## Tryptic stability of synthetic bactenecin derivatives is determined by the side chain length of cationic residues and the peptide conformation

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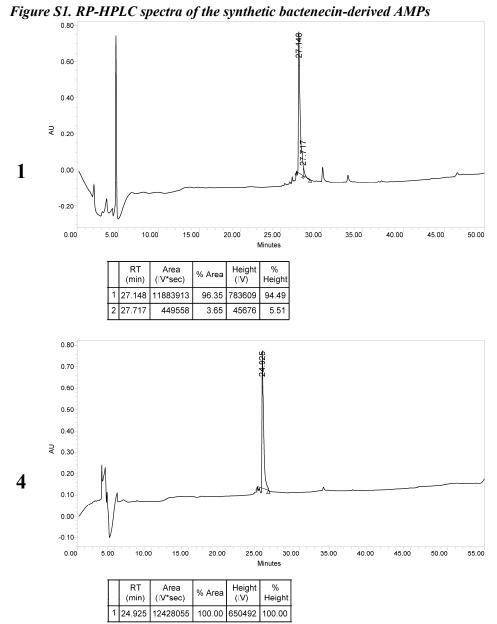
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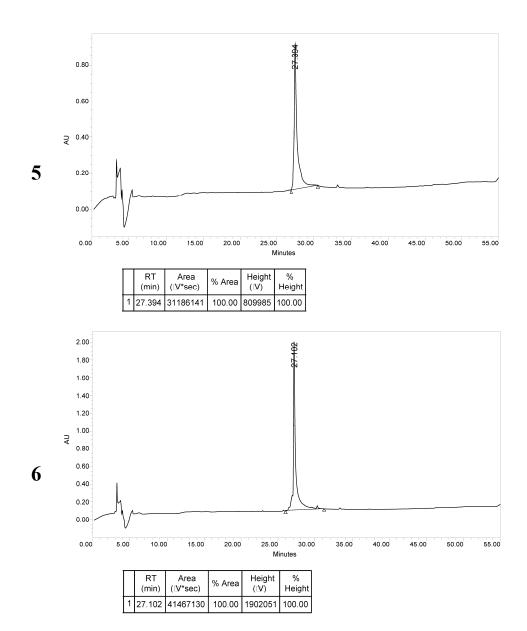
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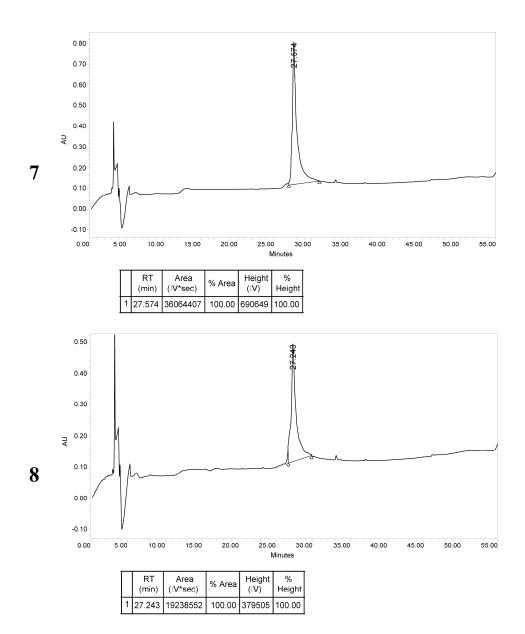
Peptide code	Sequence		
1	Lys-Arg-Trp-Trp-Lys-Trp-Ile-Arg-Trp-NH <sub>2</sub>		
$2^{a}$	Lys-Arg-Trp-Trp-Lys-Trp-Ile-Arg-Trp-NH <sub>2</sub>		
3	<u>Trp-Arg-Ile-Trp-Lys-Trp-Trp-Arg-Lys-NH</u> 2		
4	Arg-Lys-Trp-Trp-Arg-Trp-Ile-Lys-Trp-NH <sub>2</sub>		
5	Dab-Dab-Trp-Trp-Dab-Trp-Ile-Dab-Trp-NH <sub>2</sub>		
6	Orn-Orn-Trp-Trp-Orn-Trp-Ile-Orn-Trp-NH <sub>2</sub>		
7	Har-Har-Trp-Trp-Har-Trp-Ile-Har-Trp-NH <sub>2</sub>		
8	Dab-Har-Trp-Trp-Dab-Trp-Ile-Har-Trp-NH <sub>2</sub>		
9	Orn-Har-Trp-Trp-Orn-Trp-Ile-Har-Trp-NH <sub>2</sub>		
10	Lys-Arg-Trp-Trp-Lys-Trp-Trp-Arg-Arg-NH <sub>2</sub>		
11	<u>Lys-Arg-Trp-Trp-Lys-Trp-Trp-Arg-Arg</u> -NH <sub>2</sub>		
12	<u>Arg-Arg-Trp-Trp-Lys-Trp-Trp-Arg-Lys</u> -NH <sub>2</sub>		
13	Arg-Lys-Trp-Trp-Arg-Trp-Trp-Lys-Lys-NH <sub>2</sub>		
14	$Dab\text{-}Dab\text{-}Trp\text{-}Trp\text{-}Dab\text{-}Trp\text{-}Dab\text{-}Dab\text{-}NH_2$		
15	Orn-Orn-Trp-Trp-Orn-Trp-Trp-Orn-Orn-NH <sub>2</sub>		
16	Har-Har-Trp-Trp-Har-Trp-Trp-Har-Har-NH $_2$		
17	$Dab-Har-Trp-Trp-Dab-Trp-Trp-Har-Har-NH_2$		
18	$Orn-Har-Trp-Trp-Orn-Trp-Trp-Har-Har-NH_2$		

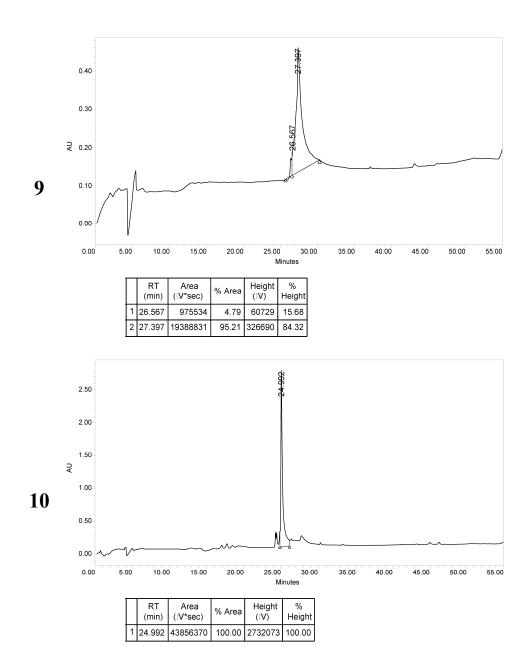
Table S1. The sequences of the synthetic bactenecin peptides andtheir analogues

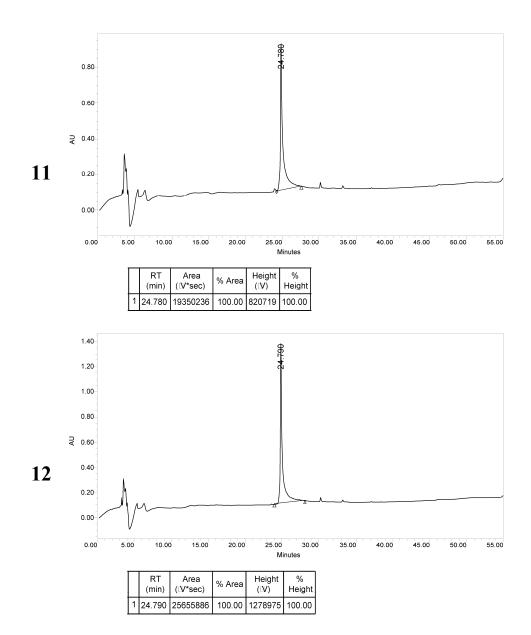
<sup>*a*</sup> *D*-amino acids are underlined.

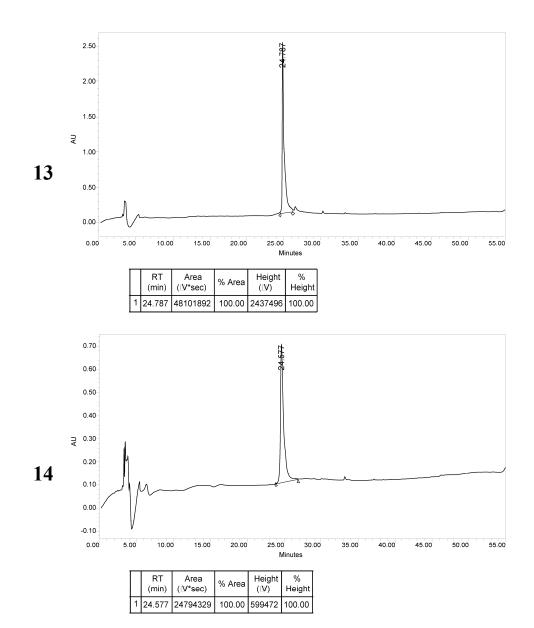




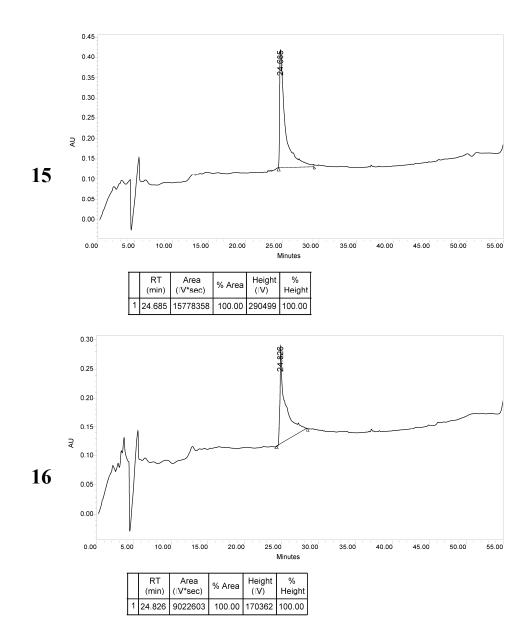


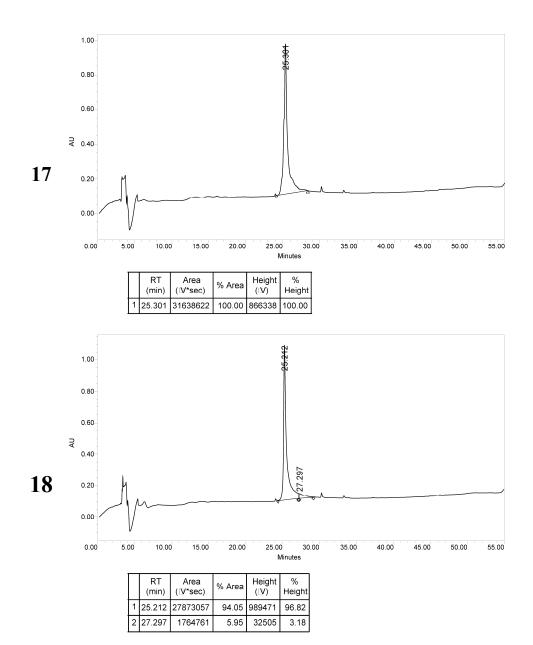






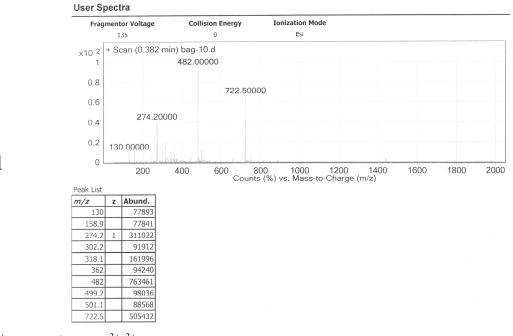
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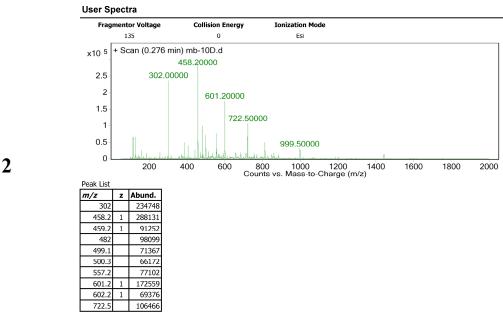


S11

*Figure S2. Mass spectra of synthetic bactenecin-derived AMPs*. The values are monoisotopic masses in positive mode.

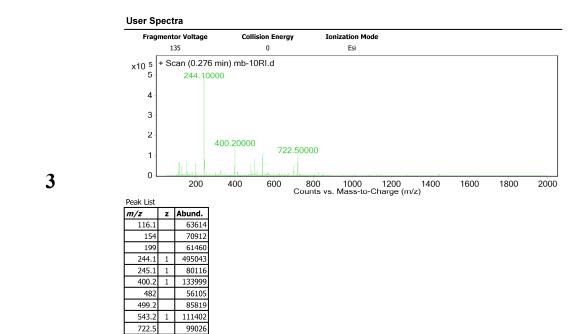


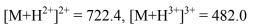
<sup>a</sup> These values are the calculated mass values for the respective peptides.

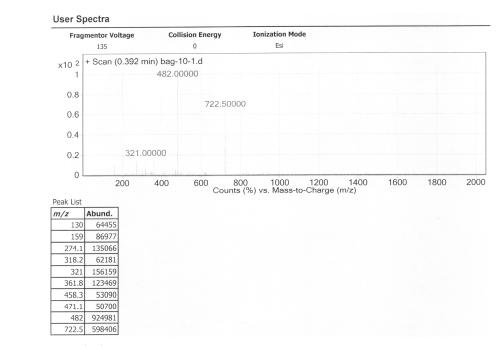


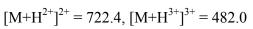
 $[M+H^{2+}]^{2+} = 722.4, [M+H^{3+}]^{3+} = 482.0, [M+2TFA+H^{3+}]^{3+} = 557.9^{b}$ 

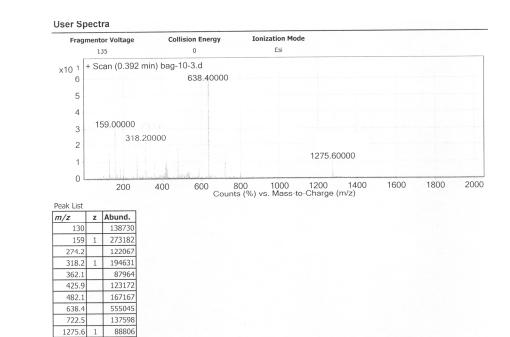
<sup>*b*</sup> The calculated masses may reflect the mass of the peptides with TFA adduct ion; e.g.,  $[M+xTFA+nH]^{n+}$ , where x is the number of TFA adduct ion, and n represents multiple-charge ionization of peptides from protonation. The monoisotopic mass of TFA is 113.99 Da.



