

## Supporting Information

### Selective Peptidomimetic Inhibitors of NTMT1/2: Rational design, synthesis, characterization, and crystallographic studies

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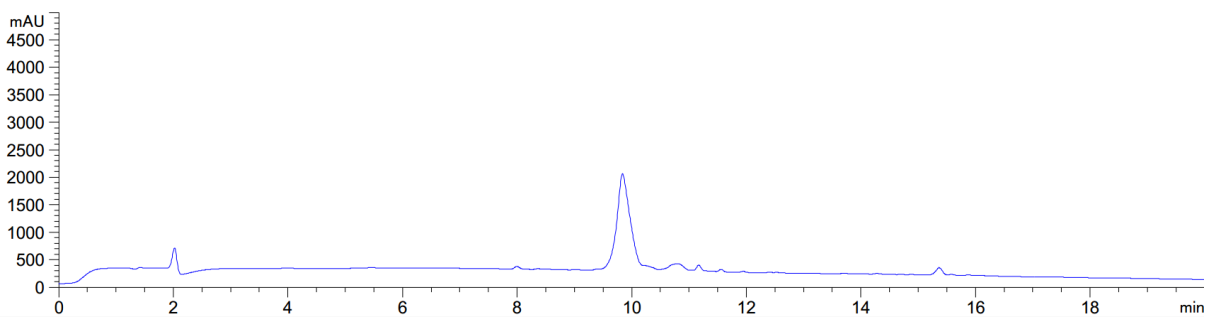
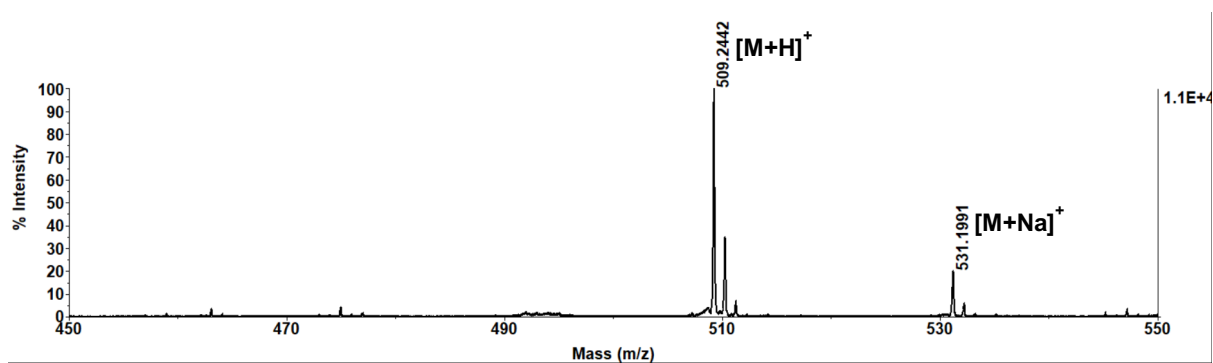
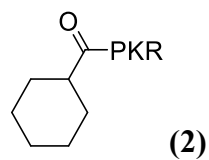
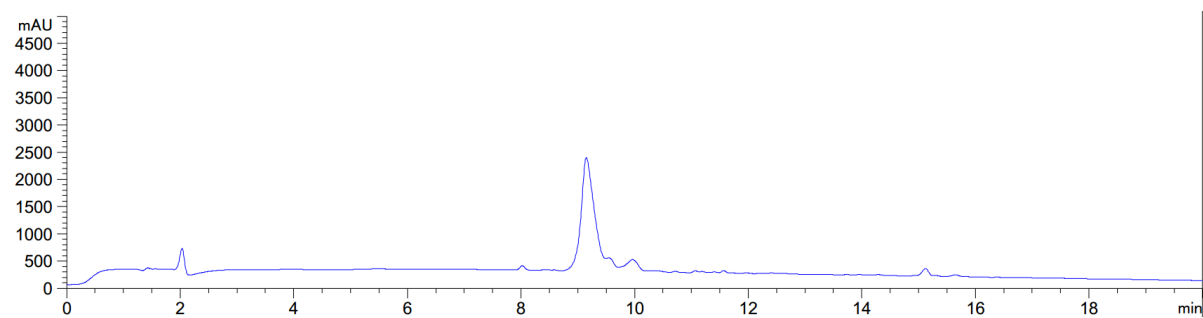
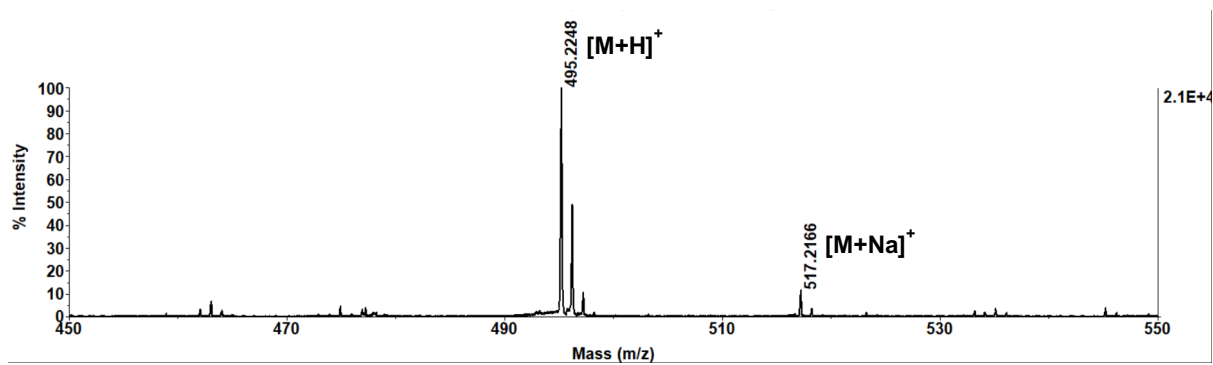
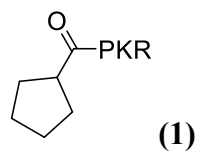
<sup>§</sup>Department of Biological Sciences, Markey Center for Structural Biology, and the Purdue Institute of Inflammation, Immunology and Infectious Disease, Purdue University, West Lafayette, IN 47907, United States

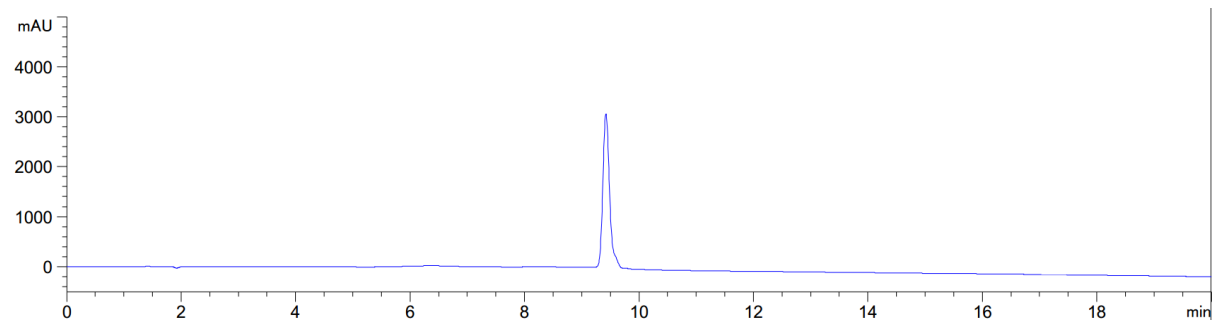
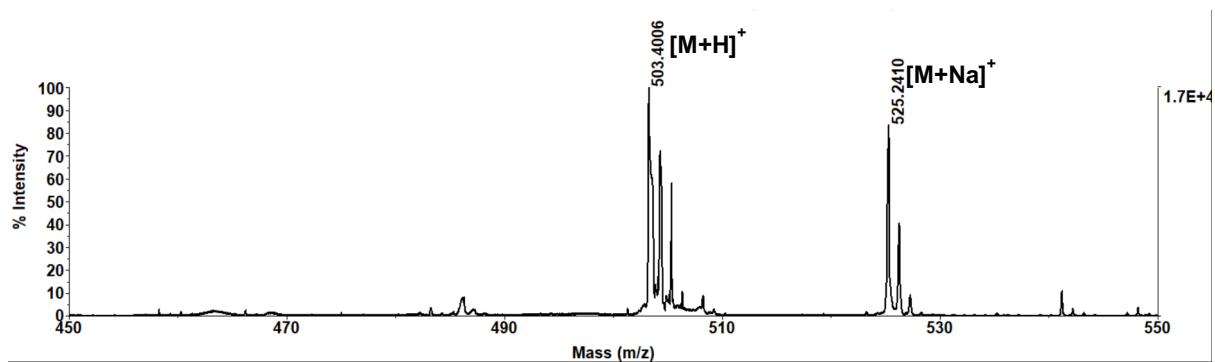
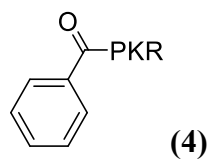
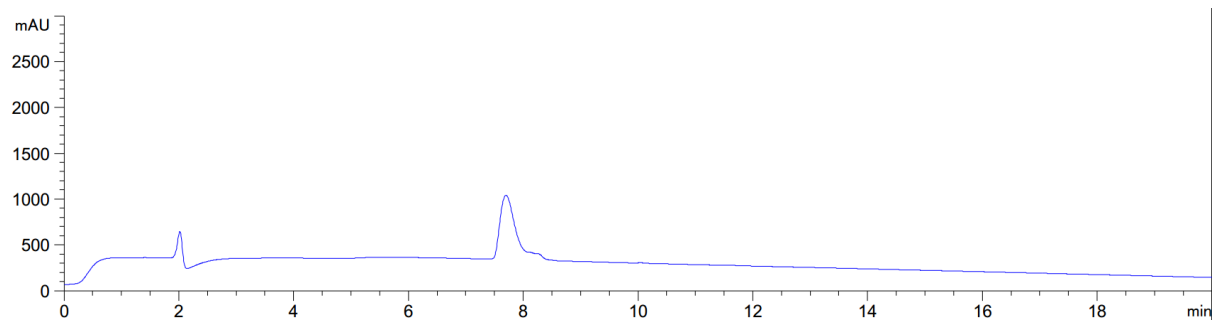
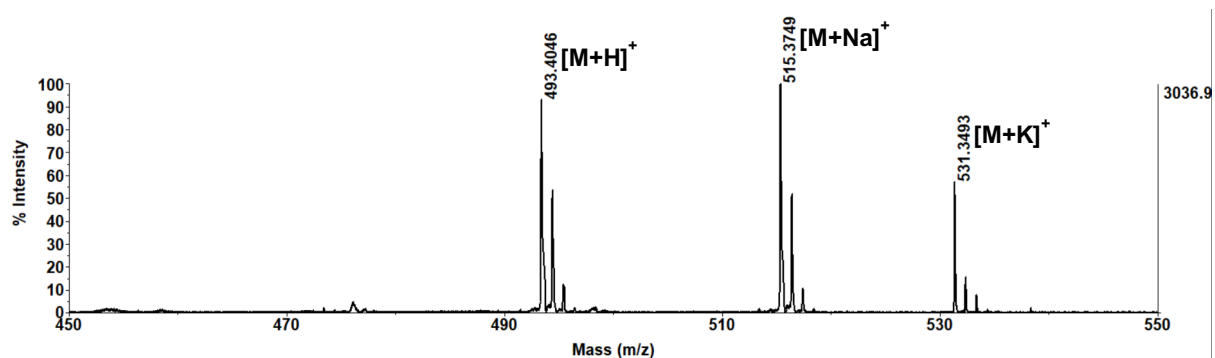
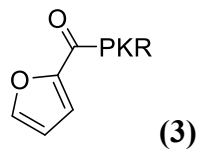
\* To whom correspondence should be addressed. E-mail: [huang-r@purdue.edu](mailto:huang-r@purdue.edu)

