

SUPPLEMENTARY MATERIALS

Rational design of novel peptidomimetics against Influenza A virus: biological and computational studies

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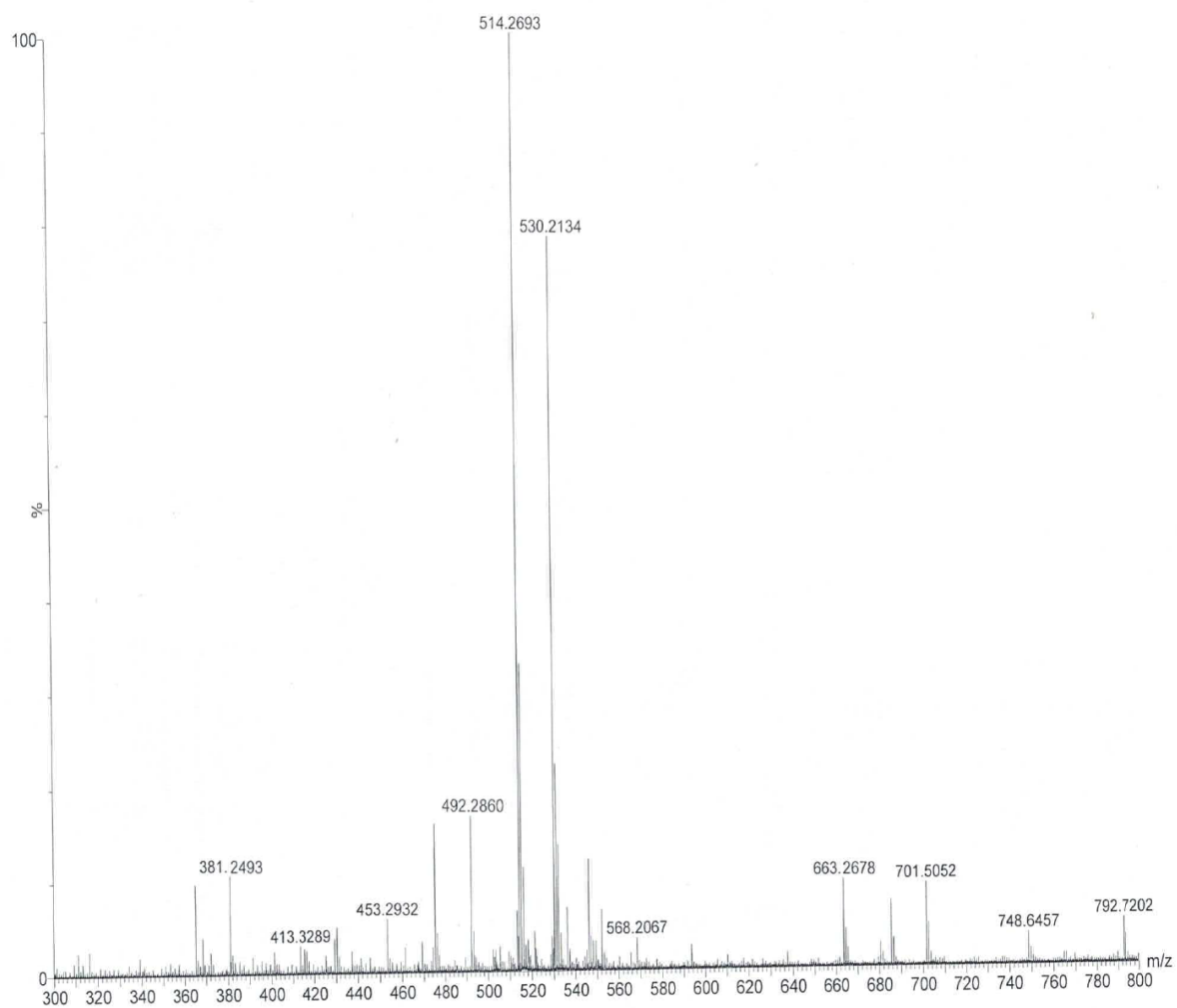
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Table S1. Analytical data of peptides **3-18**.

Pep.	Sequence	HPLC k'^a	HRMS
1^b	SLDC	3.93	477.18970
2^b	SKHS	4.68	499.26235
3	(N-Me)SLDC	8.00	492.2860
4	S(N-Me)LDC	9.33	492.2727
5	SL(N-Me)DC	5.20	493.9463
6	SLD(N-Me)C	10.50	492.9463
7	(N-Me)SKHS	7.88	513.2344
8	S(N-Me)KHS	0.44	513.2260
9	SK(N-Me)HS	0.50	513.2026
10	SKH(N-Me)S	0.58	513.2427
11	NhSLDC	4.55	492.2759
12	SMLDC	4.75	478.1846
13	SLNDC	1.15	478.3001
14	SLDNhC	1.10	493.2882
15	NhSKHS	1.15	513.2335
16	SNKHS	1.40	499.2022
17	SKNHS	2.40	498.9463
18	SKHNhS	1.20	513.2522

^a k'=[(peptide retention time-solvent retention time)/solvent retention time]; ^b Scala et al. (2017).

Supplementary figures of Mass spectrometry and HPLC of peptides used in the study



Datafile Name: Peptide 3

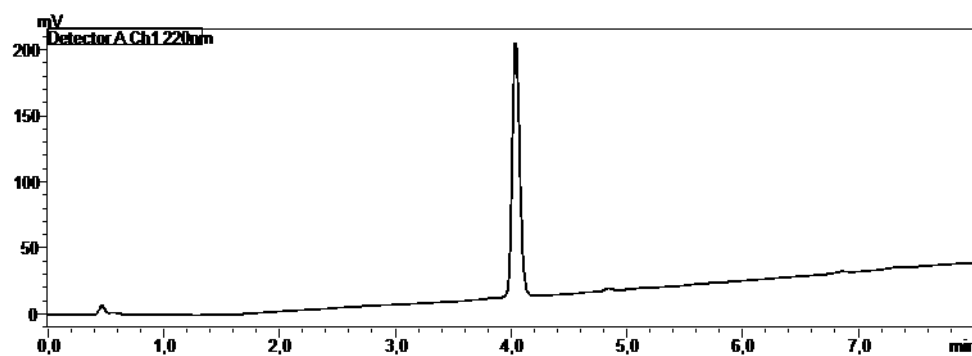


Figure S1. HR-ESI-MS of Peptide 3 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.