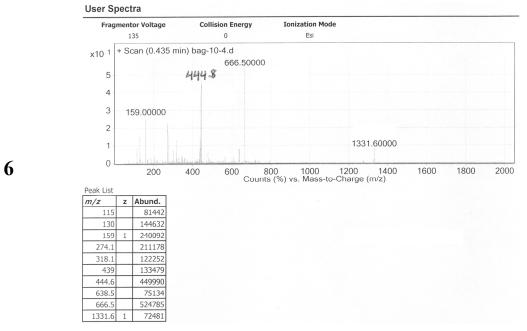






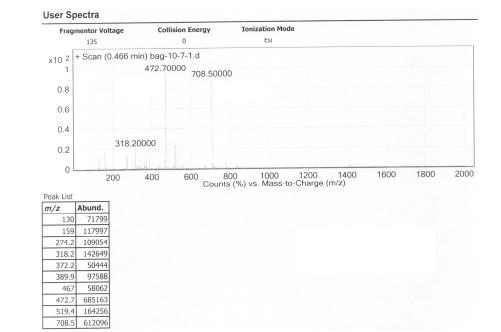


 $[M+H^{1+}]^{1+} = 1275.8, [M+H^{2+}]^{2+} = 638.4, [M+H^{3+}]^{3+} = 425.9$ 

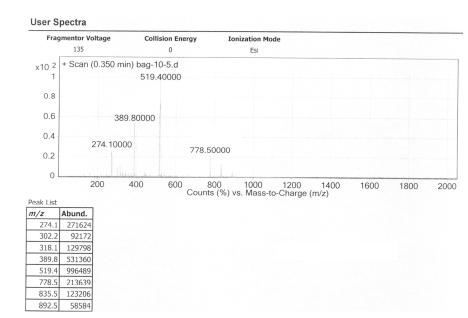


 $[M+H^{1+}]^{1+} = 1331.8, [M+H^{2+}]^{2+} = 666.4, [M+H^{3+}]^{3+} = 444.6$ 

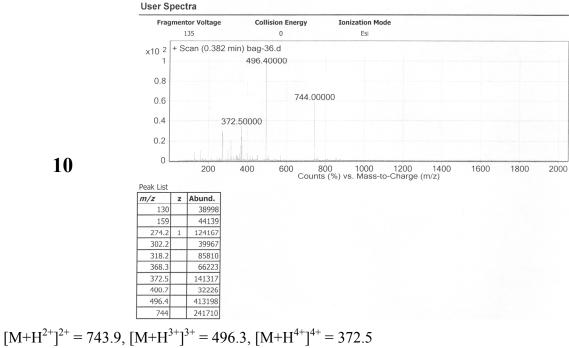
 $[M+H^{2+}]^{2+} = 708.4, [M+H^{3+}]^{3+} = 472.6$ 



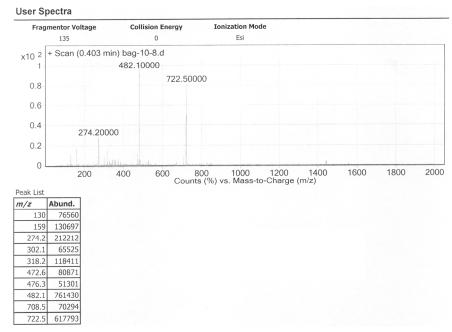
$$[M+H^{2+}]^{2+} = 778.4, [M+H^{3+}]^{3+} = 519.3, [M+H^{4+}]^{4+} = 389.7$$

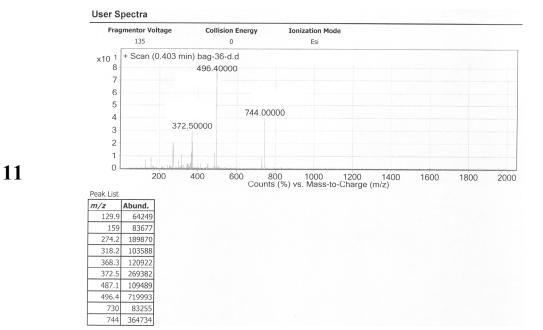


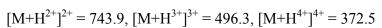
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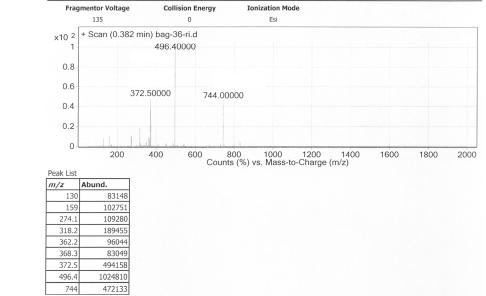
 $[M+H^{2+}]^{2+} = 722.4, [M+H^{3+}]^{3+} = 481.9$ 





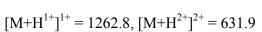


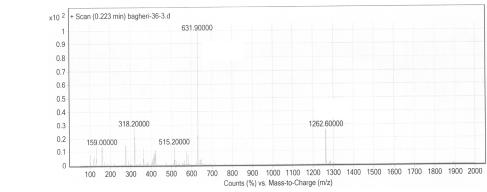
 $[M+H^{2+}]^{2+} = 743.9, [M+H^{3+}]^{3+} = 496.3, [M+H^{4+}]^{4+} = 372.5$ 

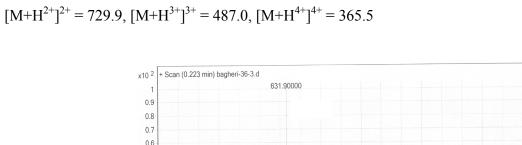




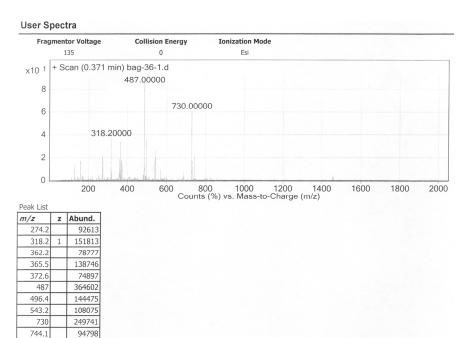


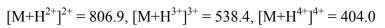


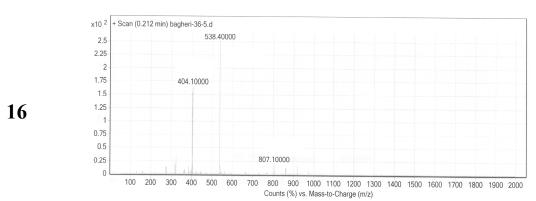




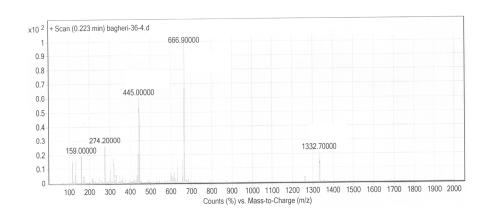


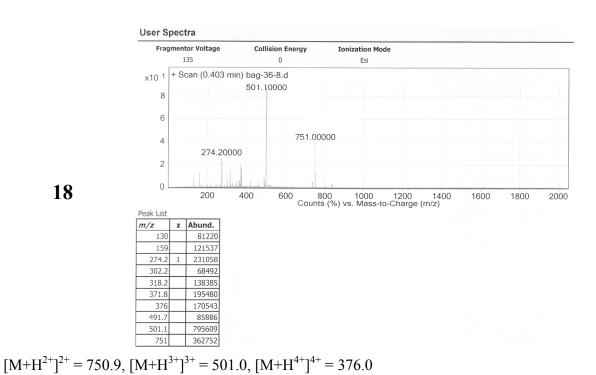






 $[M+H^{1+}]^{1+} = 1332.8, [M+H^{2+}]^{2+} = 666.9, [M+H^{4+}]^{4+} = 444.9$ 





$$[M+H^{2+}]^{2+} = 736.9, [M+H^{3+}]^{3+} = 491.6, [M+H^{4+}]^{4+} = 369.0$$

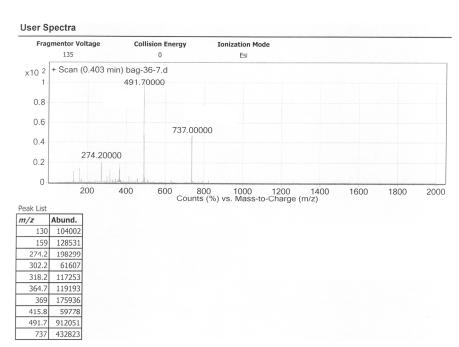




Figure S3. Ramachandran plots of each amino acid residues in the 1 derived AMPs for the structure with the highest percentage of occurrence in water. The three-letter amino acid codes from left to right represent the residues in the sequences starting from the  $2^{nd}$  residue at the peptide *N*-terminal to the 8<sup>th</sup> at the *C*-terminal.

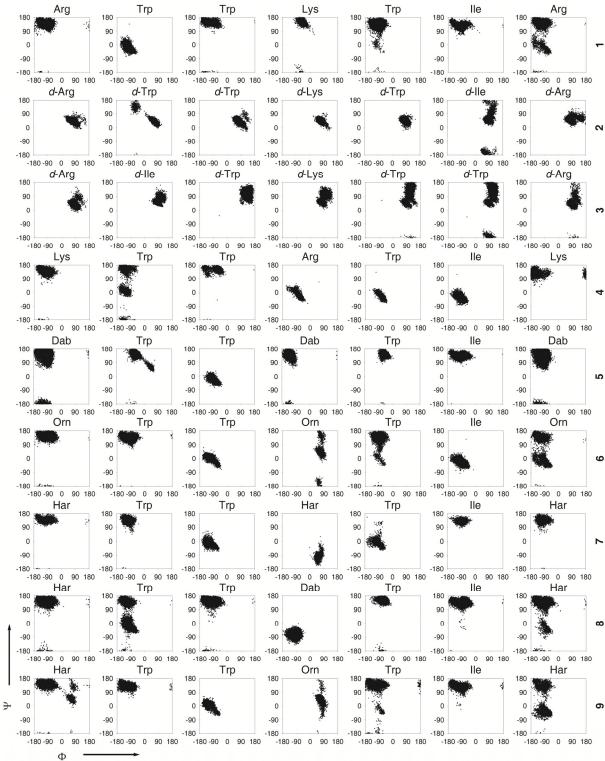


Figure S4. Ramachandran plots of each amino acid residues in the 10 derived AMPs for the structure with the highest percentage of occurrence in water. The three-letter amino acid codes from left to right represent the residues in the sequences starting from the  $2^{nd}$  residue at the peptide *N*-terminal to the 8<sup>th</sup> at the *C*-terminal.

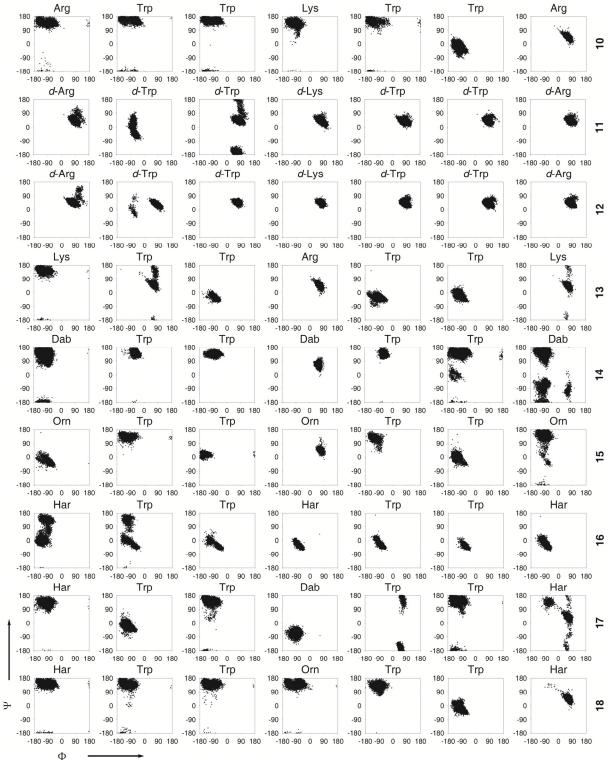
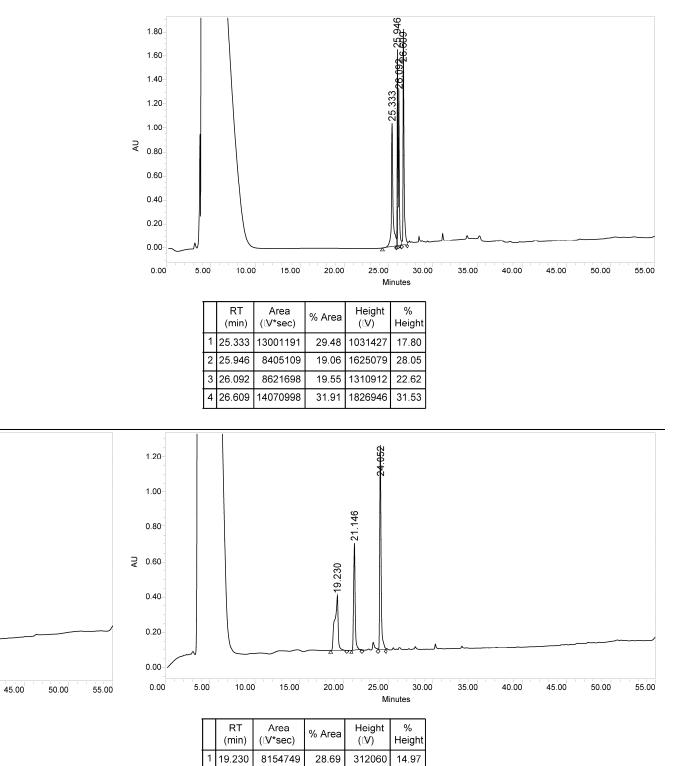


Figure S5. RP-HPLC spectra of the reaction mixture of each individual synthetic bactenecin-derived AMPs incubated with trypsin. Left and right spectra were recorded after 2 h and 24 h incubation, respectively.



26.58 608124

44.73 1164805 55.87

2 21.146 7554488

3 24.052 12711148

29.17

0.10		$\Box$				fm_	
0.00							
0.00 5.00 10.00 15.00 20.00 25.00 30.00 35.00							
Minutes							
		RT (min)	Area (Ⅳ*sec)	% Area	Height (Ⅳ)	% Height	
	1	19.611	7670579	33.04	330780	18.58	
	2	21.480	7060761	30.42	626051	35.17	
	3	24.385	8483124	36.54	823271	46.25	

