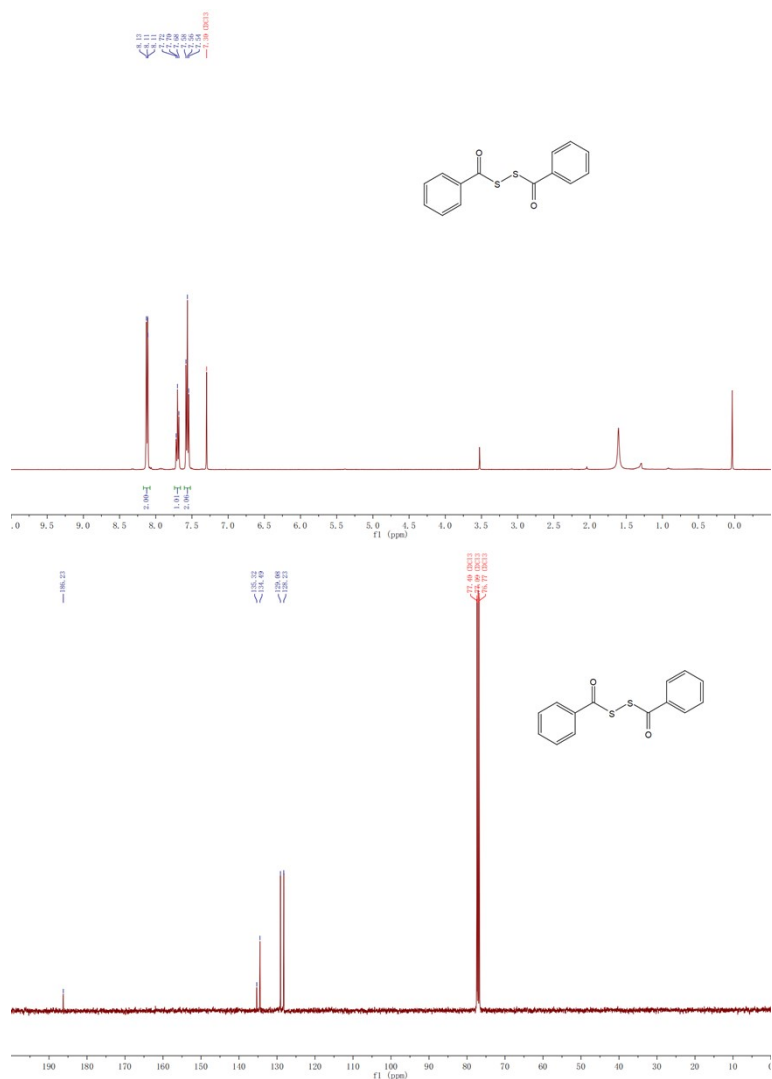
$^1\text{H}$ - $^{13}\text{C}$  HSQC spectrum of **3bj**



## 2.4 Mechanistic studies



**Figure S6** Visible-light-induced amidation of thioacid. **(A)** Screening of optimized conditions. Standard conditions: **1a** (20 mM), **2** (10 mM) and photocatalysts (5% mol) under blue LED (450 nm) for 20 min in  $\text{D}_2\text{O}$  at rt. Yield was determined by  $^1\text{H}$  NMR with dimethyl sulfone (MSM) as internal standard. **(B)** Assignment for  $^1\text{H}$  NMR analysis of the reaction.



**Figure S7**  $^1\text{H}$  and  $^{13}\text{C}$  NMR of isolated 1c intermediates.

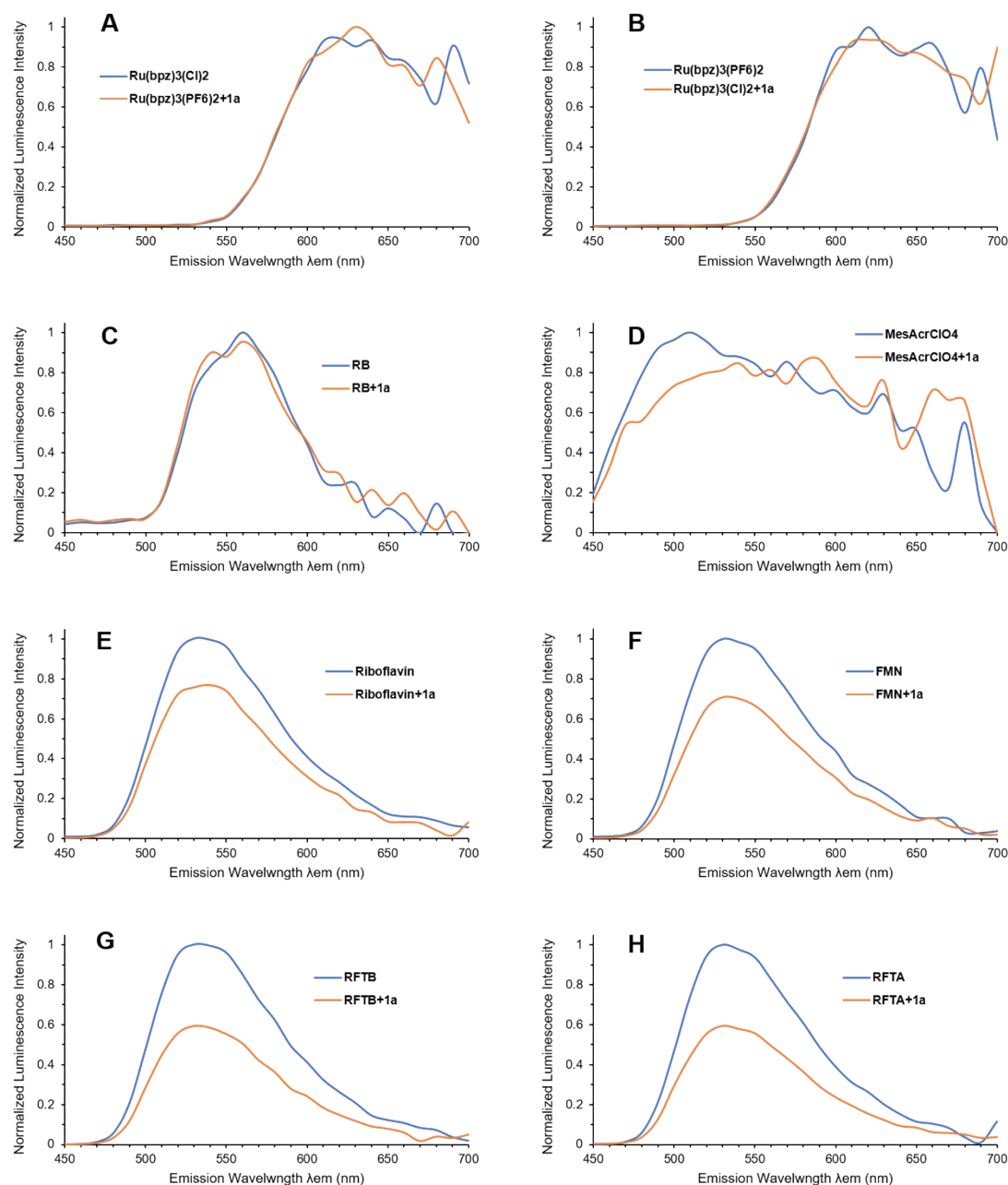
### 2.4.1 Luminescence screening

The luminescence screening was performed by following a similar procedure of previous report. In order to consistent with the reaction conditions, PBS buffer (pH 7.4, 25%MeCN) was used as the solvent for luminescence experiments. A photocatalyst concentration of 20  $\mu\text{M}$  was used throughout the experiments along with substrate concentrations of 20 mM, which equates to 1000 equivalents of each potential quencher relative to the photocatalyst. The luminescence emission spectrum of each sample excited at 450 nm was measured twice and an average was taken. The emission intensity ( $I$ ) at a predefined wavelength was noted and compared with that of the photocatalyst in isolation ( $I_0$ ). The amount of decrease in the emission intensity was then quantified as a “quenching percentage” ( $F$ ) defined by the following formula:

$$F(\%) = 100\left(1 - \frac{I}{I_0}\right)\% \quad (1)$$

The structure of the photocatalysts employed in this study are shown in **Figure S3**. The results were shown in **Figure S8**.

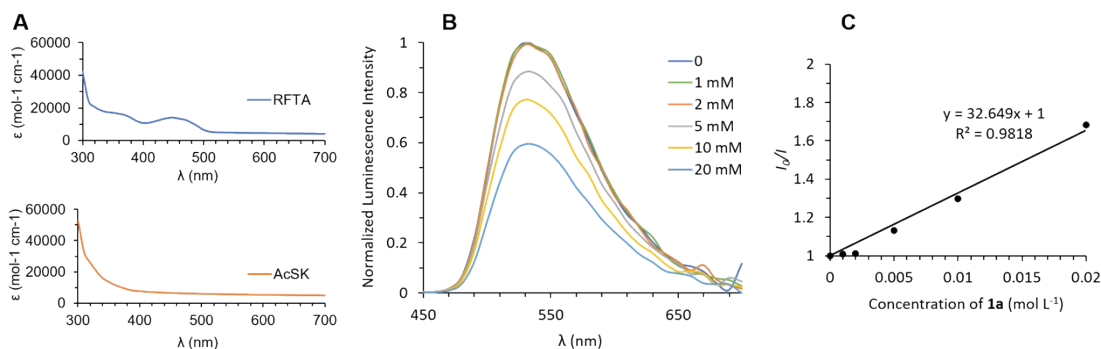




**Figure S8.** Luminescence spectra of the screening of the photocatalysts with thioacid **1a**.

### 2.4.2 Stern-Volmer luminescence quenching studies

Stern-Volmer luminescence quenching studies were carried out using a 20  $\mu\text{M}$  solution of RFTA and variable concentrations of **1a** in PBS buffer (pH 7.4, 25% MeCN). Two independent duplications were performed for two substrates. The solutions were irradiated at 420 nm and the luminescence was measured at 530 nm ( $I_0$  = emission intensity of the photocatalyst in isolation at the specified wavelength;  $I$  = observed intensity as a function of the quencher concentration). The luminescence spectra and were summarized in **Figure S9**.



**Figure S9.** Stern-Volmer luminescence quenching analysis for RFTA with thioacid **1a**.

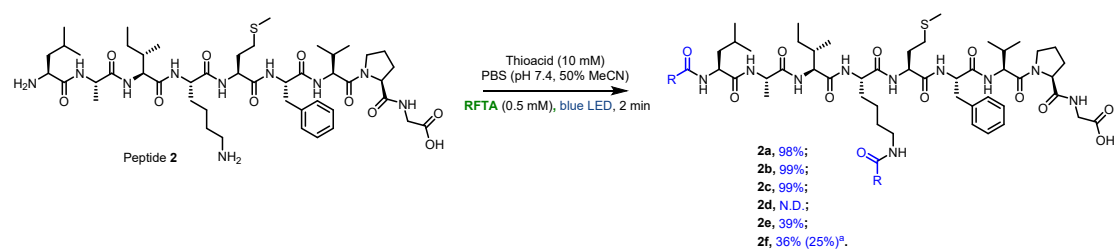
## 2.5 General procedure B for the reaction between thioacids and peptides



LC-MS yields were estimated by UV absorption at 220 nm of the peak corresponding to the thioacetal adducted product versus the internal standard (diphenyl sulfoxide): % yield =  $(A_p/A_{st}) \times k$ .  $A_p$  is the peak area of thioacetal-adducted products;  $A_{st}$  is the peak area of the internal standard;  $k$  is the quantity coefficient between specific peptide and standard. The quantity coefficients were measured by the correlation of a gradient concentration.

## 2.6 Characterization of the reaction between thioacids and peptides

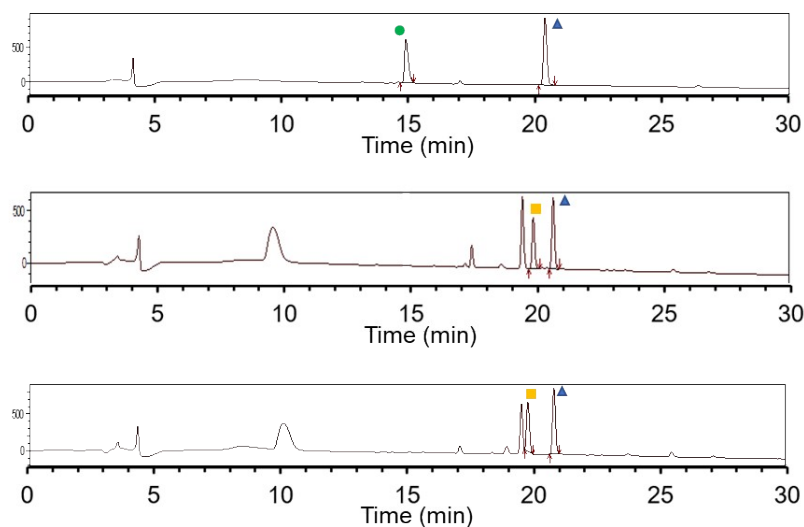
### 2.6.1 Characterization of the reaction of peptide 2



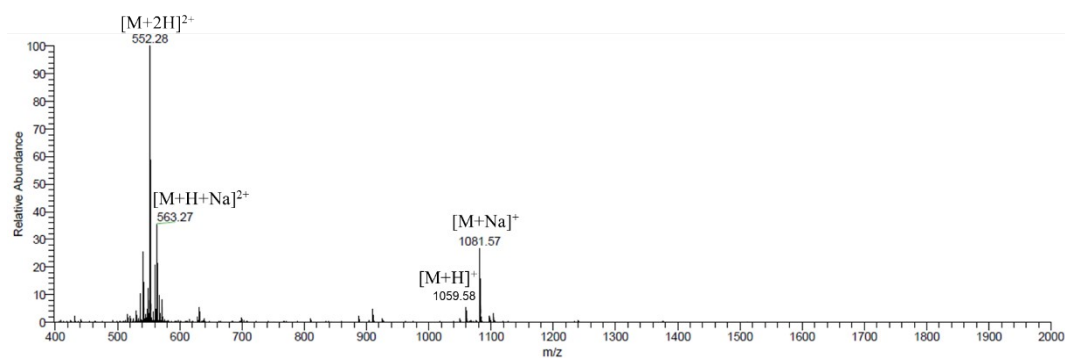
The reaction was followed **General Procedure B** using peptide **2** (1 mM), sequence: **NH<sub>2</sub>-**

LAIKMFVPG-OH, and thioacid **1a-1f**. A stock solution of peptide **2** (1 mM) was made up by 1 mL PBS buffer (pH 7.4, 50% MeCN) and 1 mg peptide **2**.

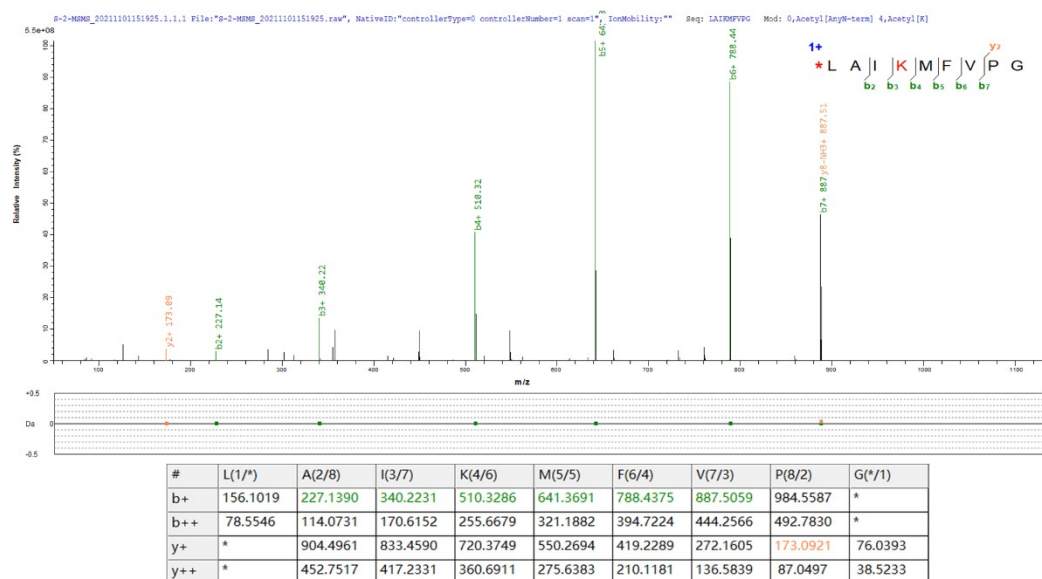
Characterization data of **2a** and **2b**



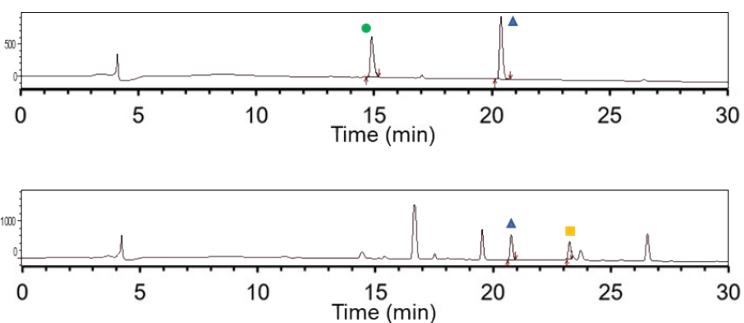
HPLC traces of the quantity relationship of matter and crude reaction of **2a** and **2b**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



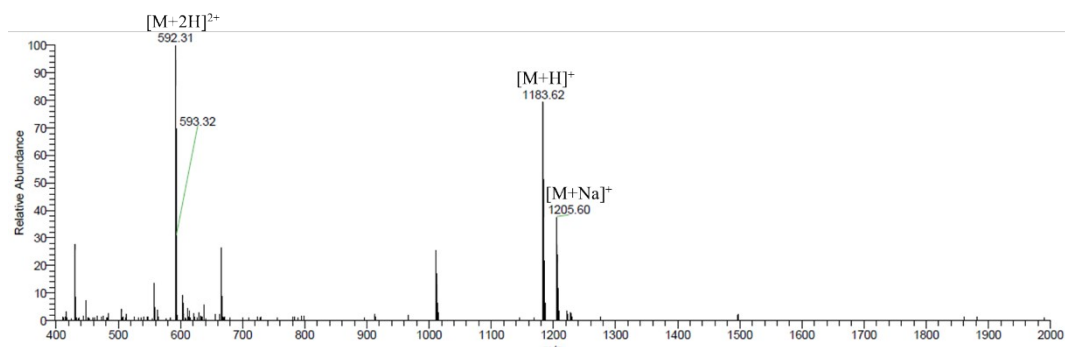
ESI Mass spectrum of purified product **2a**. Calculated Mass  $[M+H]^+$ : 1059.58,  $[M+2H]^{2+}$ : 552.28; Mass Found (ESI+)  $[M+H]^+$ : 1059.58,  $[M+2H]^{2+}$ : 552.28.



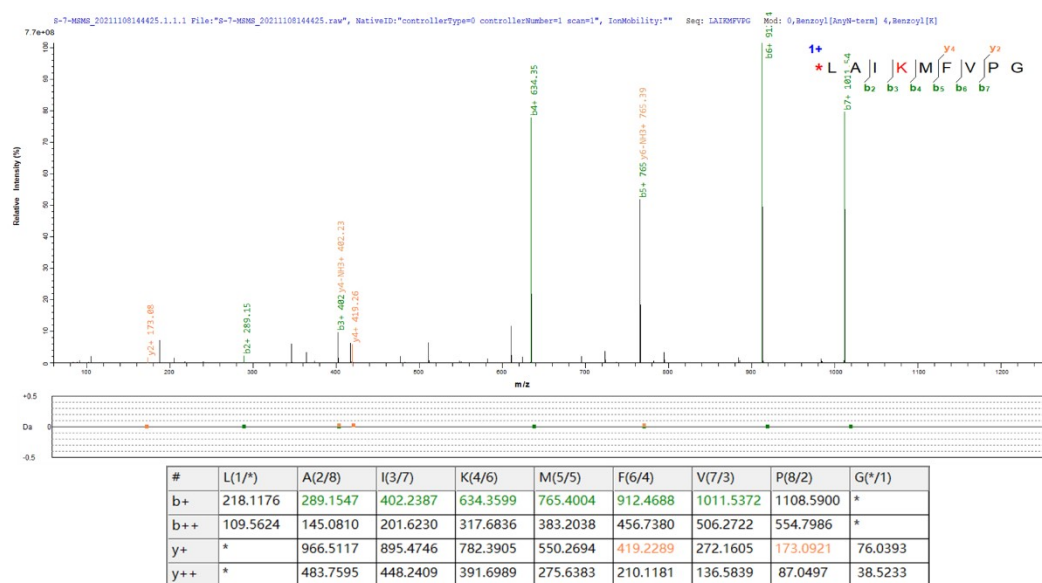
MS/MS analysis of **2a**



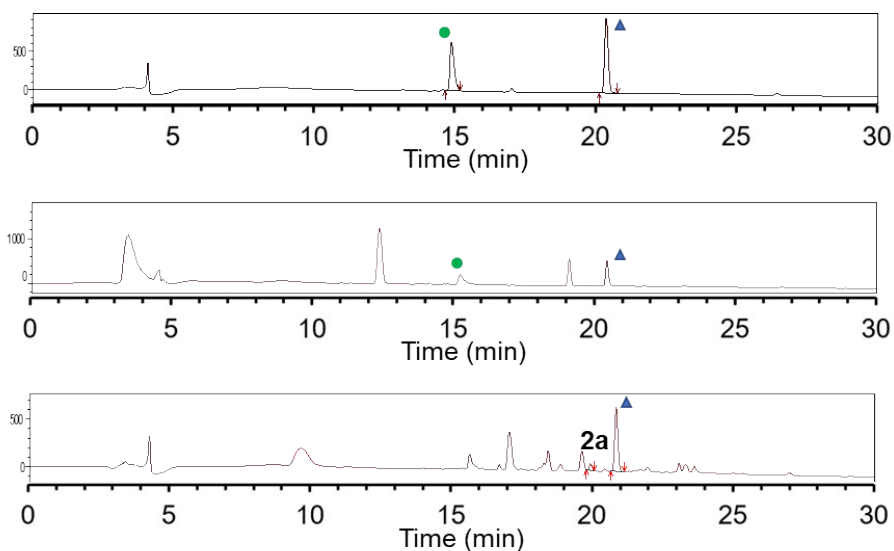
HPLC traces of the quantity relationship of matter and crude reaction of **2c**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



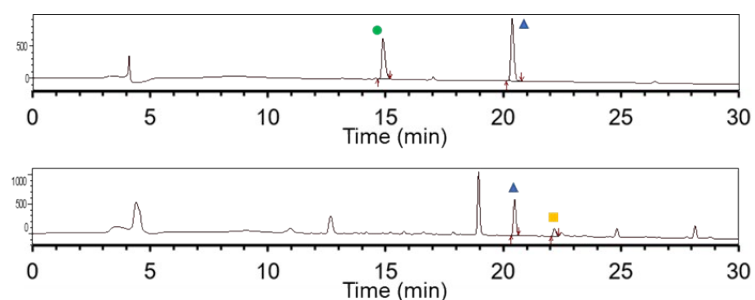
ESI Mass spectrum of purified product **2c**. Calculated Mass  $[M+H]^+$ : 1183.62,  $[M+2H]^{2+}$ : 592.31; Mass Found (ESI+)  $[M+H]^+$ : 1183.62,  $[M+2H]^{2+}$ : 592.31.