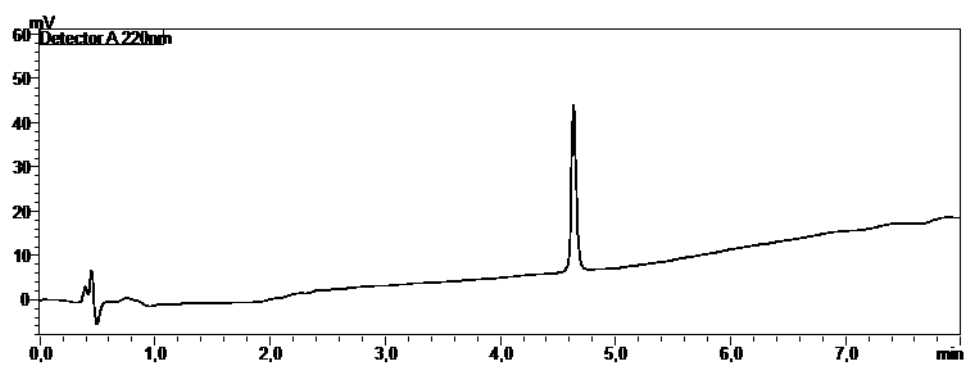
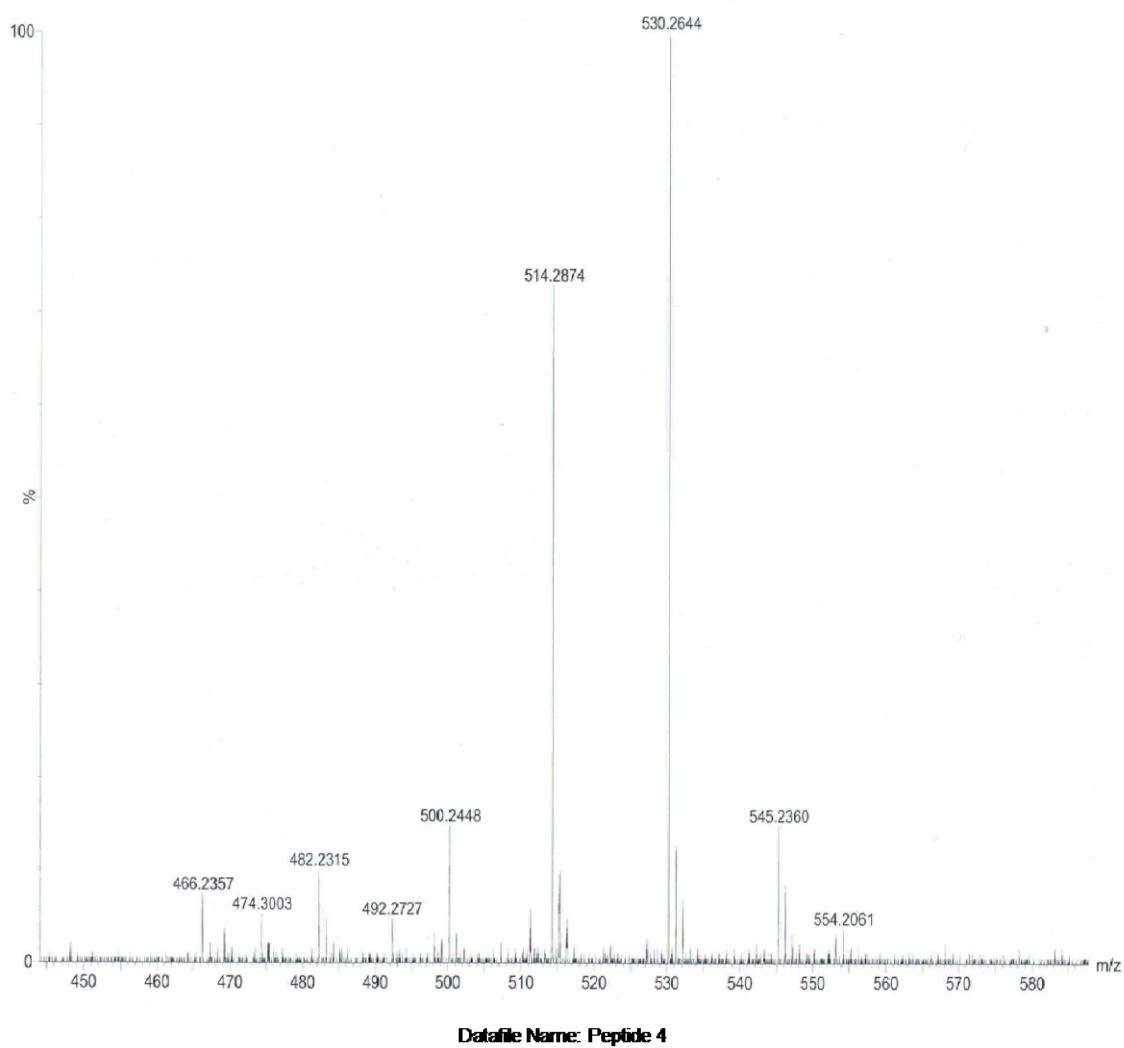


Figure S2. HR-ESI-MS of Peptide 4 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.