Not determined

21.480

19.611

1

4

0.90

0.80

0.70

0.60

0.50

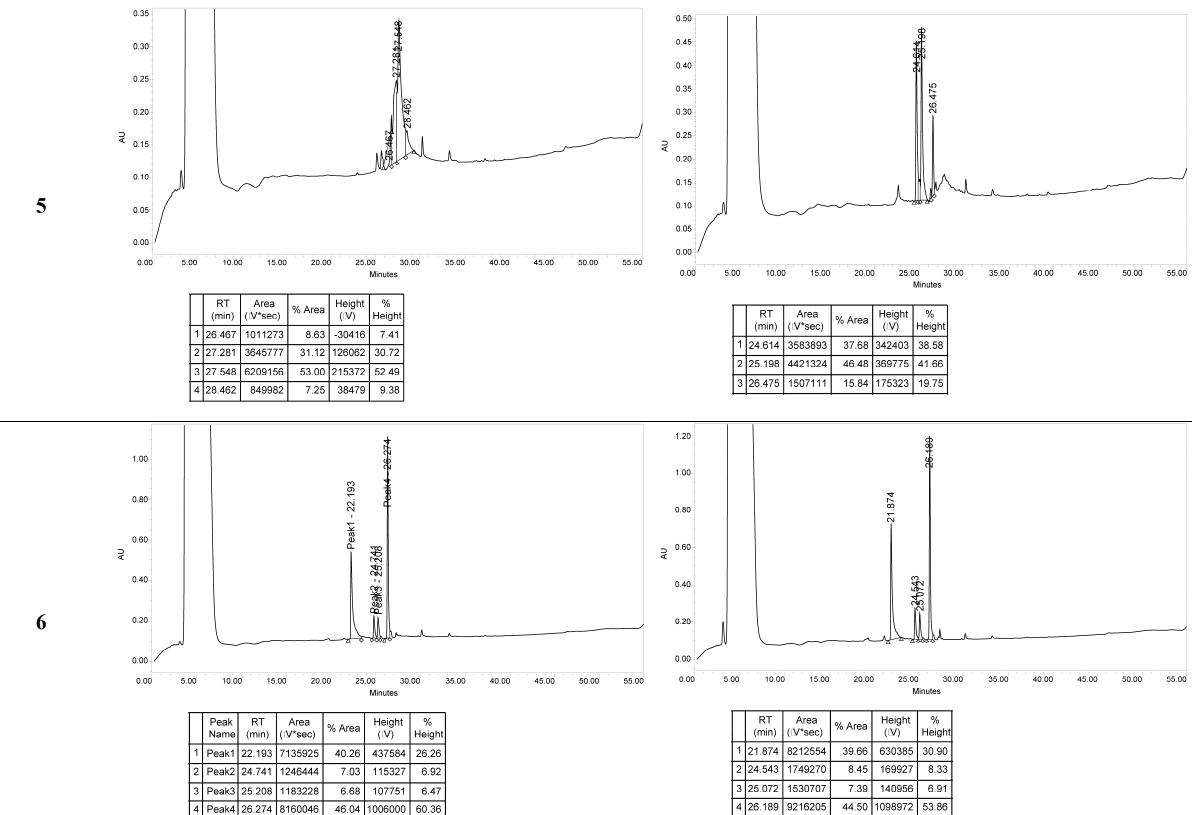
0.40

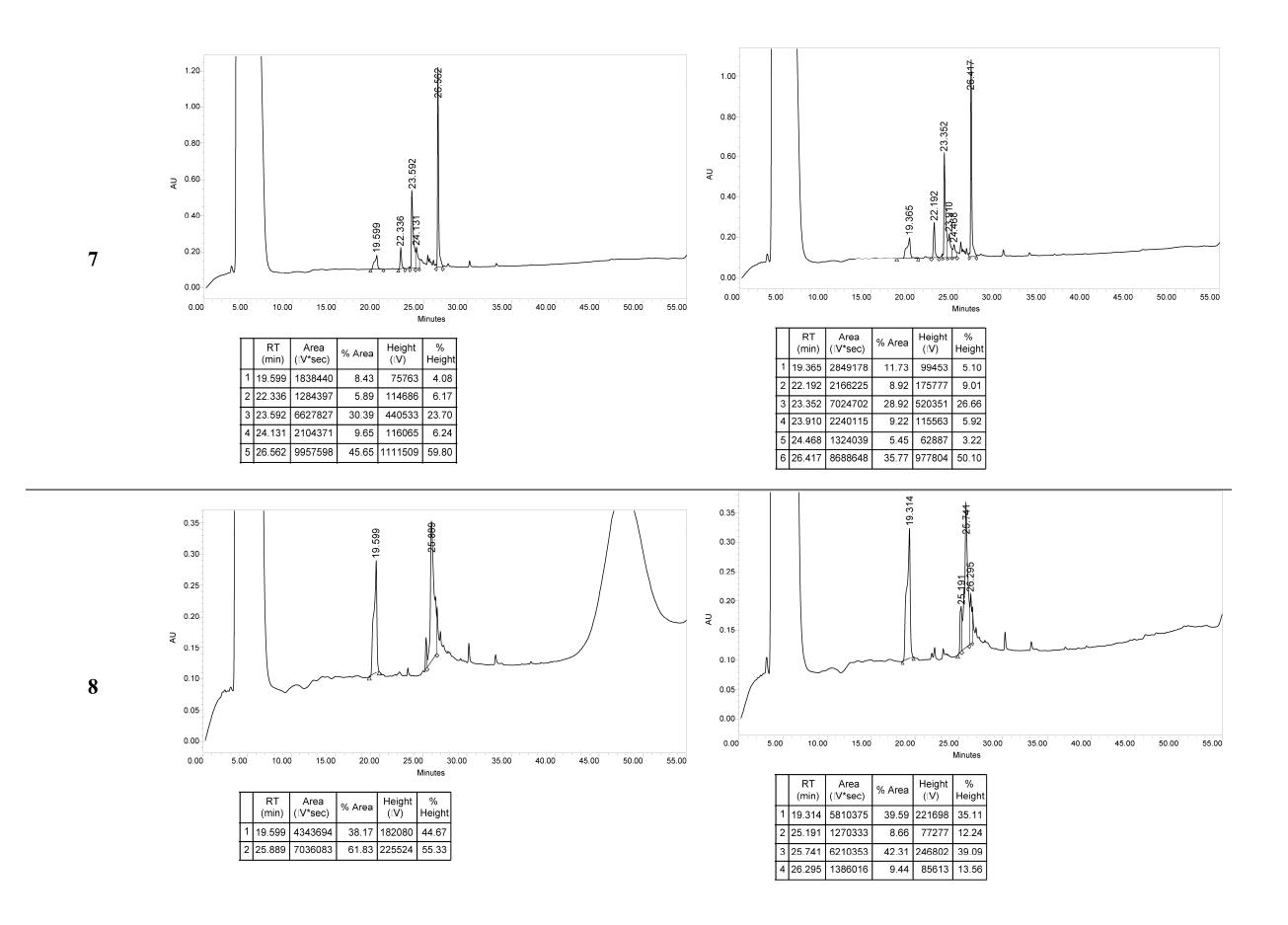
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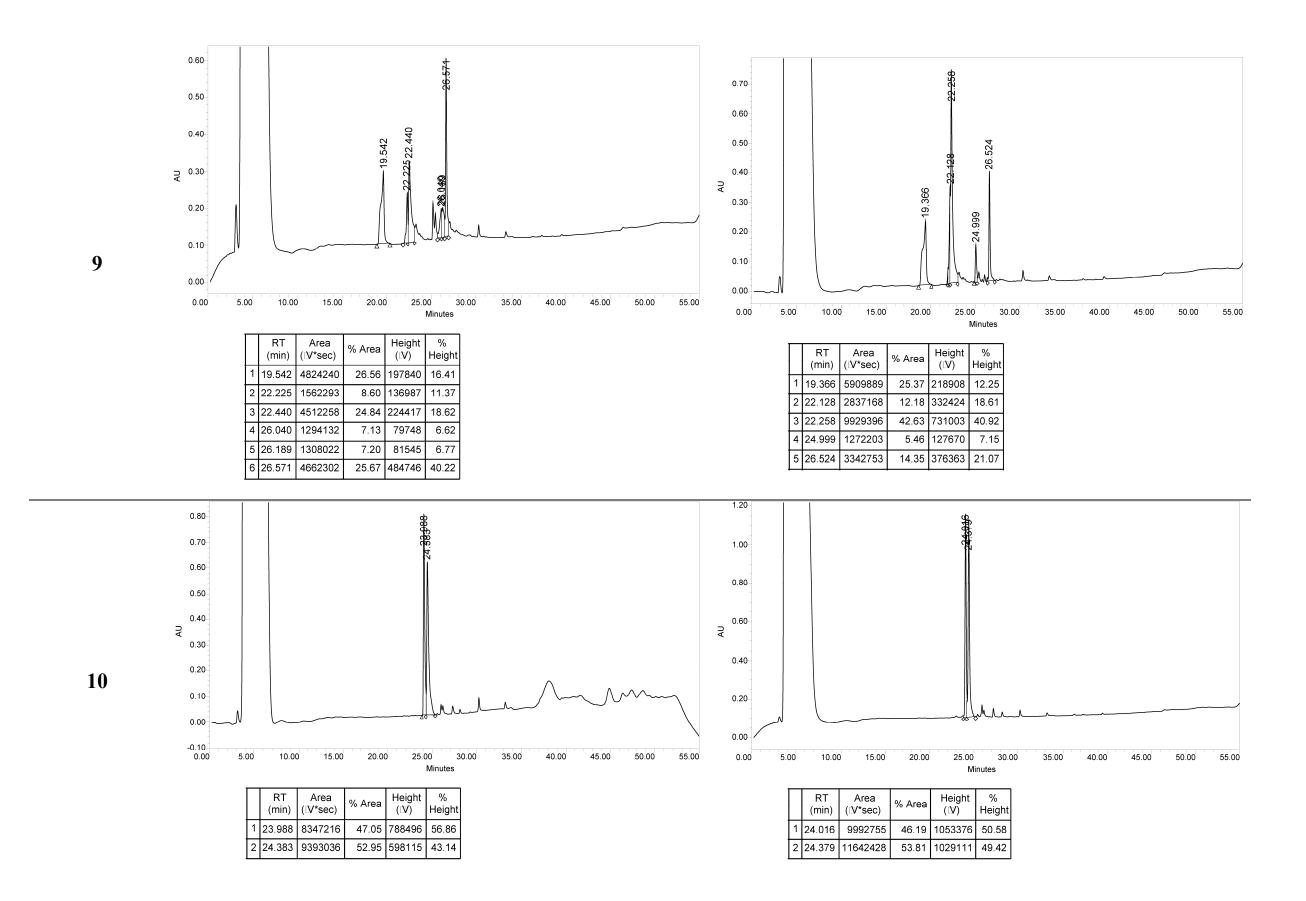
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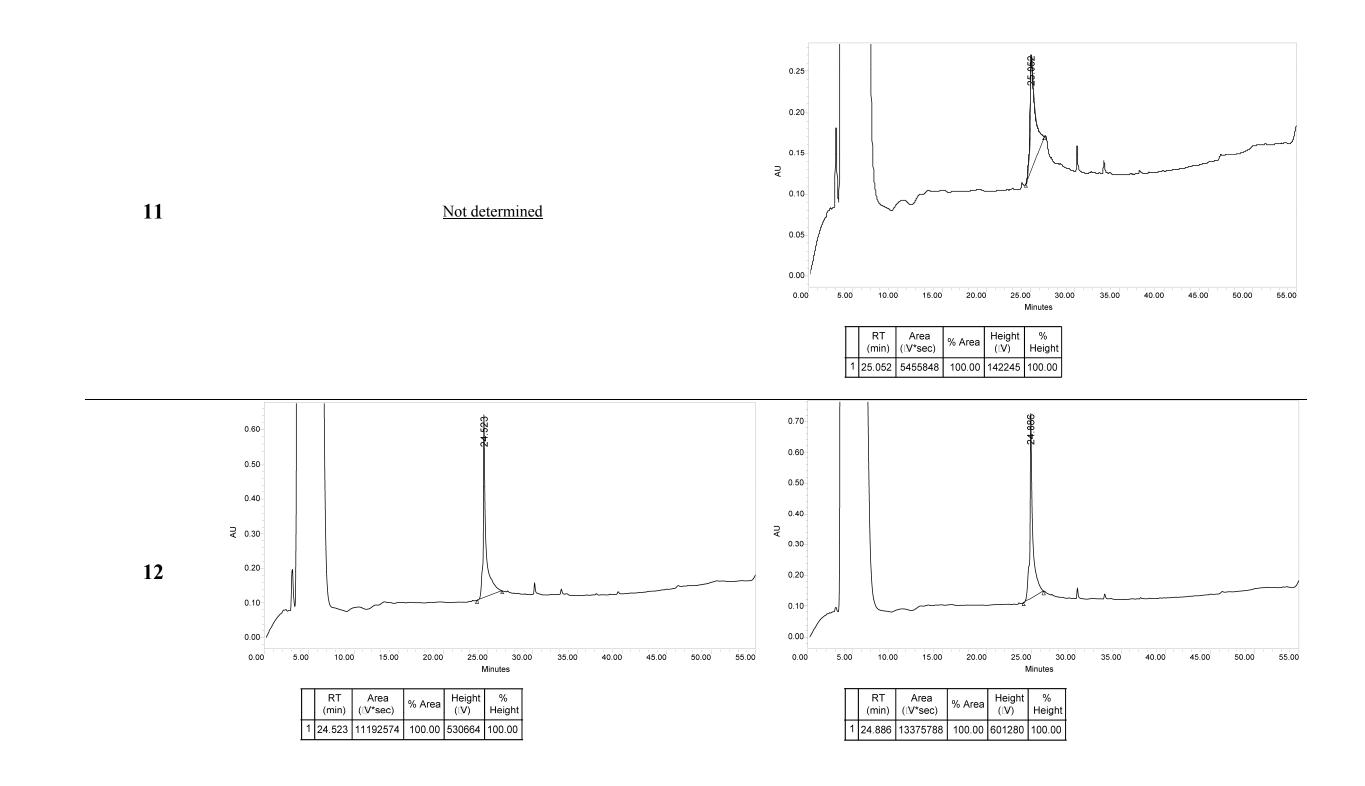
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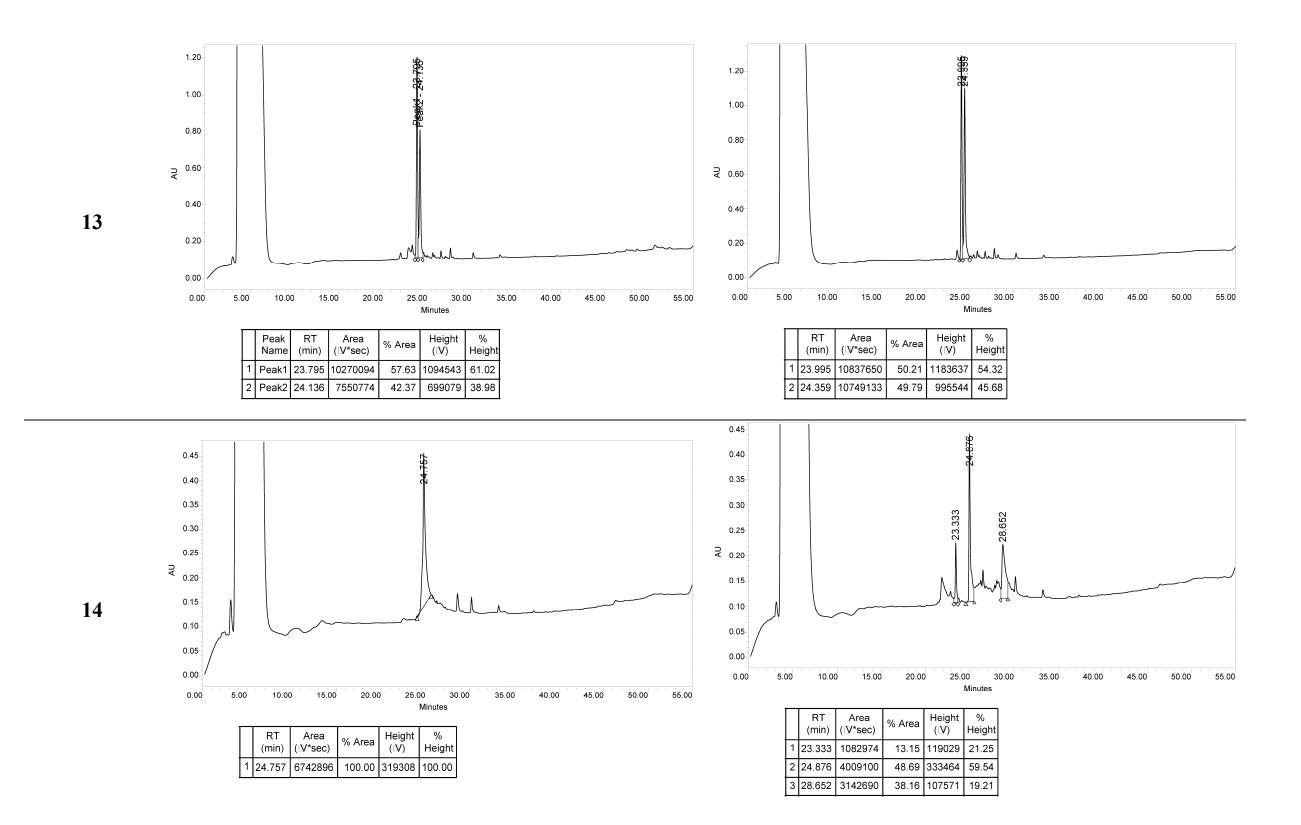