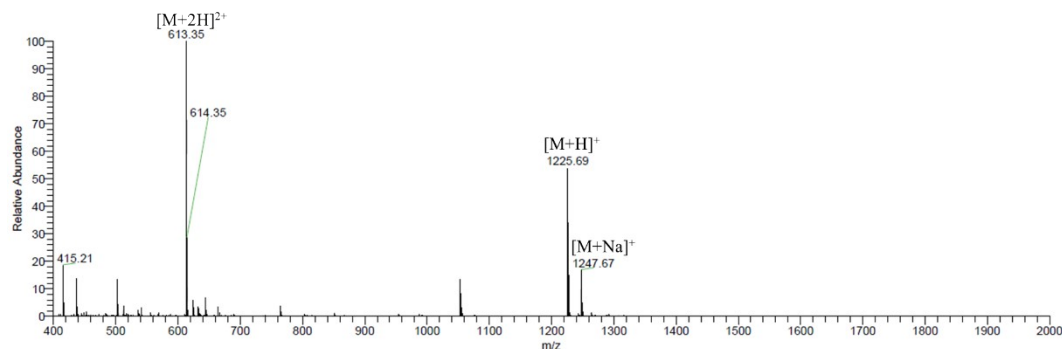
MS/MS analysis of **2c**



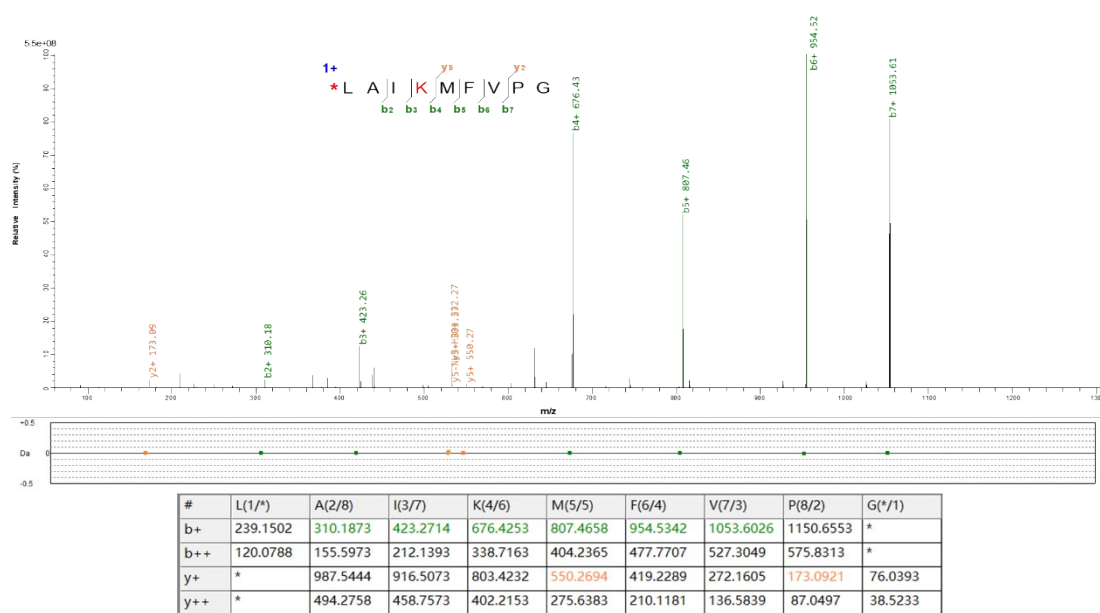
HPLC traces of the quantity relationship of matter, crude reaction of **2d** and a control reaction between peptide **2**, potassium thioacetate **1a** and alkynyl compound (pentynyl acid). (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle and blue triangle and orange square refer to the starting peptide and internal standard. No target product was detected in the reaction between **2** and **1d**. And, the adding of the alkynyl compound (pentynyl acid) decreased the conversion of the **2a** to around 10%.



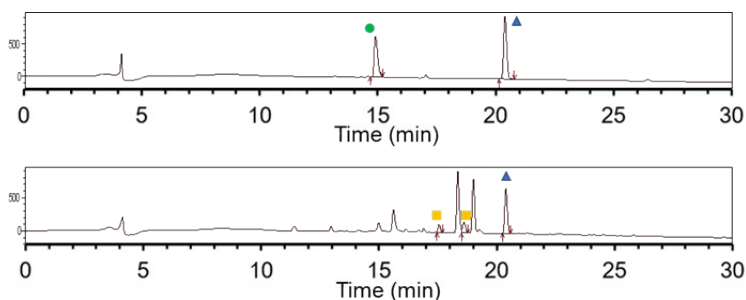
HPLC traces of the quantity relationship of matter and crude reaction of **2e**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA, λ = 220 nm, Kromasil 100-5-C18 4.6 × 250 mm, 5 μm column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



ESI Mass spectrum of purified product **2e**. Calculated Mass  $[M+H]^+$ : 1225.69,  $[M+2H]^{2+}$ : 613.35; Mass Found (ESI+)  $[M+H]^+$ : 1225.69,  $[M+2H]^{2+}$ : 613.35.

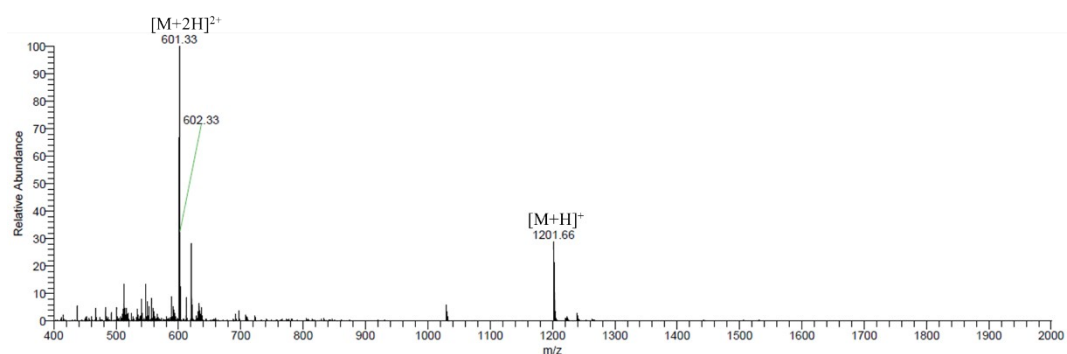


### MS/MS analysis of **2e**

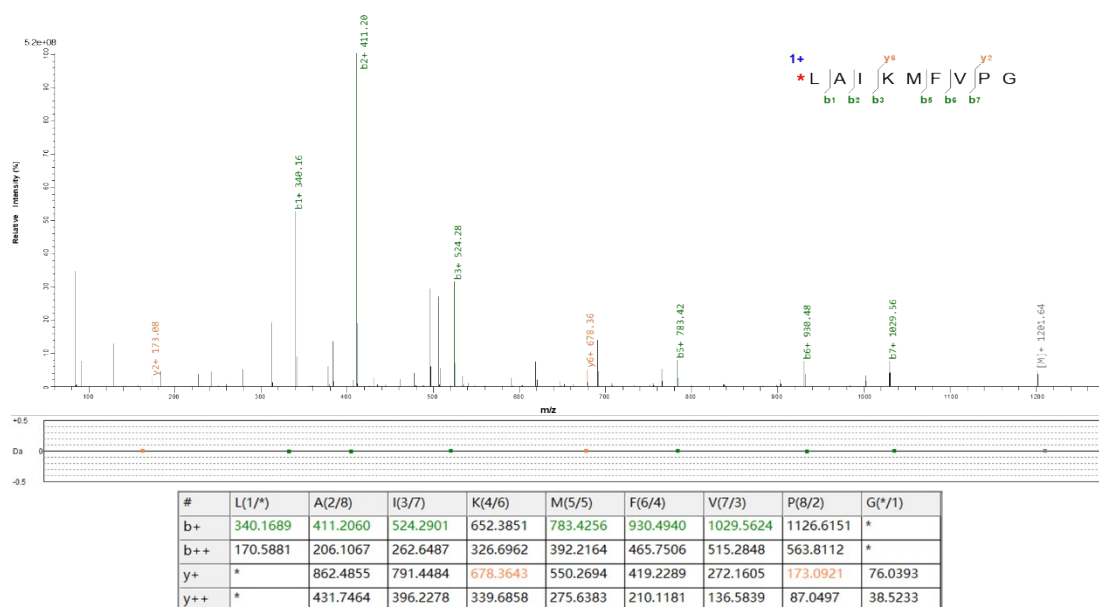


HPLC traces of the quantity relationship of matter and crude reaction of single-amidated and double-amidated **2f**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA, λ = 220 nm, Kromasil

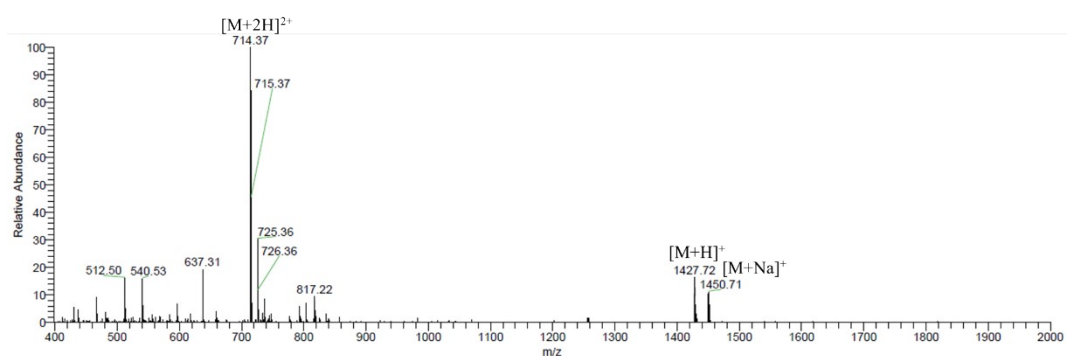
100-5-C18 4.6 × 250 mm, 5 μm column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



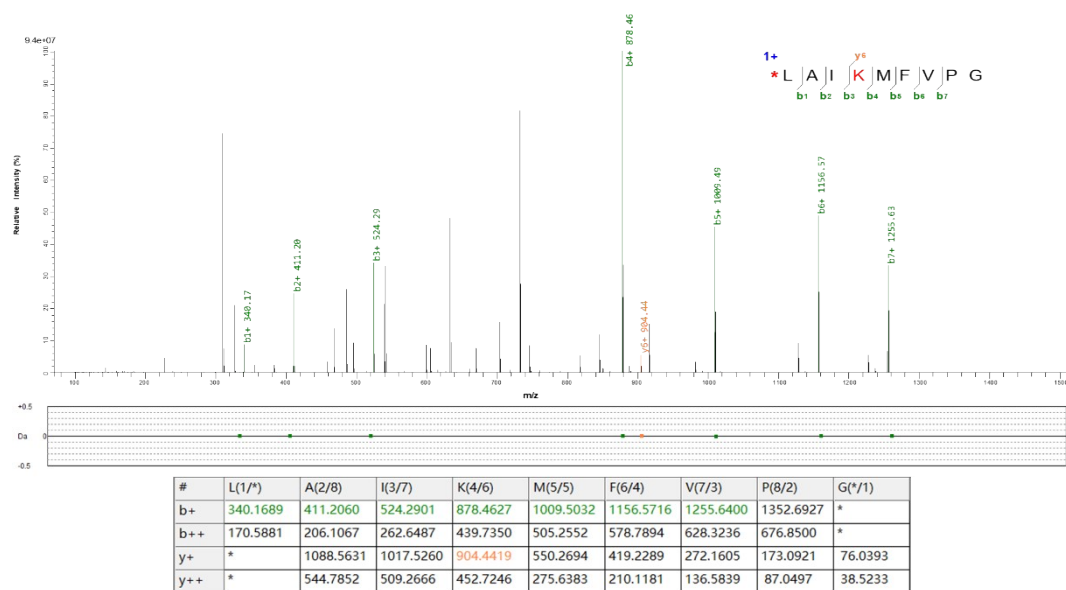
ESI Mass spectrum of purified single-amidated product **2f**. Calculated Mass  $[M+H]^+$ : 1201.66,  $[M+2H]^{2+}$ : 601.33; Mass Found (ESI+)  $[M+H]^+$ : 1201.66,  $[M+2H]^{2+}$ : 601.33.



MS/MS analysis of single-amidated **2f**

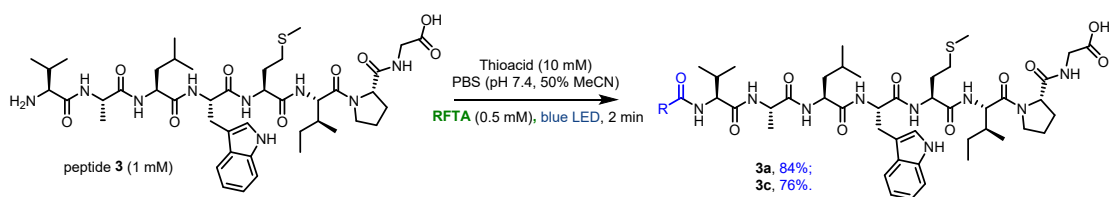


ESI Mass spectrum of purified double-amidated product **2f**. Calculated Mass  $[M+H]^+$ : 1427.72,  $[M+2H]^{2+}$ : 714.37; Mass Found (ESI+)  $[M+H]^+$ : 1427.72,  $[M+2H]^{2+}$ : 714.37.

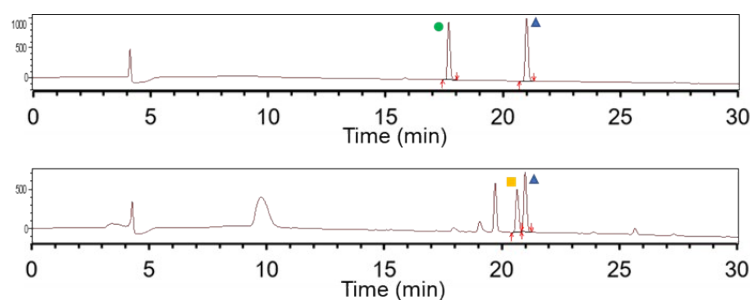


MS/MS analysis of double-amidated **2f**

## 2.6.2 Characterization of the reaction of peptide **3**

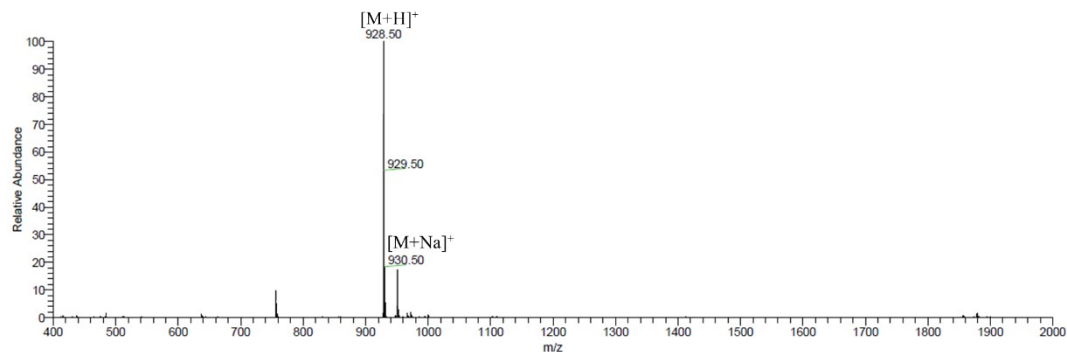


The reaction was followed **General Procedure B** using peptide **3** (1 mM), sequence: NH<sub>2</sub>-VALWMIPG-OH, and thioacid **1a** and **1c**. A stock solution of peptide **3** (1 mM) was made up by 1 mL PBS buffer (pH 7.4, 50% MeCN) and 0.9 mg peptide **3**.

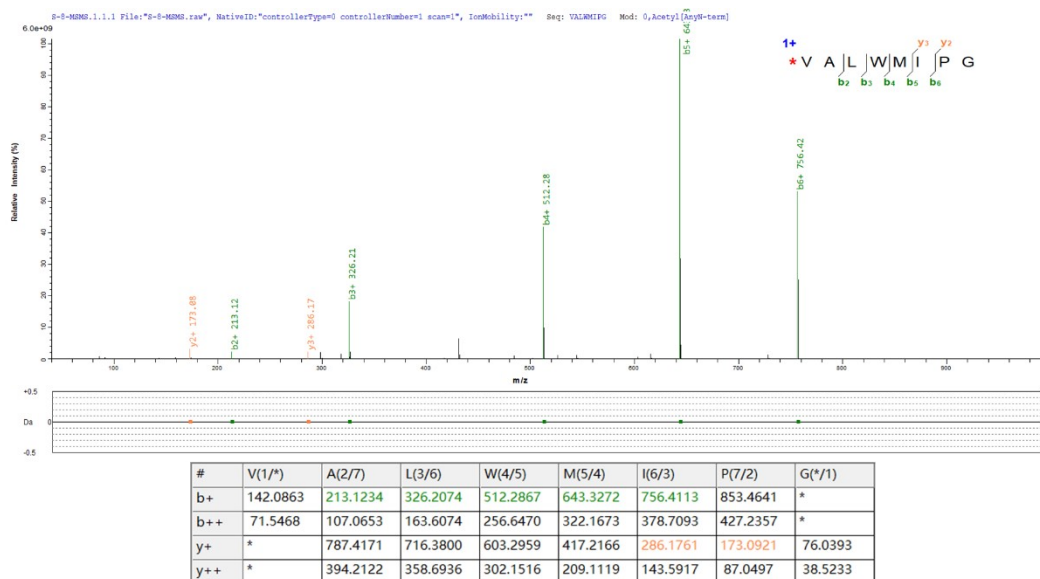


HPLC traces of the quantity relationship of matter and crude reaction of **3a**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.

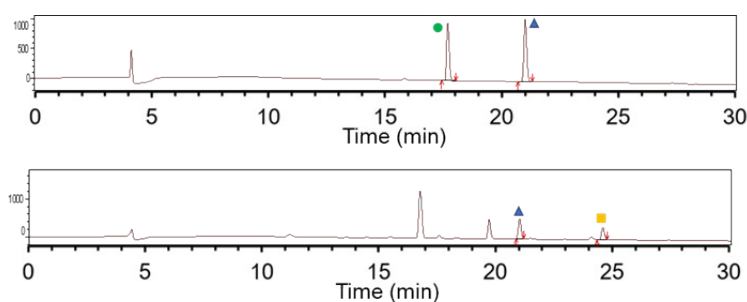




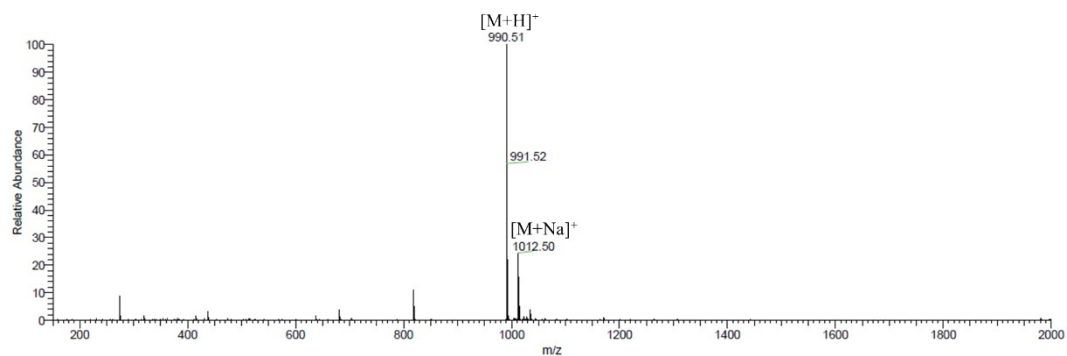
ESI Mass spectrum of purified product **3a**. Calculated Mass  $[M+H]^+$ : 928.50; Mass Found (ESI+)  $[M+H]^+$ : 928.50.