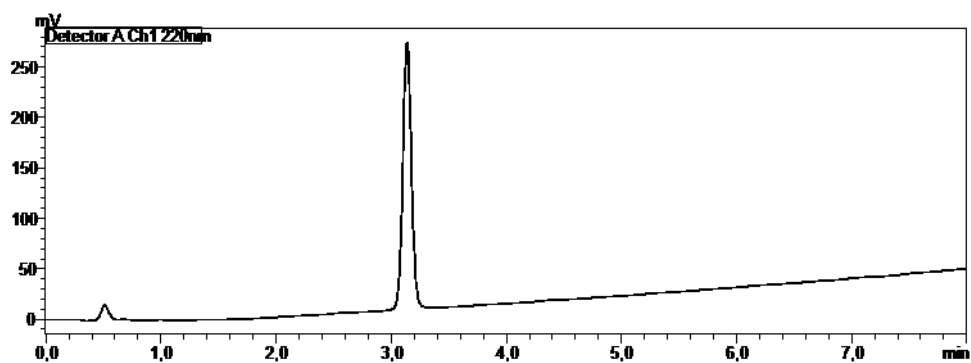
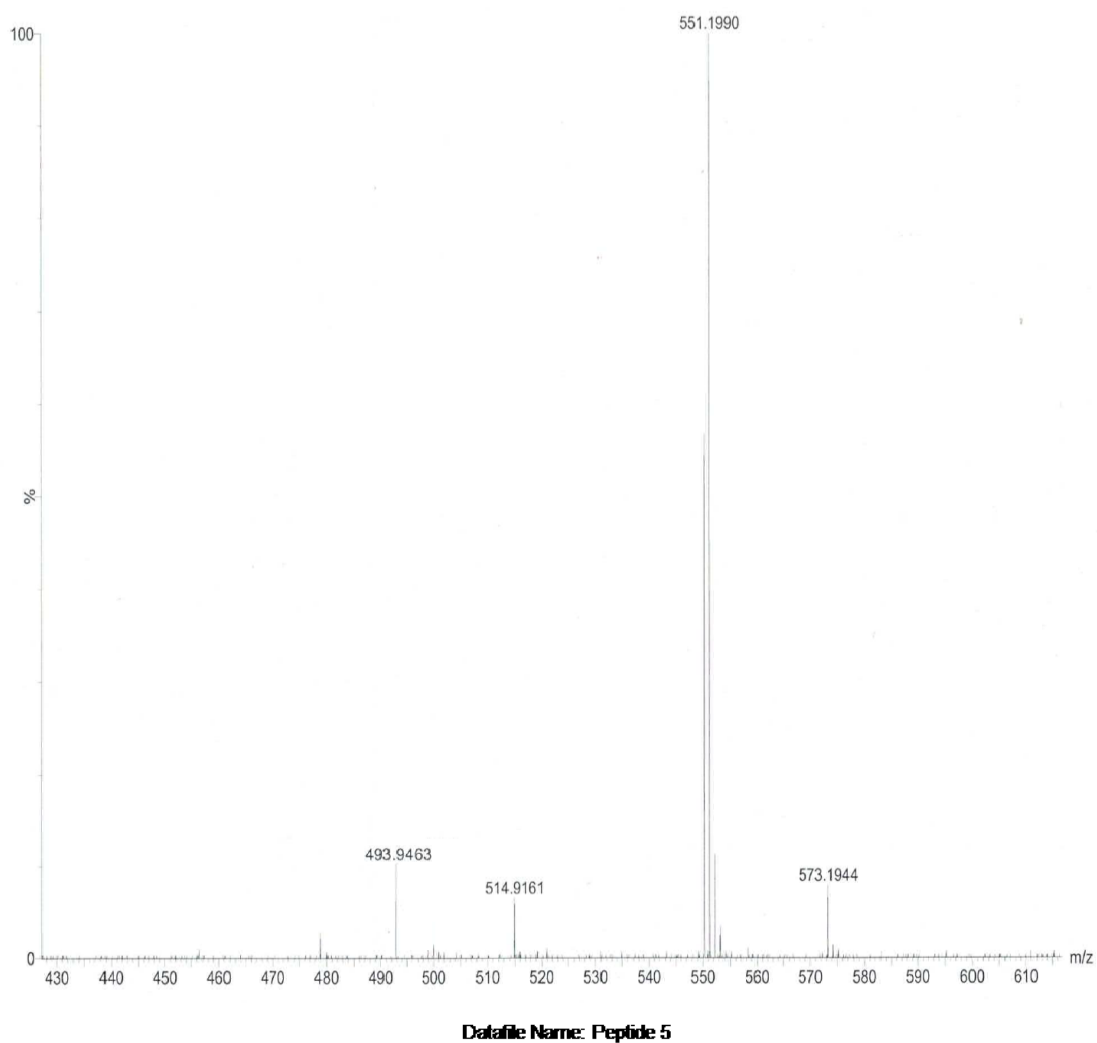


Figure S3. HR-ESI-MS of Peptide **5** ion $[M+H]^+$ and analytical HPLC trace at 220 nm.