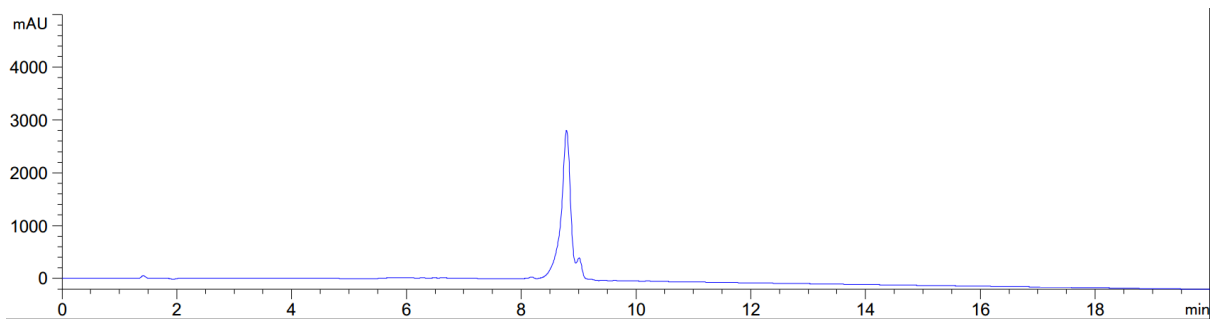
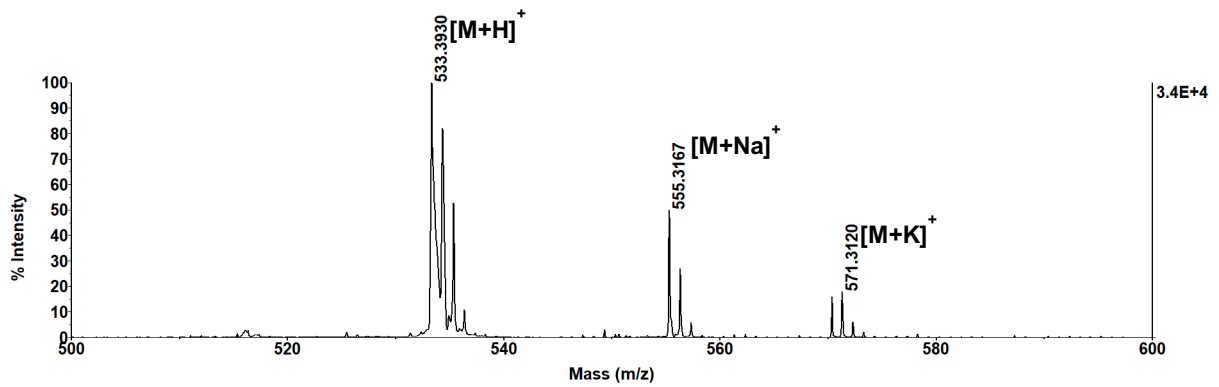
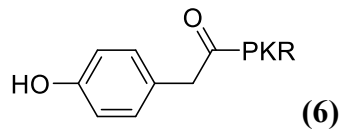
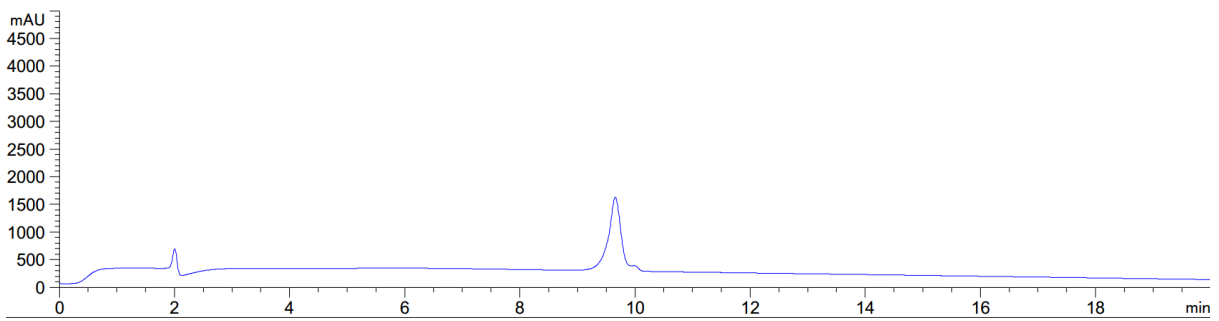
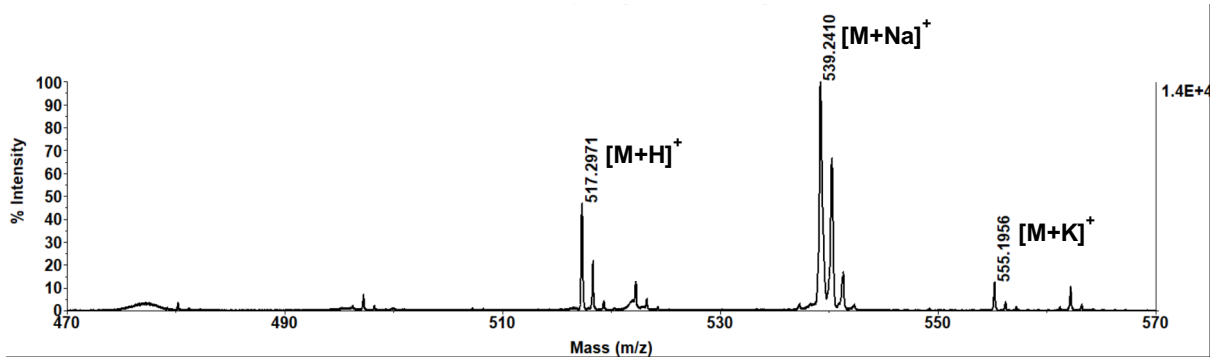
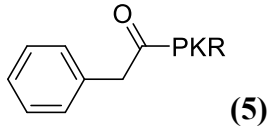
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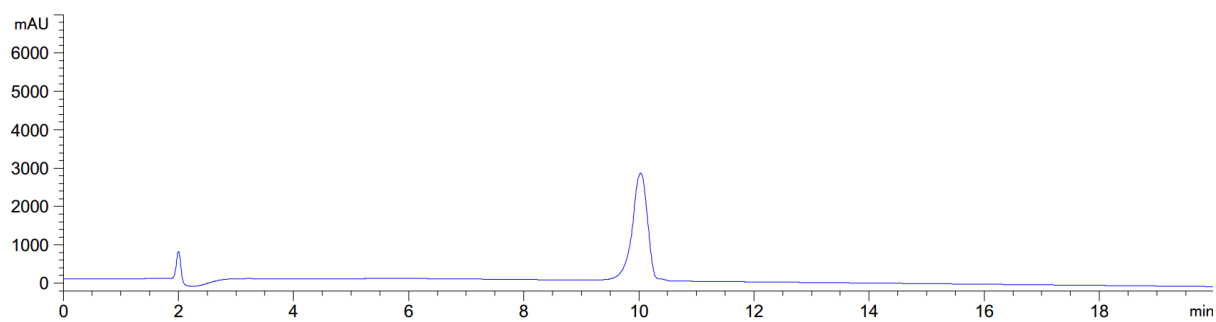
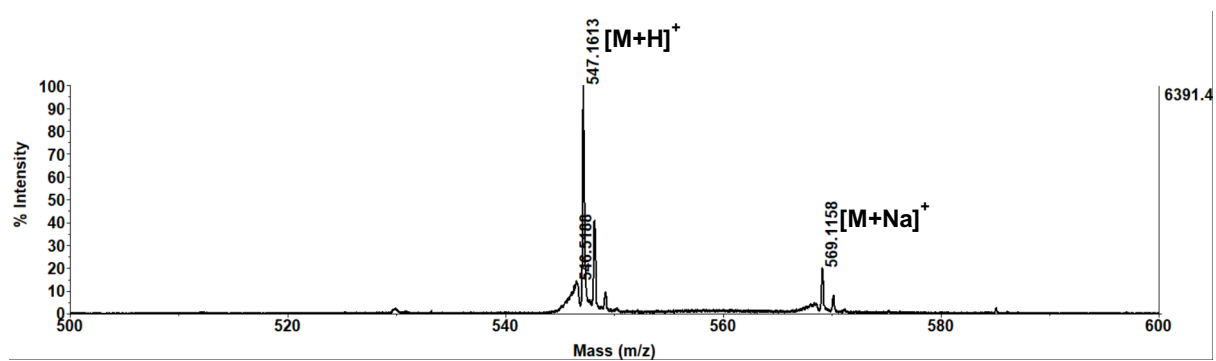
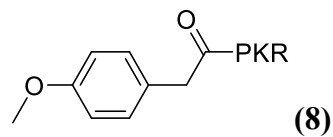
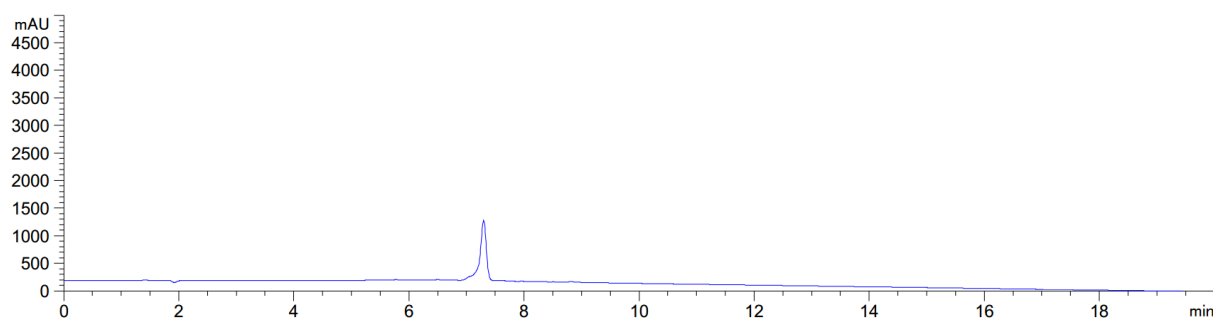
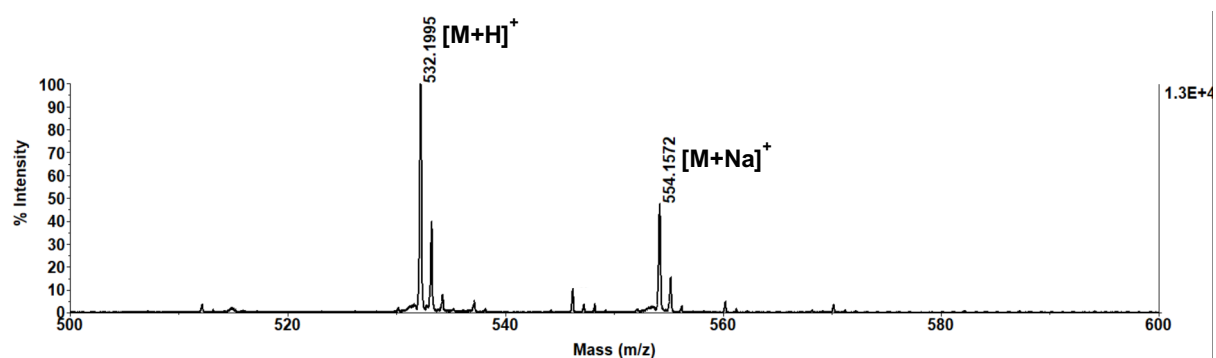
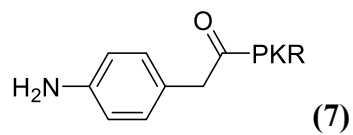
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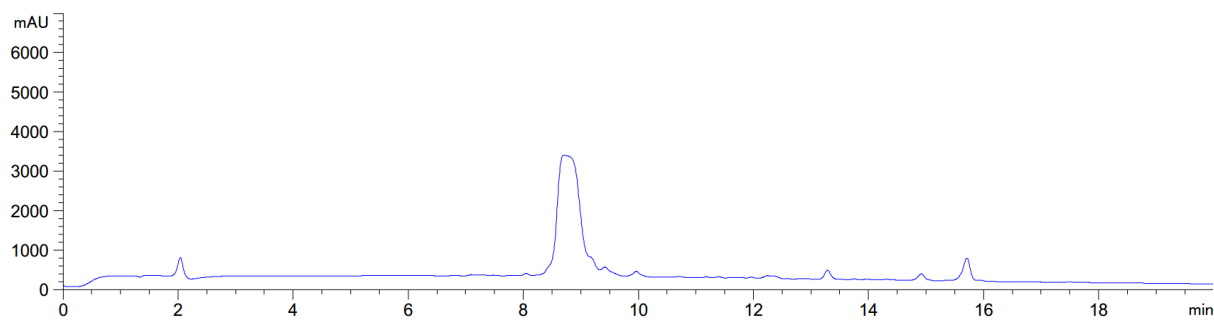
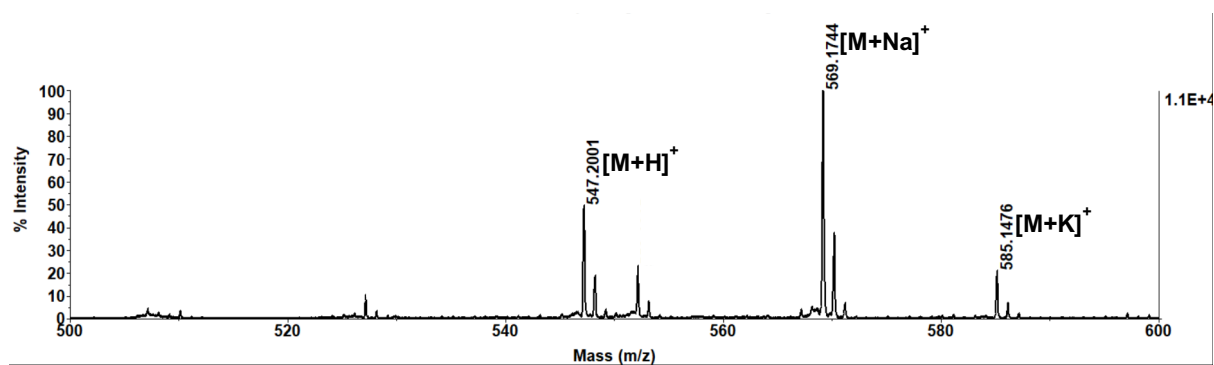
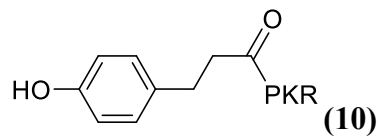
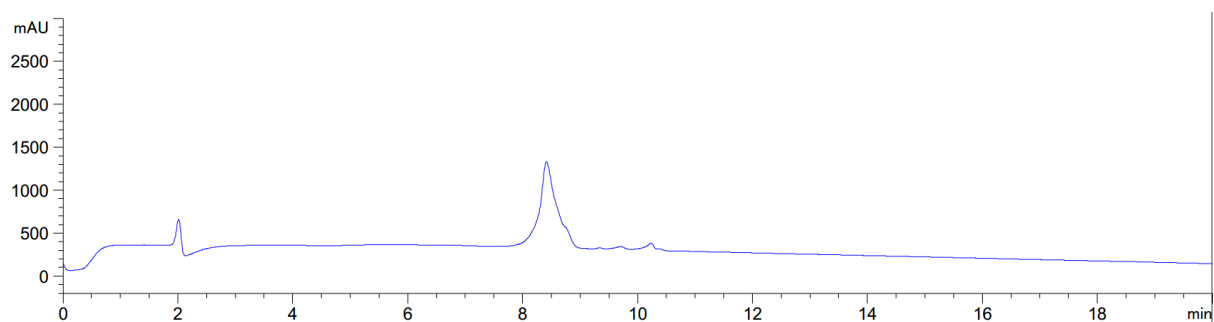
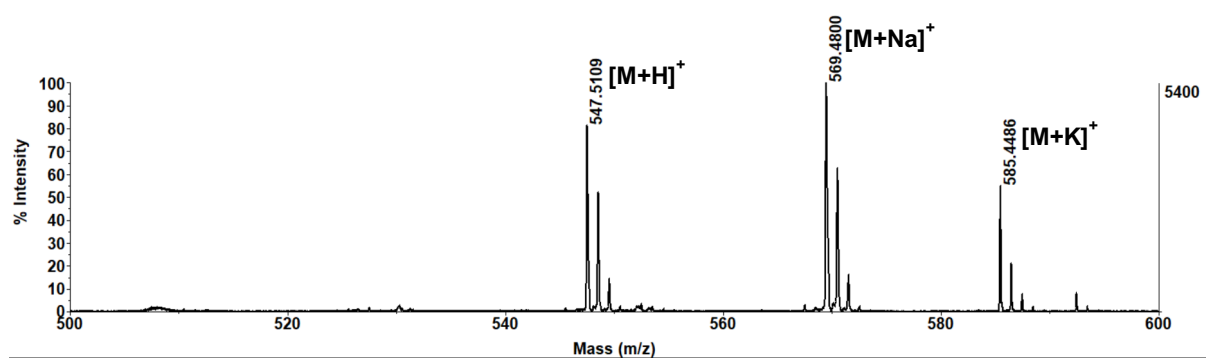
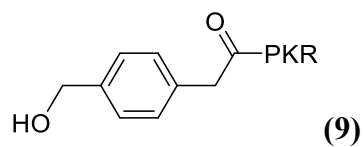
**Figure S1.** MALDI-MS and HPLC analysis of compounds 1-24, DC431 and DC432