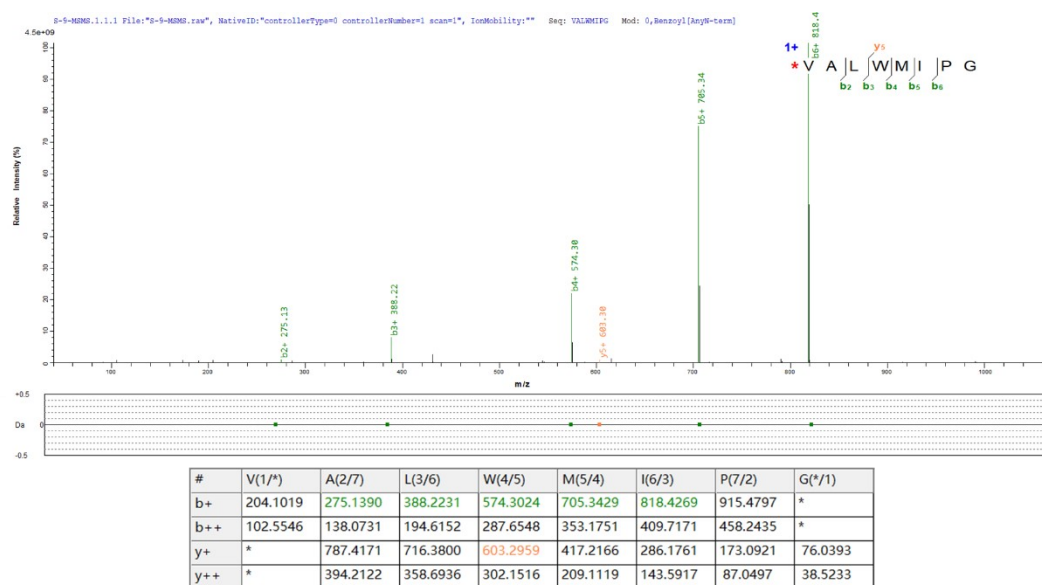
MS/MS analysis of **3a**



HPLC traces of the quantity relationship of matter and crude reaction of **3c**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.

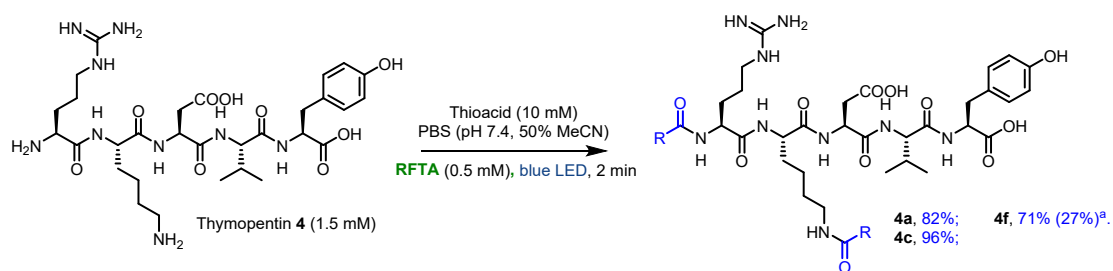


ESI Mass spectrum of purified product **3c**. Calculated Mass  $[M+H]^+$ : 990.51; Mass Found (ESI+) 990.51.

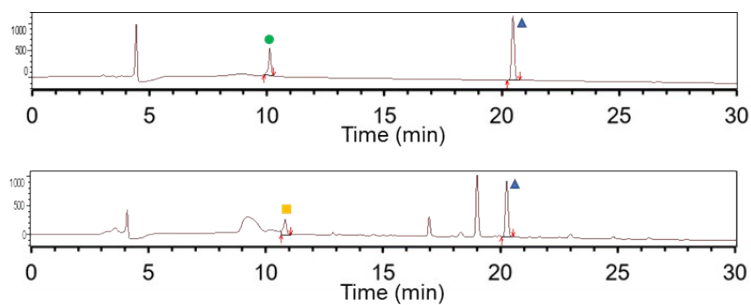


MS/MS analysis of **3c**

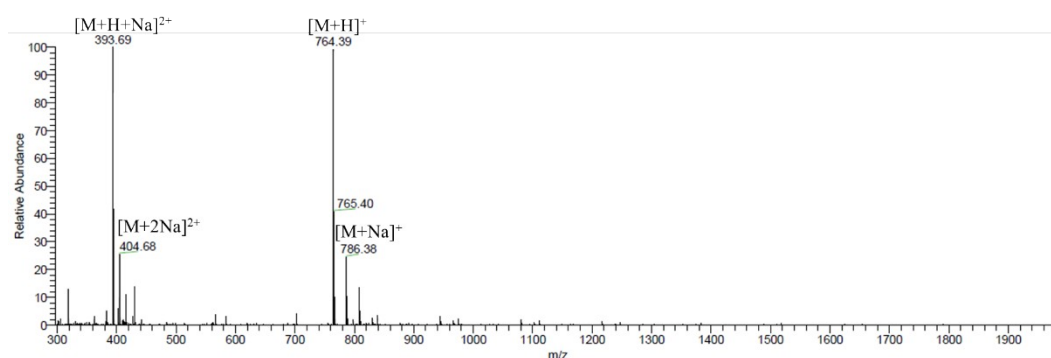
### 2.6.3 Characterization of the reaction of peptide 4



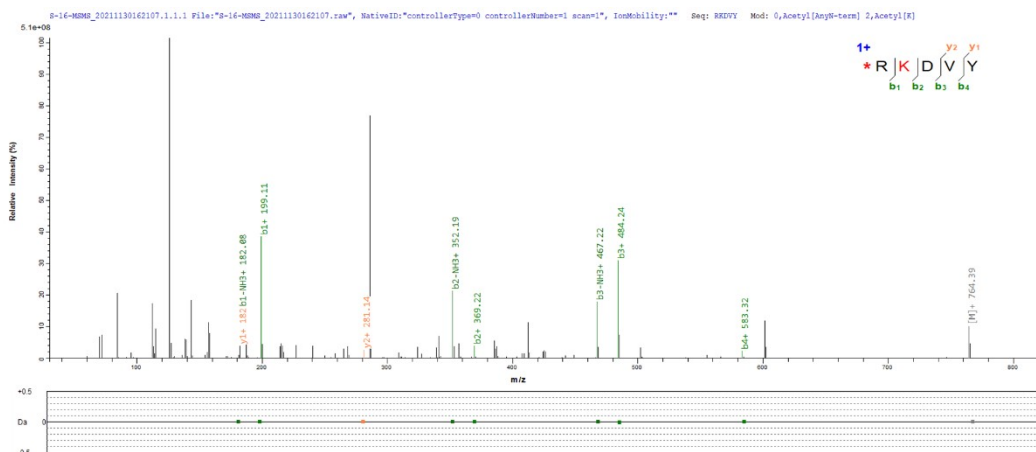
The reaction was followed **General Procedure B** using peptide **4** (1.5 mM), sequence: **NH<sub>2</sub>-RKDVY-OH**, and thioacid **1a**, **1c** and **1f**. A stock solution of peptide **4** (1.5 mM) was made up by 1 mL PBS buffer (pH 7.4, 50% MeCN) and 1 mg peptide **4**.



HPLC traces of the quantity relationship of matter and crude reaction of **4a**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA, λ = 220 nm, Kromasil 100-5-C18 4.6 × 250 mm, 5 μm column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.

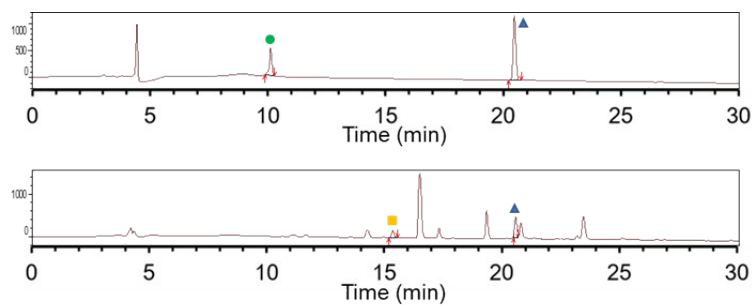


ESI Mass spectrum of purified product **4a**. Calculated Mass  $[M+H]^+$ : 764.39; Mass Found (ESI+)  $[M+H]^+$ : 764.39.

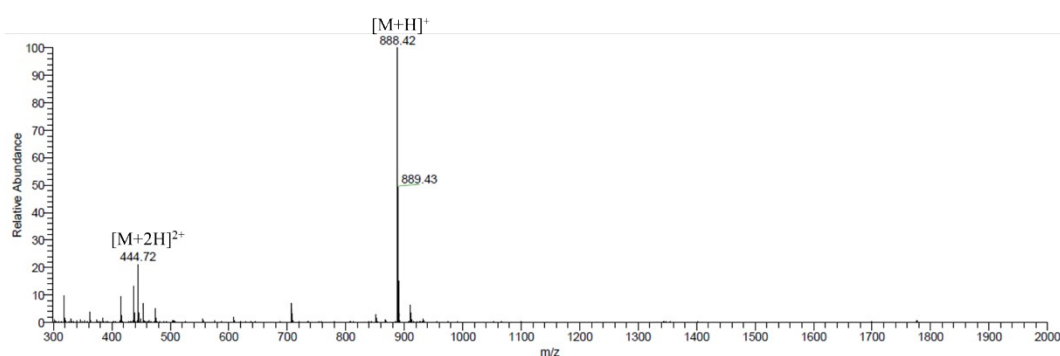


#	R(1/*)	K(2/4)	D(3/3)	V(4/2)	Y(*/1)
b+	199.1189	369.2245	484.2514	583.3198	*
b++	100.0631	185.1159	242.6293	292.1635	*
y+	*	566.2820	396.1765	281.1496	182.0812
y++	*	283.6447	198.5919	141.0784	91.5442

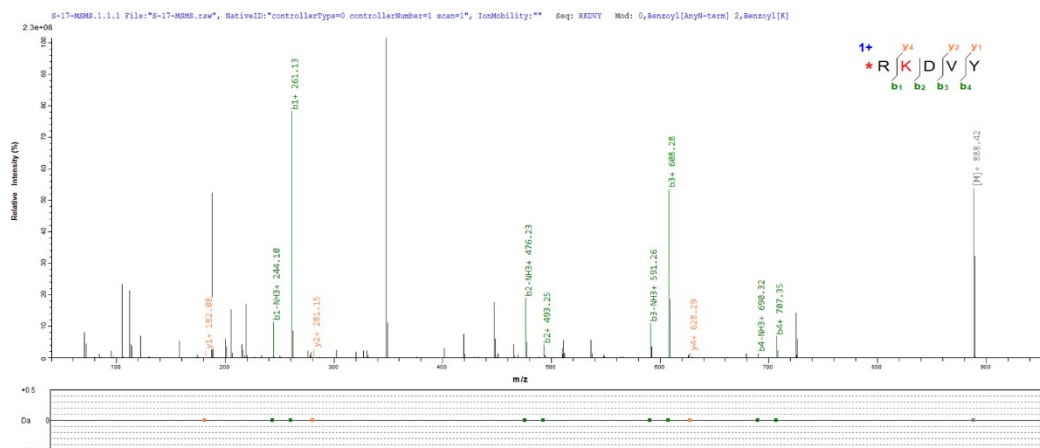
MS/MS analysis of **4a**



HPLC traces of the quantity relationship of matter and crude reaction of **4c**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA, λ = 220 nm, Kromasil 100-5-C18 4.6 × 250 mm, 5 μm column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.

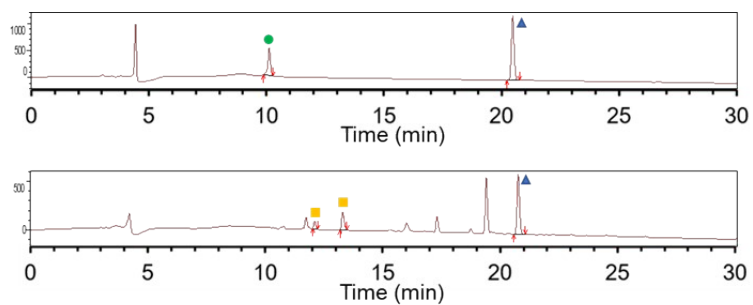


ESI Mass spectrum of purified product **4c**. Calculated Mass  $[M+H]^+$ : 888.42; Mass Found (ESI+)  $[M+H]^+$ : 888.42.

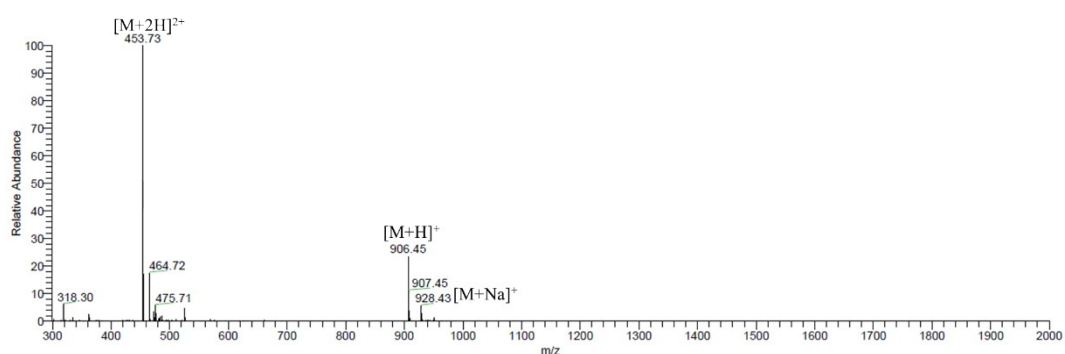


#	R(1*)	K(2/4)	D(3/3)	V(4/2)	Y(*1)
b+	261.1346	493.2558	608.2827	707.3511	*
b++	131.0709	247.1315	304.6450	354.1792	*
y+	*	628.2977	396.1765	281.1496	182.0812
y++	*	314.6525	198.5919	141.0784	91.5442

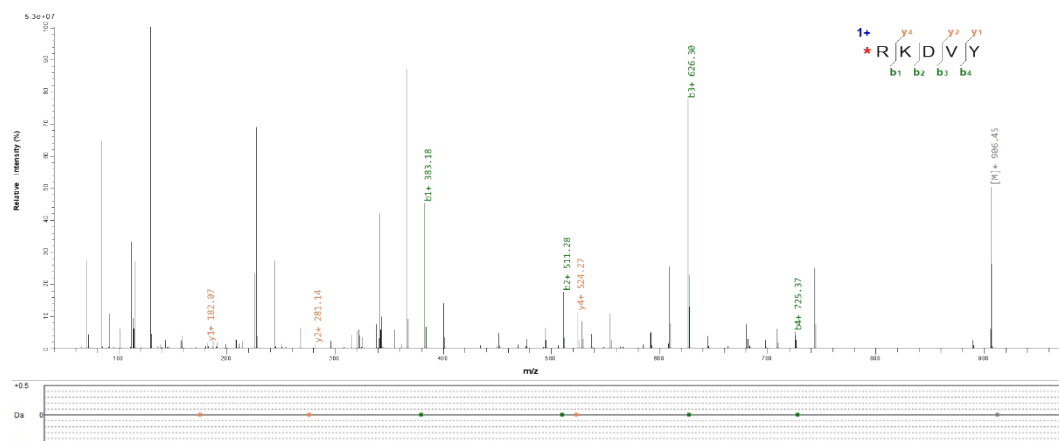
MS/MS analysis of **4c**



HPLC traces of the quantity relationship of matter and crude reaction of single-amidated and double-amidated **4f**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA, λ = 220 nm, Kromasil 100-5-C18 4.6 × 250 mm, 5 μm column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.

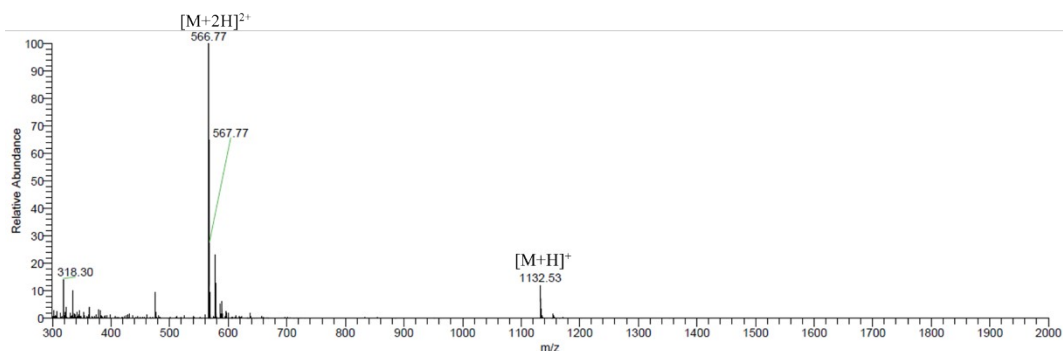


ESI Mass spectrum of purified single-amidated product **4f**. Calculated Mass [M+H]<sup>+</sup>: 906.45, [M+2H]<sup>2+</sup>: 453.73; Mass Found (ESI+) [M+H]<sup>+</sup>: 906.45, [M+2H]<sup>2+</sup>: 453.73.

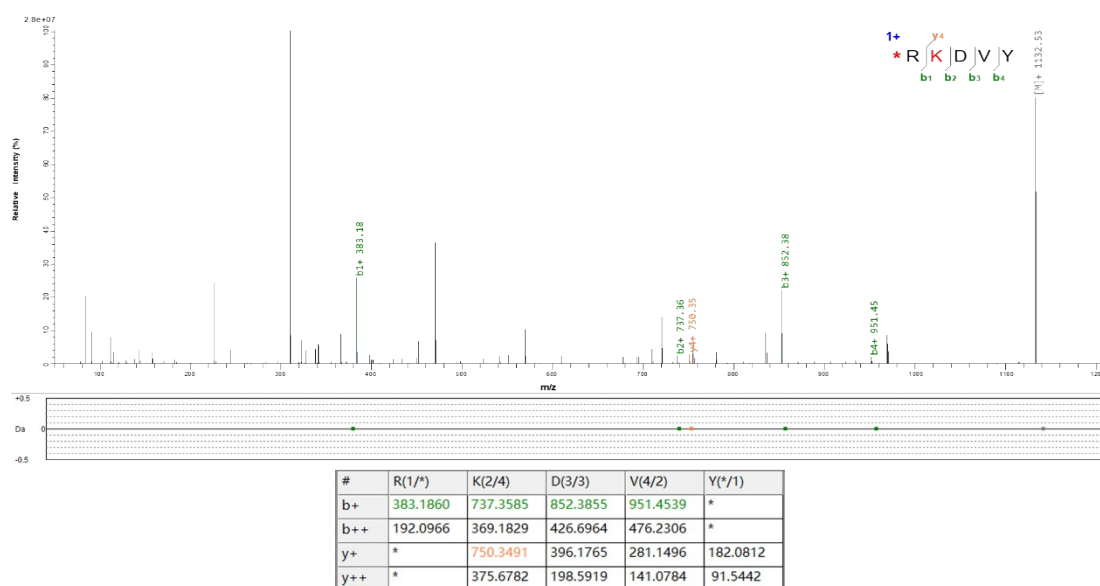


#	R(1/*)	K(2/4)	D(3/3)	V(4/2)	Y(*1)
b+	383.1860	511.2809	626.3079	725.3763	*
b++	192.0966	256.1441	313.6576	363.1918	*
y+	*	524.2715	396.1765	281.1496	182.0812
y++	*	262.6394	198.5919	141.0784	91.5442

MS/MS analysis of single-amidated **4f**

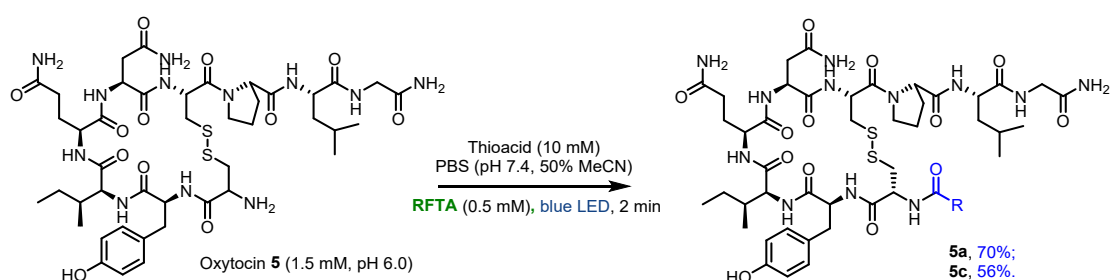


ESI Mass spectrum of purified double-amidated product **4f**. Calculated Mass  $[M+H]^+$ : 1132.53,  $[M+2H]^{2+}$ : 566.77; Mass Found (ESI+)  $[M+H]^+$ : 1132.53,  $[M+2H]^{2+}$ : 566.77.