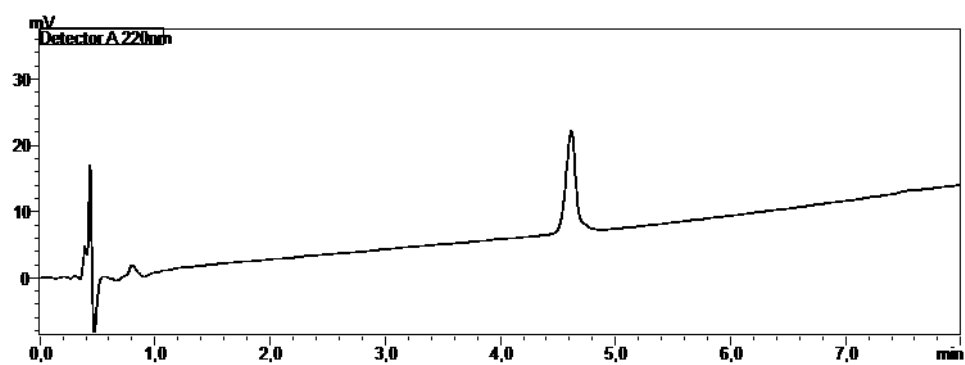
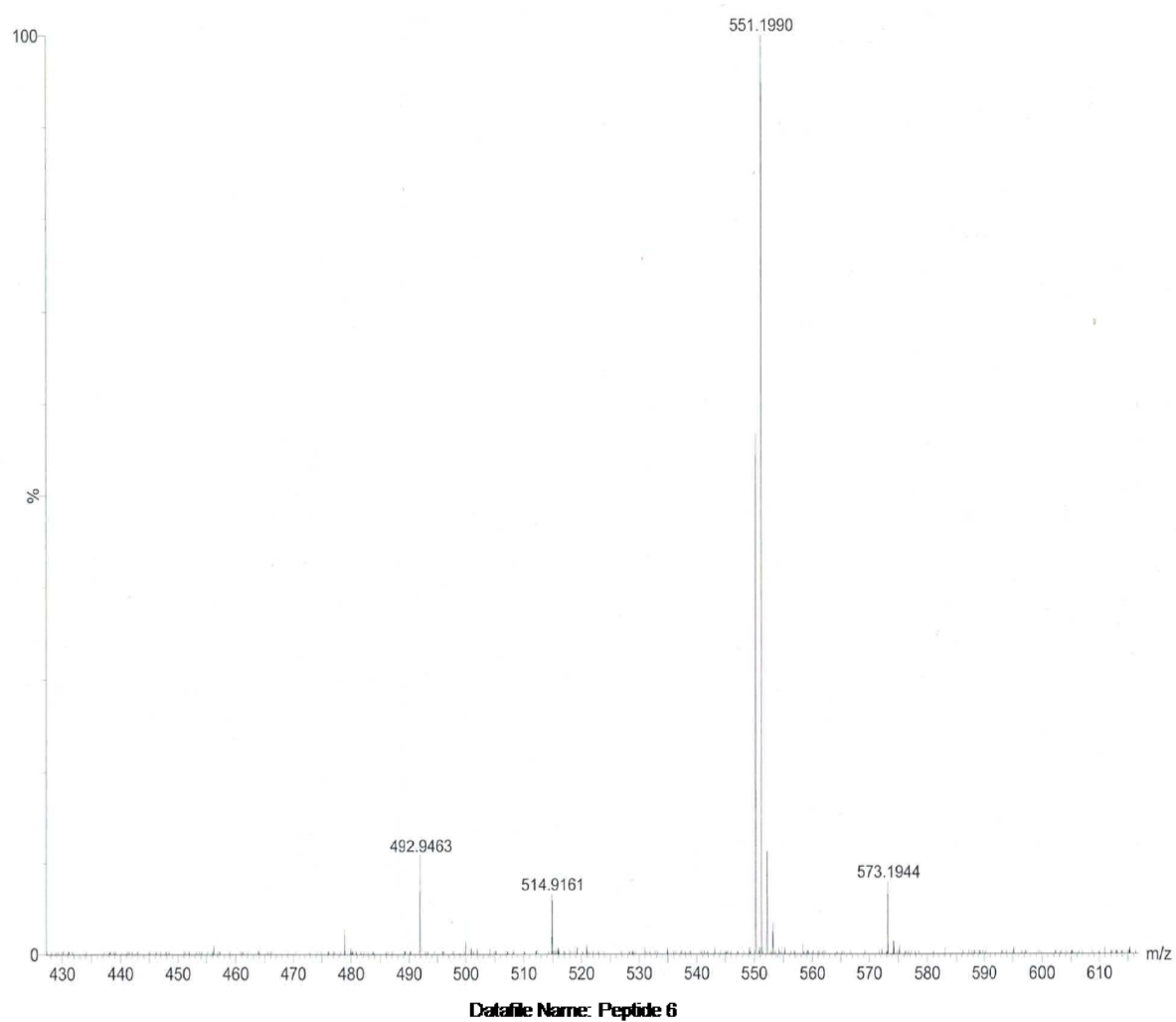
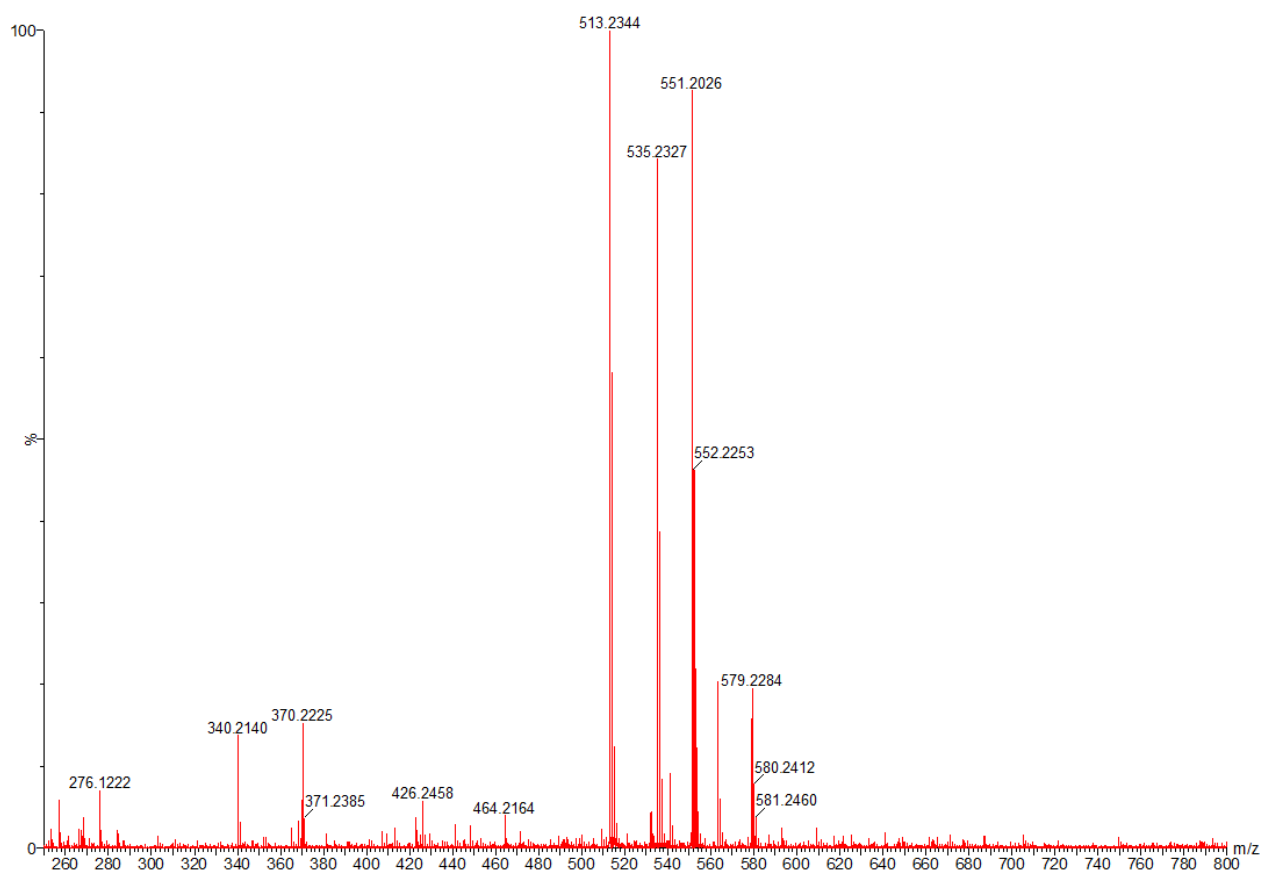


Figure S4. HR-ESI-MS of Peptide 6 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.