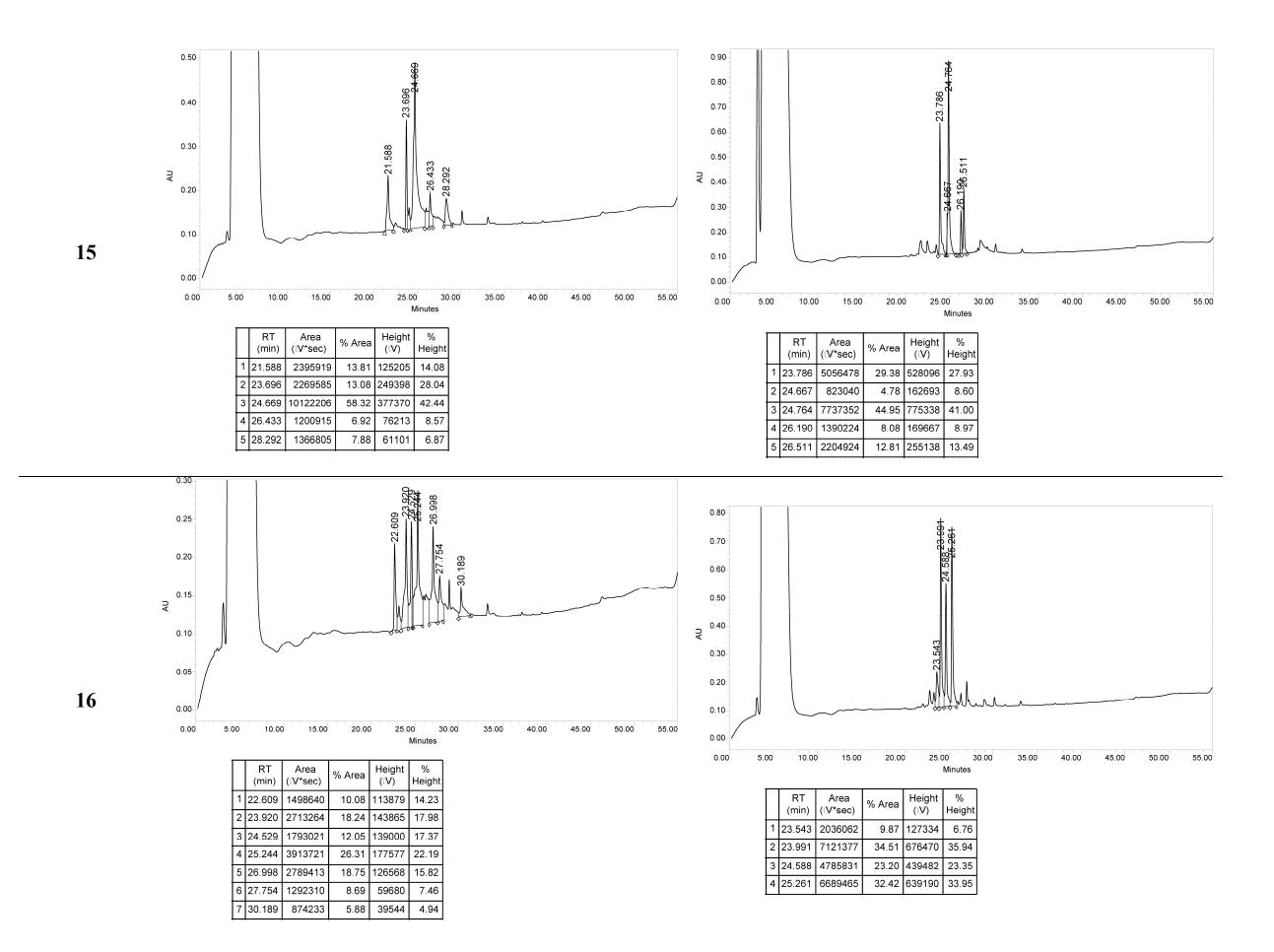




S26







S29

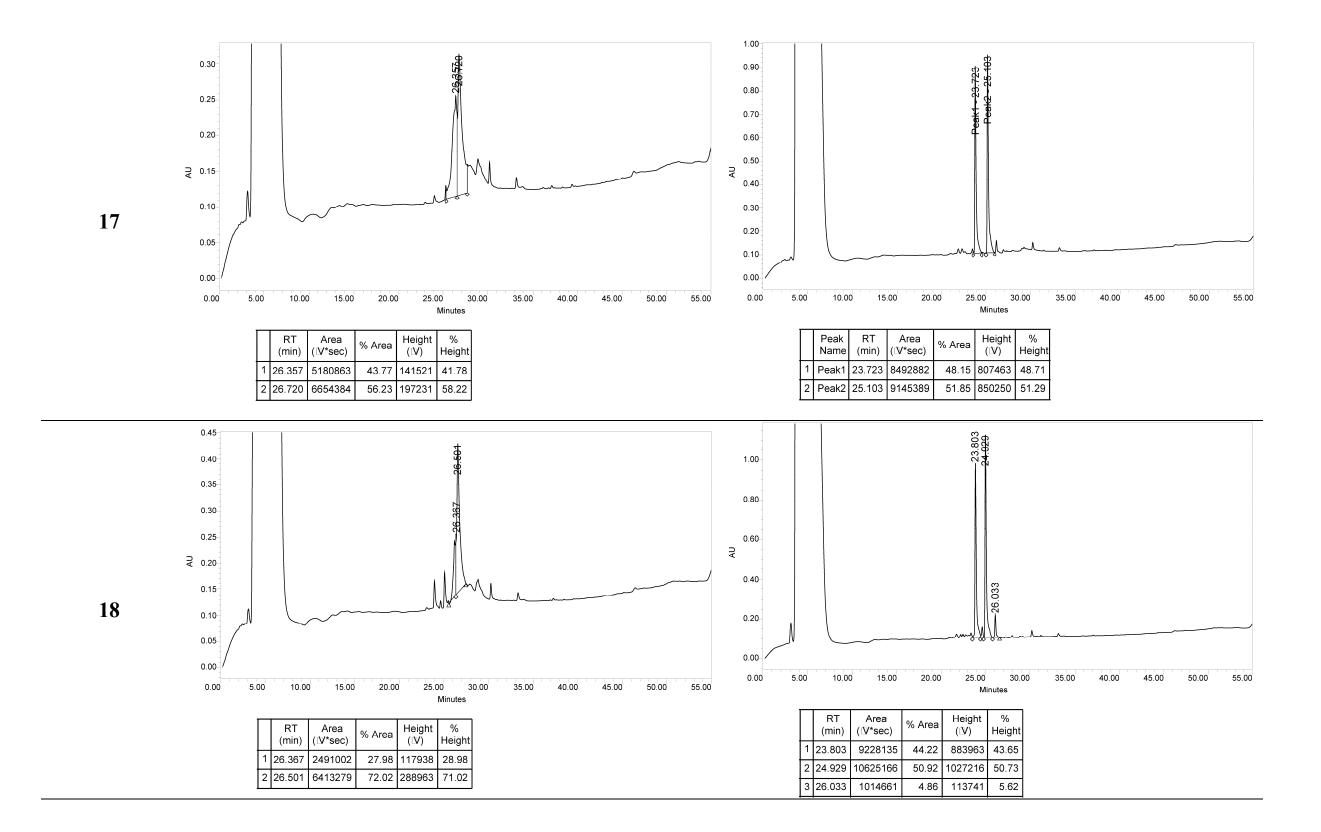
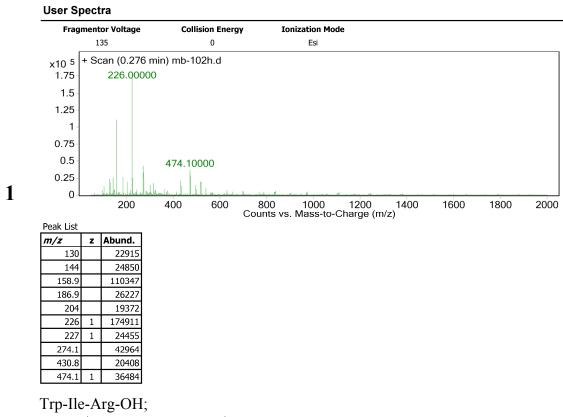
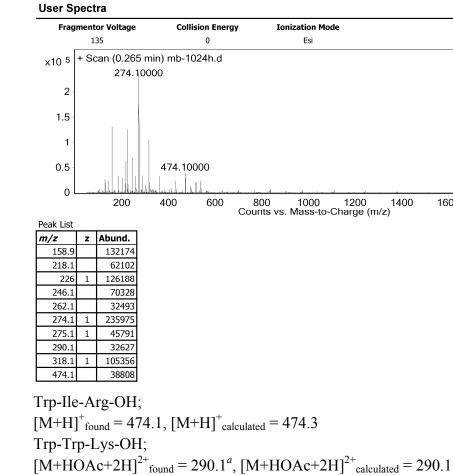


Figure S6. Mass spectra of the reaction mixture of each individual synthetic bactenecin-derived AMPs incubated with trypsin. Left and right spectra were recorded after 2 h and 24 h incubation, respectively. The values are monoisotopic masses in positive mode.

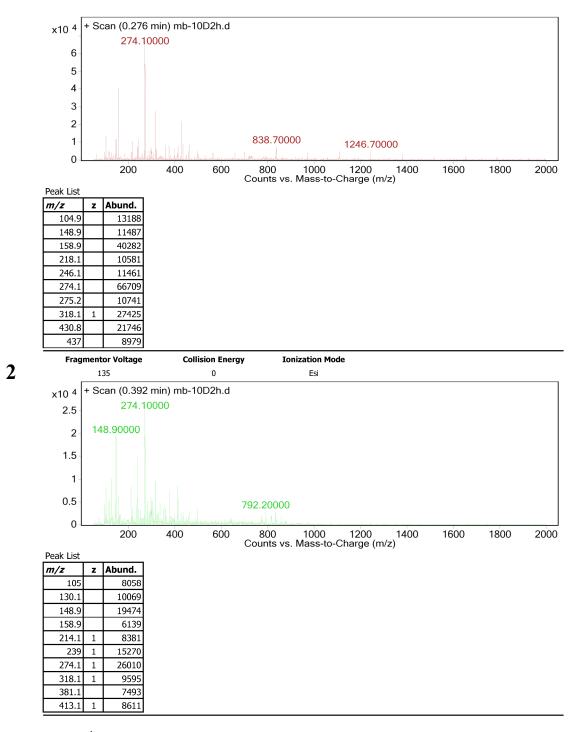


 $[M+H]^{+}_{found} = 474.1, [M+H]^{+}_{calculated} = 474.3$ 



<sup>*a*</sup> Monoisotopic mass of HOAc is 60.02 Da.

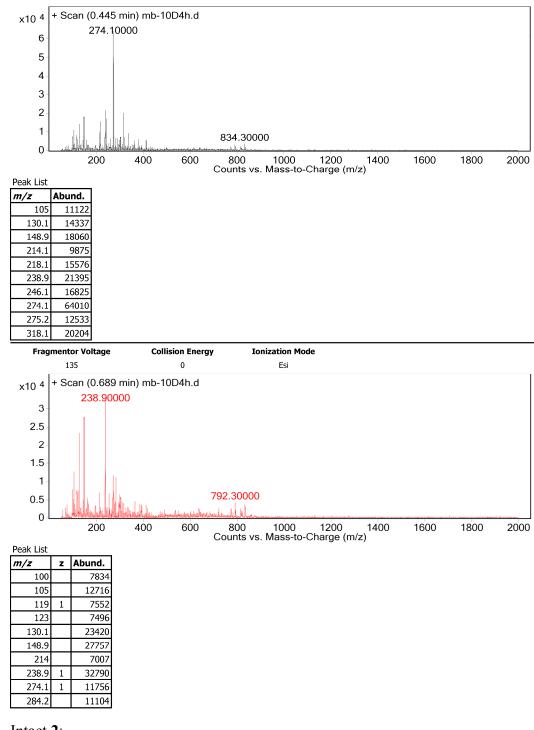
0	1600	1800	2000



Intact  $2^b$ ;

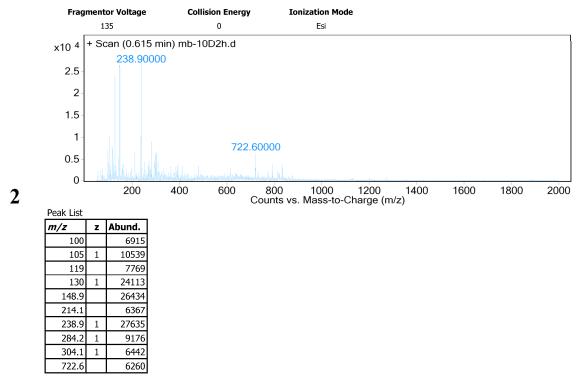
 $[M+2HOAc+TFA+2H]^{2+}_{found} = 838.7, [M+2HOAc+TFA+2H]^{2+}_{calculated} = 839.4$  $[M+6HOAc+5TFA+3H]^{3+}_{found} = 792.2, [M+6HOAc+5TFA+3H]^{3+}_{calculated} = 791.9$  $[M+5HOAc+4H]^{4+}_{found} = 437.0, [M+5HOAc+4H]^{4+}_{calculated} = 436.7$ <sup>b all-D</sup>HHC-10 and <sup>Retro-inverso</sup>HHC-10 were in impure forms.

continued in next page

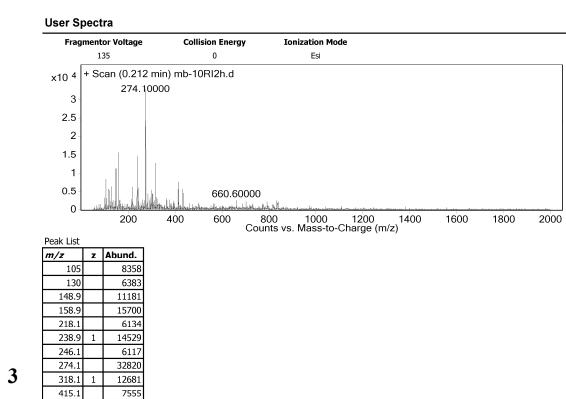


Intact 2;  $[M+10HOAc+4TFA+3H]^{3+}_{found} = 834.3, [M+10HOAc+4T]^{3+}_{found} = 792.3, [M+6HOAc+5TFA+3H]^{3+}_{found} = 792$ 

$$[FA+3H]^{3+}_{calculated} = 834.0$$
  
 $[A+3H]^{3+}_{calculated} = 791.9$ 



Intact 2;  $[M+2H]^{2+}_{found} = 722.6, [M+2H]^{2+}_{calculated} = 722.4$ 



Ionization Mode

Esi

Intact 3;  $[M+7HOAc+TFA+3H]^{3+}_{found} = 660.6, [M+7HOAc+TFA+3H]^{3+}_{calculated} = 660.0$ 

continued in next page

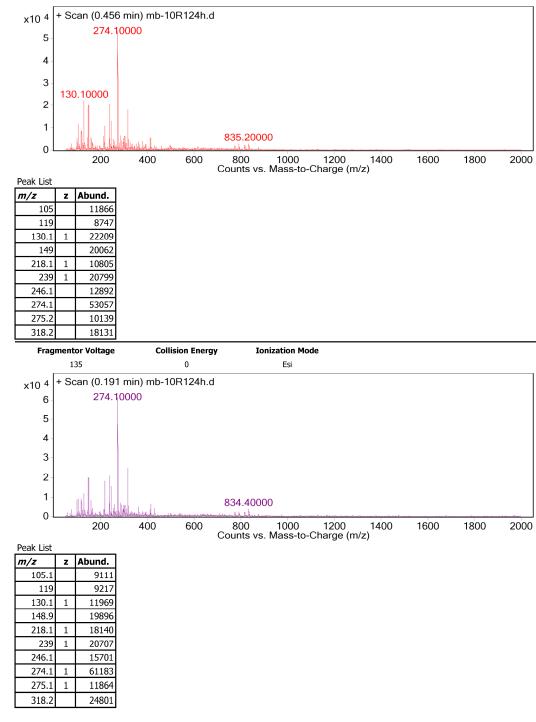
Fragr

ntor Voltage

135

**Collision Energy** 

0

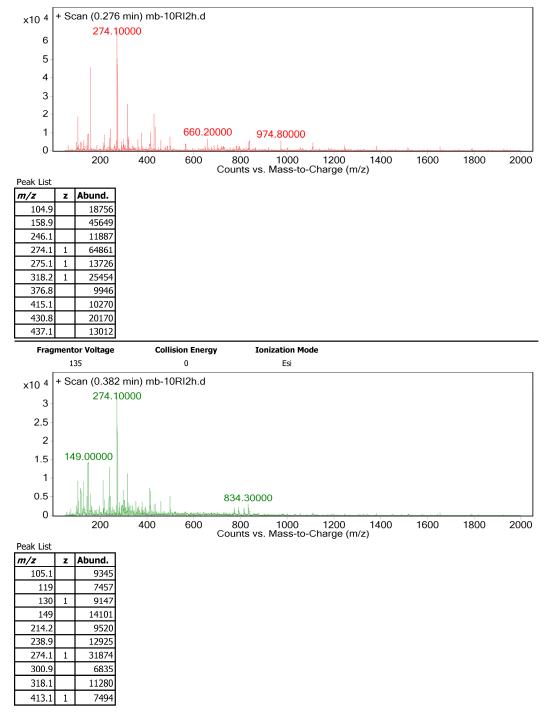


Intact **3**;