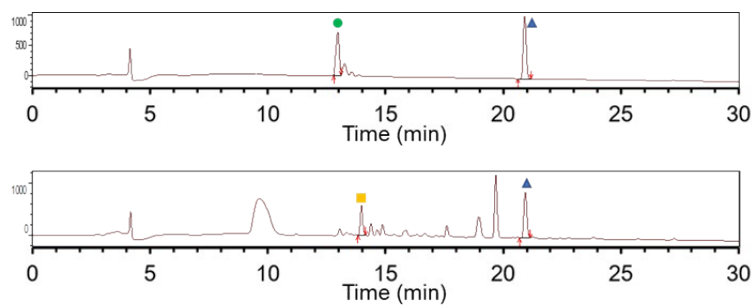


MS/MS analysis of double-amidated **4f**

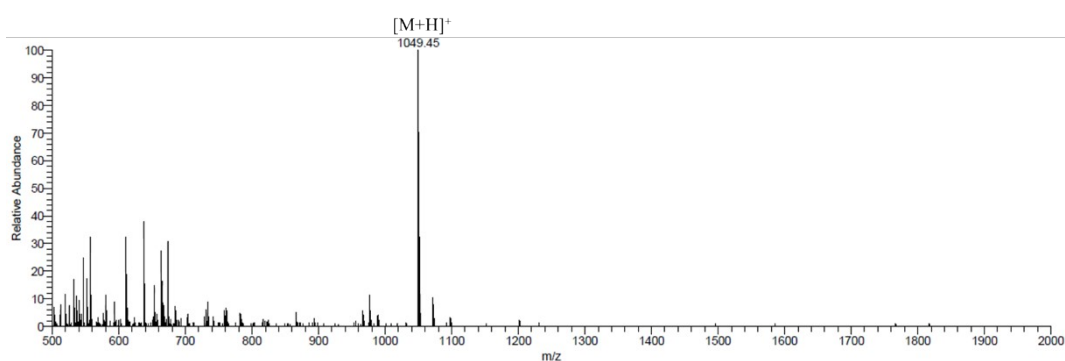
## 2.6.4 Characterization of the reaction of peptide **5**



The reaction was followed **General Procedure B** using peptide **5** (1.5 mM), sequence: **NH**<sub>2</sub>-CYIQNCPLG-NH<sub>2</sub> (disulfide: Cys1-Cys6), and thioacid **1a** and **1c**. A stock solution of peptide **5** (1.5 mM) was made up by 1 mL PBS buffer (pH 7.4, 50% MeCN) and 1.5 mg peptide **5**.



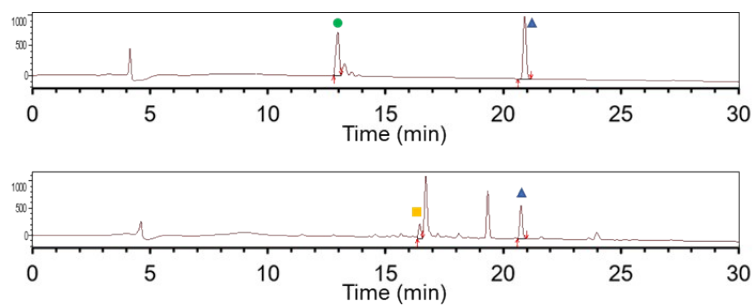
HPLC traces of the quantity relationship of matter and crude reaction of **5a**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



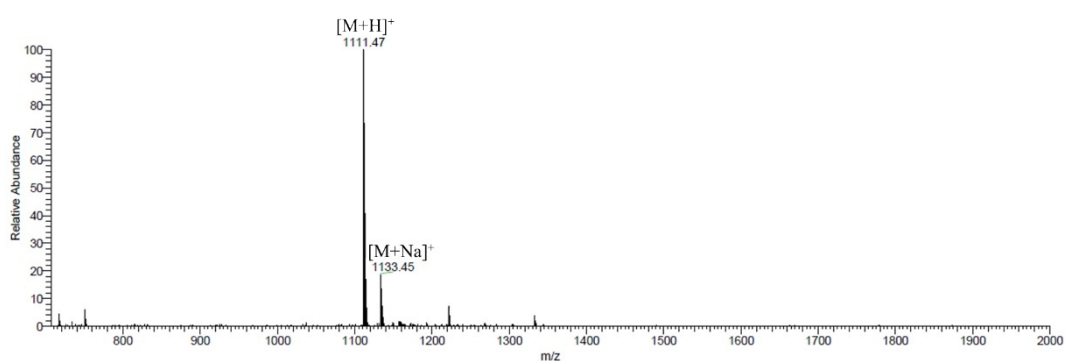
ESI Mass spectrum of purified product **5a**. Calculated Mass  $[M+H]^+$ : 1049.45; Mass Found (ESI+)  $[M+H]^+$ : 1049.45.



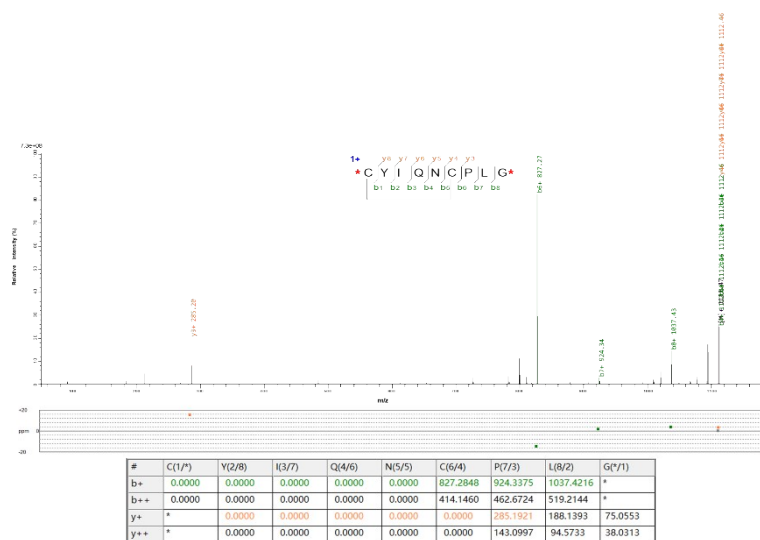
MS/MS analysis of **5a**



HPLC traces of the quantity relationship of matter and crude reaction of **5c**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA, λ = 220 nm, Kromasil 100-5-C18 4.6 × 250 mm, 5 μm column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



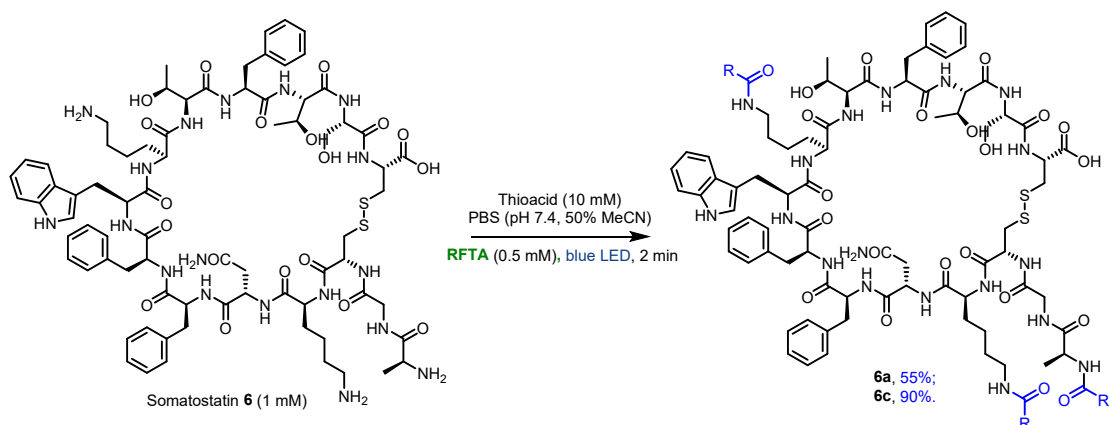
ESI Mass spectrum of purified product **5c**. Calculated Mass [M+H]<sup>+</sup>: 1111.47; Mass Found (ESI+) [M+H]<sup>+</sup>: 1111.47.



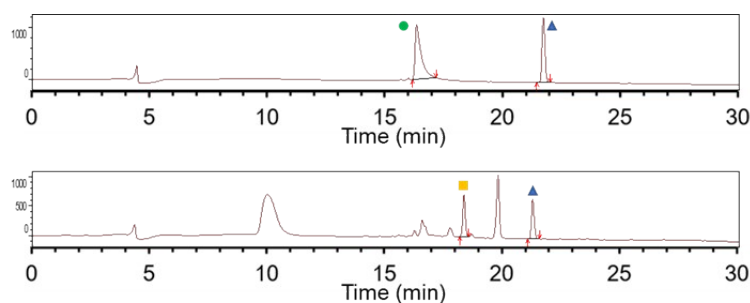
MS/MS analysis of **5c**

## 2.6.5 Characterization of the reaction of peptide **6**

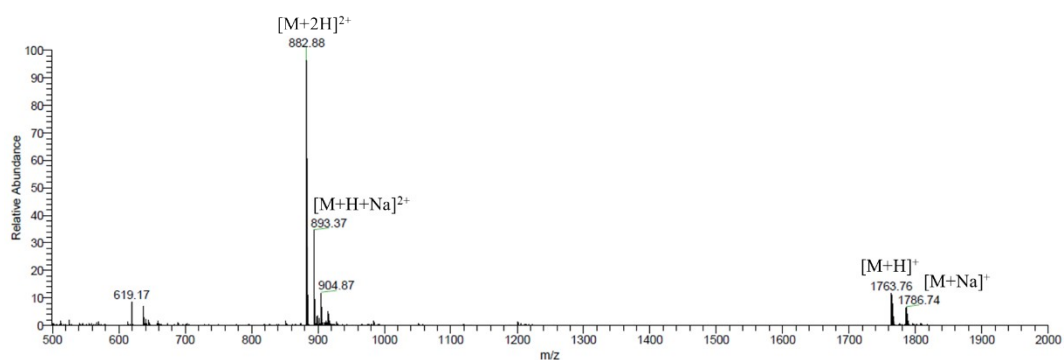




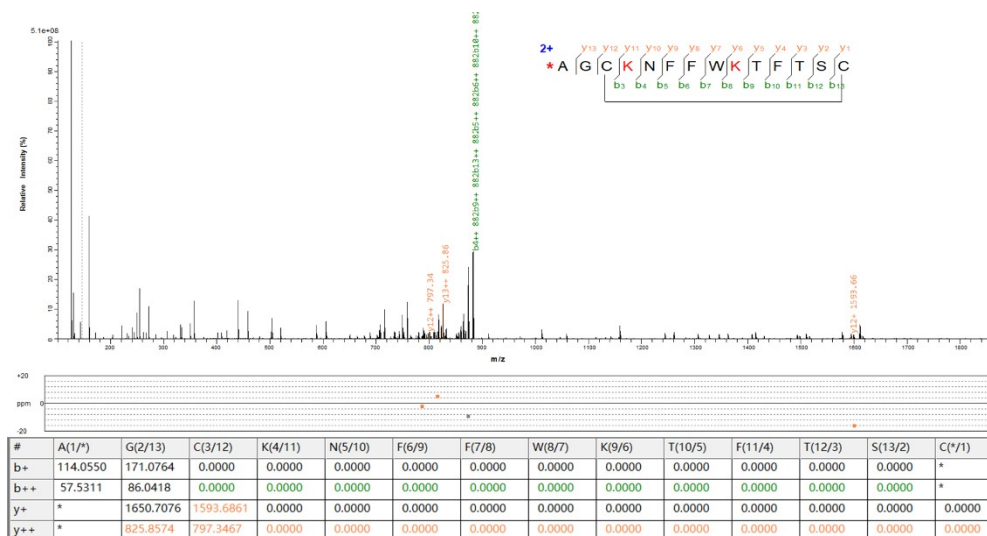
The reaction was followed **General Procedure B** using peptide **6** (1 mM), sequence: **NH<sub>2</sub>**-AGCK**N**FFW**K**TFTSC-OH (disulfide: Cys3-Cys14), and thioacid **1a** and **1c**. A stock solution of peptide **6** (1 mM) was made up by 1 mL PBS buffer (pH 7.4, 50% MeCN) and 1.6 mg peptide **6**.



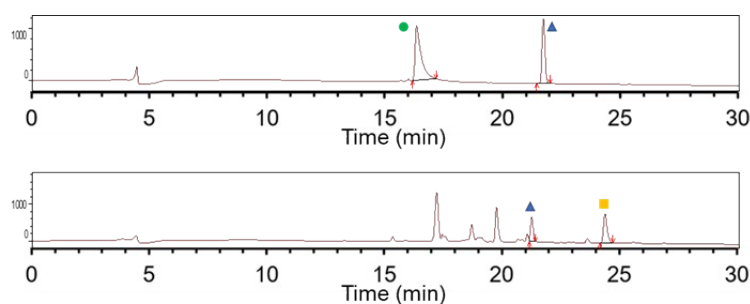
HPLC traces of the quantity relationship of matter and crude reaction of **6a**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



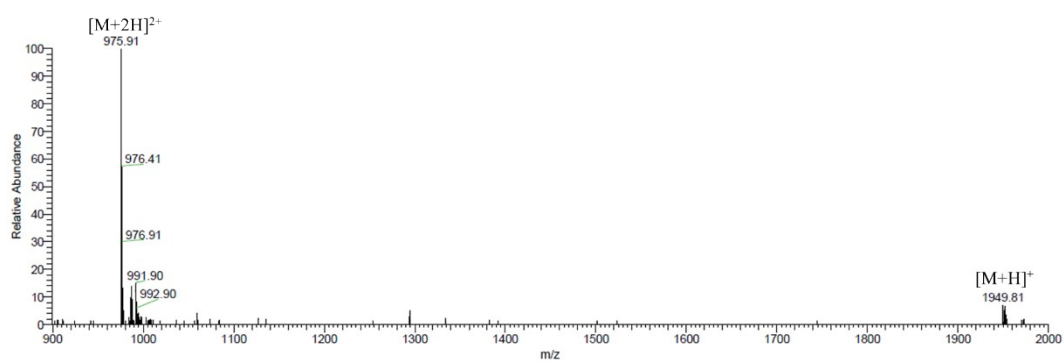
ESI Mass spectrum of purified product **6a**. Calculated Mass  $[M+H]^+$ : 1763.76,  $[M+2H]^{2+}$ : 882.88; Mass Found (ESI+)  $[M+H]^+$ : 1763.76,  $[M+2H]^{2+}$ : 882.88.



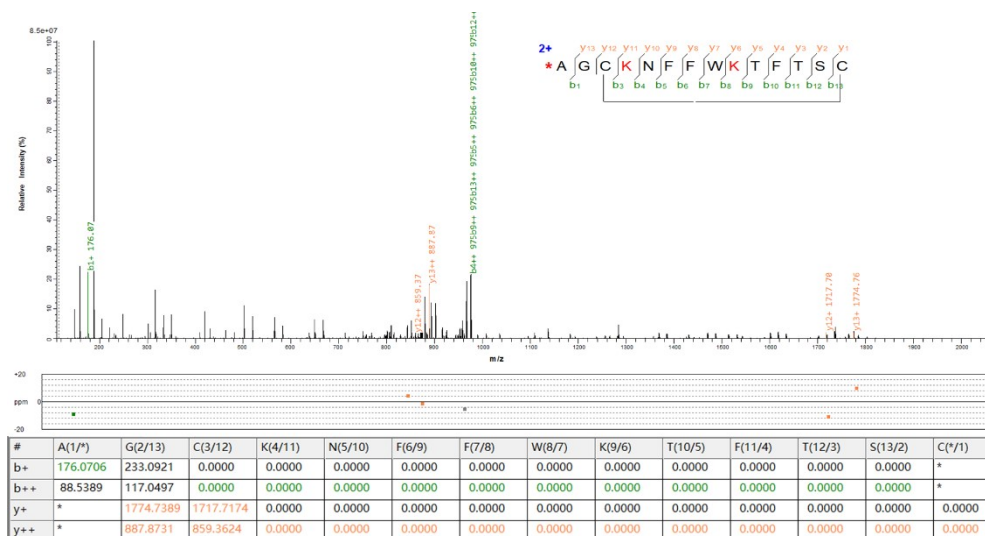
### MS/MS analysis of 6a



HPLC traces of the quantity relationship of matter and crude reaction of **6c**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.

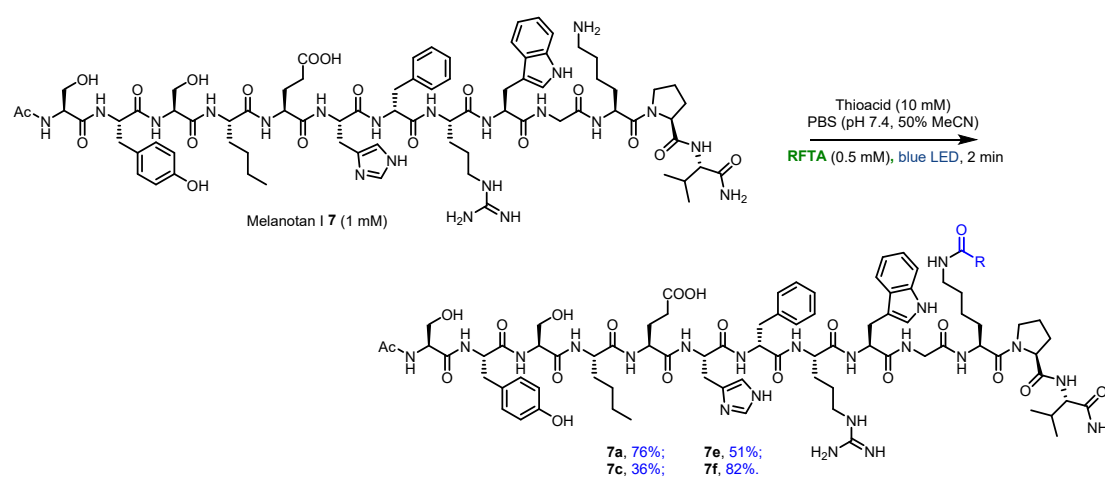


ESI Mass spectrum of purified product **6c**. Calculated Mass  $[M+H]^+$ : 1949.81,  $[M+2H]^{2+}$ : 975.91; Mass Found (ESI+)  $[M+H]^+$ : 1949.81,  $[M+2H]^{2+}$ : 975.91.

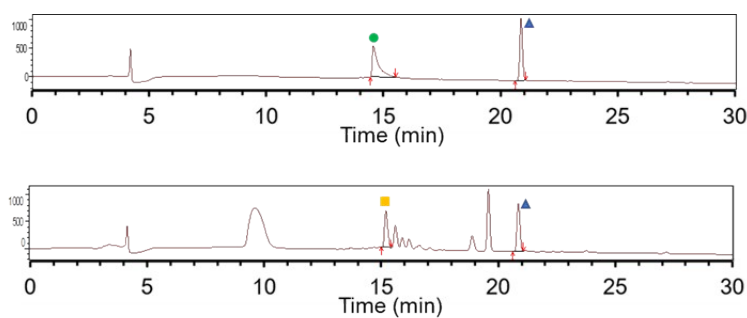


MS/MS analysis of **6c**

## 2.6.6 Characterization of the reaction of peptide **7**

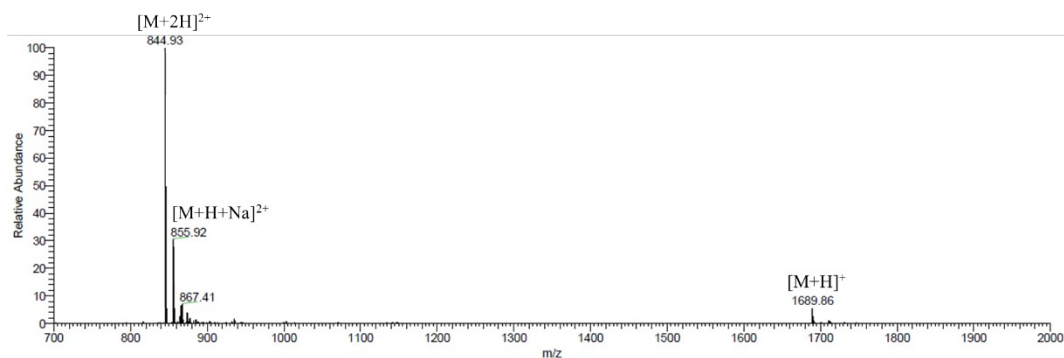


The reaction was followed **General Procedure B** using peptide **7** (1 mM), sequence: Ac-SYS(Nle)EHFRWGKPV-NH<sub>2</sub>, and thioacid **1a**, **1b**, **1e** and **1f**. A stock solution of peptide **7** (1 mM) was made up by 1 mL PBS buffer (pH 7.4, 50% MeCN) and 1.6 mg peptide **7**.