Datafile Name: Peptide 7

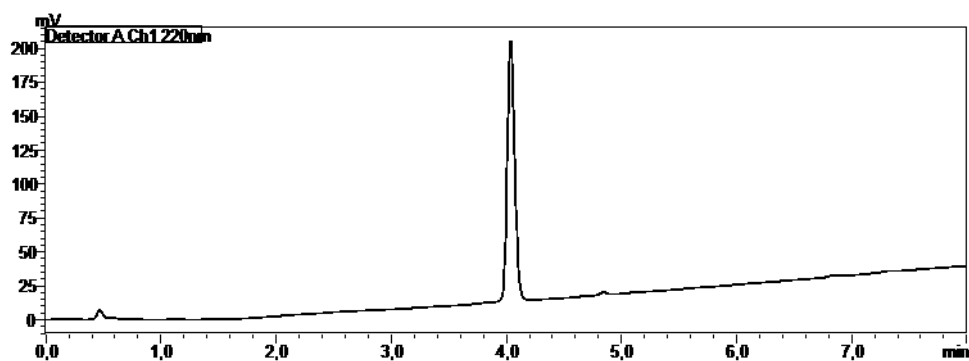
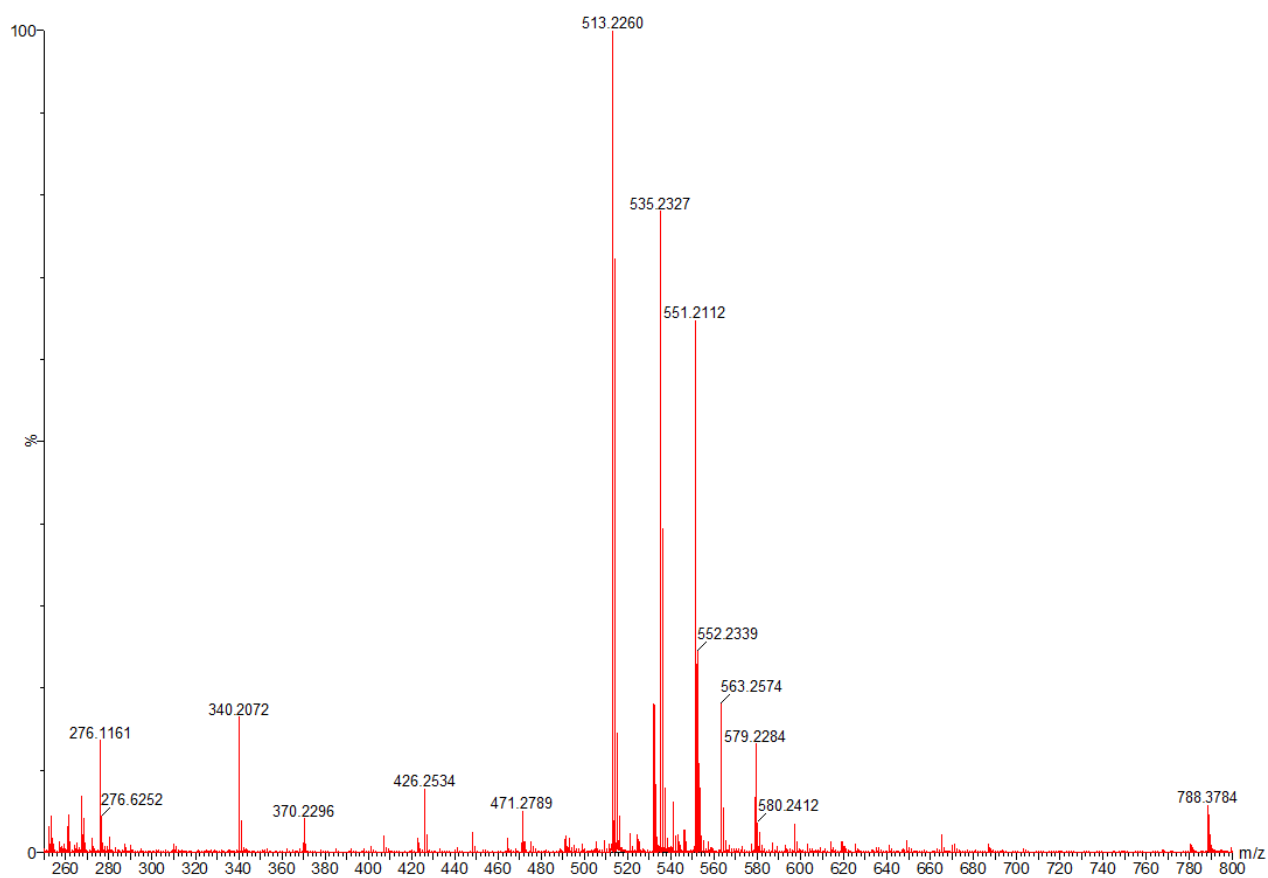


Figure S5. HR-ESI-MS of Peptide 7 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.



Datafile Name: Peptide 8

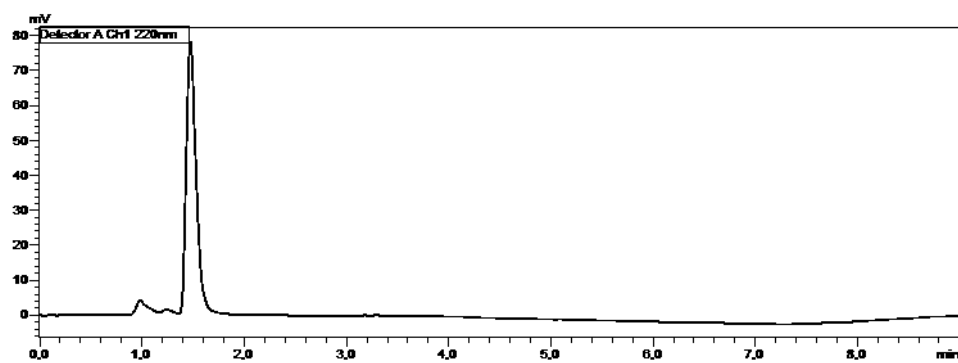
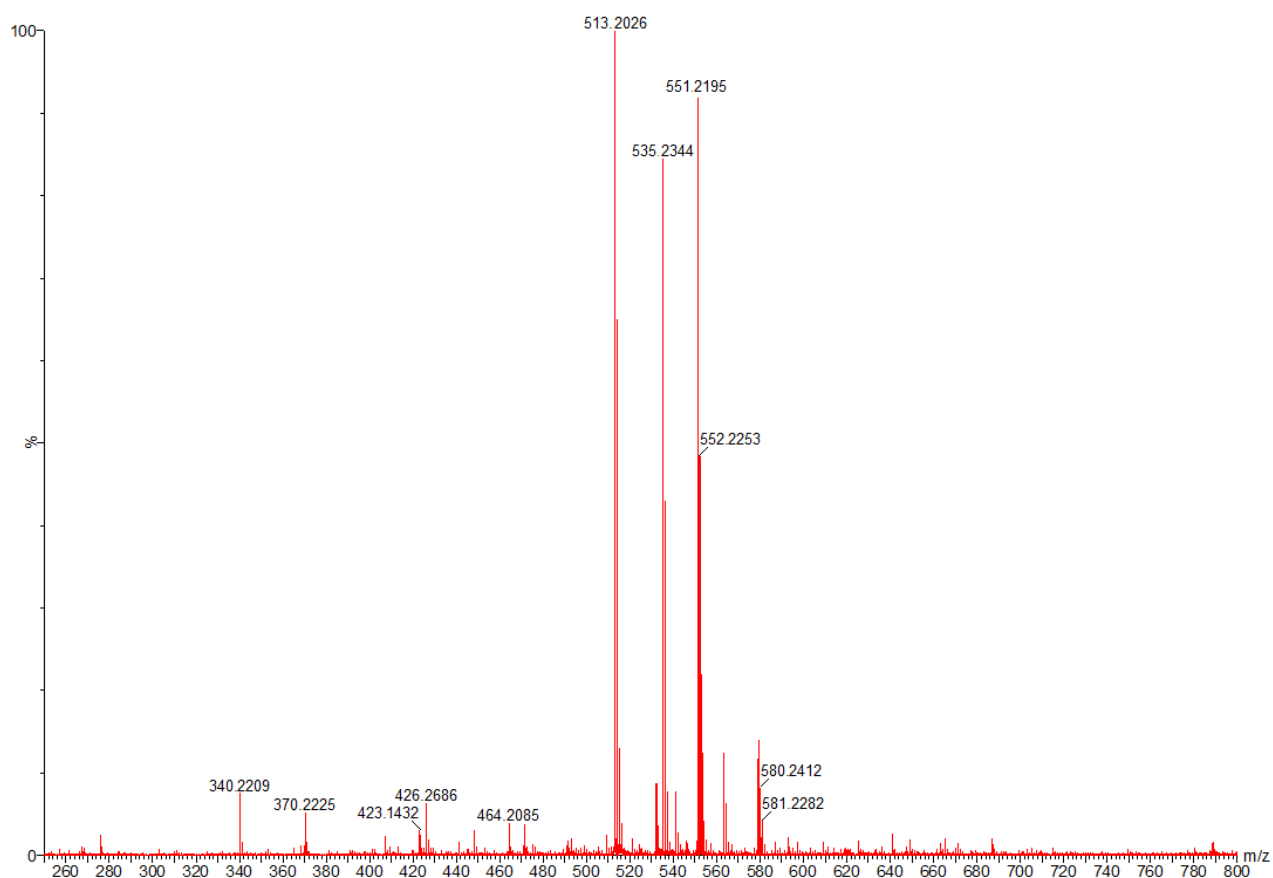


Figure S6. HR-ESI-MS of Peptide 8 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.