 $[M+12HOAc+3TFA+3H]^{3+}_{found} = 835.2, [M+12HOAc+3T]$  $[M+10HOAc+4TFA+3H]^{3+}_{found} = 834.4, [M+10HOAc+4T]$ 

0	1600	1800	2000

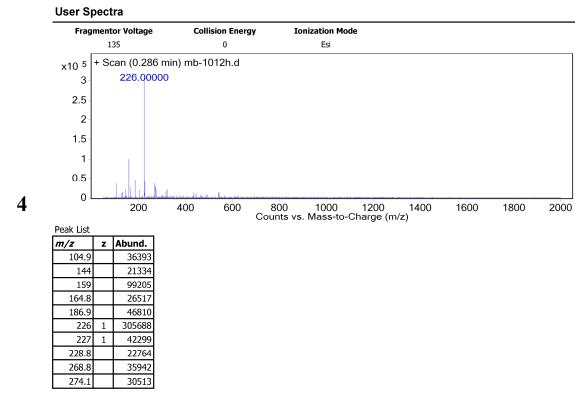
$$[FA+3H]^{3+}_{calculated} = 836.0$$
  
 $[FA+3H]^{3+}_{calculated} = 834.0$ 



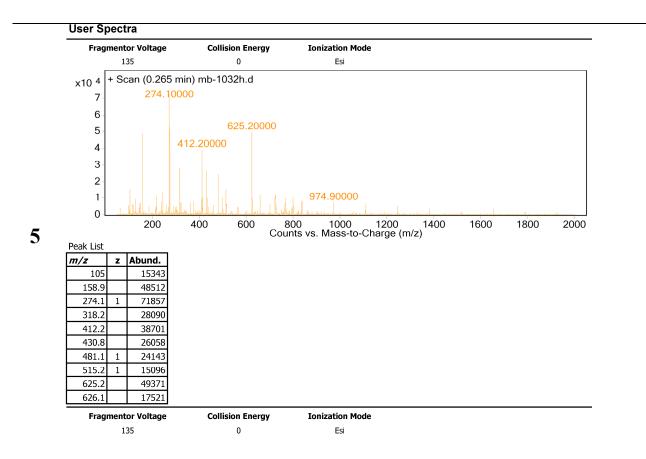
Intact 3;

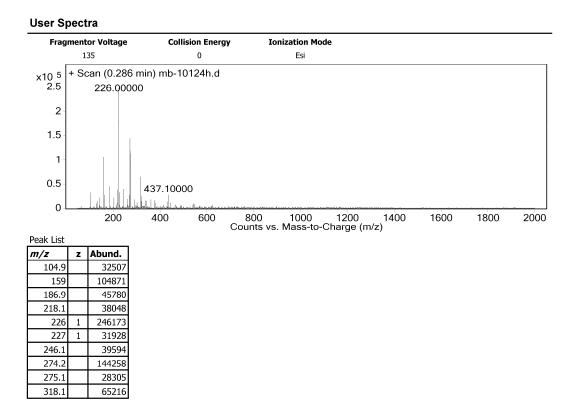
3

 $[M+7HOAc+TFA+3H]^{3+}_{found} = 660.6, [M+7HOAc+TFA+3H]^{3+}_{calculated} = 660.0$  $[M+10HOAc+4TFA+3H]^{3+}_{found} = 834.3, [M+10HOAc+4TFA+3H]^{3+}_{calculated} = 834.0$ 

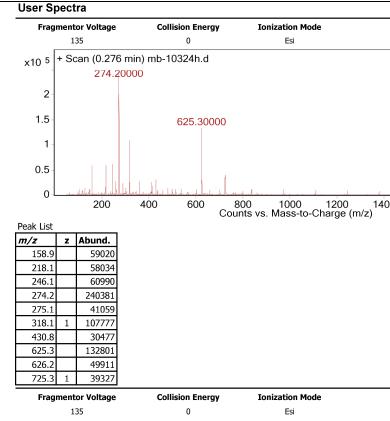


not detectable





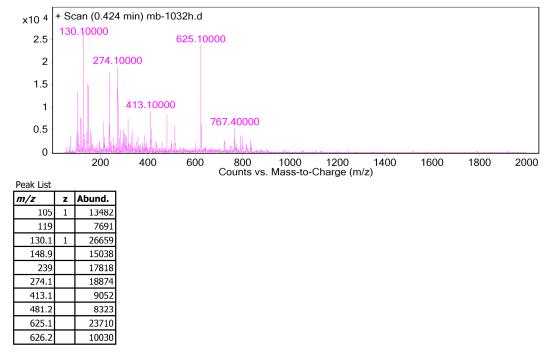
### Lys-Trp-Trp-Arg-OH; $[M+3HOAc+4TFA+3H]^{3+}_{found} = 437.1, [M+3HOAc+4TFA]^{3+}$



$$[A+3H]^{3+}_{calculated} = 437.8$$

	a i	*	
00	1600	1800	2000

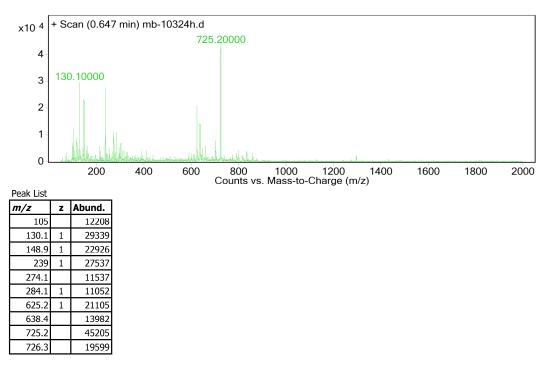
continued in next page Dab-Trp-Trp-Dab-Trp-Ile-Dab-Trp-NH<sub>2</sub>;  $[M+1HOAc+3H]^{3+}_{found} = 412.2, [M+1HOAc+3H]^{3+}_{calculated} = 412.6$ Trp-Trp-Dab-Trp-Ile-Dab-Trp-NH<sub>2</sub>;  $[M+HOAc+TFA+2H]^{2+}_{found} = 625.2, [M+HOAc+TFA+2H]^{2+}_{calculated} = 625.3$ 



5

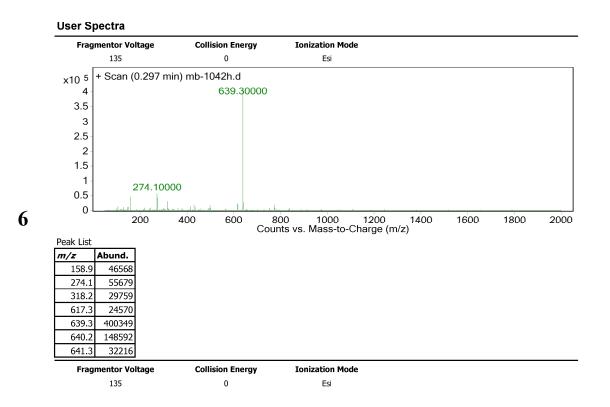
Dab-Trp-Trp-Dab-Trp-Ile-Dab-Trp-NH<sub>2</sub>;  $[M+HOAc+3H]^{3+}_{found} = 412.2, [M+HOAc+3H]^{3+}_{calculated} = 412.6$ Trp-Trp-Dab-Trp-Ile-Dab-Trp-NH<sub>2</sub>;  $[M+HOAc+TFA+2H]^{2+}_{found} = 625.2, [M+HOAc+TFA+2H]^{2+}_{calculated} = 625.3$ 

continued in next page Trp-Trp-Dab-Trp-Ile-Dab-Trp-NH<sub>2</sub>;  $[M+1HOAc+1TFA+2H]^{2+}_{found} = 625.3, [M+1HOAc+1TFA]^{2+}$ Trp-Trp-Dab-OH;  $[M+2HOAc+TFA+H]^{+}_{found} = 725.3, [M+2HOAc+TFA+H]^{+}_{calculated} = 725.2$ 



Trp-Trp-Dab-OH;  $[M+2HOAc+TFA+H]^{+}_{found} = 725.2, [M+2HOAc+TFA+H]^{+}_{calculated} = 725.2$ 

$$(+2H]^{2+}_{calculated} = 625.3$$

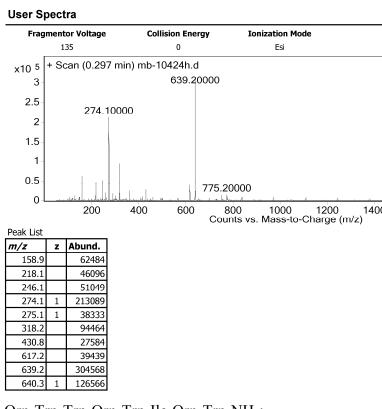


Orn-Trp-Trp-Orn-Trp-Ile-Orn-Trp-NH<sub>2</sub>;

 $[M+HOAc+2H]^{2+}_{found} = 639.3, [M+HOAc+2H]^{2+}_{calculated} = 639.4$ Trp-Ile-Orn-Trp-NH<sub>2</sub>;

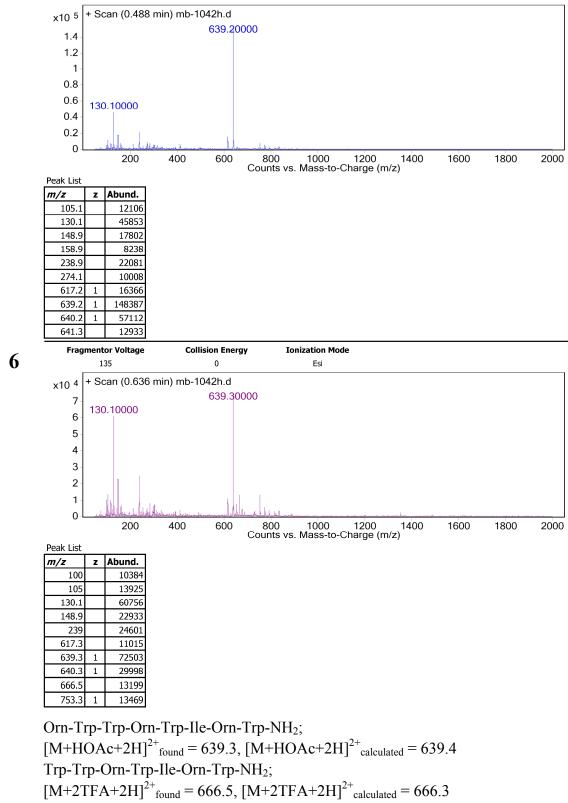
 $[M+H]^{+}_{found} = 617.3, [M+H]^{+}_{calculated} = 617.4$ 

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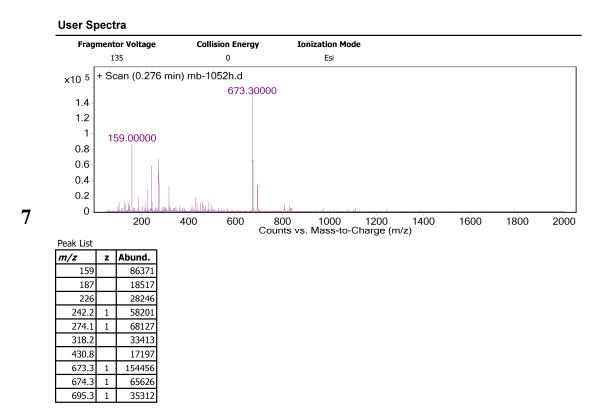
Orn-Trp-Trp-Orn-Trp-Ile-Orn-Trp-NH<sub>2</sub>;  $[M+HOAc+2H]^{2+}_{found} = 639.3, [M+HOAc+2H]^{2+}_{calculated} = 639.4$ Trp-Ile-Orn-Trp-NH<sub>2</sub>;  $[M+H]^{+}_{found} = 617.2, [M+H]^{+}_{calculated} = 617.4$ 

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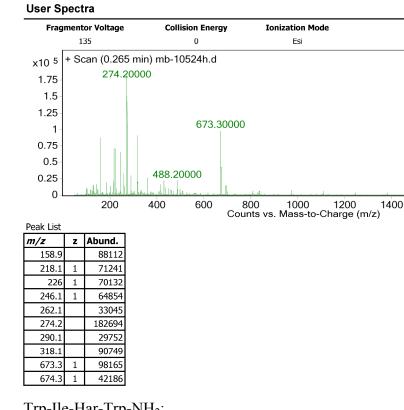


[M+21FA+2H] found = 666.5, [M+21FA+2H] calcu Trp-Ile-Orn-Trp-NH<sub>2</sub>;

 $[M+H]^{+}_{found} = 617.3, [M+H]^{+}_{calculated} = 617.4$ 

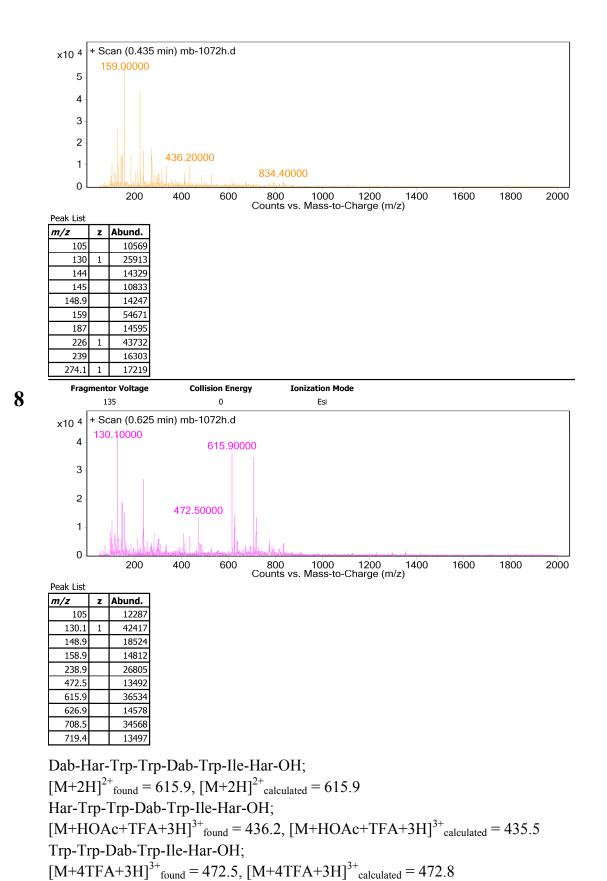


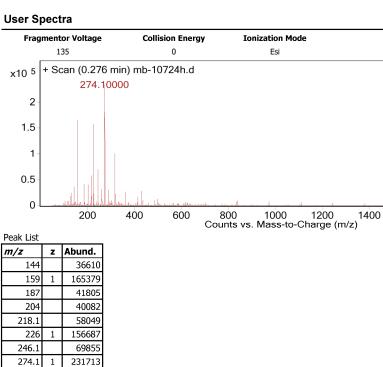
Trp-Ile-Har-Trp-NH<sub>2</sub>;  $[M+H]^{+}_{found} = 673.3, [M+H]^{+}_{calculated} = 673.4$ 