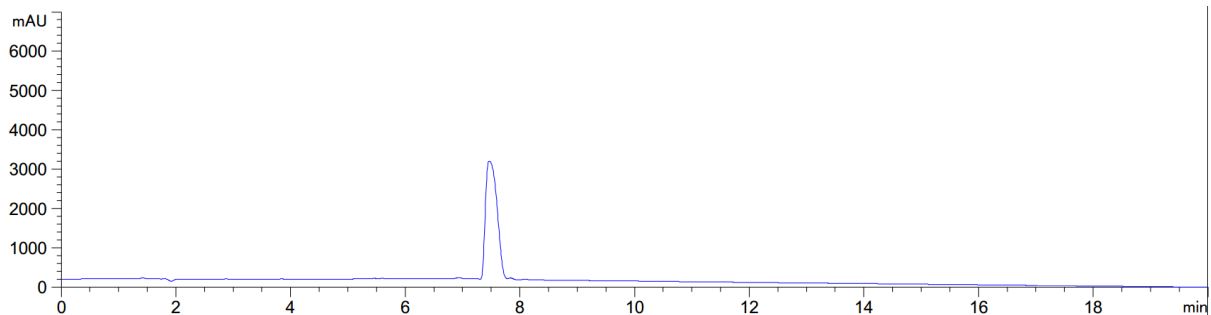
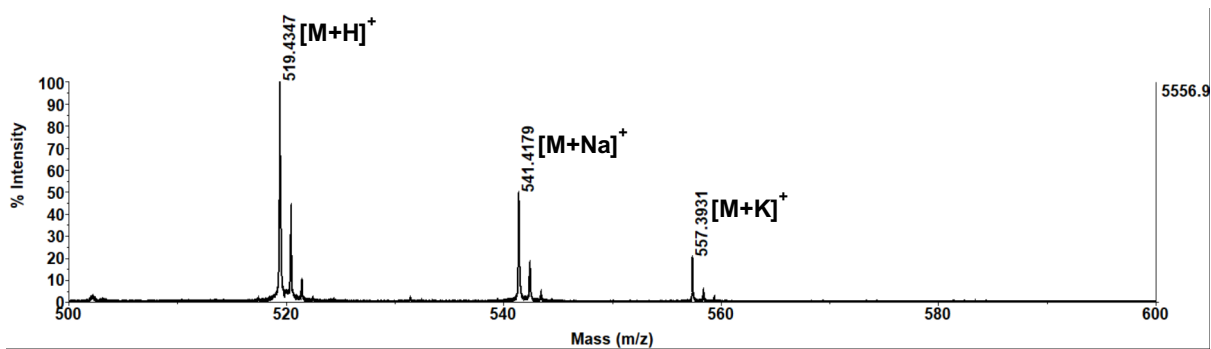
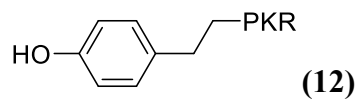
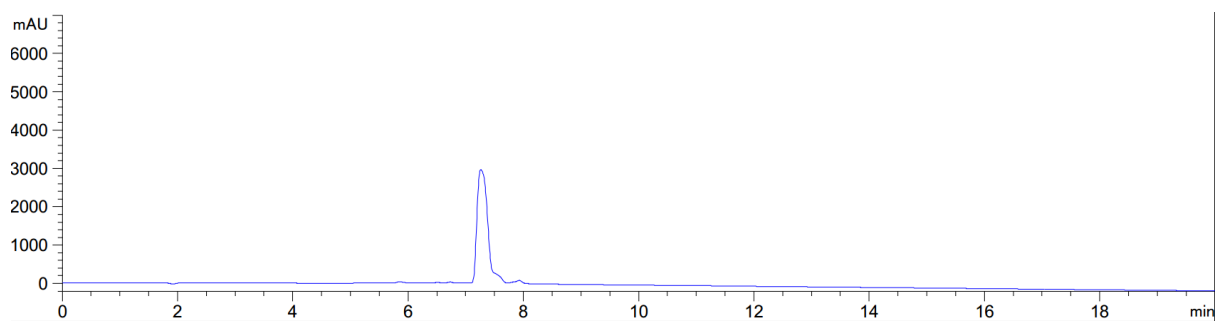
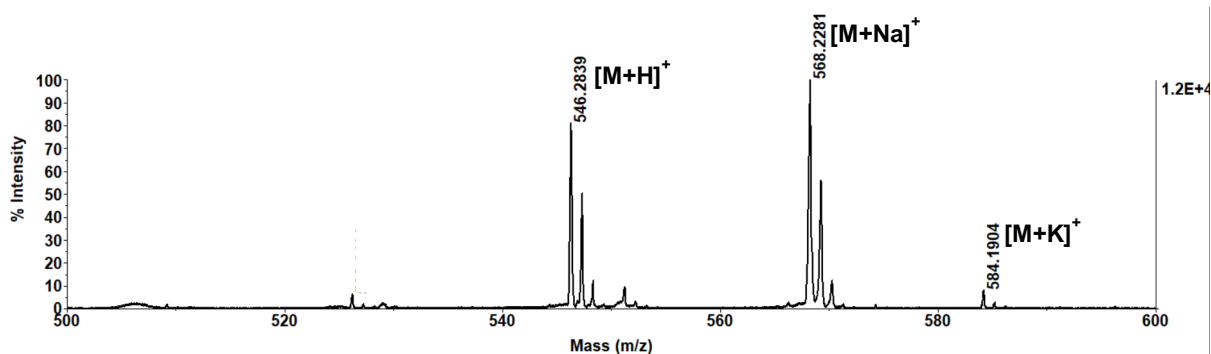
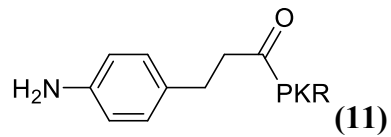