Datafile Name: Peptide 9

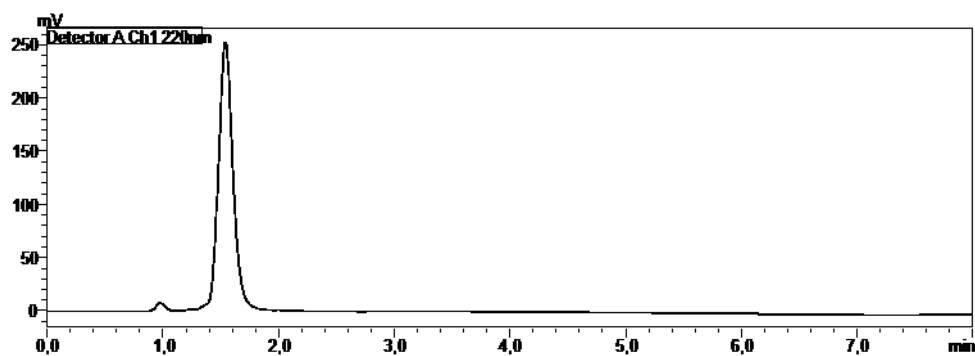


Figure S7. HR-ESI-MS of Peptide 9 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.

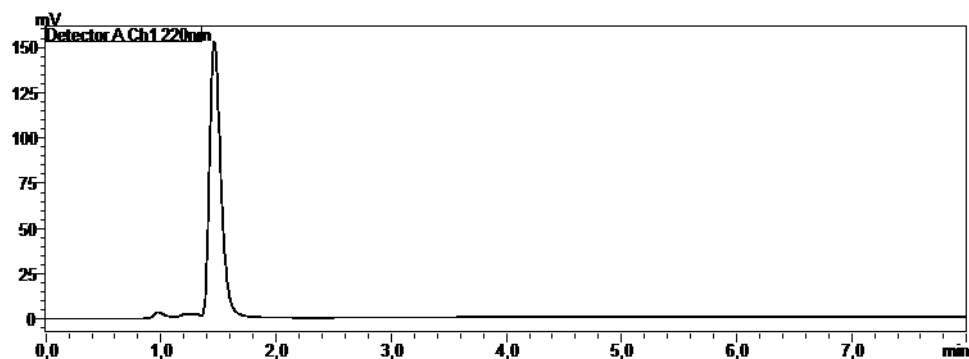
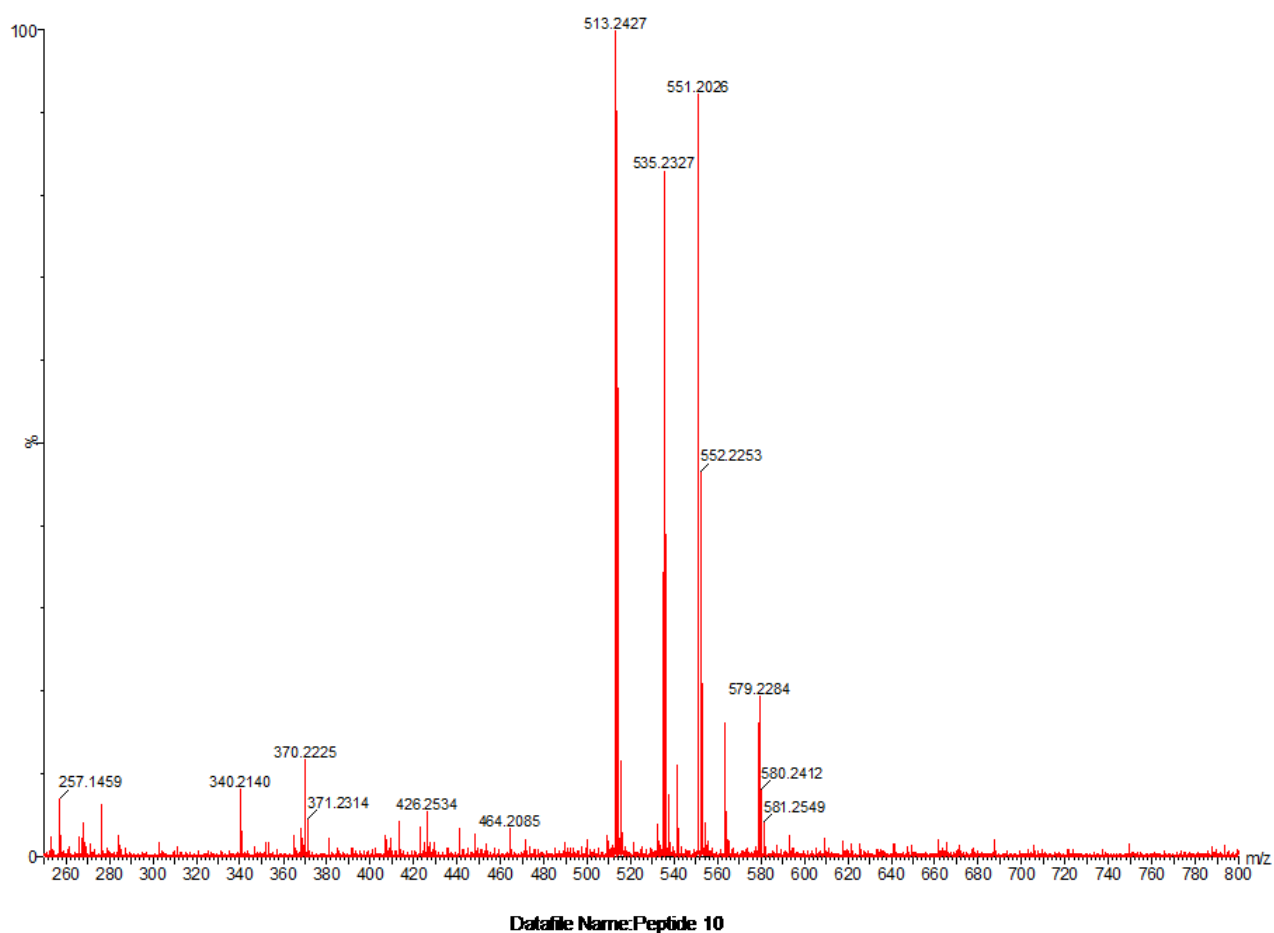
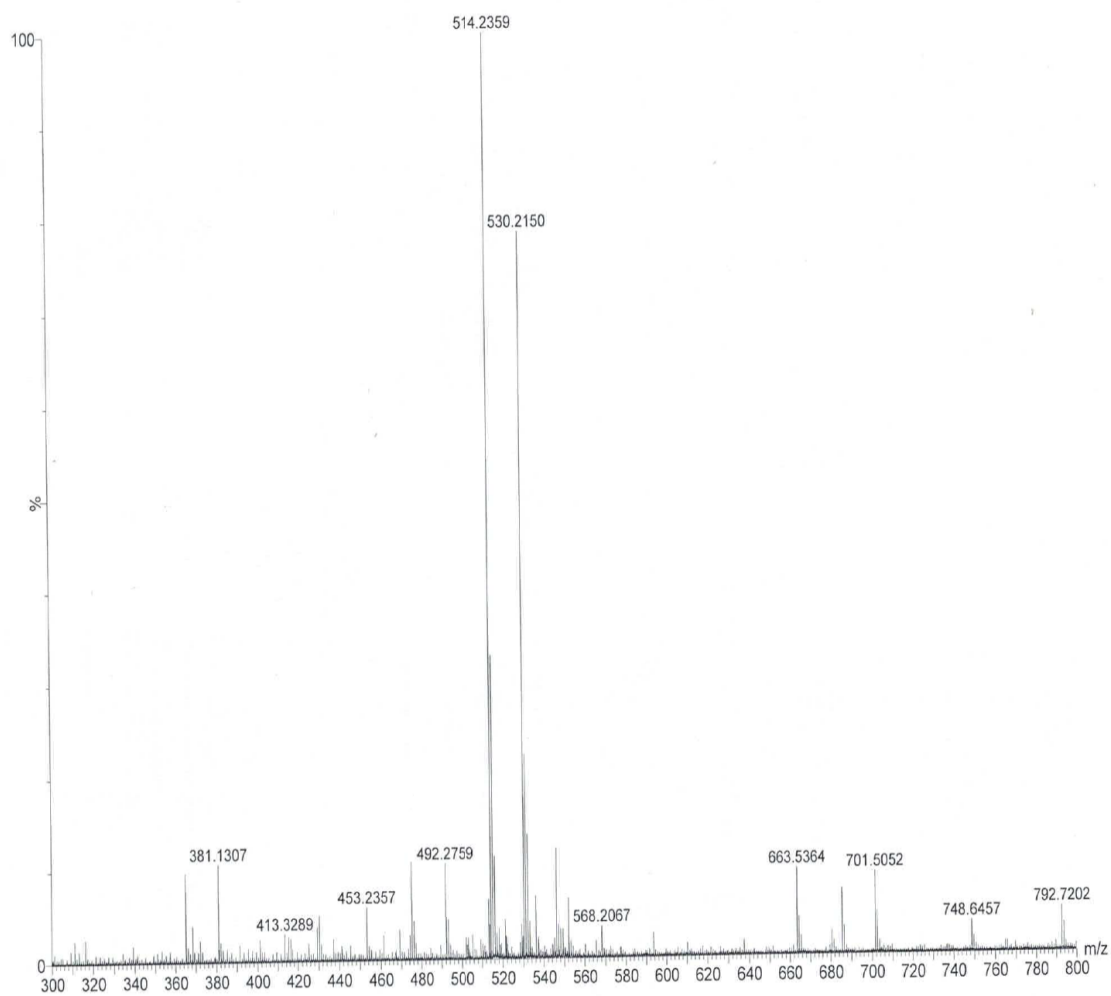