Trp-Ile-Har-Trp-NH<sub>2</sub>;  $[M+H]^{+}_{found} = 673.3, [M+H]^{+}_{calculated} = 673.4$ Trp-Ile-Har-OH;  $[M+H]^{+}_{found} = 488.2, [M+H]^{+}_{calculated} = 488.3$ 

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not detectable

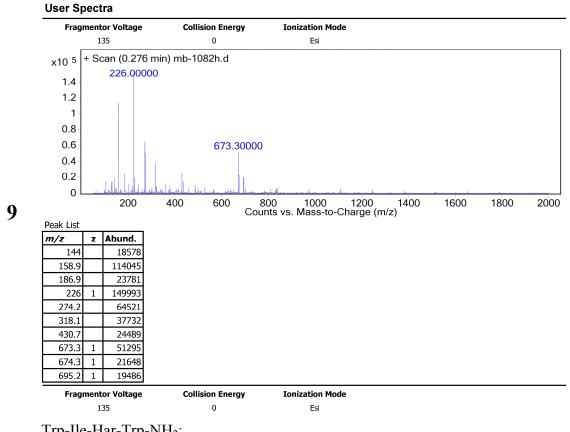
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318.1

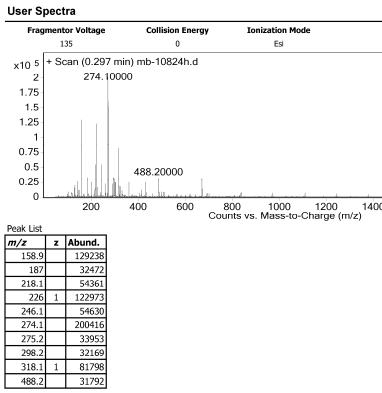
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99774

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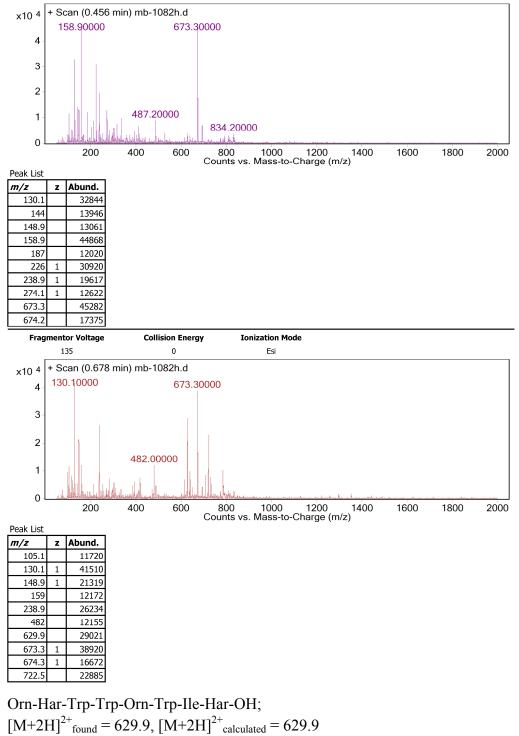


Trp-Ile-Har-Trp-NH<sub>2</sub>;  $[M+H]^{+}_{found} = 673.3, [M+H]^{+}_{calculated} = 673.4$ Trp-Trp-Orn-OH  $[M+4HOAc+TFA+2H]^{2+}_{found} = 430.7, [M+4HOAc+TFA+2H]^{2+}_{calculated} = 430.1$ 



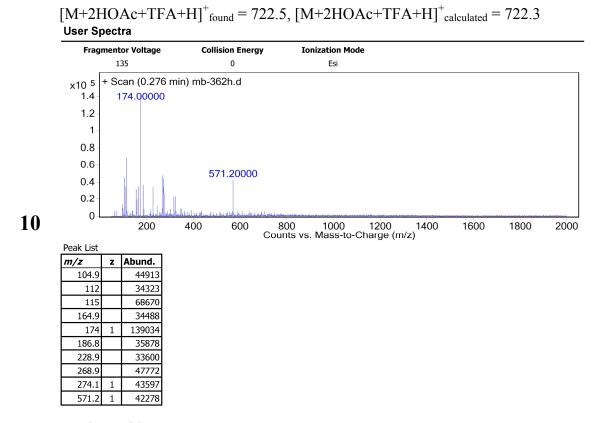
Trp-Trp-Orn-Trp-Ile-Har-OH;  $[M+2H]^{2+}_{found} = 488.2, [M+2H]^{2+}_{calculated} = 487.8$ 

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0	1600	1800	2000



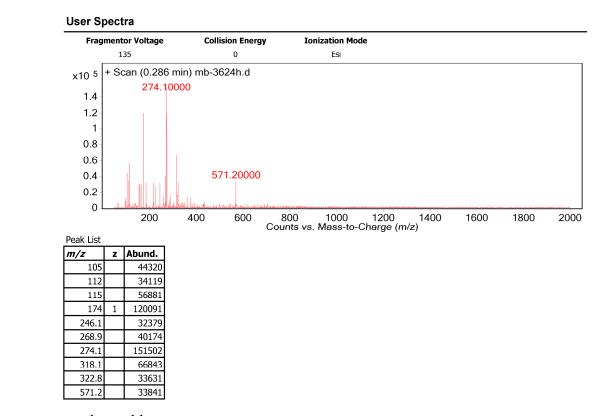
9

 $[M+2H]^{2+}_{found} = 629.9, [M+2H]^{2+}_{calculated} = 629.9$ Har-Trp-Trp-Orn-Trp-Ile-Har-OH;  $[M+5HOAc+3H]^{3+}_{found} = 482.0, [M+5HOAc+3H]^{3+}_{calculated} = 482.2$ Trp-Trp-Orn-Trp-Ile-Har-OH;  $[M+2H]^{2+}_{found} = 487.2, [M+2H]^{2+}_{calculated} = 487.8$ Trp-Ile-Har-Trp-NH<sub>2</sub>;  $[M+H]^{+}_{found} = 673.3, [M+H]^{+}_{calculated} = 673.3$ Trp-Ile-Har-OH

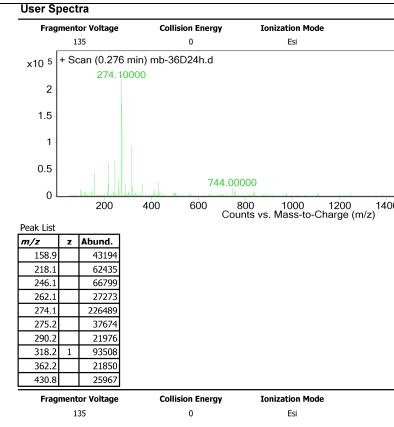


## not detectable

## User Spectra Collision Energy Fragmentor Voltage Ionization Mode 135 Esi x10 4 + Scan (0.254 min) mb-36D2h.d 274.10000 3 2 755.00000 1246.50000 0 800 1000 1200 1 Counts vs. Mass-to-Charge (m/z) 200 400 600 1800 1400 1600 2000 11 Peak List *m/z* Abund. 12700 105 158.9 44555 274.1 53511 275.2 12037 318.1 20657 430.8 19412 496.5 11372 503.7 10988 744 12604 755 14479 Fragmentor Voltage **Collision Energy** Ionization Mode 135 0 Esi

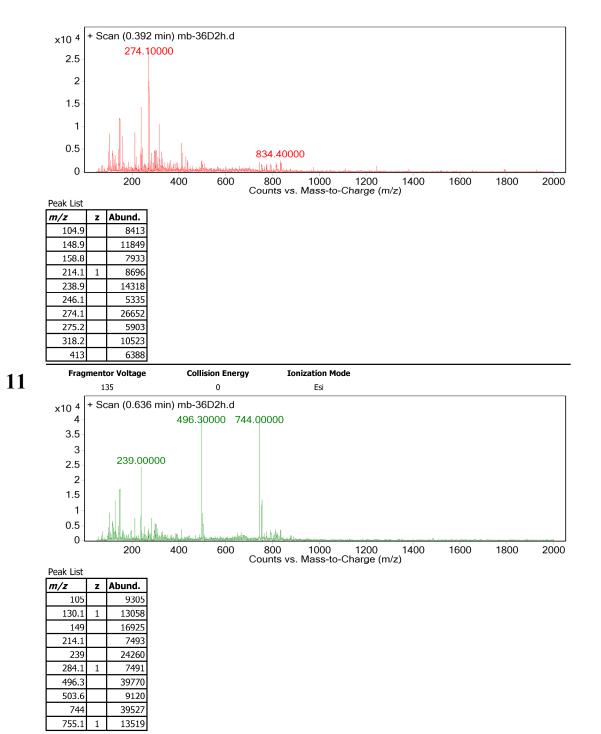




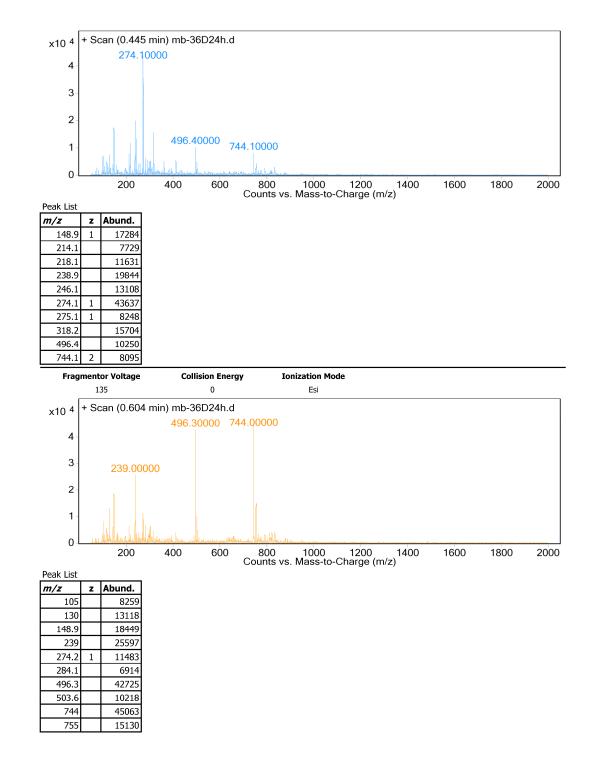


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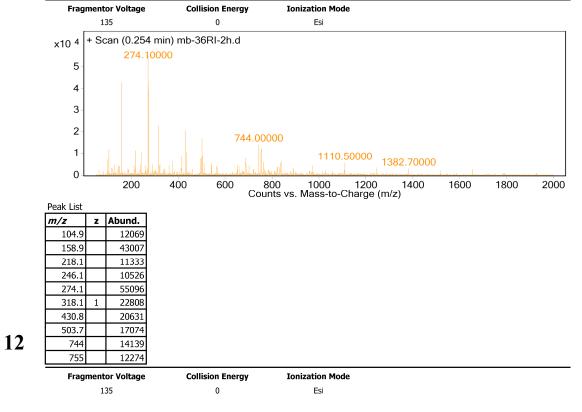
continued in next page Intact 11;  $[M+2H]^{2+}_{found} = 744.0, [M+2H]^{2+}_{calculated} = 743.9$   $[M+3H]^{3+}_{found} = 496.5, [M+3H]^{3+}_{calculated} = 496.3$  $[M+3HOAc+3TFA+4H]^{4+}_{found} = 503.7, [M+3HOAc+3TFA+4H]^{4+}_{calculated} = 503.0$ 



continued in next page Intact 11;  $[M+2H]^{2+}_{found} = 744.0, [M+2H]^{2+}_{calculated} = 743.9$ 

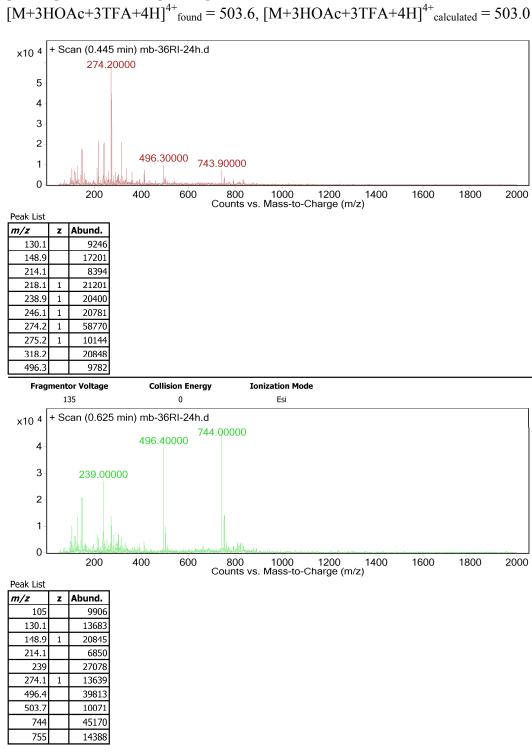


Intact 11;  $[M+3HOAc+2H]^{2+}_{found} = 834.4, [M+3HOAc+2H]^{2+}_{calculated} = 833.9$  $[M+2H]^{2+}_{\text{found}} = 744.0, [M+2H]^{2+}_{\text{calculated}} = 743.9$  $[M+3H]^{3+}_{\text{found}} = 496.3, [M+3H]^{3+}_{\text{calculated}} = 496.3$  $[M+3HOAc+3TFA+4H]^{4+}_{found} = 503.6, [M+3HOAc+3TFA+4H]^{4+}_{calculated} = 503.0$ **User Spectra** 



Intact 12;  $[M+2H]^{2+}_{found} = 744.0, [M+2H]^{2+}_{calculated} = 743.9$  $[M+3HOAc+3TFA+4H]^{4+}_{found} = 503.7, [M+3HOAc+3TFA+4H]^{4+}_{calculated} = 503.0$ 

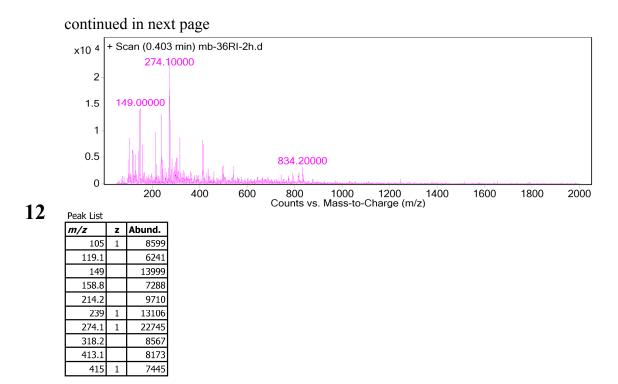
Intact 11;  $[M+2H]^{2+}_{\text{found}} = 744.0, [M+2H]^{2+}_{\text{calculated}} = 743.9$  $[M+3H]^{3+}_{\text{found}} = 496.3, [M+3H]^{3+}_{\text{calculated}} = 496.3$ 