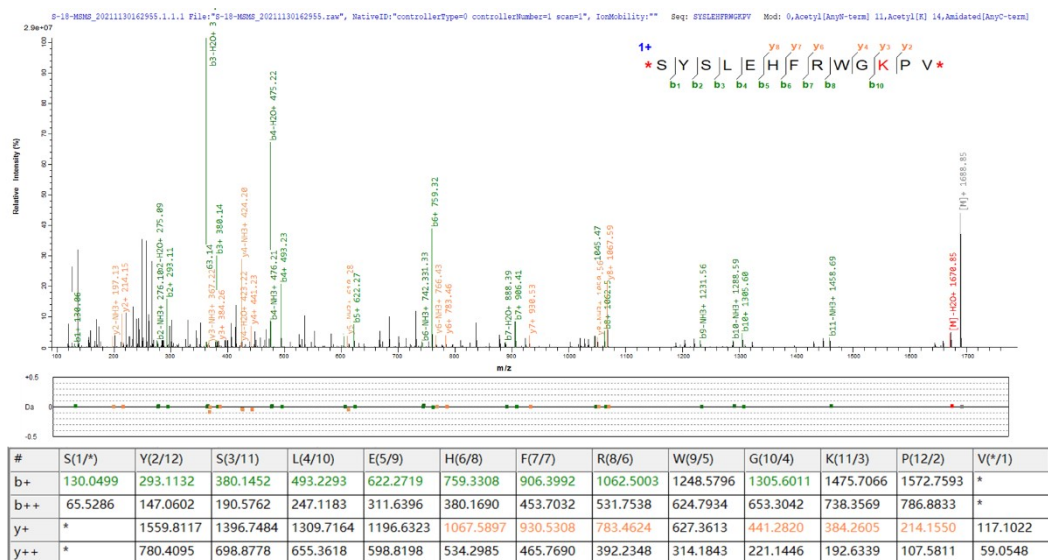


HPLC traces of the quantity relationship of matter and crude reaction of **7a**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA, λ = 220 nm, Kromasil 100-5-C18 4.6 × 250 mm, 5 μm column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target

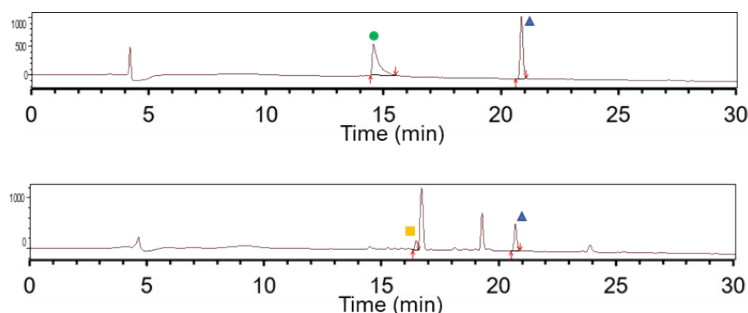
product.



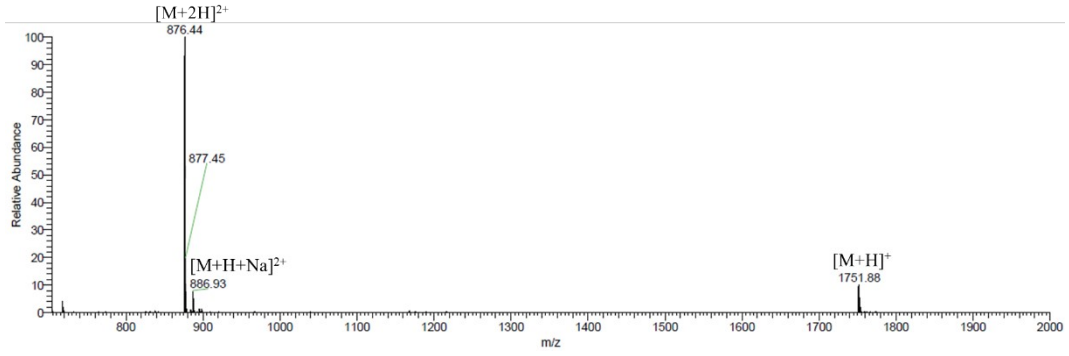
ESI Mass spectrum of purified product **7a**. Calculated Mass  $[M+H]^+$ : 1689.86,  $[M+2H]^{2+}$ : 844.93; Mass Found (ESI+)  $[M+H]^+$ : 1689.86,  $[M+2H]^{2+}$ : 844.93.



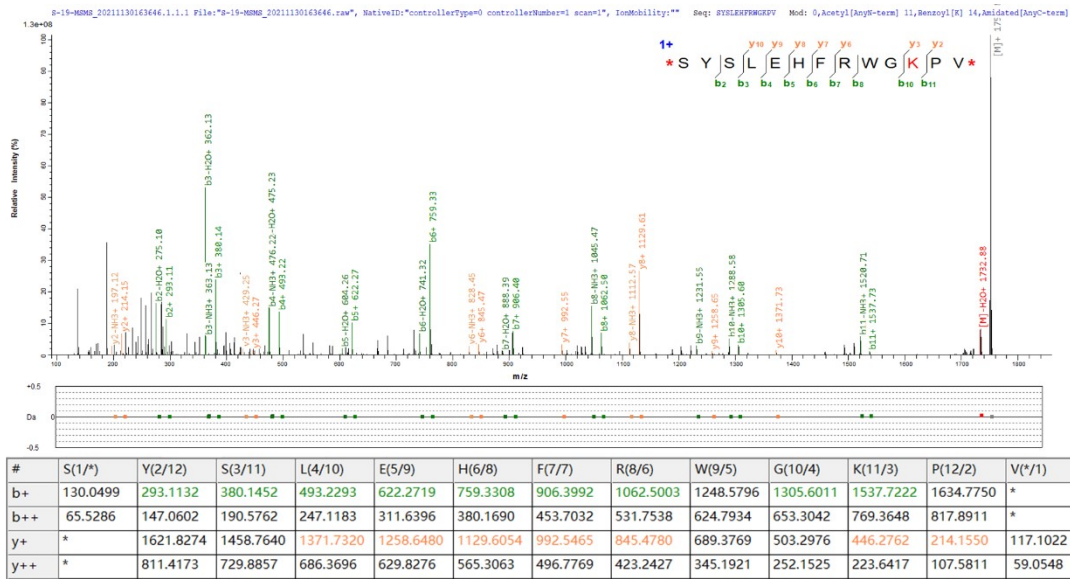
### MS/MS analysis of **7a**



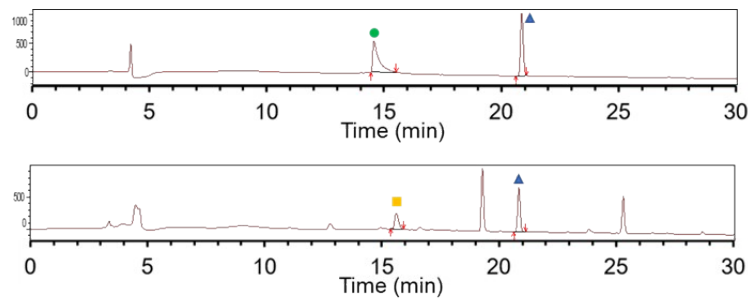
HPLC traces of the quantity relationship of matter and crude reaction of **7c**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda$  = 220 nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



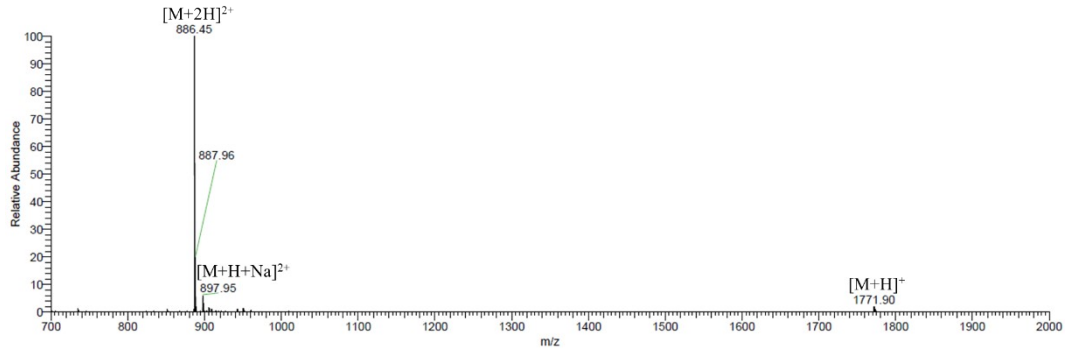
ESI Mass spectrum of purified product **7c**. Calculated Mass  $[M+H]^+$ : 1751.88,  $[M+2H]^{2+}$ : 876.44; Mass Found (ESI+)  $[M+H]^+$ : 1751.88,  $[M+2H]^{2+}$ : 876.44.



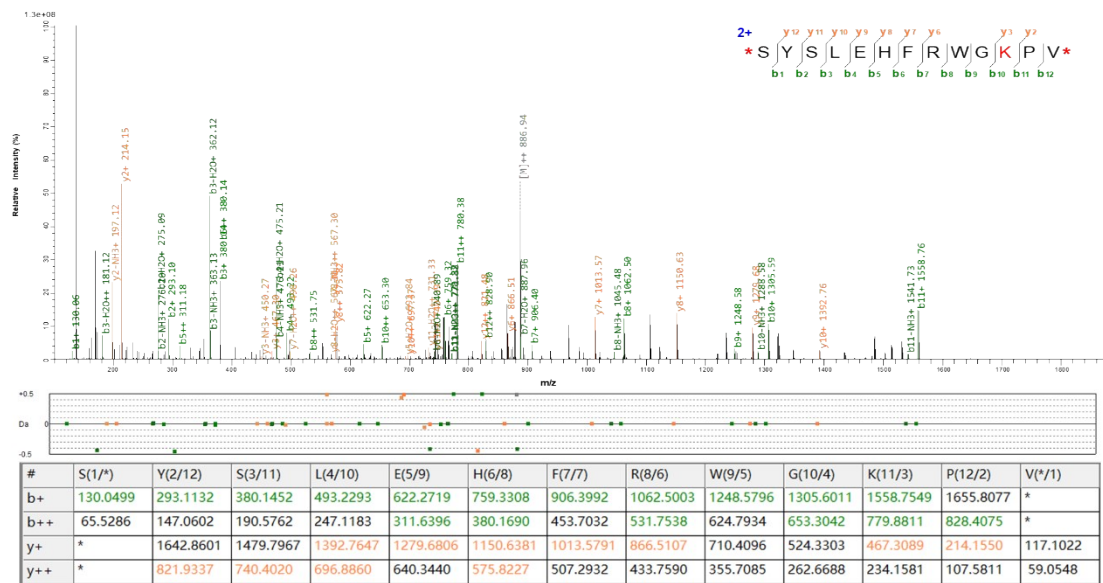
### MS/MS analysis of **7c**



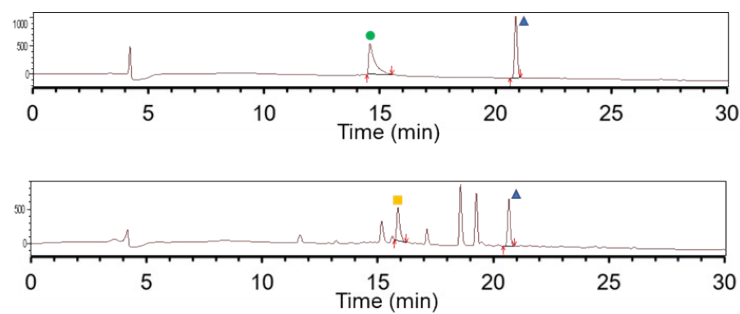
HPLC traces of the quantity relationship of matter and crude reaction of **7e**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



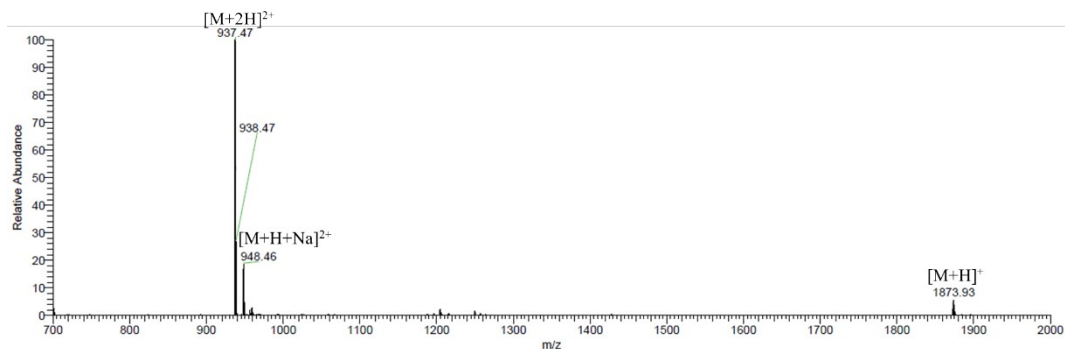
ESI Mass spectrum of purified product **7e**. Calculated Mass  $[M+H]^+$ : 1771.90,  $[M+2H]^{2+}$ : 886.45; Mass Found (ESI+)  $[M+H]^+$ : 1771.90,  $[M+2H]^{2+}$ : 886.45.



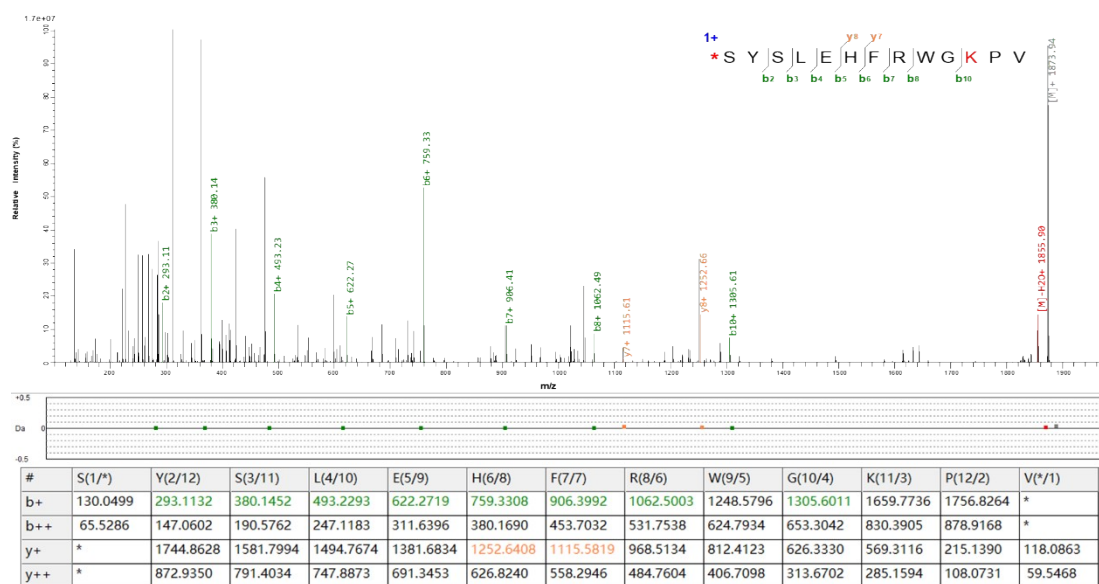
MS/MS analysis of **7e**



HPLC traces of the quantity relationship of matter and crude reaction of **7f**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.

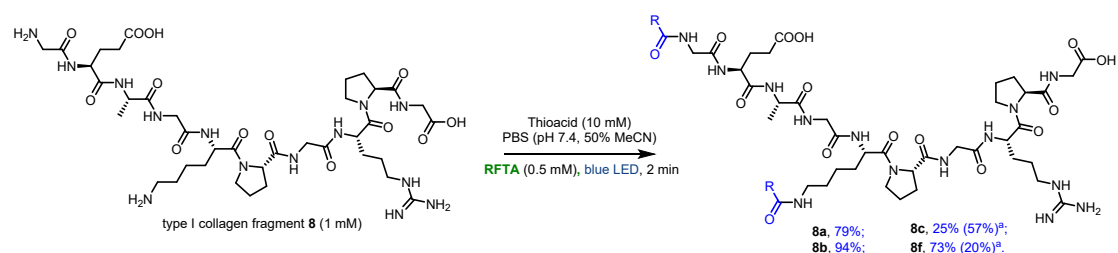


ESI Mass spectrum of purified product **7f**. Calculated Mass  $[M+H]^+$ : 1873.93,  $[M+2H]^{2+}$ : 937.47; Mass Found (ESI+)  $[M+H]^+$ : 1873.93,  $[M+2H]^{2+}$ : 937.47.

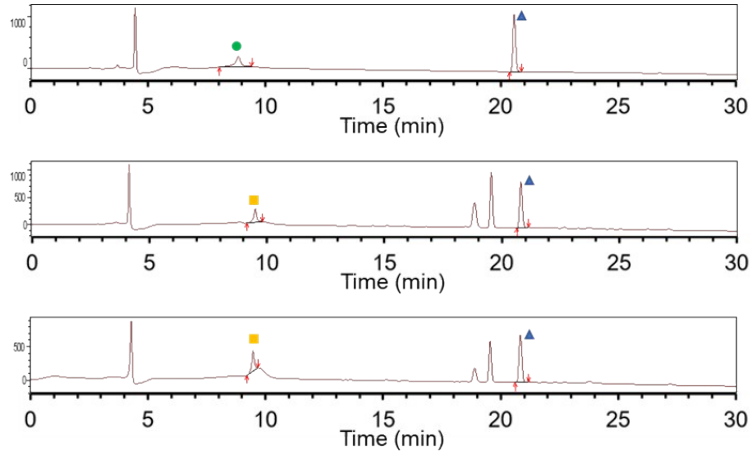


MS/MS analysis of **7f**

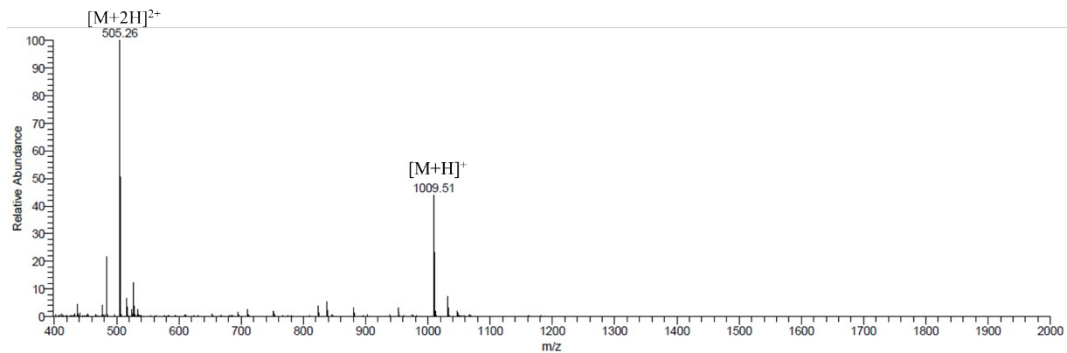
## 2.6.7 Characterization of the reaction of peptide **8**



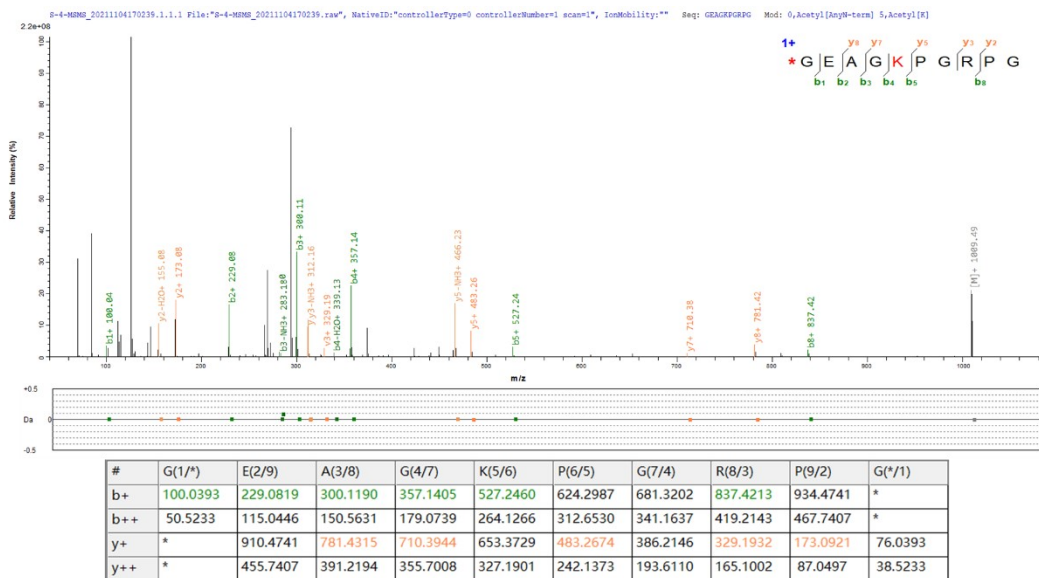
The reaction was followed **General Procedure B** using peptide **8** (1 mM), sequence: **NH**<sub>2</sub>-GEAG**K**PGRPG-OH, and thioacid **1a**, **1b**, **1c** and **1f**. A stock solution of peptide **8** (1 mM) was made up by 1 mL PBS buffer (pH 7.4, 50% MeCN) and 0.9 mg peptide **8**.



HPLC traces of the quantity relationship of matter and crude reaction of **8a** and **8b**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA, λ = 220 nm, Kromasil 100-5-C18 4.6 × 250 mm, 5 μm column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.

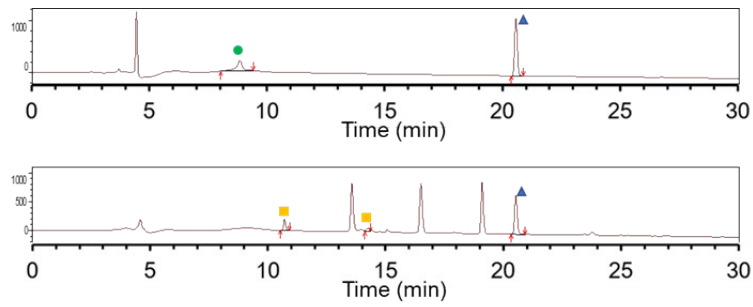


ESI Mass spectrum of purified product **8a**. Calculated Mass  $[M+H]^+$ : 1009.51,  $[M+2H]^{2+}$ : 505.26; Mass Found (ESI+)  $[M+H]^+$ : 1009.51,  $[M+2H]^{2+}$ : 505.26.