Figure S8. HR-ESI-MS of Peptide 10 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.



Datafile Name: Peptide 11

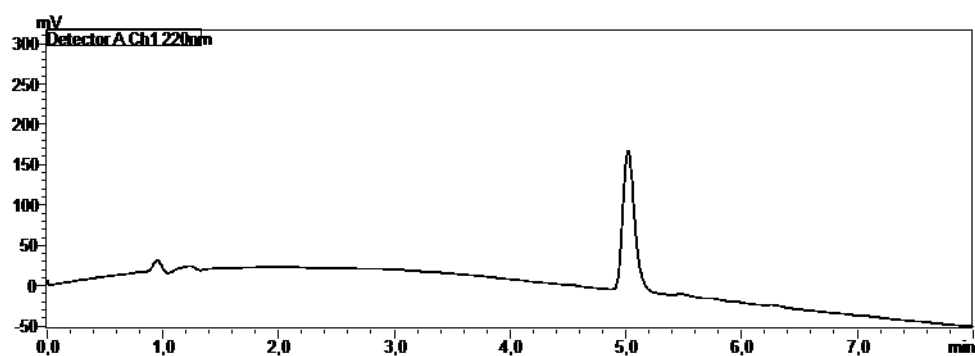
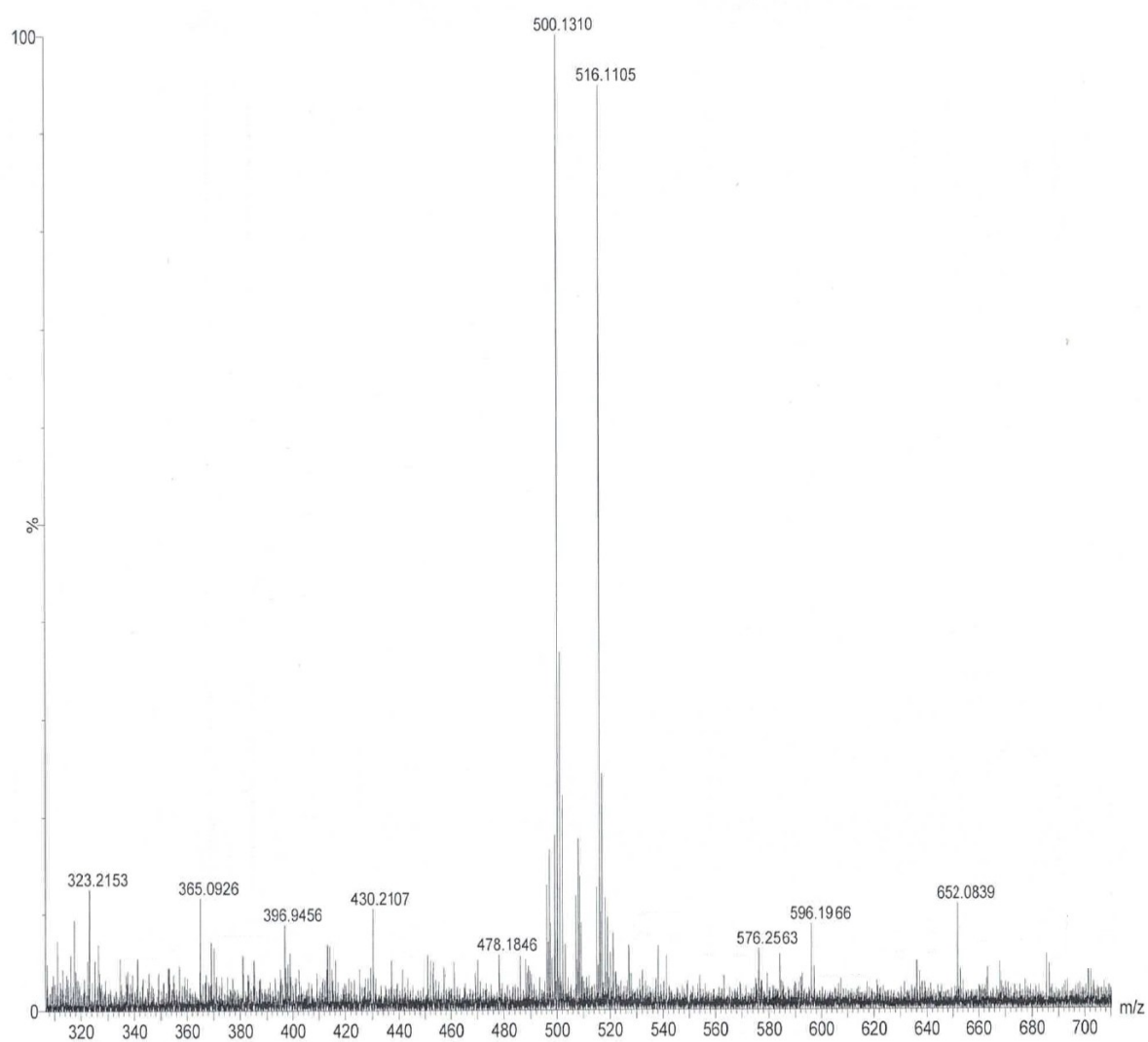