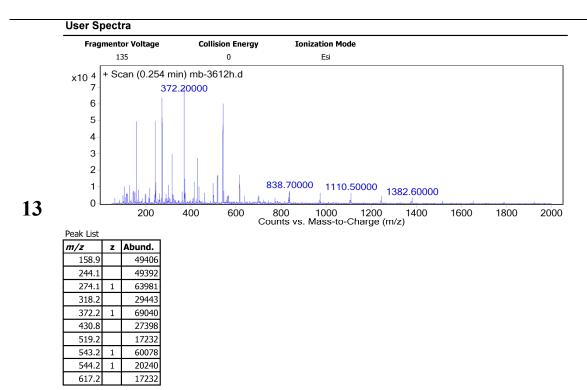
Intact 12;

 $[M+2H]^{2+}_{\text{found}} = 744.0 \text{ or } 743.9, [M+2H]^{2+}_{\text{calculated}} = 743.9$  $[M+3H]^{3+}_{\text{found}} = 496.4, [M+3H]^{3+}_{\text{calculated}} = 496.3$ 

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Intact 12;  $[M+3HOAc+2H]^{2+}_{found} = 834.2, [M+3HOAc+2H]^{2+}_{calculated} = 833.9$ 

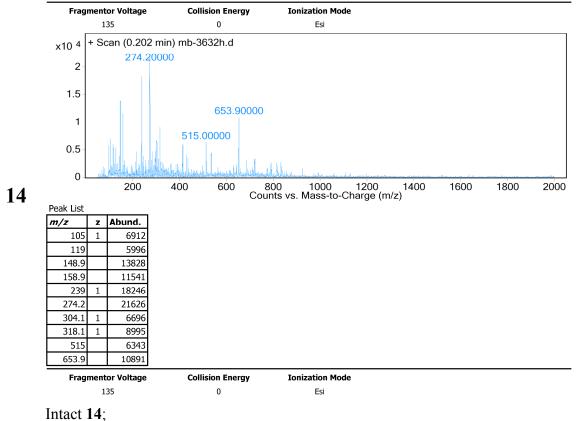


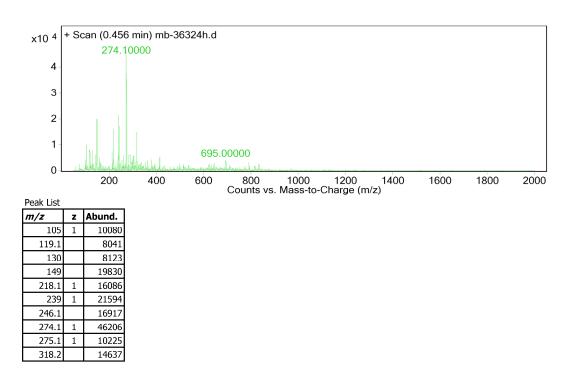
Trp-Trp-Arg-Trp-Trp-Lys-Lys-NH<sub>2</sub>;  $[M+HOAc+2H]^{2+}_{found} = 617.2, [M+HOAc+2H]^{2+}_{calculated} = 617.8$ 

not determined

Trp-Trp-Arg-Trp-Trp-Lys-OH;  $[M+HOAc+5TFA+2H]^{2+}_{found} = 838.7, [M+HOAc+5TFA+2H]^{2+}_{calculated} = 839.3$ Trp-Trp-Lys-OH  $[M+H]^{+}_{found} = 519.2, [M+H]^{+}_{calculated} = 519.3$ 

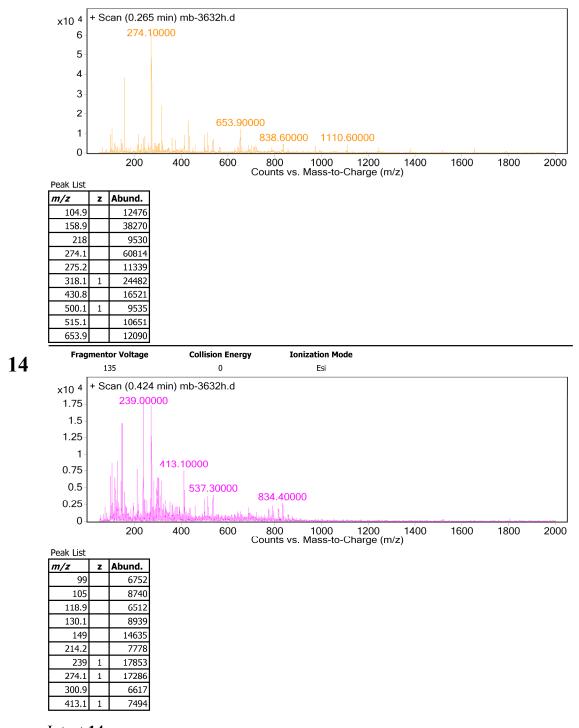
User Spectra





 $[M+4HOAc+4TFA+3H]^{3+}_{found} = 653.9, [M+4HOAc+4TFA+3H]^{3+}_{calculated} = 653.6$ 

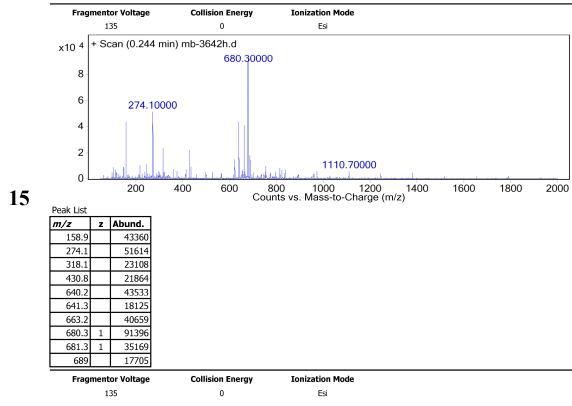
Dab-Trp-Trp-Dab-Trp-Trp-Dab-Dab-NH<sub>2</sub>;  $[M+2TFA+2H]^{2+}_{found} = 695.0, [M+2TFA+2H]^{2+}_{calculated} = 695.9$ 



Intact 14;

 $[M+5HOAc+TFA+2H]^{2+}_{found} = 838.6, [M+5HOAc+TFA+2H]^{2+}_{calculated} = 838.9$  $[M+2HOAc+2TFA+3H]^{3+}_{found} = 537.3, [M+2HOAc+2TFA+3H]^{3+}_{calculated} = 537.6$ 

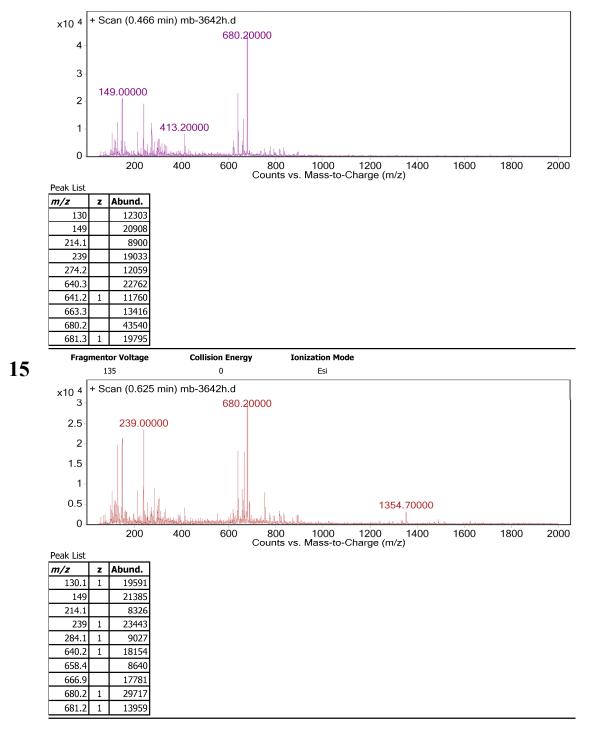




Trp-Trp-Orn-Trp-Trp-Orn-Orn-NH<sub>2</sub>;

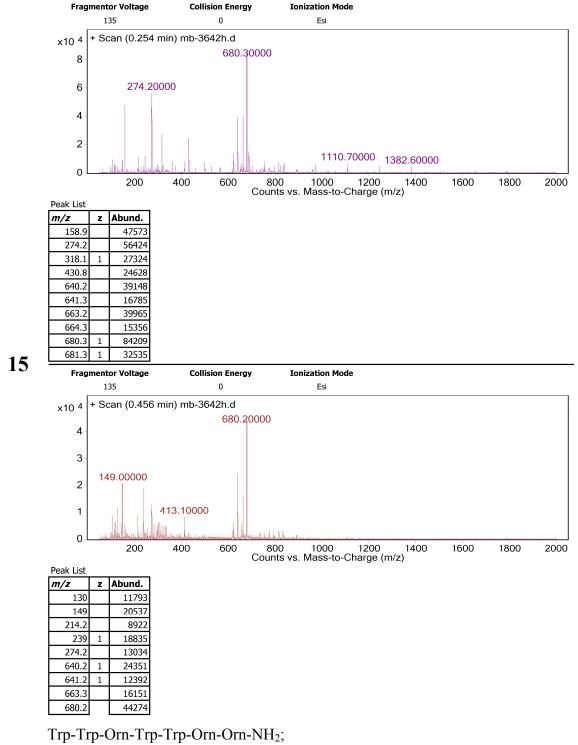
 $[M+HOAc+TFA+2H]^{2+}_{found} = 640.2, [M+HOAc+TFA+2H]^{2+}_{calculated} = 639.8$ Trp-Trp-Orn-OH  $[M+HOAc+TFA+H]^{+}_{found} = 680.3, [M+HOAc+TFA+H]^{+}_{calculated} = 679.6$ 



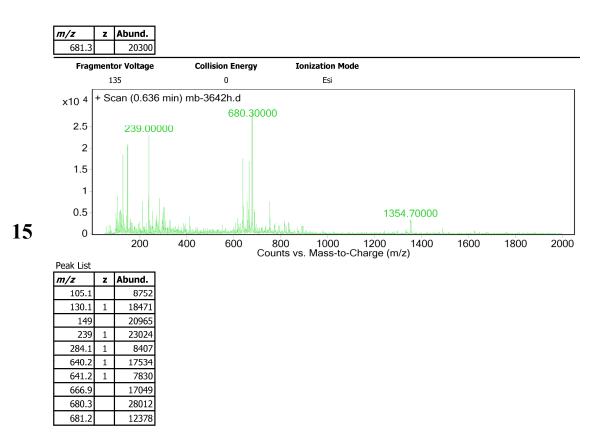


Orn-Trp-Trp-Orn-Trp-Trp-Orn-Orn-NH<sub>2</sub>;

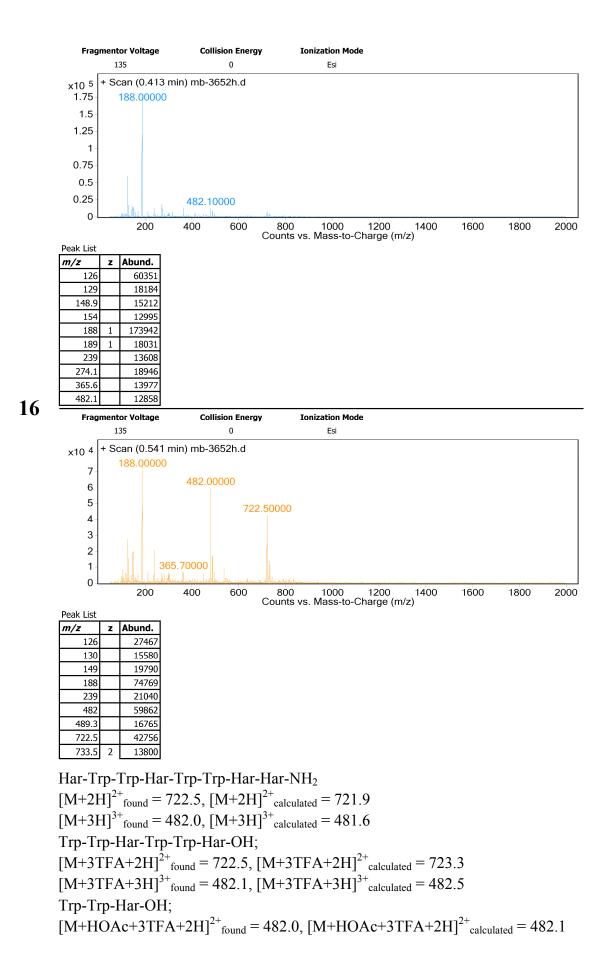
 $[M+TFA+2H]^{2+}_{found} = 666.9, [M+TFA+2H]^{2+}_{calculated} = 666.9$ Trp-Trp-Orn-Trp-Trp-Orn-Orn-NH<sub>2</sub>;  $[M+HOAc+TFA+2H]^{2+}_{found} = 640.3, [M+HOAc+TFA+2H]^{2+}_{calculated} = 639.8$ Trp-Trp-Orn-OH  $[M+HOAc+TFA+H]^{+}_{found} = 680.2, [M+HOAc+TFA+H]^{+}_{calculated} = 679.6$ 

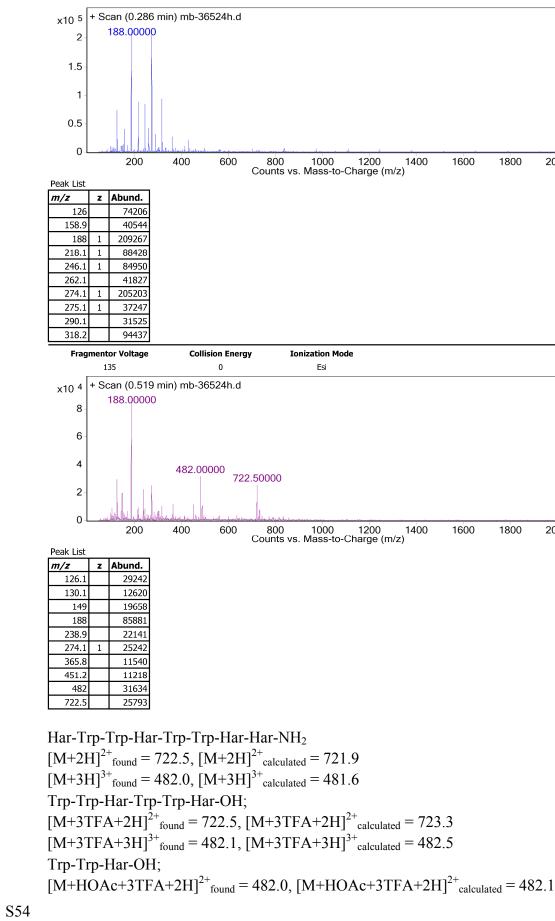


Trp-Trp-Orn-Trp-Trp-Orn-Orn-NH<sub>2</sub>;  $[M+HOAc+TFA+2H]^{2+}_{found} = 640.2$ ,  $[M+HOAc+TFA+2H]^{2+}_{calculated} = 639.8$ Trp-Trp-Orn-OH  $[M+HOAc+TFA+H]^{+}_{found} = 680.2$ ,  $[M+HOAc+TFA+H]^{+}_{calculated} = 679.6$ 