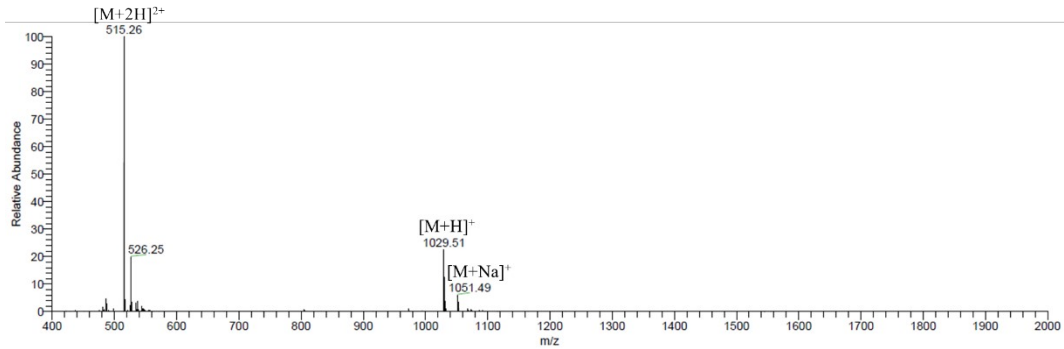


MS/MS analysis of **8a**

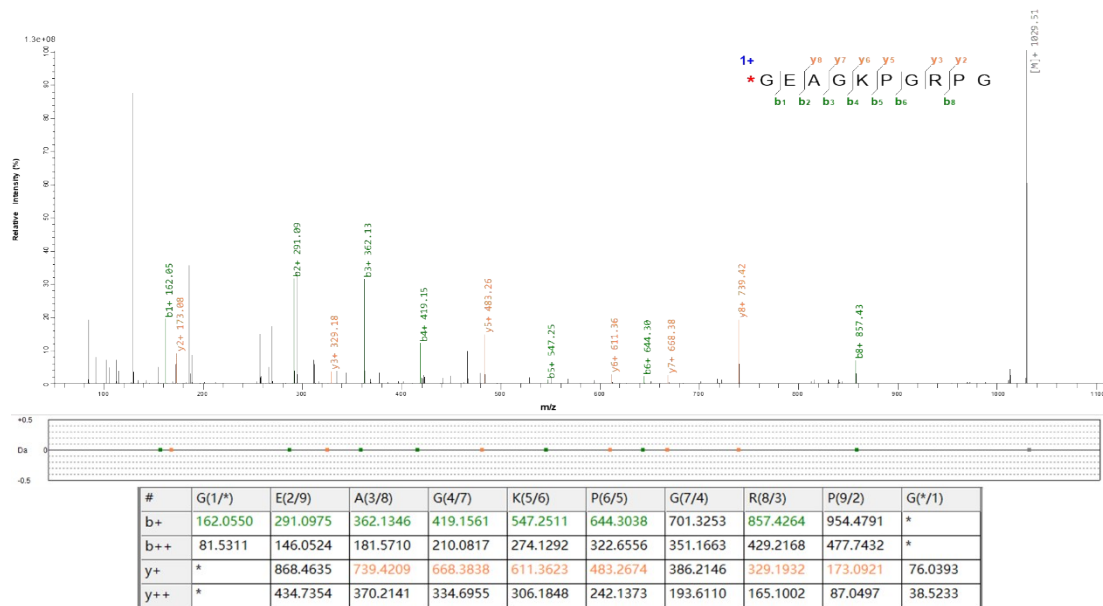




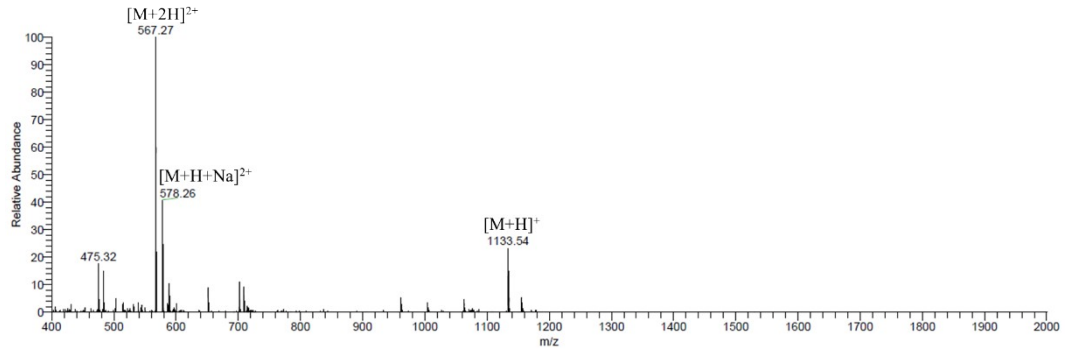
HPLC traces of the quantity relationship of matter and crude reaction **8c**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



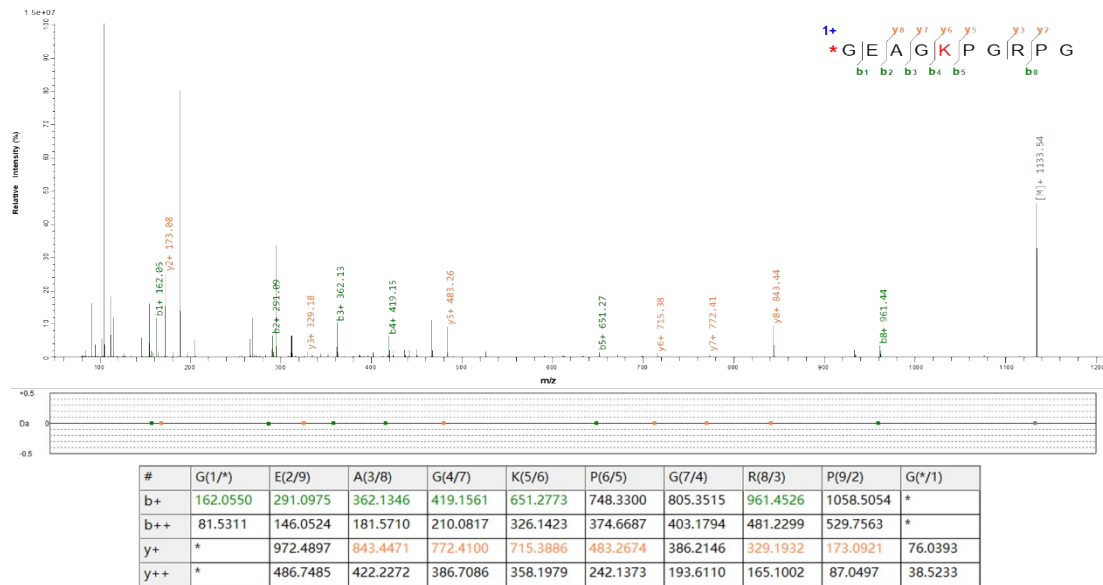
ESI Mass spectrum of purified single-amidated product **8c**. Calculated Mass  $[M+H]^+$ : 1029.51,  $[M+2H]^{2+}$ : 515.26; Mass Found (ESI+)  $[M+H]^+$ : 1029.51,  $[M+2H]^{2+}$ : 515.26.



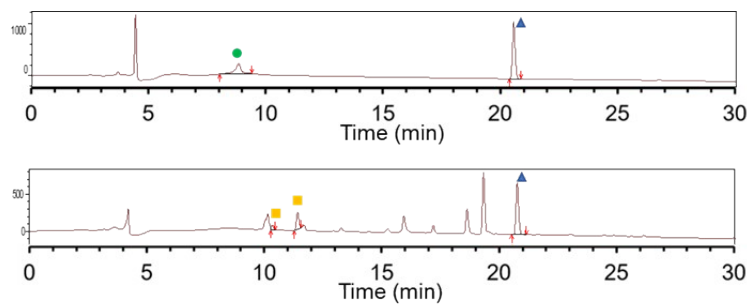
MS/MS analysis of single-amidated **8c**



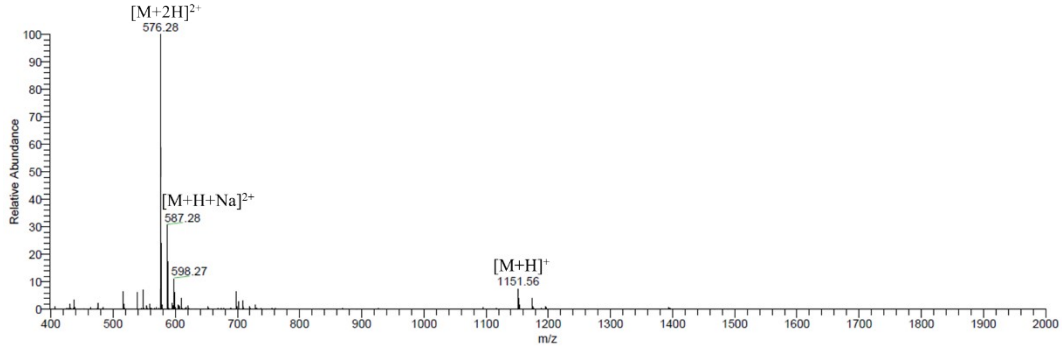
ESI Mass spectrum of purified double-amidated product **8c**. Calculated Mass  $[M+H]^+$ : 1133.54,  $[M+2H]^{2+}$ : 567.27; Mass Found (ESI+)  $[M+H]^+$ : 1133.54,  $[M+2H]^{2+}$ : 567.27.



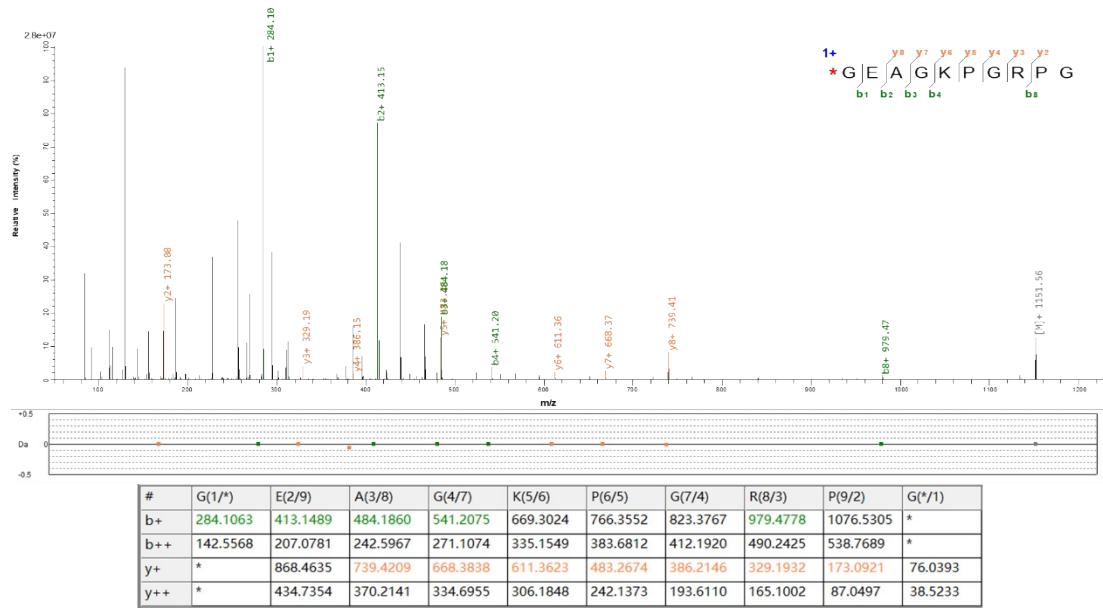
MS/MS analysis of double-amidated **8c**



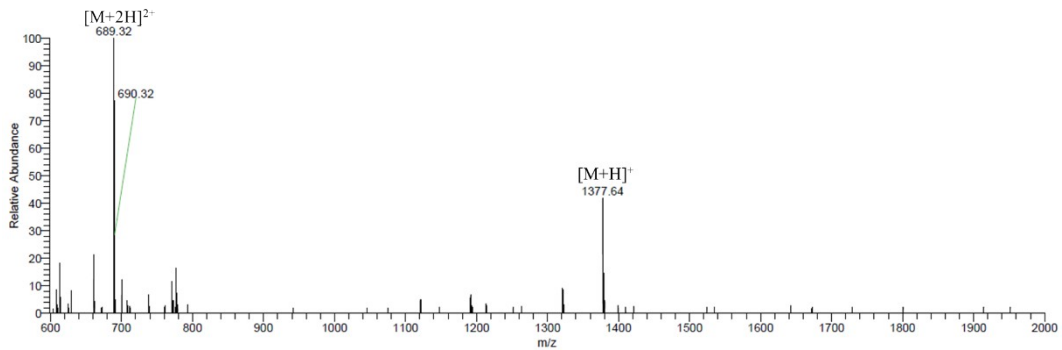
HPLC traces of the quantity relationship of matter and crude reaction **8f**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



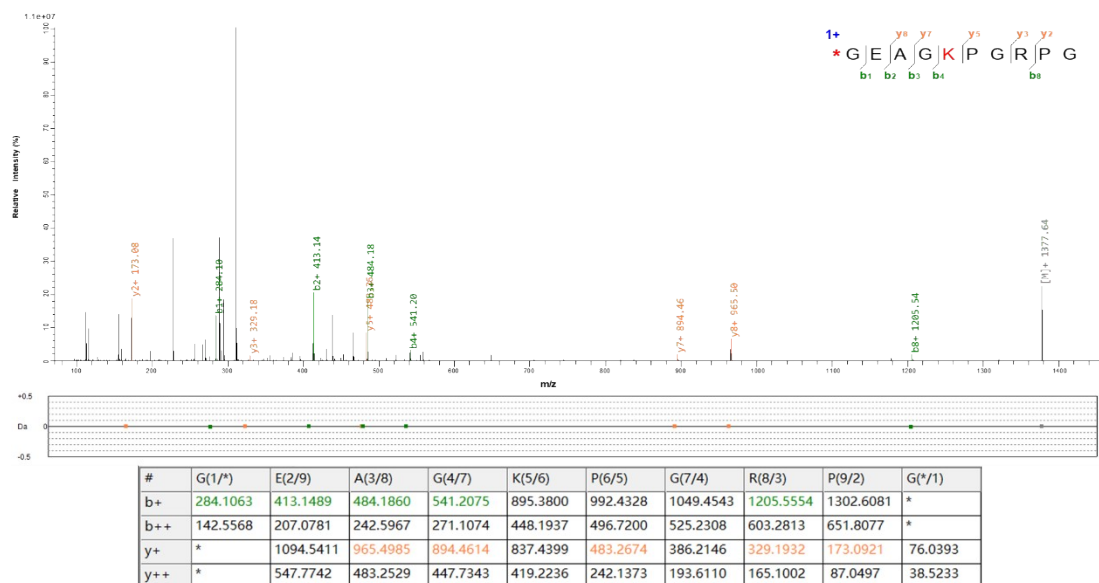
ESI Mass spectrum of purified single-amidated product **8f**. Calculated Mass  $[M+H]^+$ : 1151.56,  $[M+2H]^{2+}$ : 576.28; Mass Found (ESI+)  $[M+H]^+$ : 1151.56,  $[M+2H]^{2+}$ : 576.28.



MS/MS analysis of single-amidated **8f**

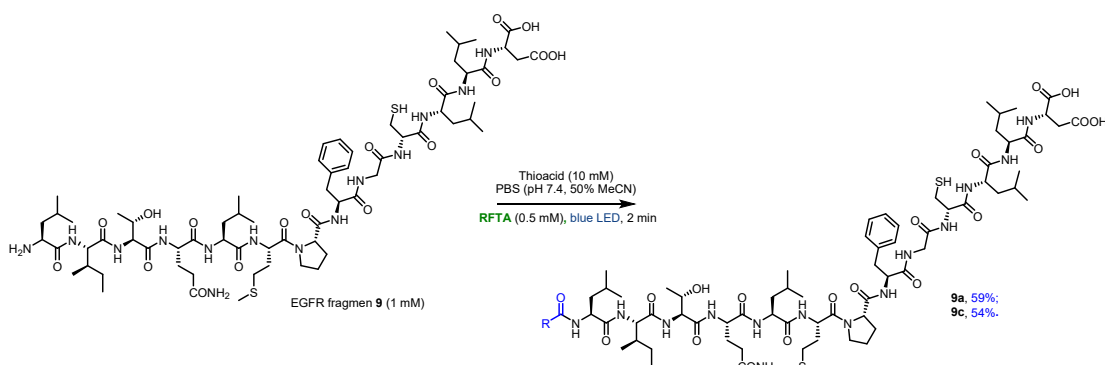


ESI Mass spectrum of purified double-amidated product **8f**. Calculated Mass  $[M+H]^+$ : 1377.64,  $[M+2H]^{2+}$ : 689.32; Mass Found (ESI+)  $[M+H]^+$ : 1377.64,  $[M+2H]^{2+}$ : 689.32.

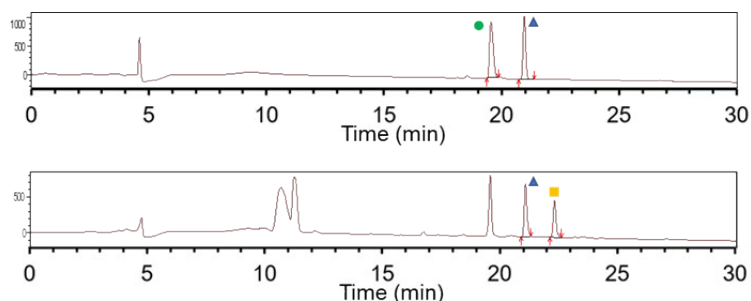


MS/MS analysis of double-amidated **8f**

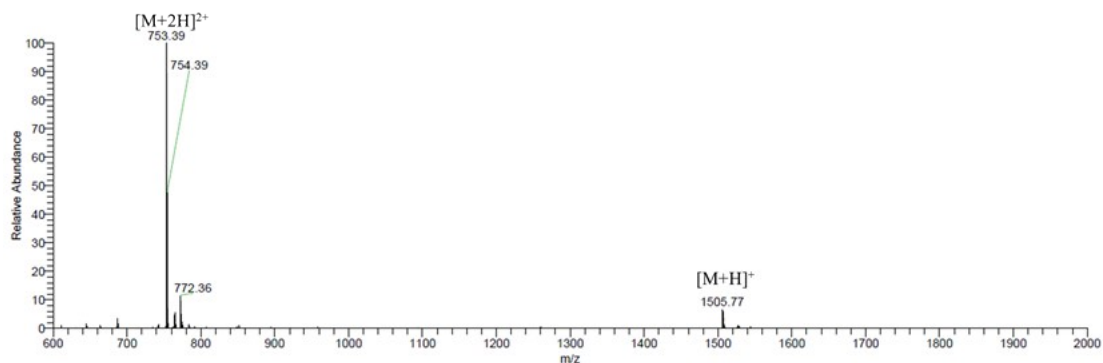
## 2.6.8 Characterization of the reaction of peptide **9**



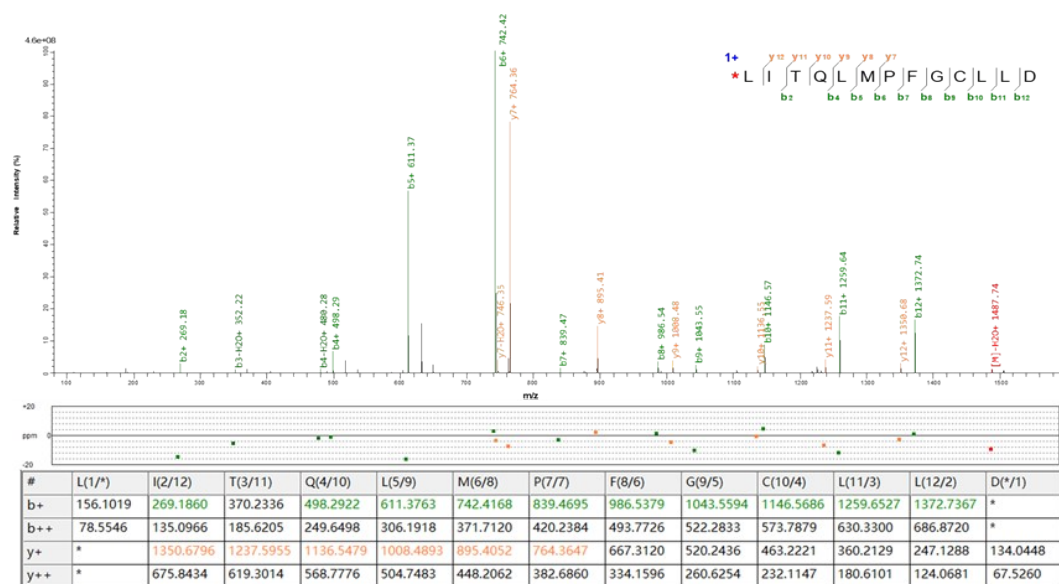
The reaction was followed **General Procedure B** using peptide **9** (1 mM), sequence: **NH<sub>2</sub>-LITQLMPFGCLLD-OH**, and thioacid **1a** and **1c**. A stock solution of peptide **9** (1 mM) was made up by 1 mL PBS buffer (pH 7.4, 50% MeCN) and 1.5 mg peptide **9**.