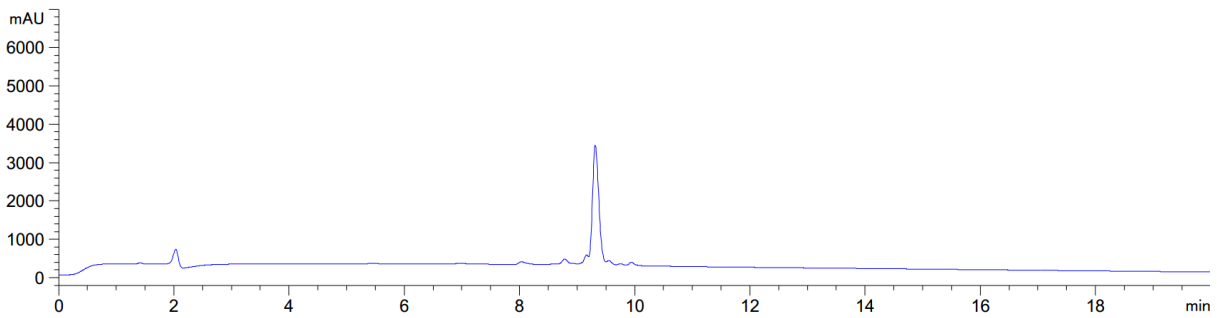
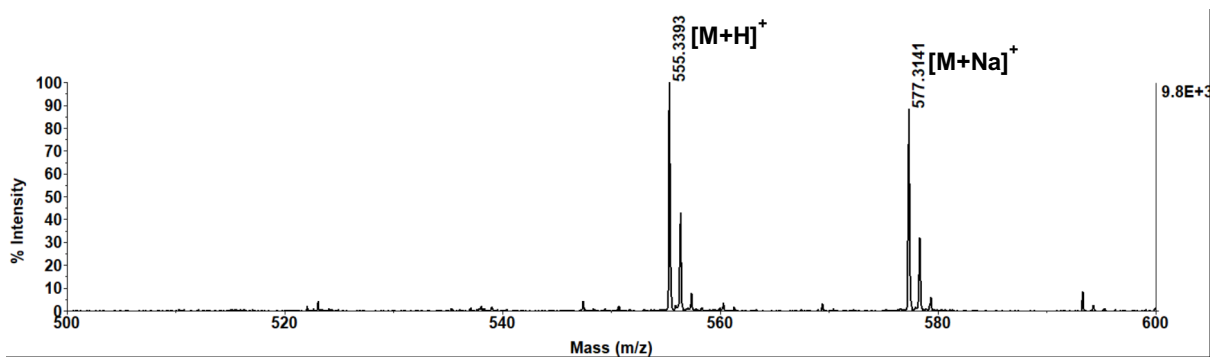
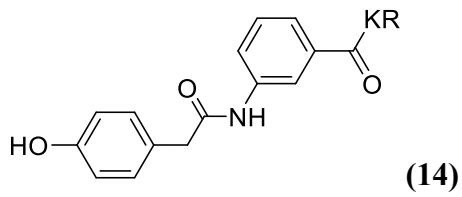
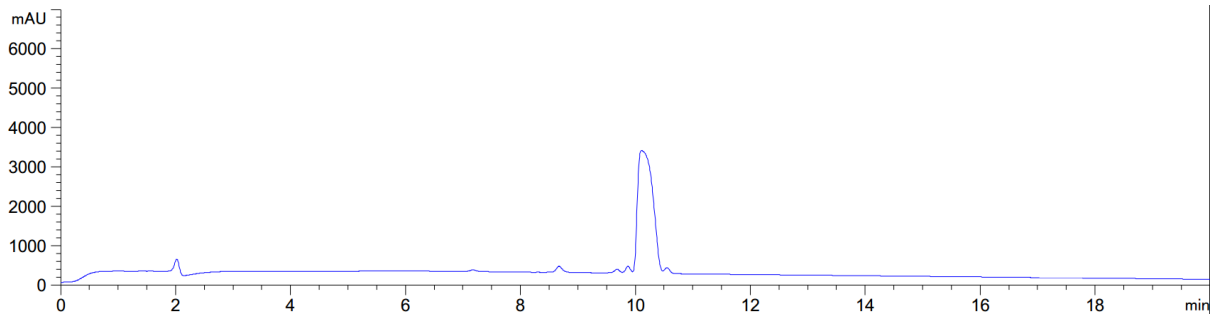
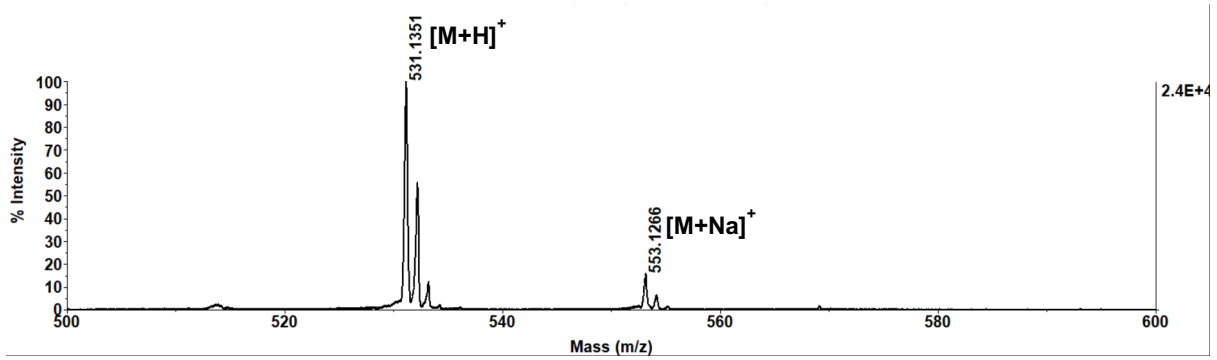
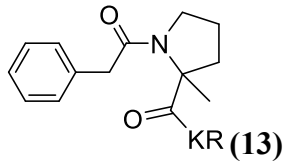


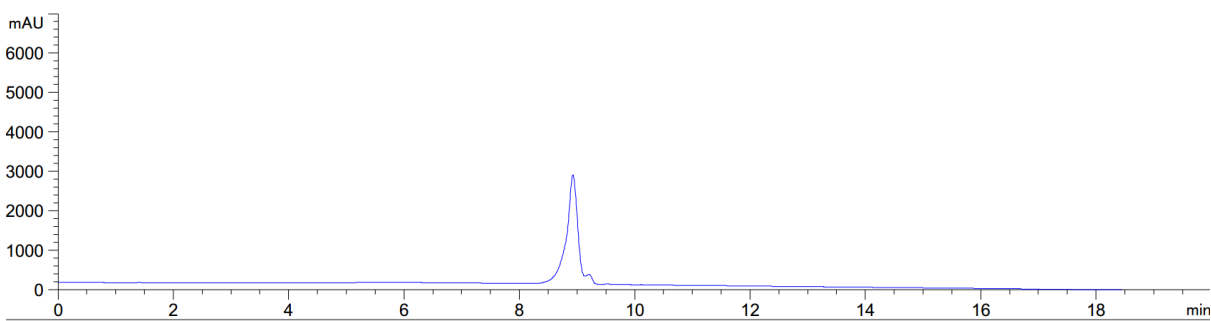
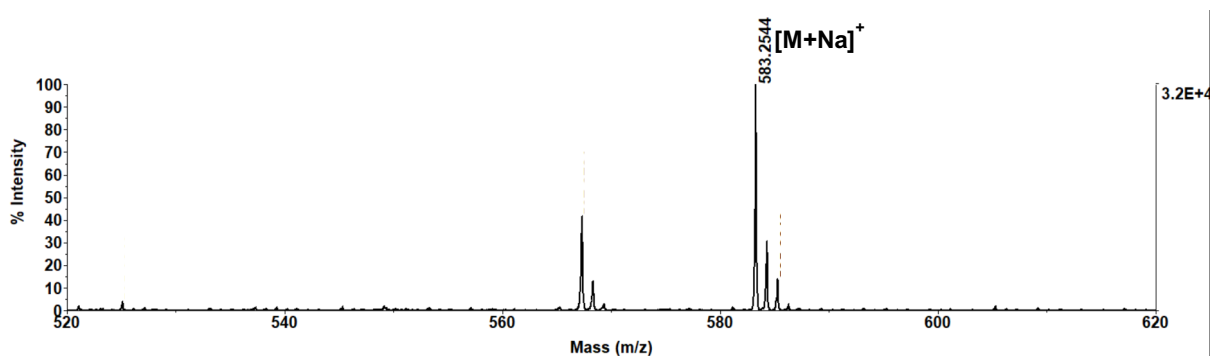
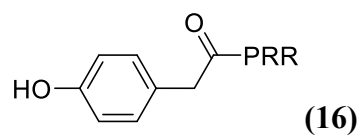
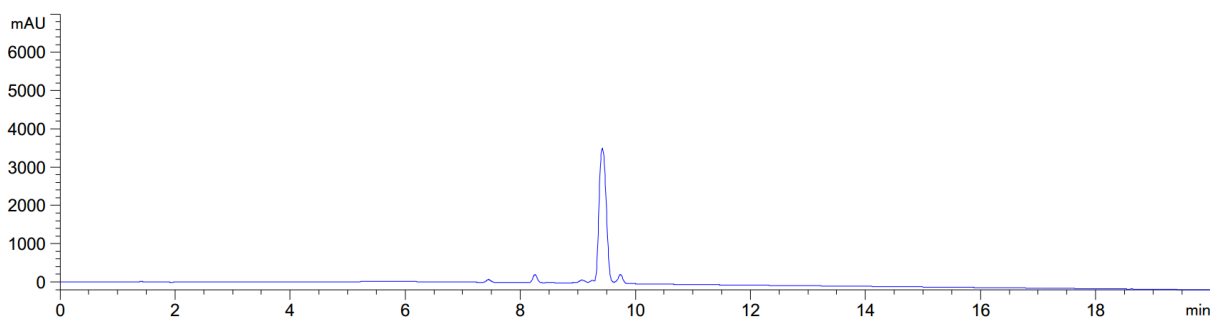
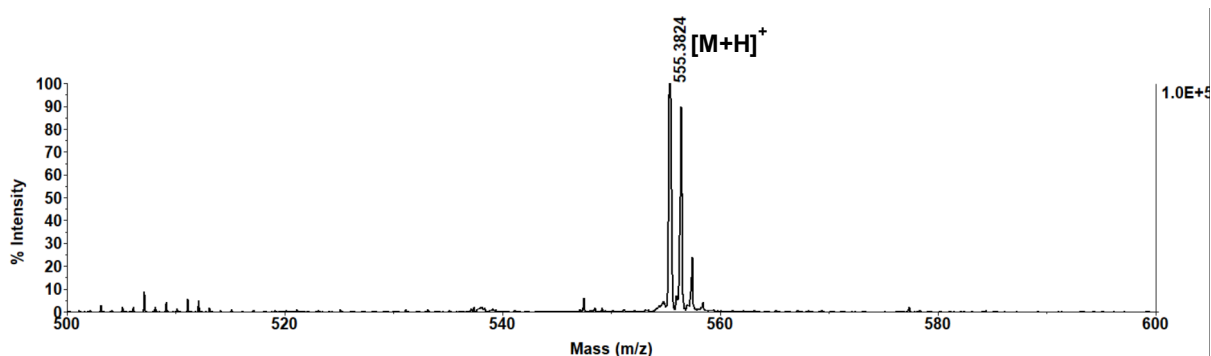
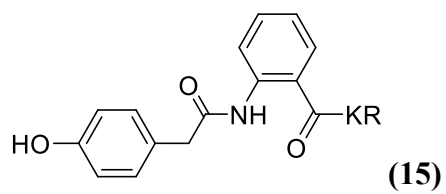