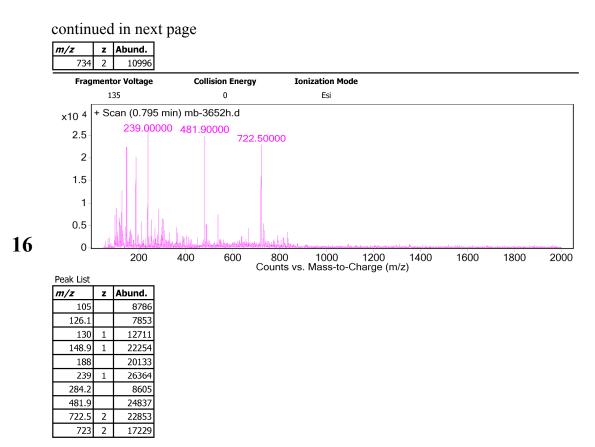
Orn-Trp-Trp-Orn-Trp-Trp-Orn-Orn-NH<sub>2</sub>;  $[M+TFA+2H]^{2+}_{found} = 666.9, [M+TFA+2H]^{2+}_{calculated} = 666.9$ Trp-Trp-Orn-OH  $[M+HOAc+TFA+H]^{+}_{found} = 680.3, [M+HOAc+TFA+H]^{+}_{calculated} = 679.6$ 



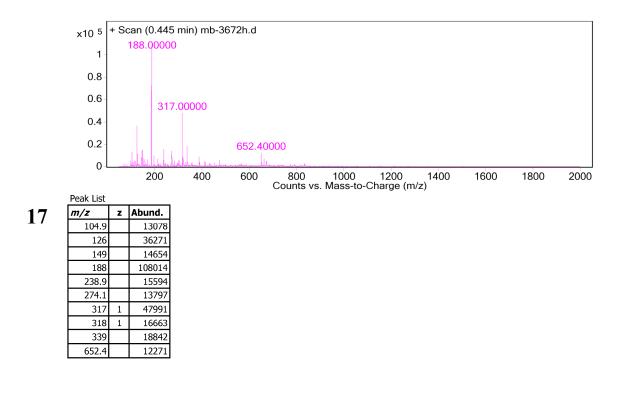


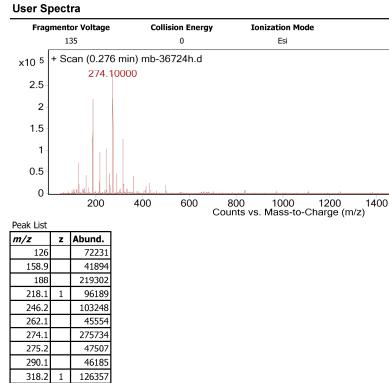
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0 1600 1	800 2000



Har-Trp-Trp-Har-Trp-Trp-Har-Har-NH<sub>2</sub>  $[M+2H]^{2+}_{found} = 722.5, [M+2H]^{2+}_{calculated} = 721.9$   $[M+3H]^{3+}_{found} = 481.9, [M+3H]^{3+}_{calculated} = 481.6$ Trp-Trp-Har-Trp-Trp-Har-Har-NH<sub>2</sub>;  $[M+HOAc+TFA+2H]^{2+}_{found} = 723.0, [M+HOAc+TFA+2H]^{2+}_{calculated} = 723.8$ 

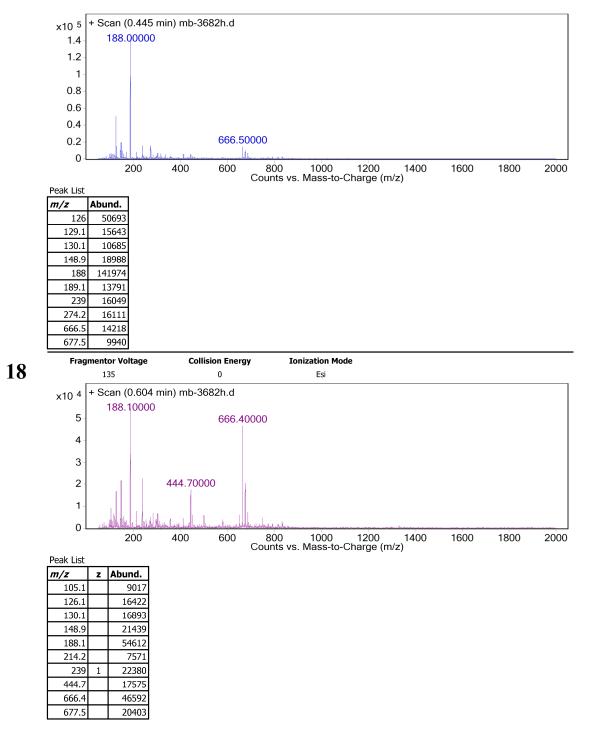




Har-Trp-Trp-Dab-Trp-Trp-Har-Har-NH<sub>2</sub>;  $[M+4HOAc+3TFA+3H]^{3+}_{found} = 652.4, [M+4HOAc+3TFA+3H]^{3+}_{calculated} = 652.5$ 

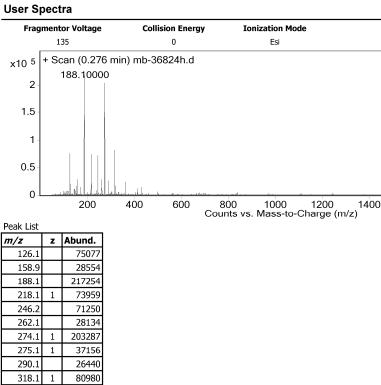
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Trp-Trp-Orn-Trp-Trp-Har-Har-NH<sub>2</sub>

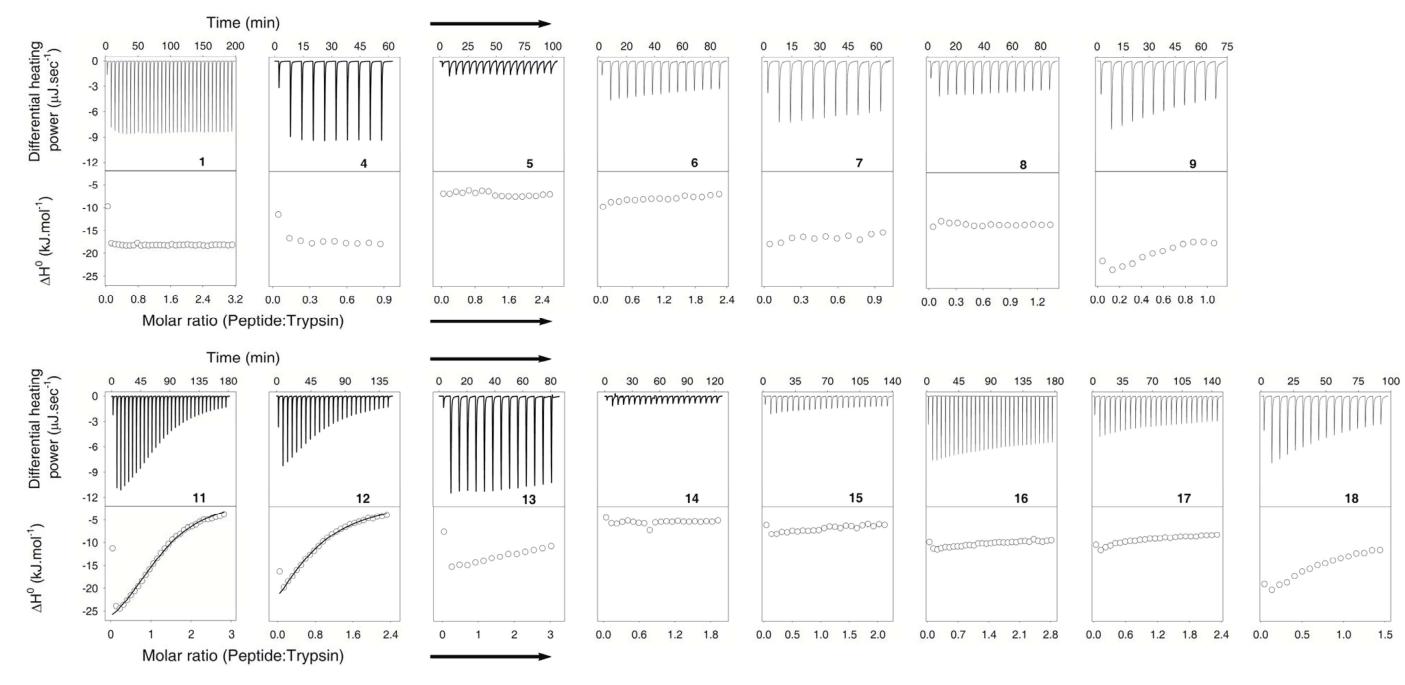
 $[M+TFA+2H]^{2+}_{found} = 666.4, [M+TFA+2H]^{2+}_{calculated} = 666.2$  $[M+TFA+3H]^{3+}_{found} = 444.7, [M+TFA+3H]^{3+}_{calculated} = 444.5$ 



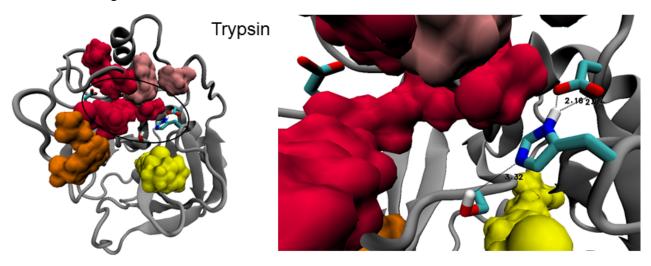
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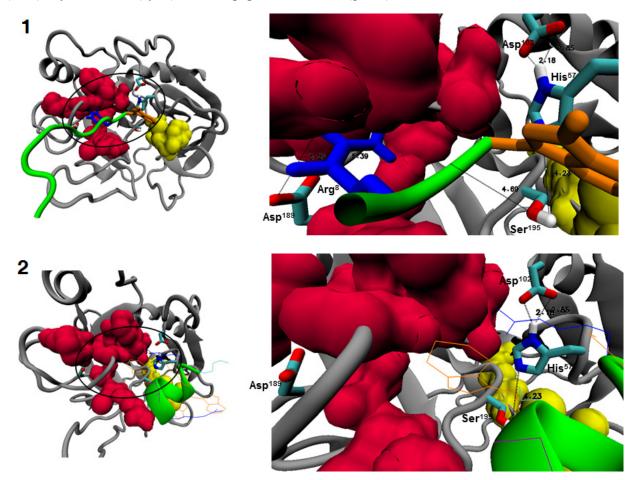
Figure S7. The raw ITC data (power vs. time) and the integrated data for injection of the 1 and 10 derived peptides into the calorimeter cell containing trypsin at 310 °K. The fit parameters are  $\Delta H^\circ = -34.6 \text{ kJ.mol}^{-1}$ ,  $T\Delta S^\circ = -$ 1.2 kJ.mol<sup>-1</sup>,  $K^{\circ} = 2.4 \times 10^{+4} M^{-1}$ , n = 1.3 for **11** and  $\Delta H^{\circ} = -49.4 kJ.mol<sup>-1</sup>$ ,  $T\Delta S^{\circ} = -3.3 kJ.mol<sup>-1</sup>$ ,  $K^{\circ} = 1.1 \times 10^{+4} M^{-1}$ , n = 0.7 for **12**.

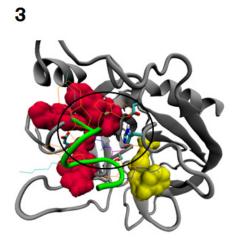


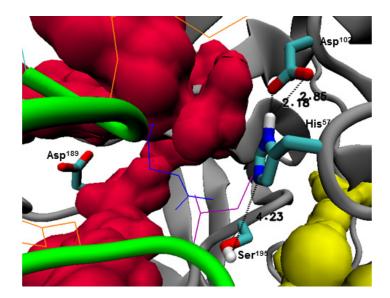
*Figure S8. The representative structure of trypsin used in the docking studies*. The structure with the highest percentage of occurrence generated from cluster analysis of trypsin (PDB ID: 4I8G) MD simulation in water for 20 ns. The left image shows enzyme binding pockets; e.g., S1 (composed of amino acid residues 189-192, 214-216, 224-228), S1' (composed of amino acid residues 41-45), S2 (composed of amino acid residues 57, 215, 99) and S2' (composed of amino acid residues 142-143, 151) in red, yellow, pink and orange colors, respectively. The right image shows the position of histidine-57, aspartate-102 and serin-195 in the enzyme catalytic triad with respect to aspartate-189 in the S1 binding site.

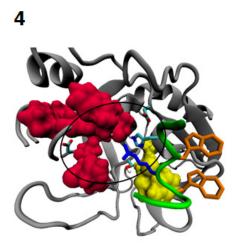


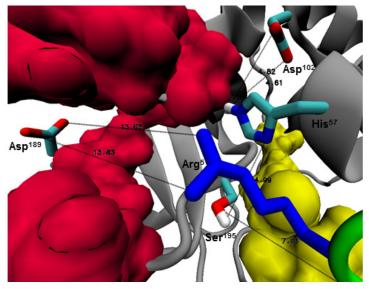
*Figure S9. The molecular docked models of synthetic bactenecin 1 and its analogues with trypsin*. The left image is the interaction mode between the peptides and trypsin and right panel is the inset shows the interaction from a close view. The enzyme binding pockets S1 (red color) and S1' (yellow color) are shown here. The colors in the peptide structures define as follow: Trp (orange), Ile (violet), Arg/Har (blue), Lys/Dab/Orn (cyan), and the peptide backbone (green).



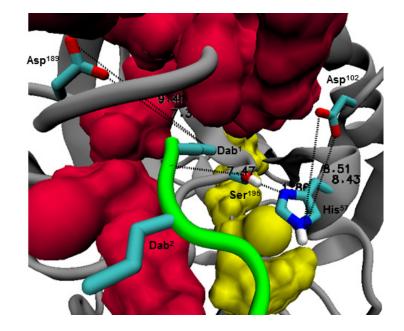


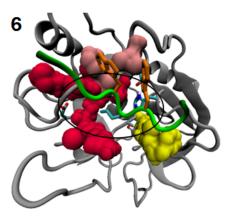


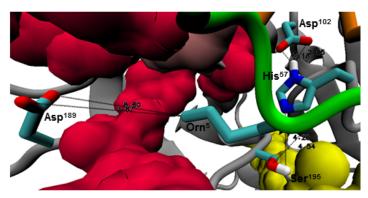


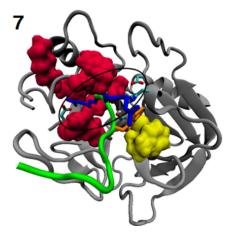


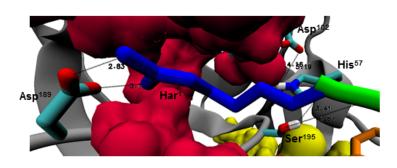
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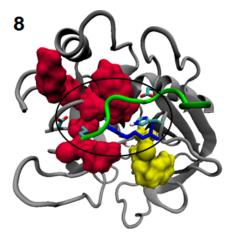


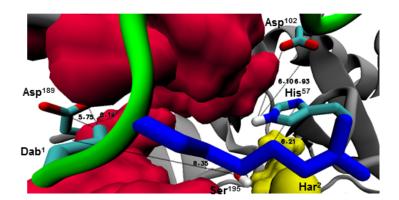


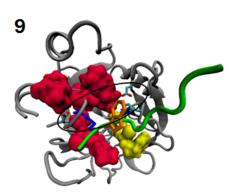


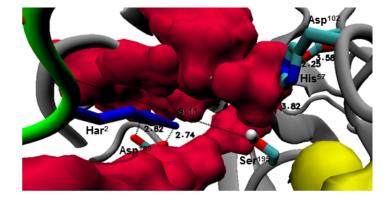












*Figure S10. The molecular docked model of synthetic bactenecin 10 and its analogues with trypsin.* The left image is the interaction mode between the peptides and trypsin and right panel is the inset shows the interaction from a close view. The enzyme binding pockets S1 (red color) and S1' (yellow color) are shown here. The colors in the peptide structures define as follow: Trp (orange), Arg/Har (blue), Lys/Dab/Orn (cyan) and the peptide backbone (green).