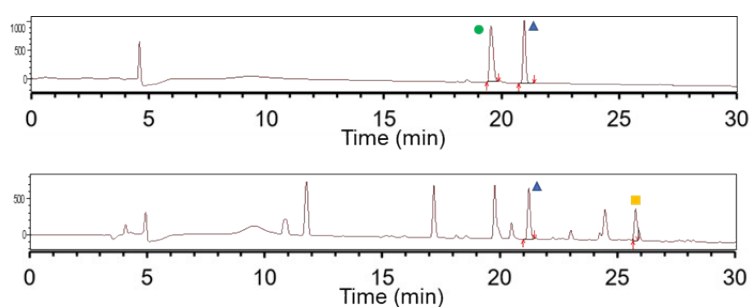
HPLC traces of the quantity relationship of matter and crude reaction **9a**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



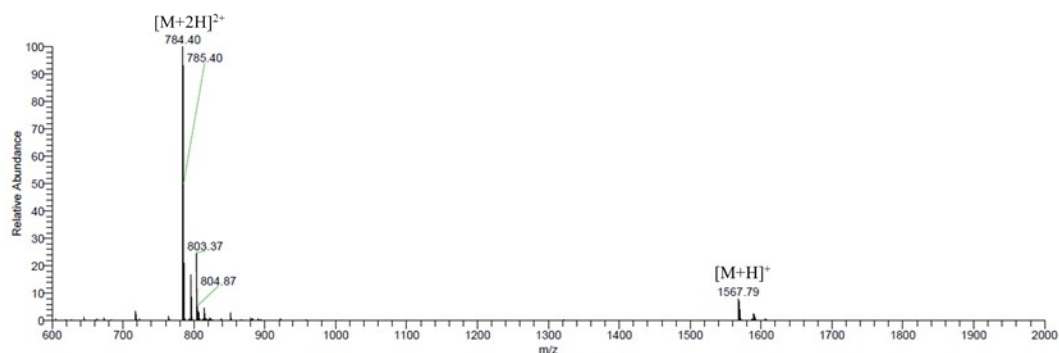
ESI Mass spectrum of purified product **9a**. Calculated Mass  $[M+H]^+$ : 1505.77,  $[M+2H]^{2+}$ : 753.39; Mass Found (ESI+)  $[M+H]^+$ : 1505.77,  $[M+2H]^{2+}$ : 753.39.



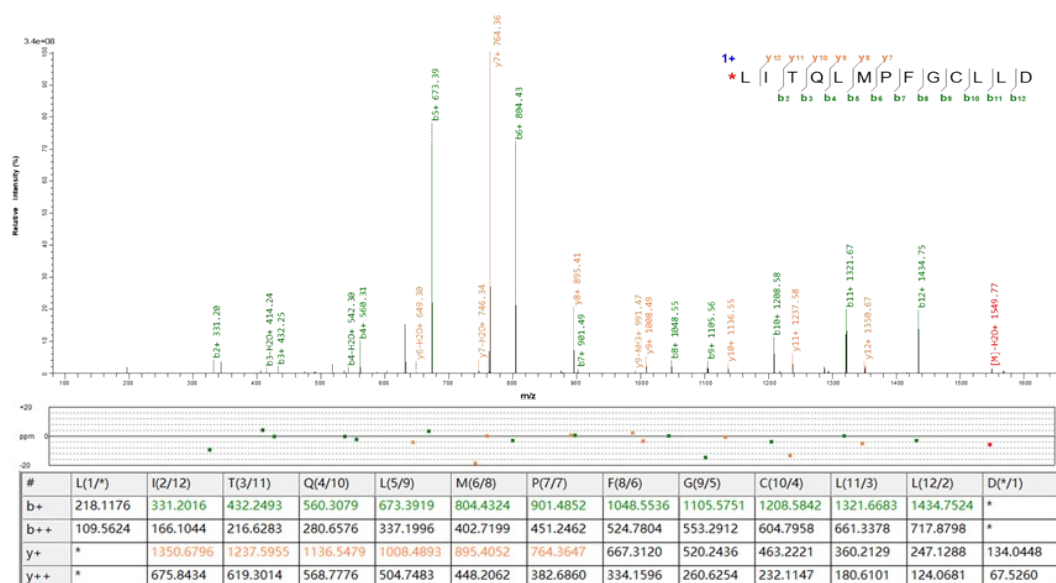
MS/MS analysis of **9a**



HPLC traces of the quantity relationship of matter and crude reaction **9c**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.

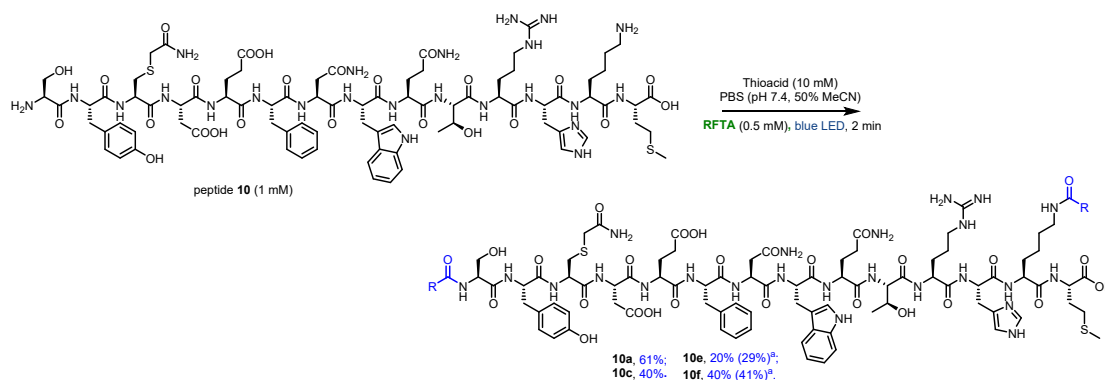


ESI Mass spectrum of purified product **9c**. Calculated Mass  $[M+H]^+$ : 1567.79,  $[M+2H]^{2+}$ : 784.40; Mass Found (ESI+)  $[M+H]^+$ : 1567.79,  $[M+2H]^{2+}$ : 784.40.

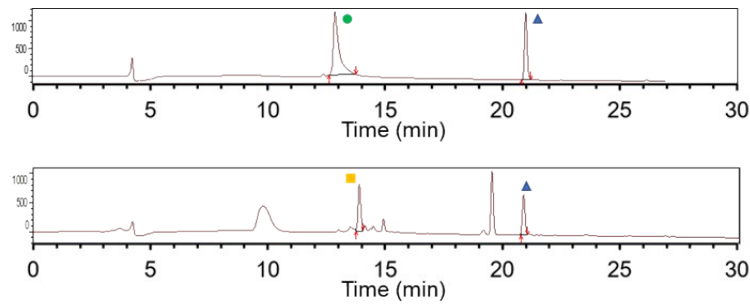


MS/MS analysis of **9c**

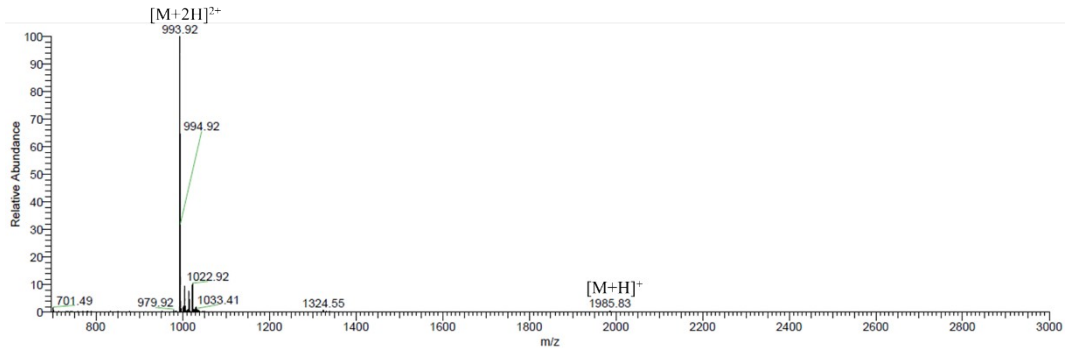
## 2.6.9 Characterization of the reaction of peptide 10



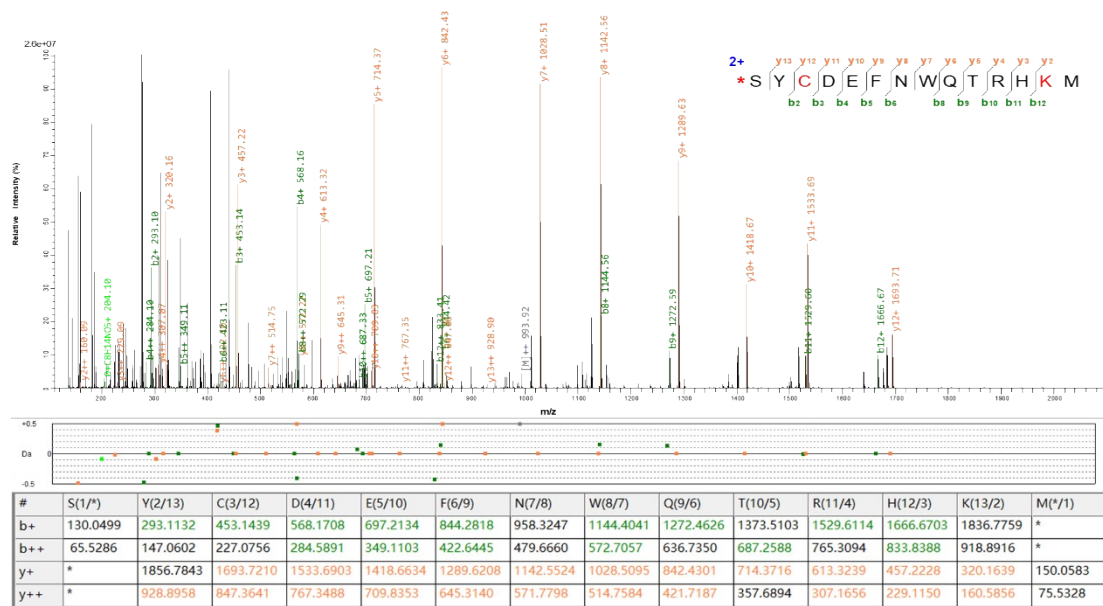
The reaction was followed **General Procedure B** using peptide **10** (1 mM), sequence: **NH<sub>2</sub>**-SYC(AM)DEFNWQTRHKM-OH, and thioacid **1a**, **1c**, **1e** and **1f**. A stock solution of peptide **10** (1 mM) was made up by 1 mL PBS buffer (pH 7.4, 50% MeCN) and 1.9 mg peptide **10**.



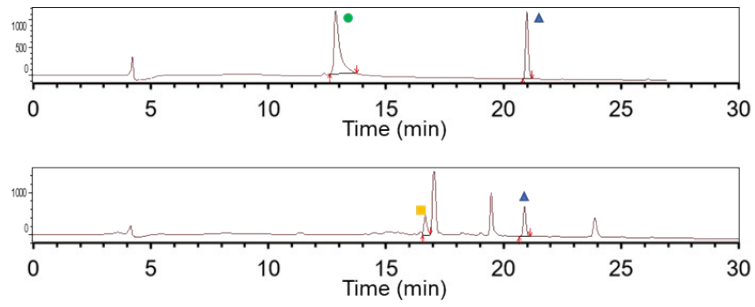
HPLC traces of the quantity relationship of matter and crude reaction **10a**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA, λ = 220 nm, Kromasil 100-5-C18 4.6 × 250 mm, 5 μm column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



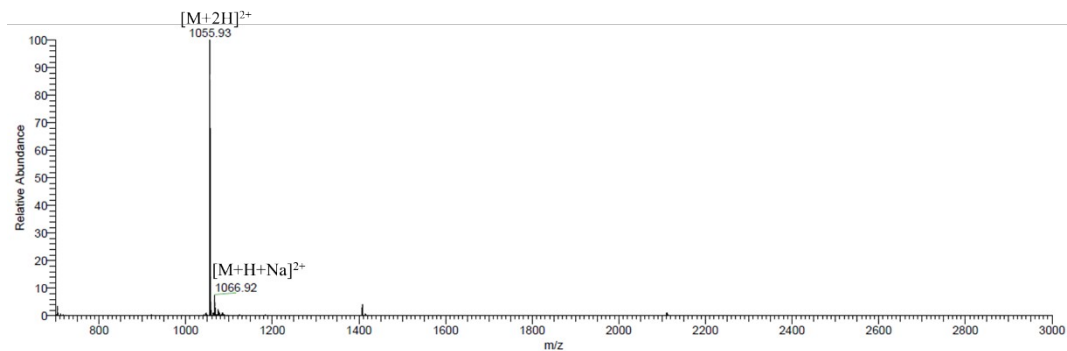
ESI Mass spectrum of purified product **10a**. Calculated Mass  $[M+H]^+$ : 1985.83,  $[M+2H]^{2+}$ : 993.92; Mass Found (ESI+)  $[M+H]^+$ : 1985.83,  $[M+2H]^{2+}$ : 993.92.



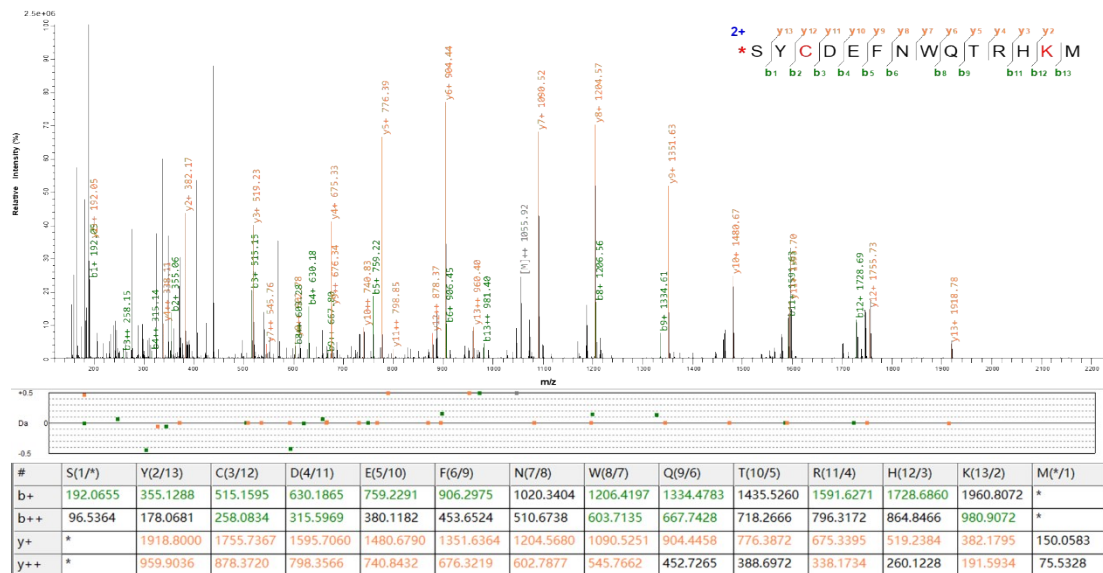
MS/MS analysis of **10a**



HPLC traces of the quantity relationship of matter and crude reaction of **10c**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA, λ = 220 nm, Kromasil 100-5-C18 4.6 × 250 mm, 5 μm column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.

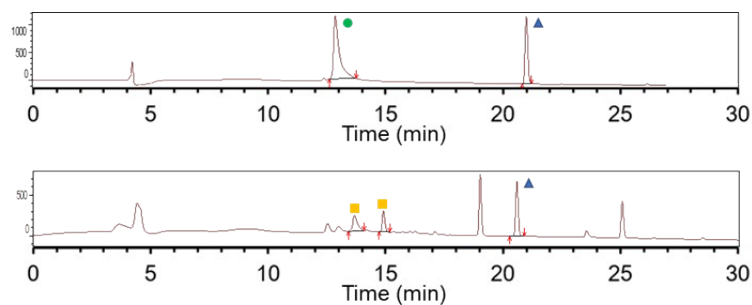


ESI Mass spectrum of purified product **10c**. Calculated Mass  $[M+2H]^{2+}$ : 1055.93; Mass Found (ESI+)  $[M+2H]^{2+}$ : 1055.93.

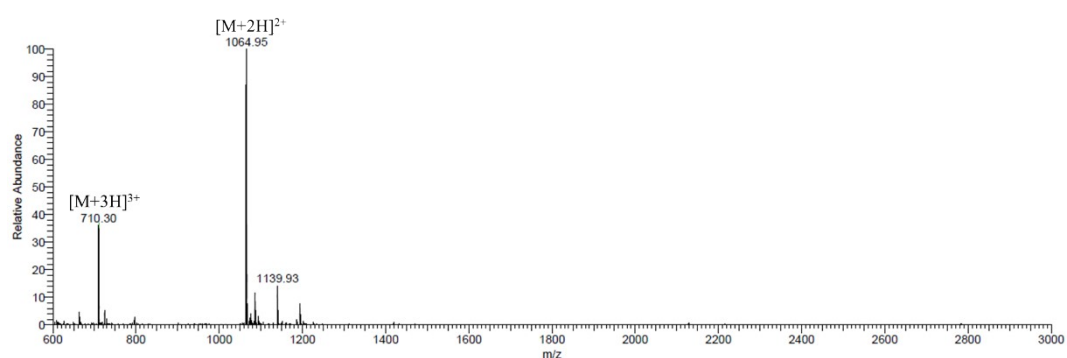


MS/MS analysis of **10c**

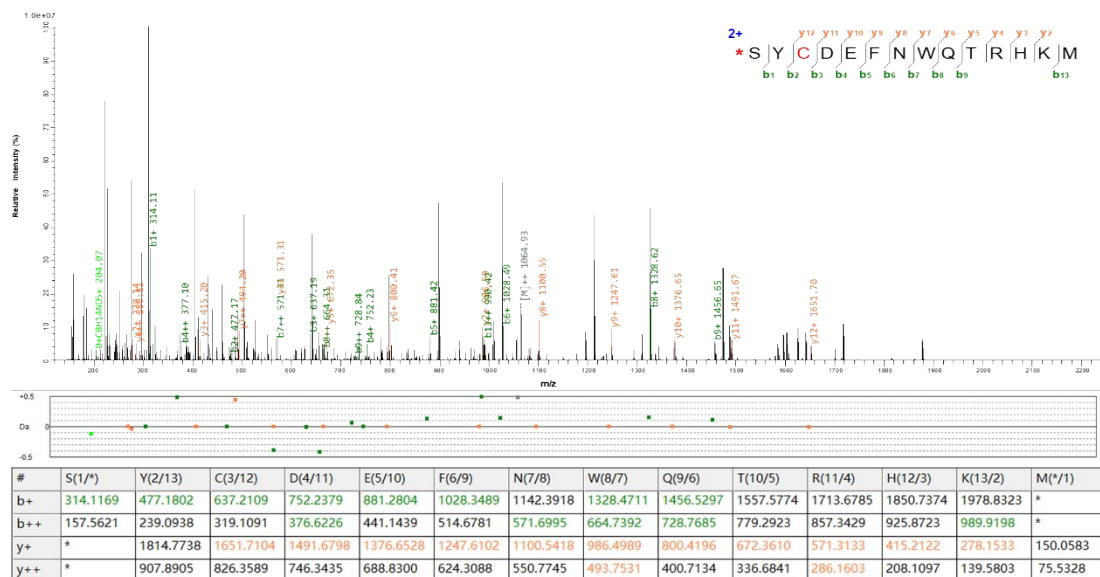




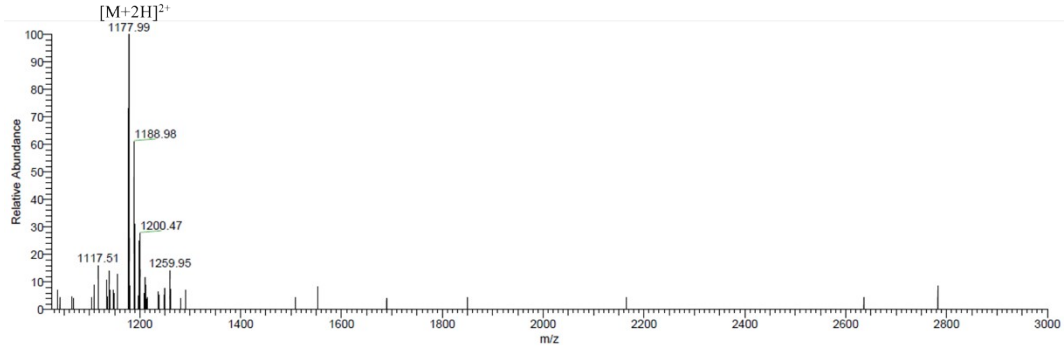
HPLC traces of the quantity relationship of matter and crude reaction of **10e**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA, λ = 220 nm, Kromasil 100-5-C18 4.6 × 250 mm, 5 μm column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



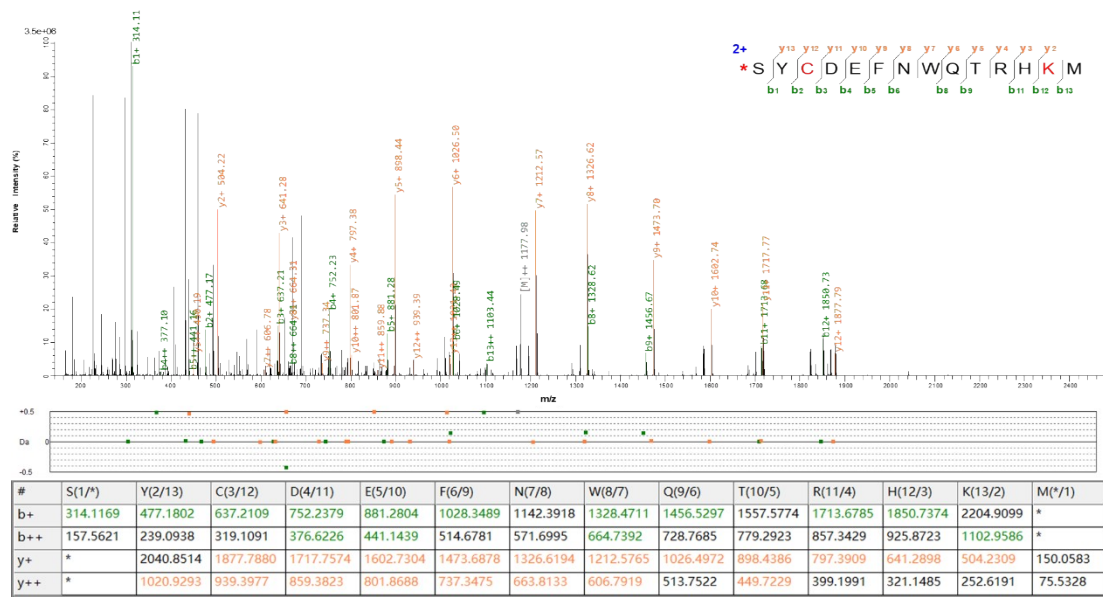
ESI Mass spectrum of purified single-amidated product **10e**. Calculated Mass  $[M+2H]^{2+}$ : 1064.95,  $[M+3H]^{3+}$ : 710.30; Mass Found (ESI+)  $[M+2H]^{2+}$ : 1064.95,  $[M+3H]^{3+}$ : 710.30.