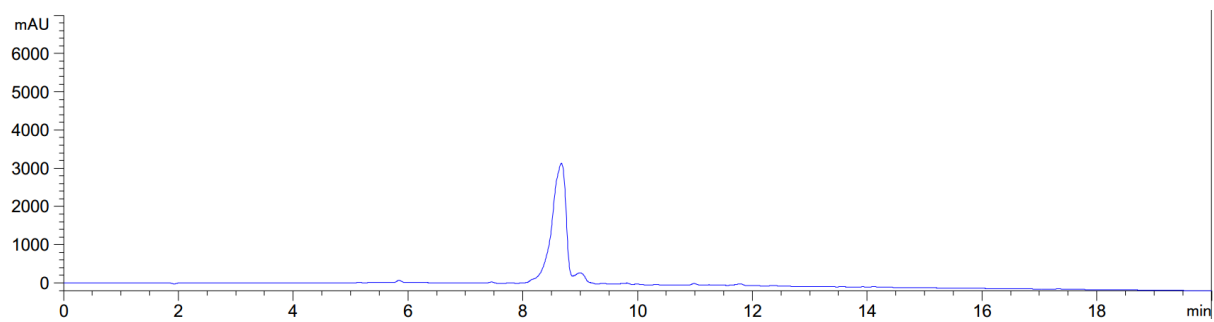
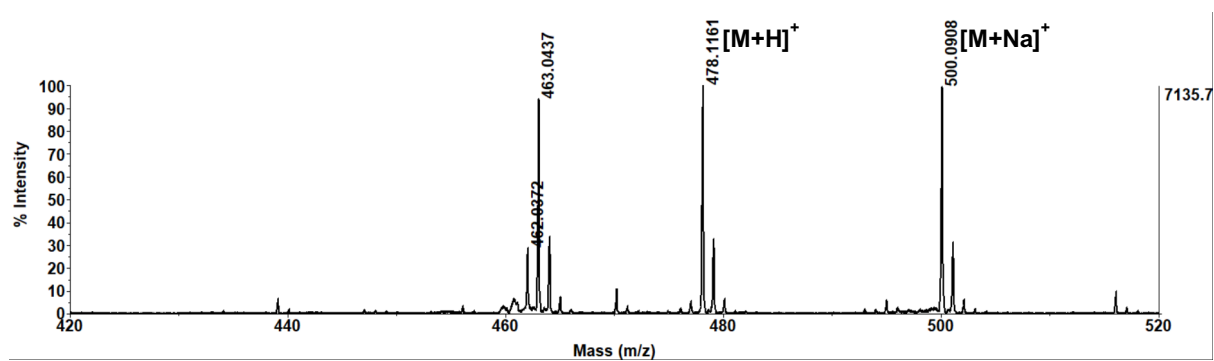
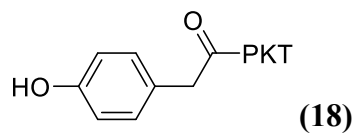
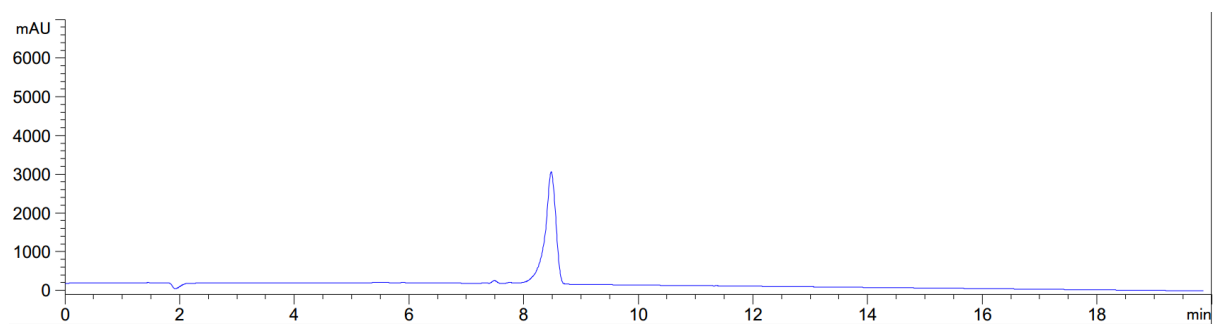
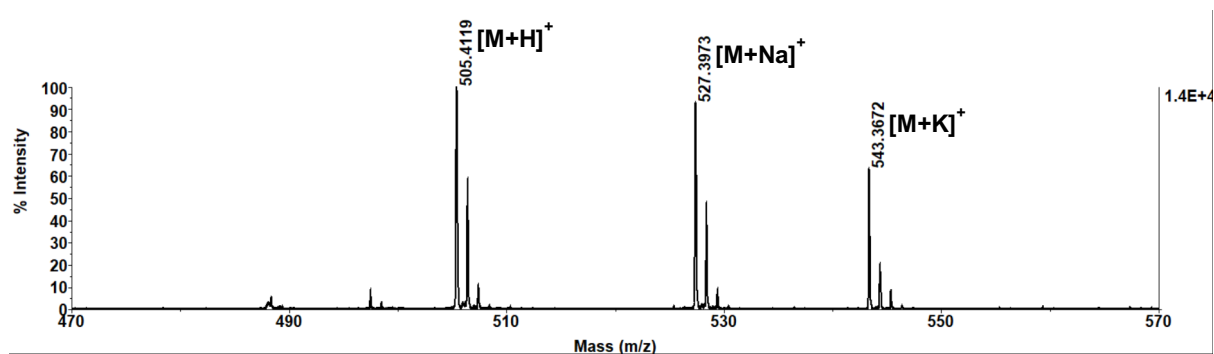
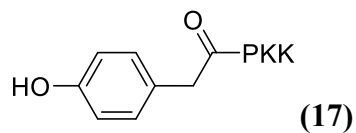


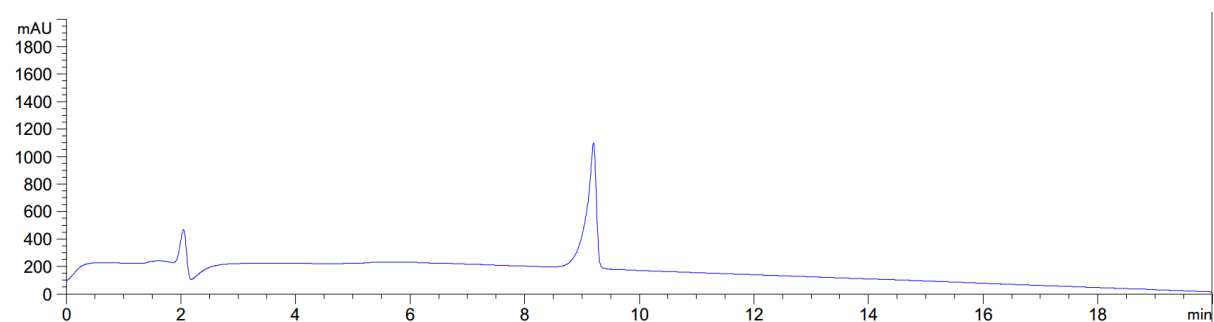
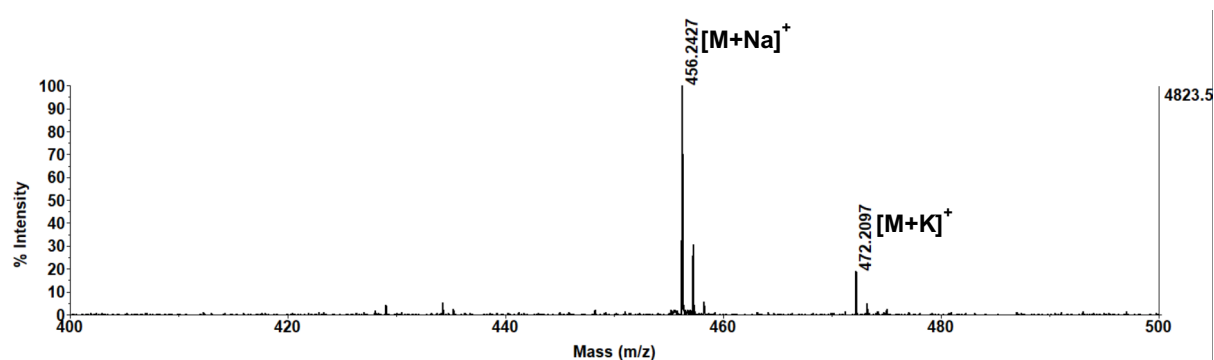
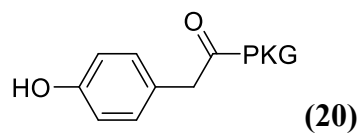
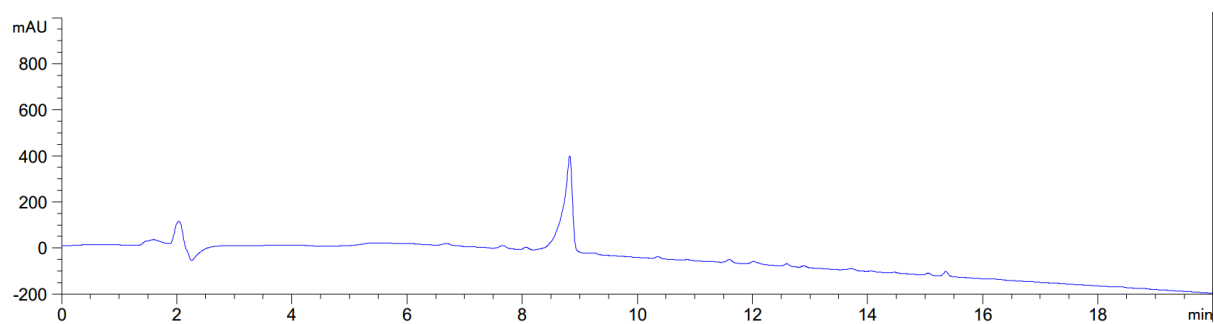
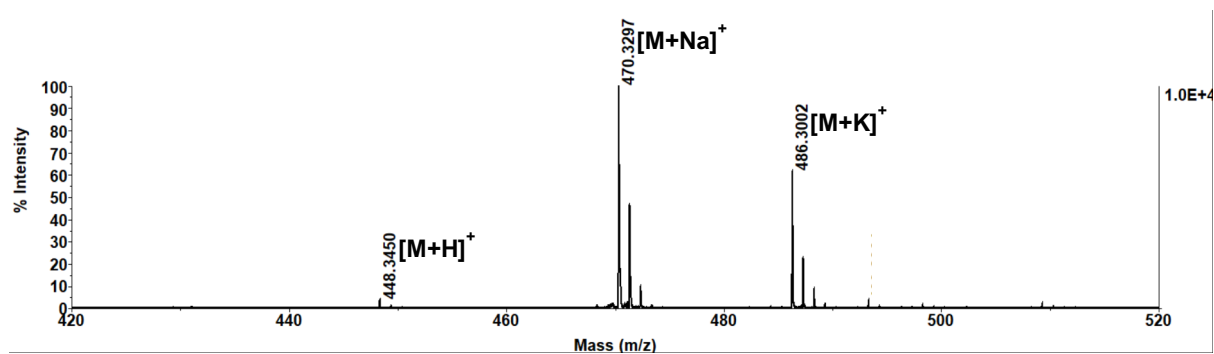
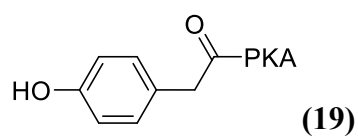


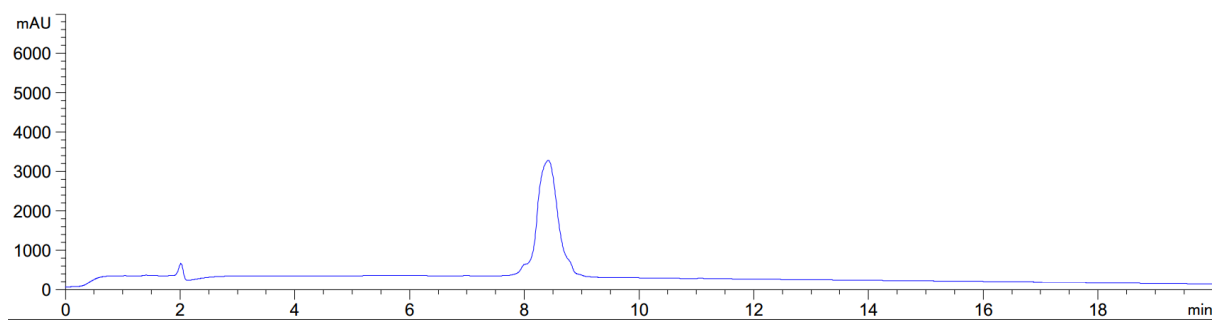
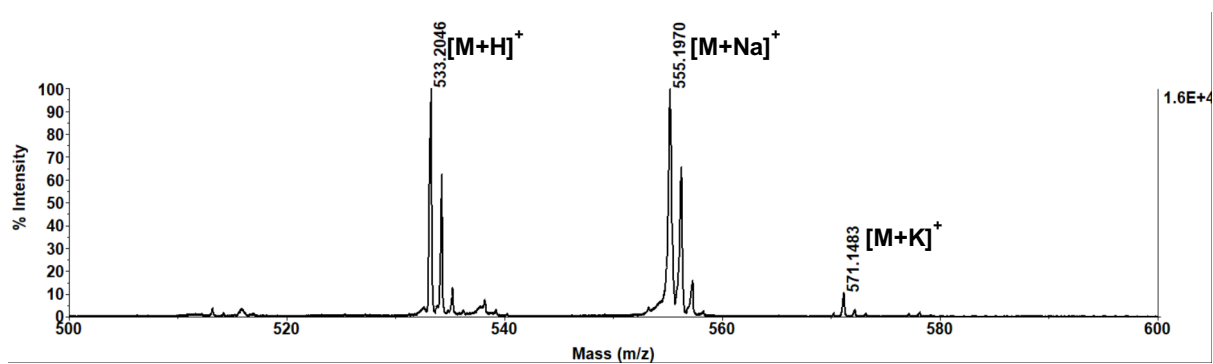
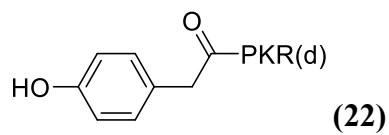
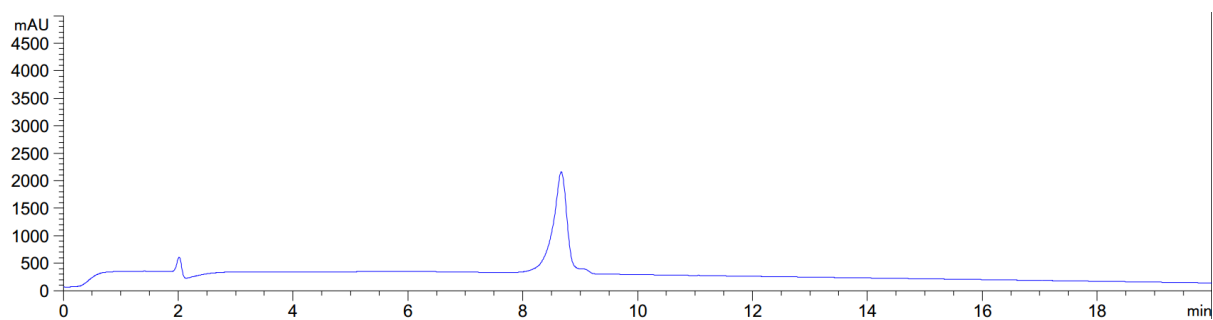
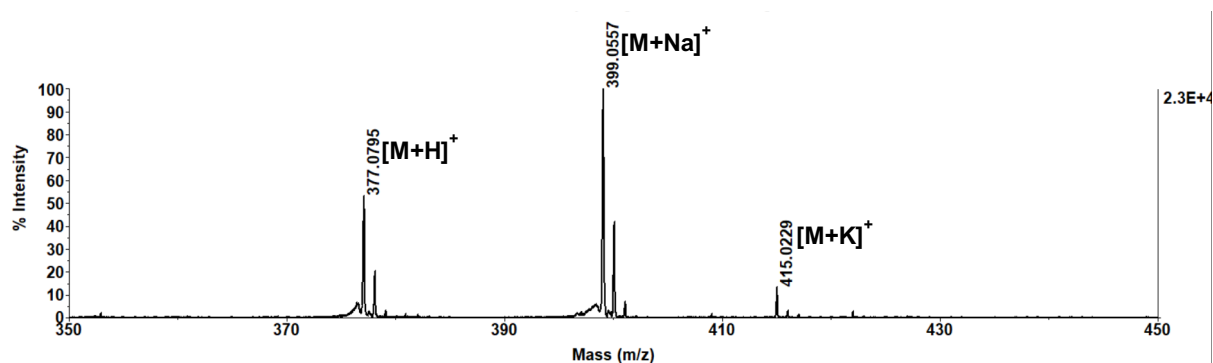
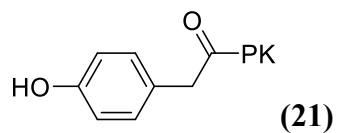


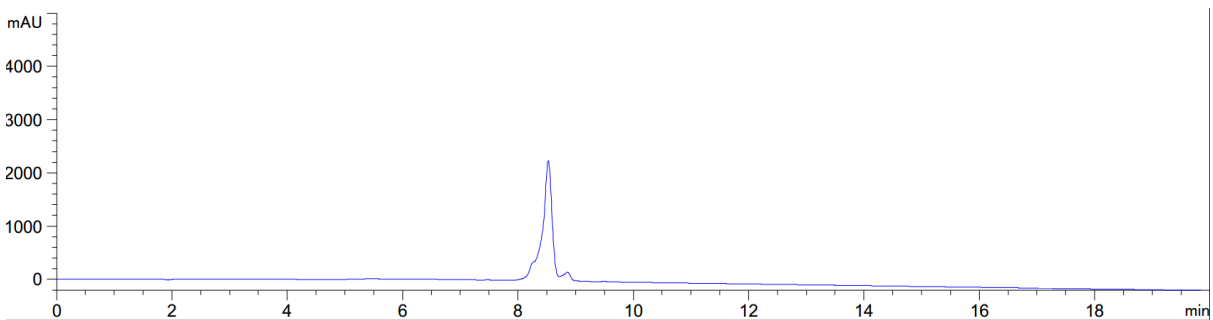
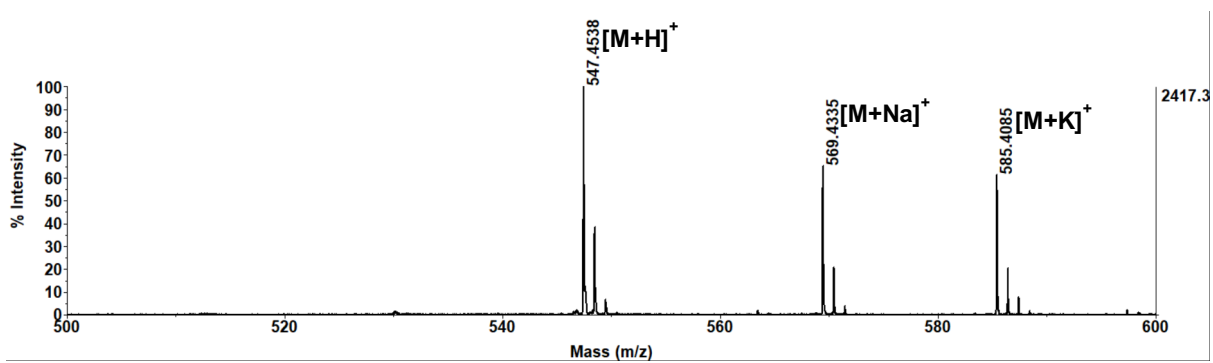
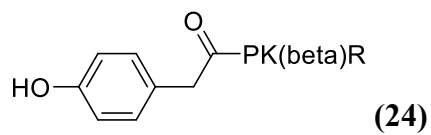
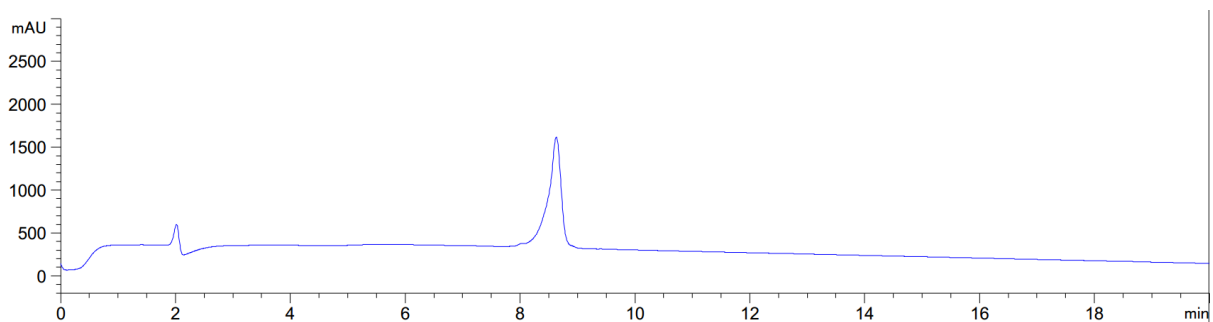
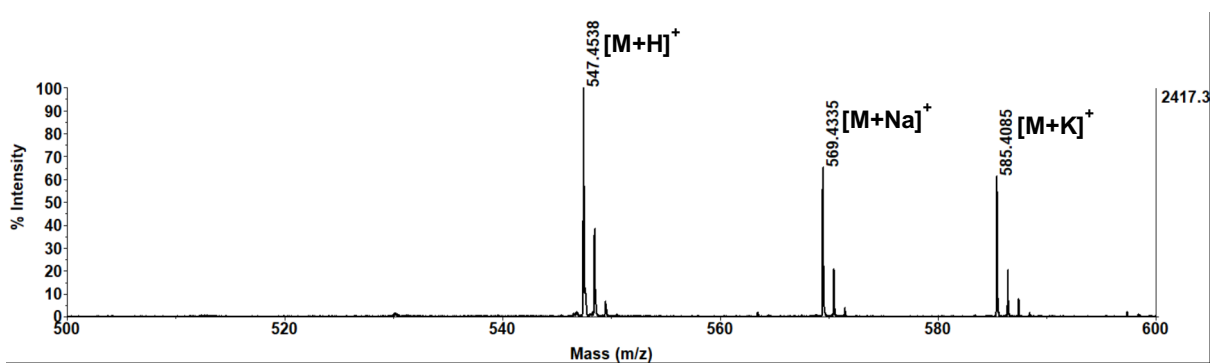
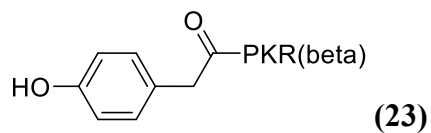


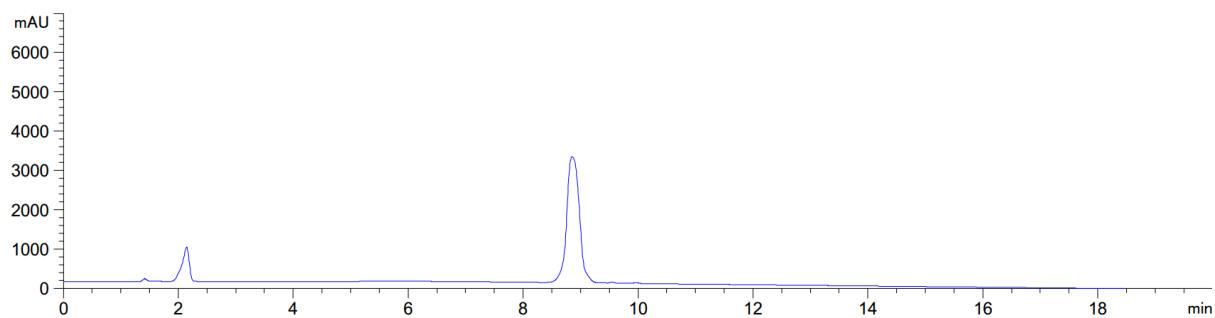
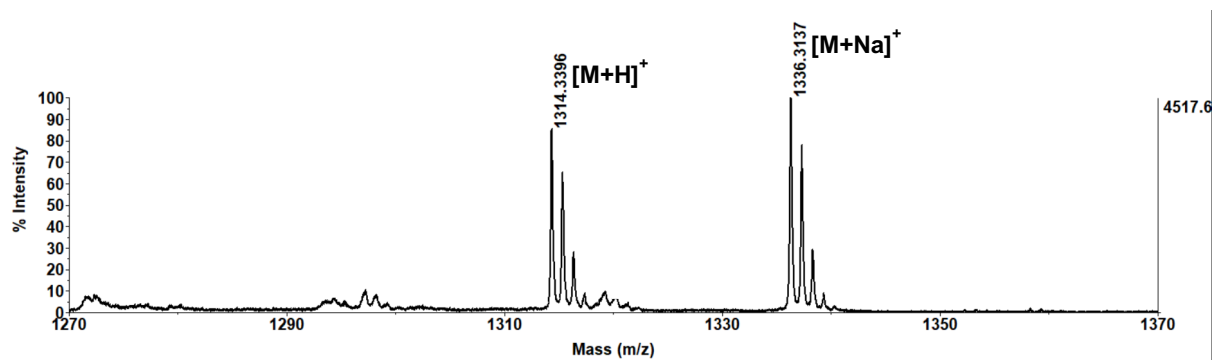
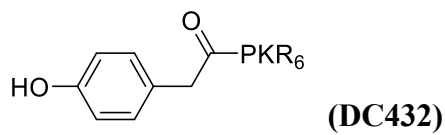
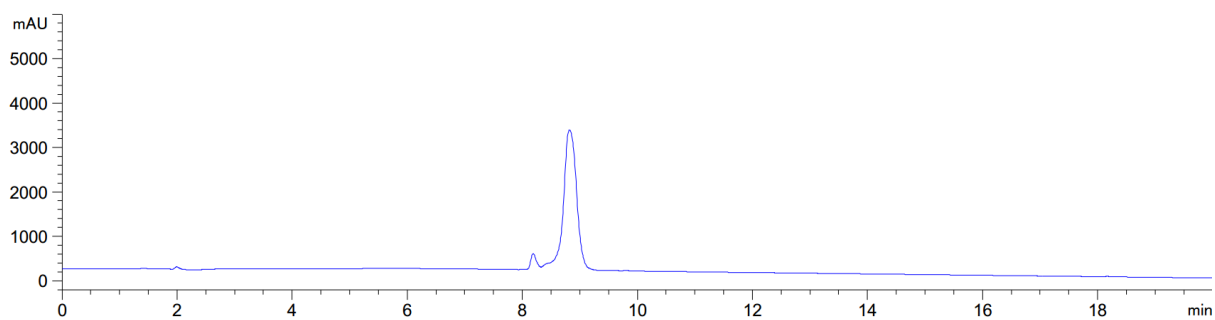
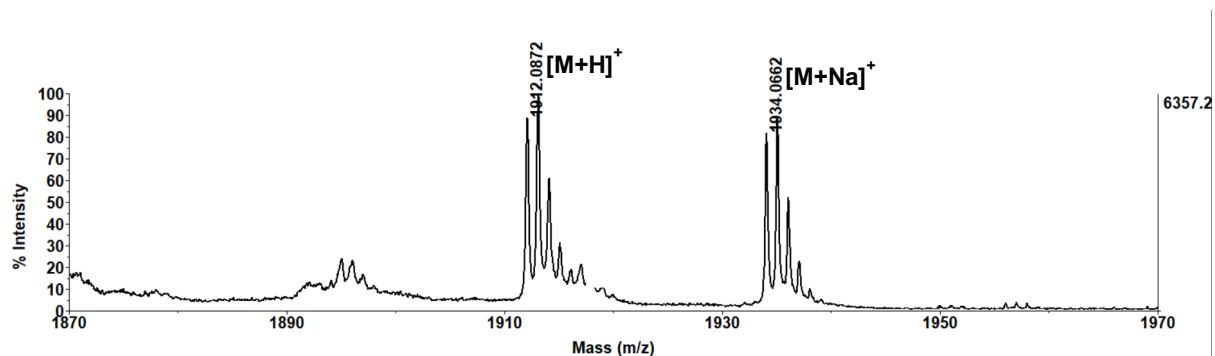
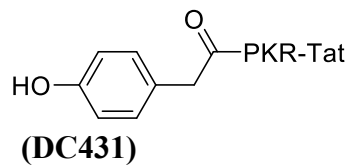