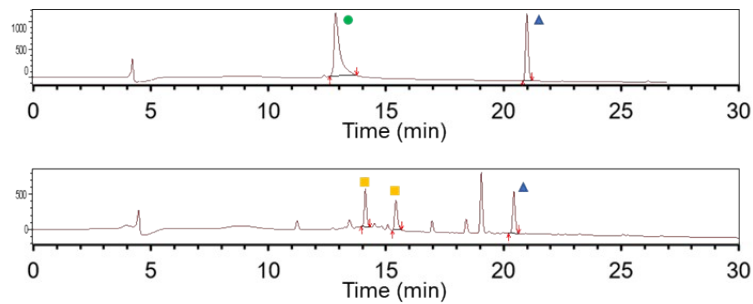
MS/MS analysis of single-amidated **10e**



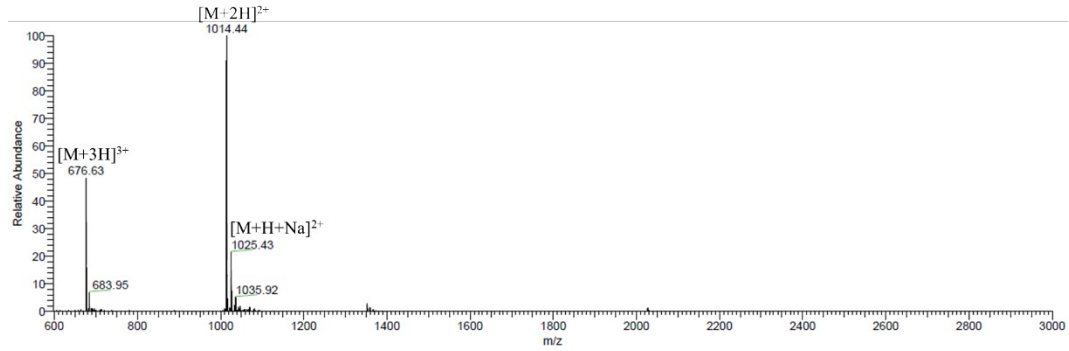
ESI Mass spectrum of purified double-amidated product **10e**. Calculated Mass  $[M+2H]^{2+}$ : 1177.99; Mass Found (ESI+)  $[M+2H]^{2+}$ : 1177.99.



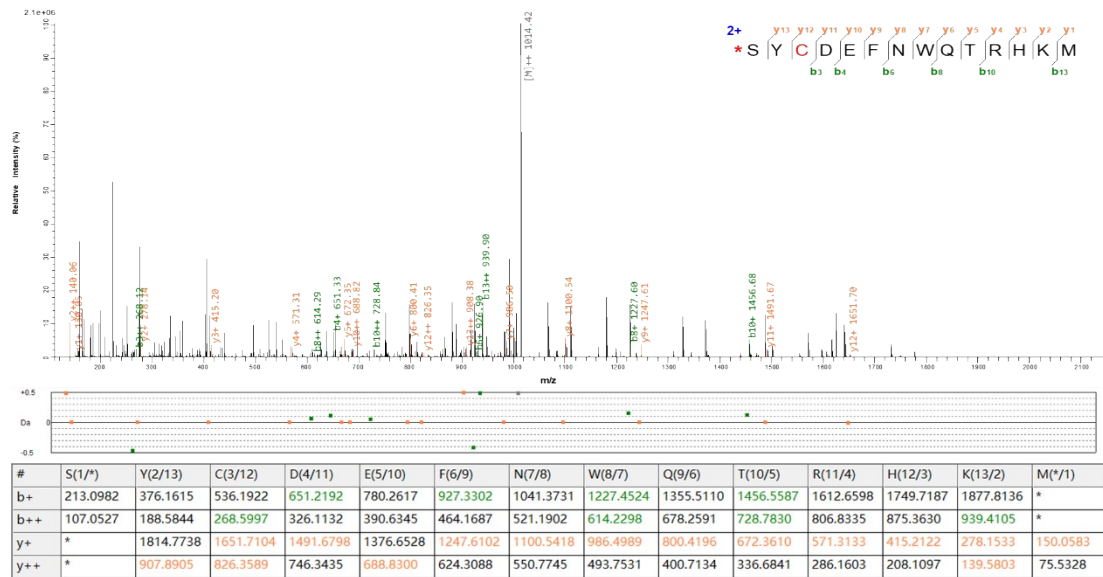
MS/MS analysis of double-amidated **10e**



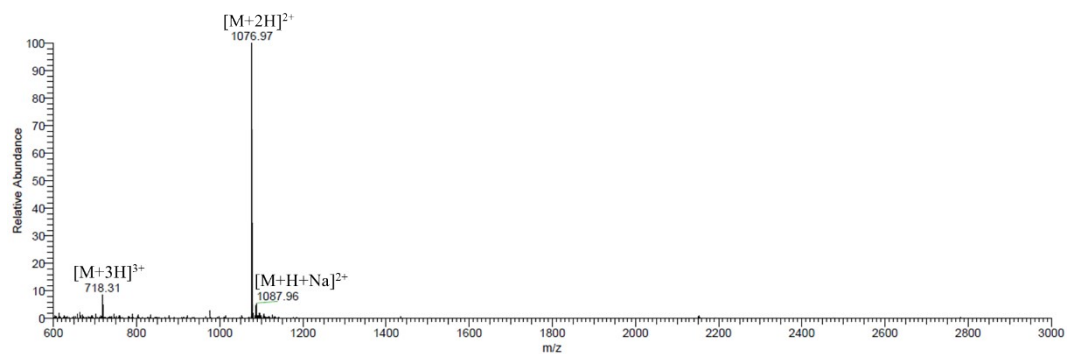
HPLC traces of the quantity relationship of matter and crude reaction of **10f**. (10-80% B phase over 25 min, 1 mL·min<sup>-1</sup> flow rate, 0.1% TFA,  $\lambda = 220$  nm, Kromasil 100-5-C18 4.6 × 250 mm, 5  $\mu$ m column). The green circle, blue triangle and orange square refer to the starting peptide, internal standard and target product.



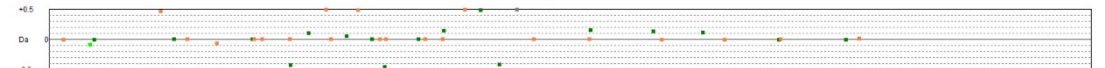
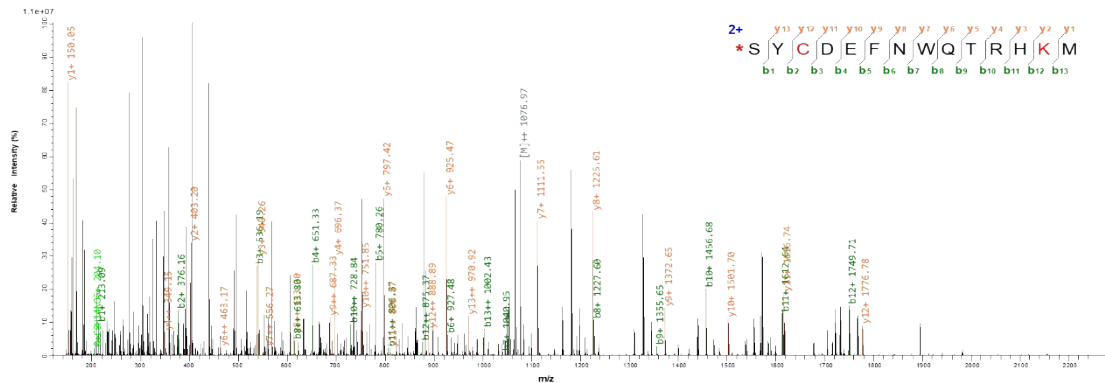
ESI Mass spectrum of purified single-amidated product **10f**. Calculated Mass  $[M+2H]^{2+}$ : 1014.44,  $[M+3H]^{3+}$ : 676.63; Mass Found (ESI+)  $[M+2H]^{2+}$ : 1014.44,  $[M+3H]^{3+}$ : 676.63.



MS/MS analysis of single-amidated **10f**



ESI Mass spectrum of purified single-amidated product **10f**. Calculated Mass  $[M+2H]^{2+}$ : 1076.97,  $[M+3H]^{3+}$ : 718.31; Mass Found (ESI+)  $[M+2H]^{2+}$ : 1076.97,  $[M+3H]^{3+}$ : 718.31.



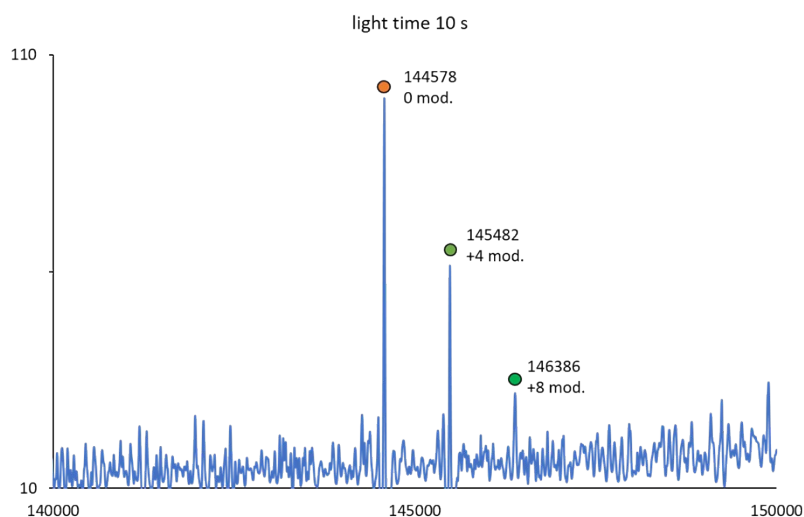
#	S(1*)	Y(2/13)	C(3/12)	D(4/11)	E(5/10)	F(6/9)	N(7/8)	W(8/7)	Q(9/6)	T(10/5)	R(11/4)	H(12/3)	K(13/2)	M(* /1)
b+	213.0982	376.1615	536.1922	651.2192	780.2617	927.3302	1041.3731	1227.4524	1355.5110	1456.5587	1612.6598	1749.7187	2002.8725	*
b++	107.0527	188.5844	268.5997	326.1132	390.6345	464.1687	521.1902	614.2298	678.2591	728.7830	806.8335	875.3630	1001.9399	*
y+	*	1939.8327	1776.7693	1616.7387	1501.7117	1372.6691	1225.6007	1111.5578	925.4785	797.4199	696.3722	540.2711	403.2122	150.0583
y++	*	970.4200	888.8883	808.8730	751.3595	686.8382	613.3040	556.2825	463.2429	399.2136	348.6897	270.6392	202.1097	75.5328

MS/MS analysis of single-amidated 10f

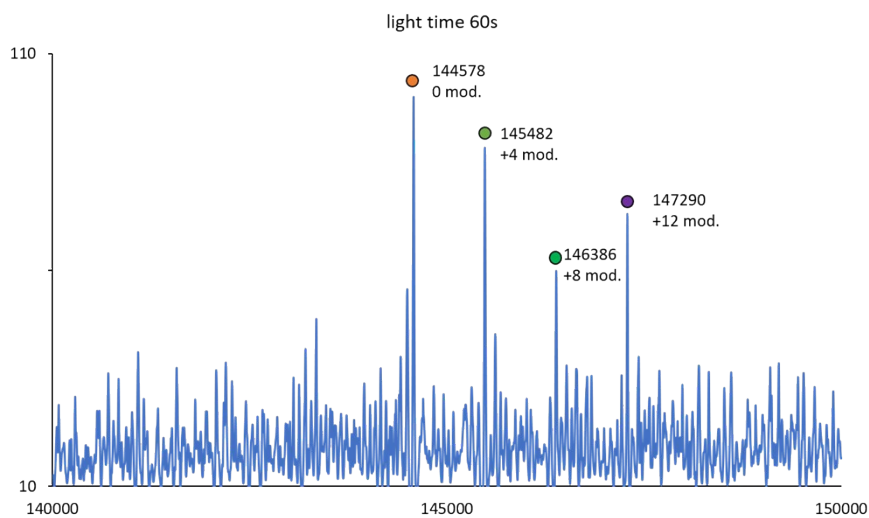
### 3. Supporting information for protein conjugates

#### 3.1 Antibody modifications at different light time

We analyzed the molecular weight of trastuzumab conjugates at different light time (10s and 60s) by protein mass spectrometry. The trastuzumab was de-glycosylated with PNGase F only, and was not reduced.



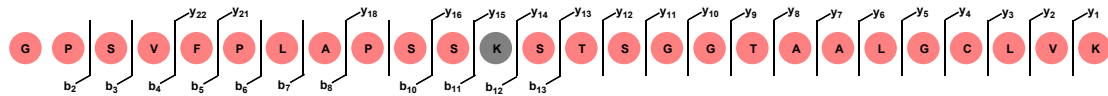
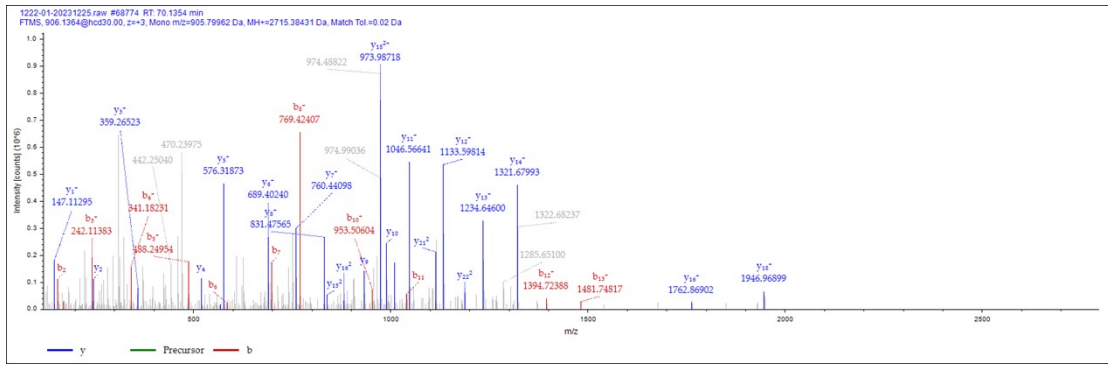
**Figure S10** Trastuzumab was illuminated for 10s.



**Figure S11** Trastuzumab was illuminated for 60s.

Sequence: GPSVFPLAPSSKSTSGGTAALGCLVK, C23-Carbamidomethyl (57.02146 Da), K12-biotin-COSH (226.07760 Da)

Charge: +3, Monoisotopic m/z: 905.79962 Da (-0.04 mmu/-0.05 ppm), MH+: 2715.38431 Da, RT: 70.1354 min,



Sequence: DSTYLSSTLTLSKADYEKHK, K14-biotin-COSH (226.07760 Da), K19-biotin-COSH (226.07760 Da)

Charge: +3, Monoisotopic m/z: 942.78113 Da (-1.21 mmu/-1.28 ppm), MH+: 2826.32883 Da, RT: 69.8761min

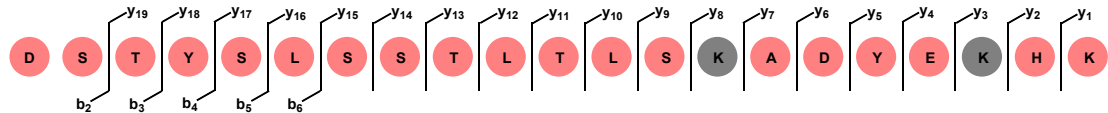
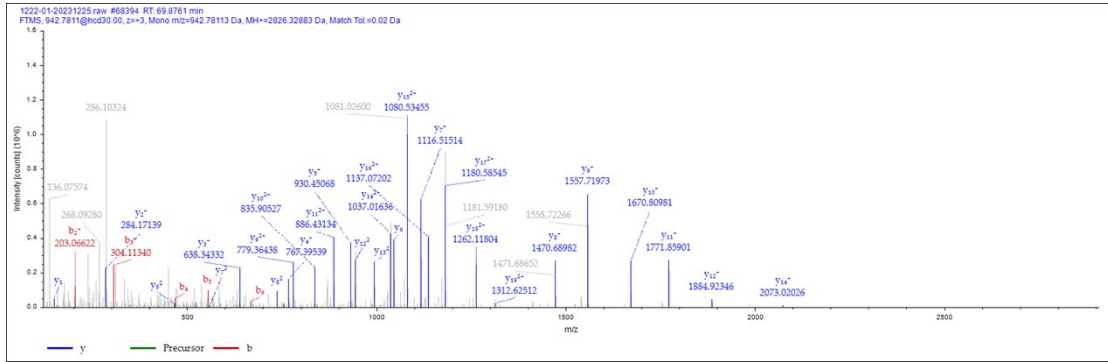
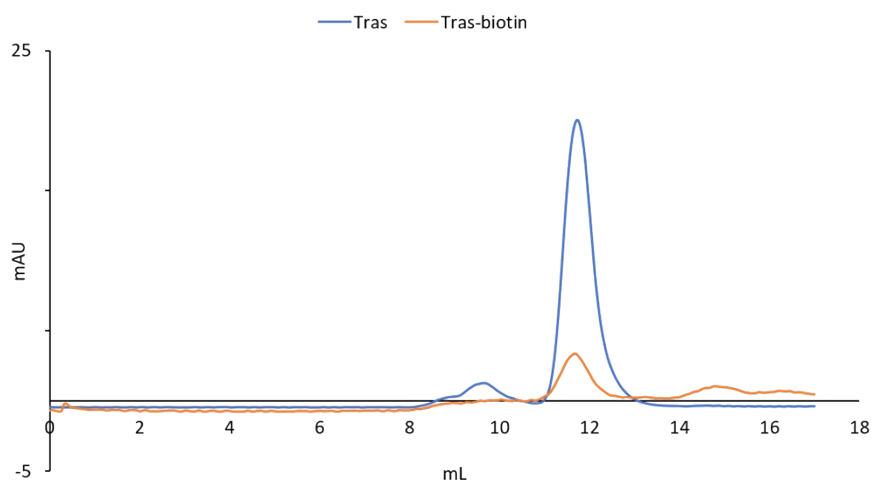


Figure S12 MS/MS analysis of trastuzumab-biotin

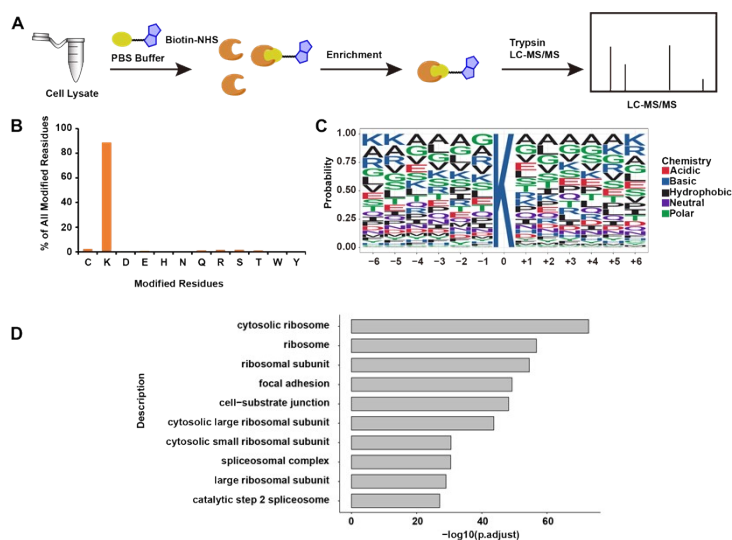
### 3.2 Antibody aggregation assay

Trastuzumab (0.4 mg/mL) and trastuzumab-biotin (40 µg/mL) were analyzed with Superdex 200 increase 10 300 GL.



**Figure S13** Comparison antibody aggregation of Tras and Tras-biotin with SEC.

### 3.3 Sample processing of LC-MS/MS to determine protein modification site



**Figure S14** (A) Schematic representation of the labeling proteome. (B) **Biotin-NHS** preferentially labels lysine in SK-BR-3 cells. (E) Frequency plots showing the conserved motifs from SK-BR-3 cells using **Biotin-NHS**. (D) GO-Cellular Component (GO-CC) annotation of highly enriched protein targeted by **Biotin-NHS**.