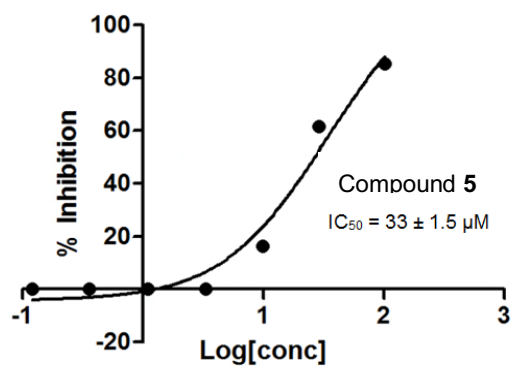








**Figure S2.** IC<sub>50</sub> curves of compounds **5**. IC<sub>50</sub> values were determined in triplicates (n = 3) and presented as mean ± SD





**Figure S3.** IC<sub>50</sub> curve of **BM30** (6). IC<sub>50</sub> values were determined in triplicates (n = 3) and presented as mean ± SD

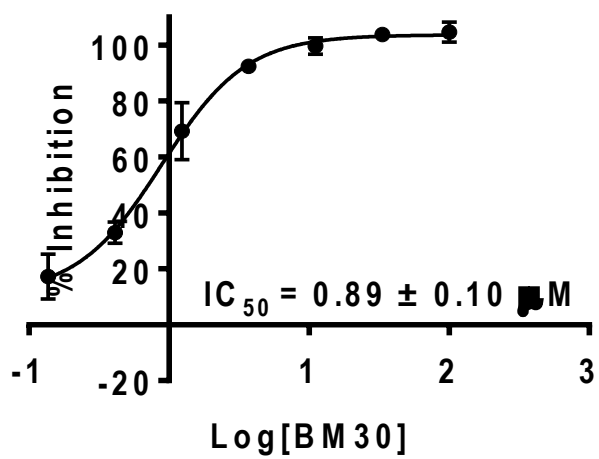
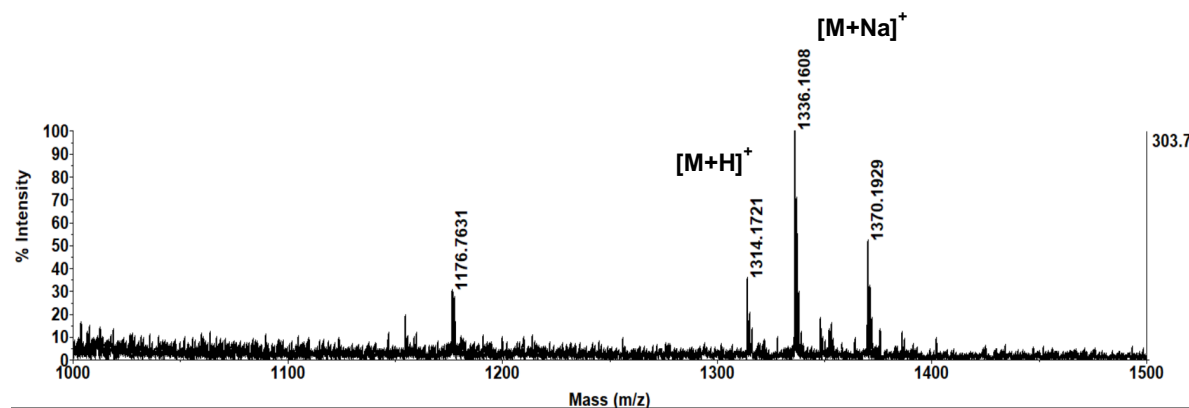
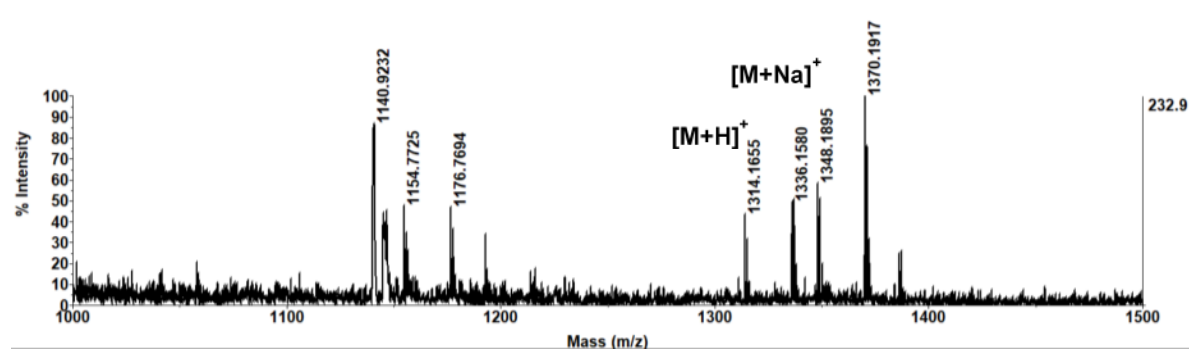


Figure S4. Cell permeability evaluation

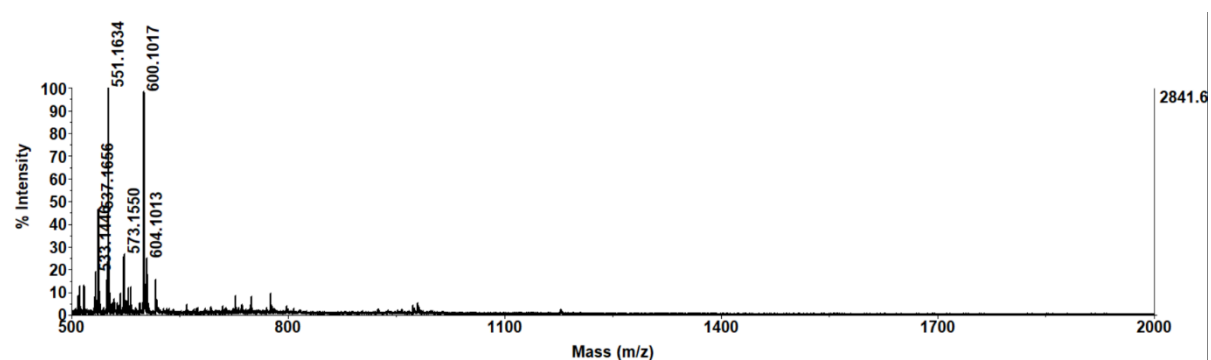
10  $\mu$ M DC432



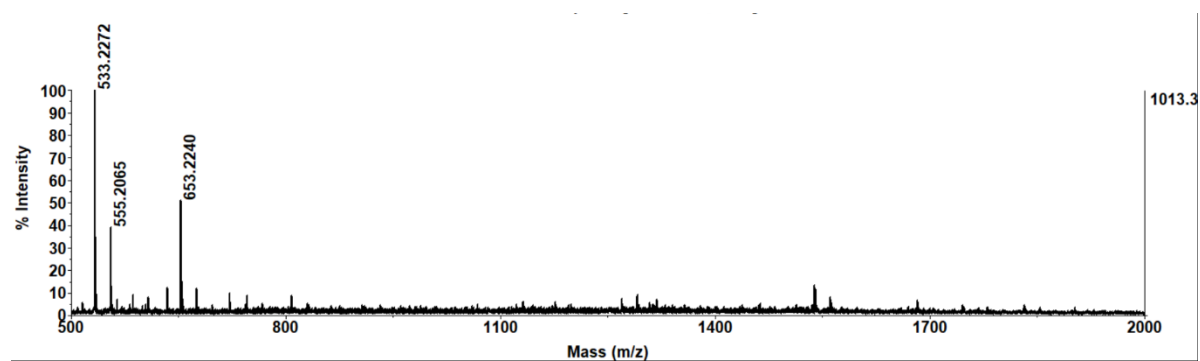
1  $\mu$ M DC432



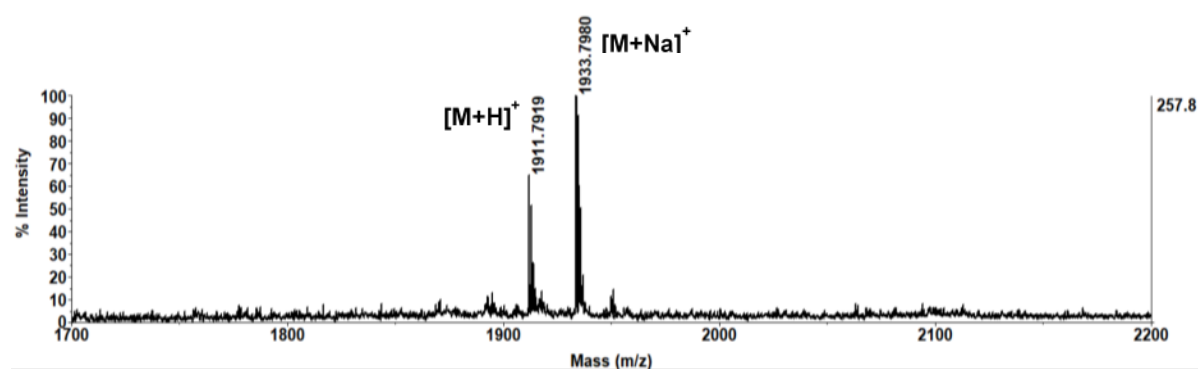
Last wash of cells incubated with 10  $\mu$ M DC432



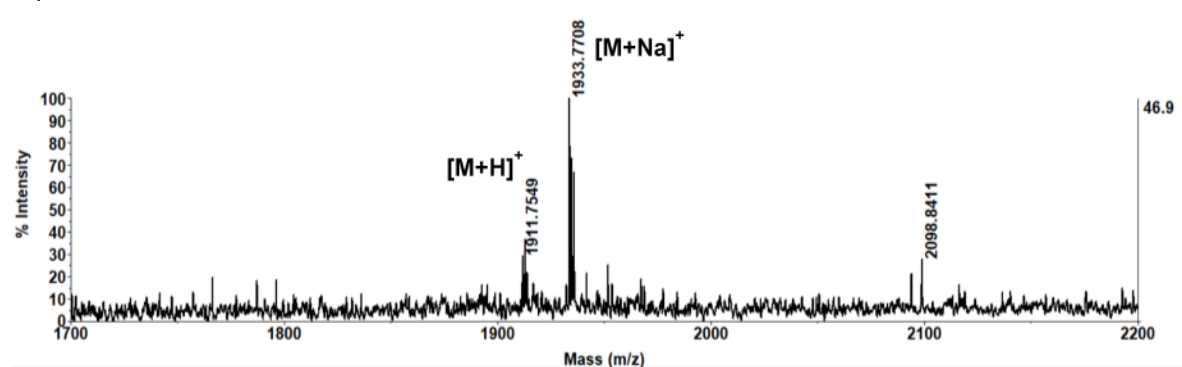
Last wash of cells incubated with 1  $\mu$ M DC432



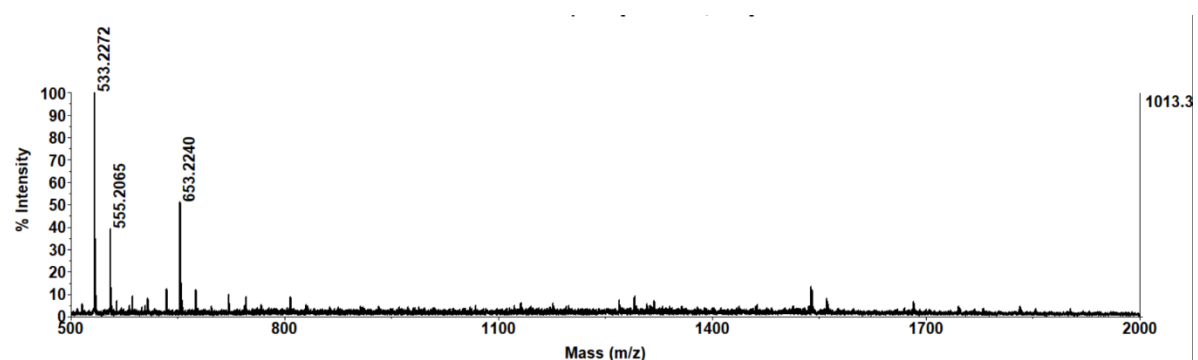
10  $\mu$ M DC431



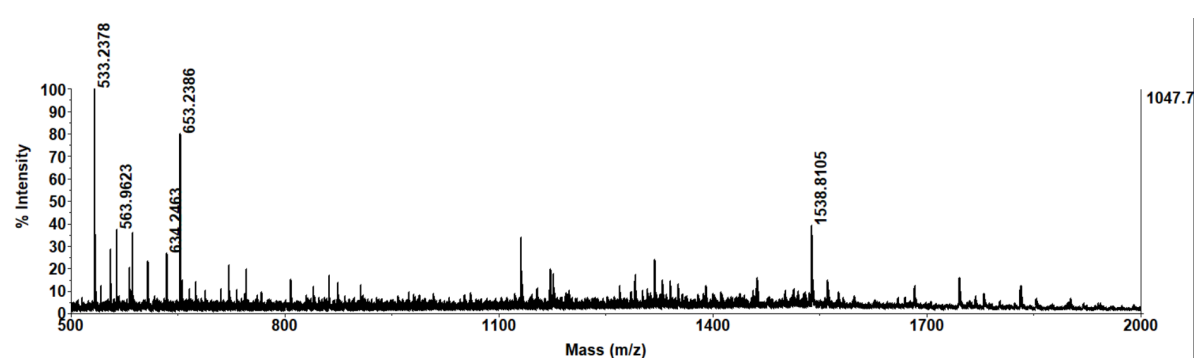
1  $\mu$ M DC431



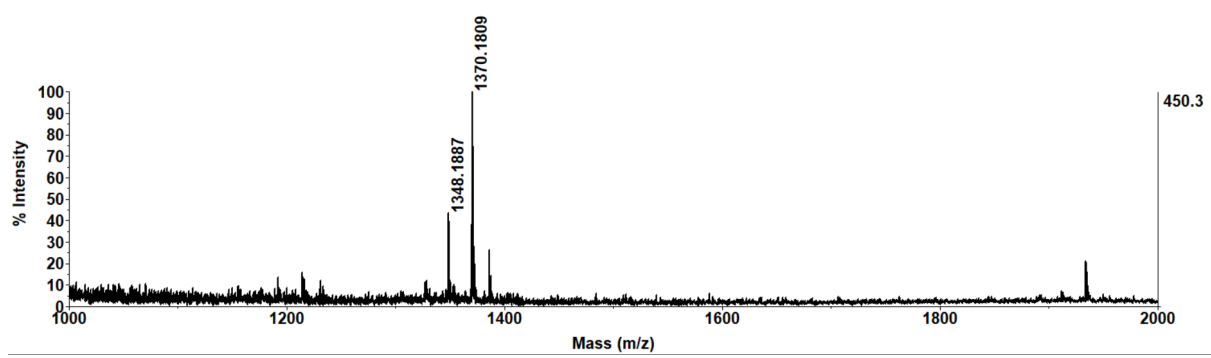
Last wash of cells incubated with 10  $\mu$ M DC431



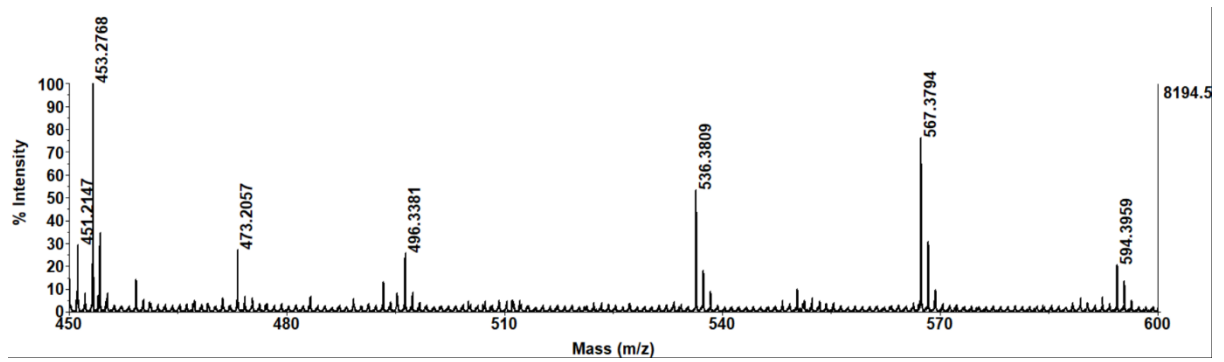
Last wash of cells incubated with 1  $\mu$ M DC431



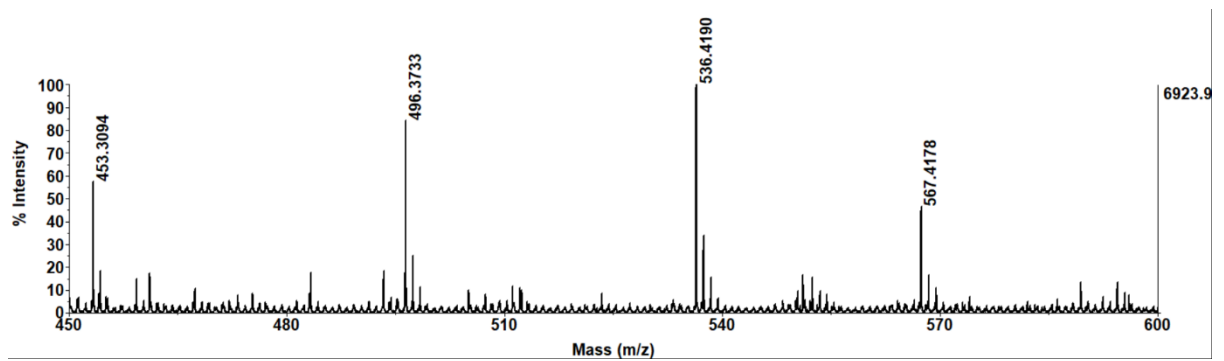
Cell lysate alone



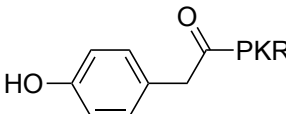
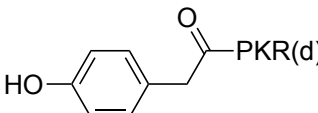
100  $\mu$ M BM-30



Cell lysate alone



**Table S1.** Selectivity study of **BM30** and **22**

Compound	Structure	IC <sub>50</sub> (μM)		
		NTMT1	G9a	PRMT1
<b>BM30</b>		0.32±0.06	>100	>100
<b>22</b>		4.2±1.2	13±4.1	>100

**Table S2.** Selectivity study of compound BM30 against a panel of 41 MTases (Reaction Biology)<sup>a</sup>

Enzyme	Activity (mean, %)	SD (%)	n
ASH1L	92	4.6	2
DNMT1	100	0.4	2
DNMT3a	100	3.4	2
DNMT3b	103	2.2	2
DNMT3b/3L	118	0.6	2
DOT1L	92	1.9	2
EZH1 Complex	112	0.9	2
EZH2 Complex	104	2.1	2
EZH2 (Y641F)	100	1.0	2
G9a	101	0.1	2
GLP	97	6.8	2
METTL21A-GST	95	10.6	2
MLL1 Complex	75	0.9	2
MLL2 Complex	85	1.0	2
MLL3 Complex	96	0.4	2
MLL4 Complex	84	2.4	2
NTMT1	11	0.1	2
NTMT2	12	0.1	2
NSD1	95	0.4	2
NSD2	102	0.7	2
NSD2 (E1099K)	98	2.7	2
NSD2 (T1150A)	97	5.4	2
NSD3	91	1.2	2
PRDM9	100	0.3	2
PRMT1	112	0.3	2
PRMT3	98	2.4	2
PRMT4	104	3.7	2
PRMT5	106	7.6	2
PRMT5/MEP50 Complex	106	2.3	2
PRMT6	98	8.0	2
PRMT7	104	7.6	2
PRMT8	100	10.8	2
SET1b Complex	94	5.5	2
SET7/9	90	4.2	2
SET8	96	5.1	2
SETD2	100	3.2	2
SMYD1	97	0.7	2
SMYD2	96	0.6	2
SUV39H1	99	6.1	2
SUV39H2	93	1.8	2
SUV420H1TV2	99	3.4	2

<sup>a</sup> Selectivity of **BM30** was determined at concentration of 100  $\mu$ M for duplicate (n=2).

**Table S3.** Crystallography data and refinement statistics

<b>Data Collection</b>	<b>NTMT1-BM30</b>
$\lambda$ (Å)	1.0332
Space group	P6 <sub>5</sub> 22
a, b, c (Å)	106.9, 106.9, 205.4
$\alpha$ , $\beta$ , $\gamma$ (°)	90, 90, 120
Resolution (Å)*	30 – 1.73 (1.76 – 1.73)
Completeness (%)*	99.9 (98.1)
Redundancy*	19.4 (18.7)
$R_{\text{sym}}$ †*	0.21 (4.5)
$I / \sigma(I)$ *	12.8 (0.7)
CC <sub>1/2</sub>	1.0 (0.36)
<b>Refinement</b>	
Resolution (Å)	30 – 1.73
No. reflections	72,828
$R^{\S}/R_{\text{free}}^{\P}$	0.18/0.20
<b>r.m.s. deviations</b>	
Bonds (Å)	0.008
Angles (°)	0.879
No. Protein atoms	7088
No. Ligand atoms	246
No. Waters	564
<b>B-factors (Å<sup>2</sup>)</b>	
Wilson B	26.81
Protein	32.53
Ligands	41.43
Waters	40.42
<b>Ramachandran Analysis<sup>¥</sup></b>	
Favored (%)	98.9
Allowed (%)	1.1
Outliers (%)	0
PDB code	6WH8

†  $R_{\text{sym}} = \sum_{hkl,j} (|I_{hkl} - \langle I_{hkl} \rangle|) / \sum_{hkl,j} I_{hkl}$ , where  $\langle I_{hkl} \rangle$  is the average intensity for a set of  $j$  symmetry related reflections and  $I_{hkl}$  is the value of the intensity for a single reflection within a set of symmetry-related reflections.

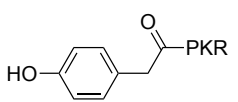
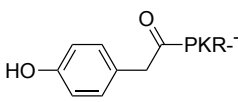
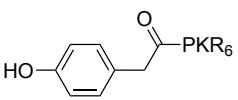
§  $R$  factor =  $\sum_{hkl} (|F_o| - |F_c|) / \sum_{hkl} F_o$  where  $F_o$  is the observed structure factor amplitude and  $F_c$  is the calculated structure factor amplitude.

¶  $R_{\text{free}} = \sum_{hkl,T} (|F_o| - |F_c|) / \sum_{hkl,T} F_o$ , where a test set,  $T$  (5% of the data), is omitted from the refinement.

¥ Performed using Molprobity within PHENIX.

\* Indicates statistics for last resolution shell shown in parenthesis.

**Table S4.** IC<sub>50</sub> values and binding affinities of BM30 and its cell-permeable analogs<sup>a</sup>

Compound	Structure	IC <sub>50</sub> (μM) for NTMT1	K <sub>d</sub> (μM) for NTMT1	K <sub>d</sub> (μM) for NTMT2
<b>BM30</b>		0.89±0.10	3, 2.8	3.7
<b>DC431</b>		0.23± 0.03	0.6, 0.8	3.4
<b>DC432</b>		0.054± 0.004	0.3, 0.4	1

<sup>a</sup> IC<sub>50</sub> = mean±SD (n=3)