Figure S9. HR-ESI-MS of Peptide 11 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.



Datafile Name: Peptide 12

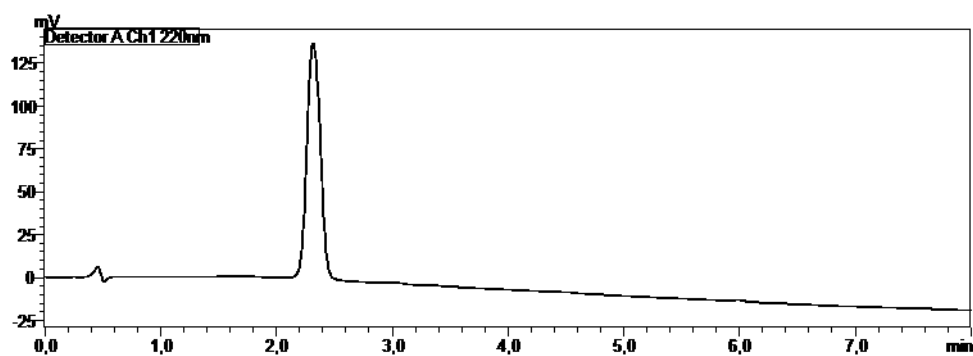
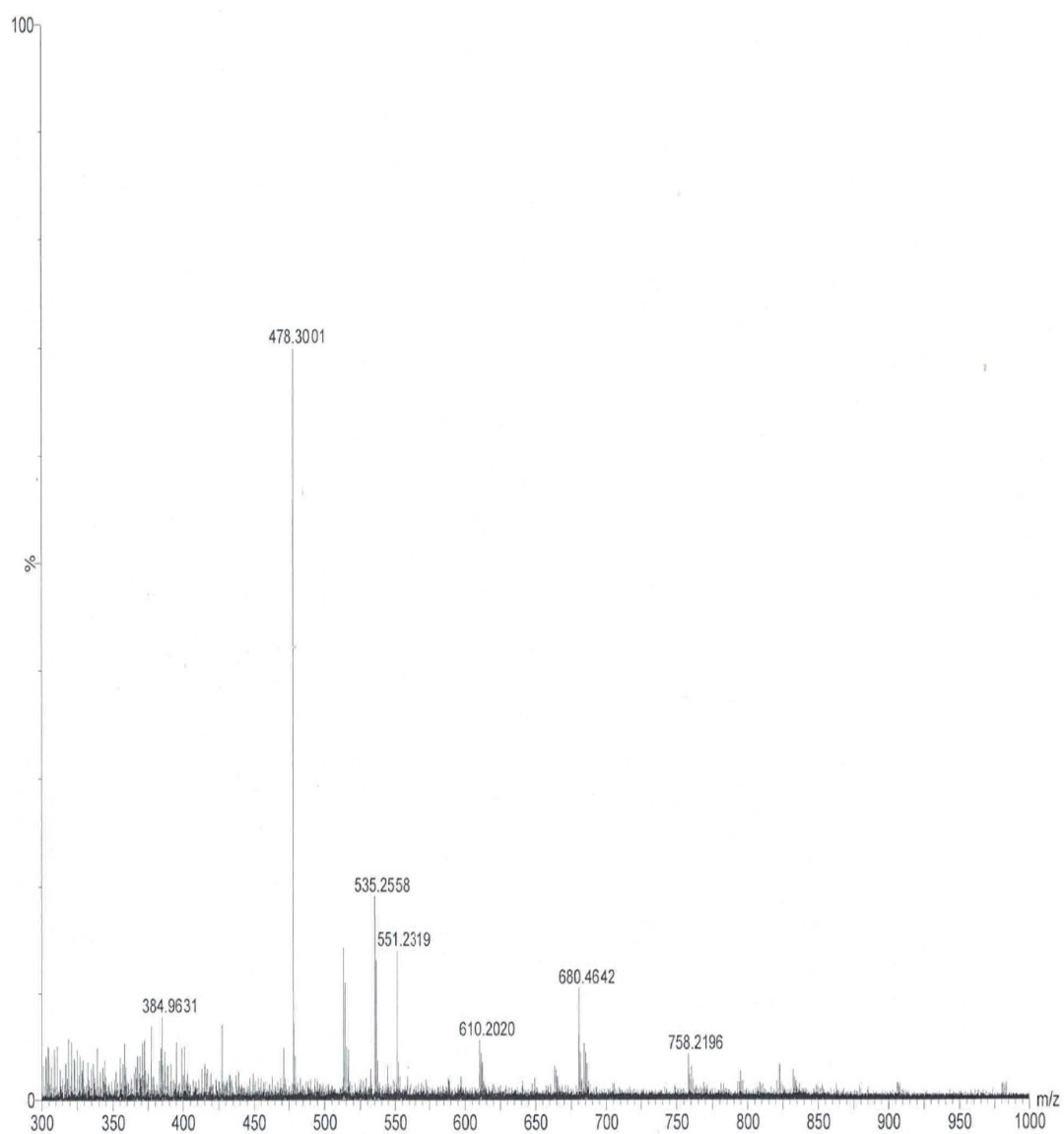


Figure S10. HR-ESI-MS of Peptide 12 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.



Datafile Name: Peptide 13

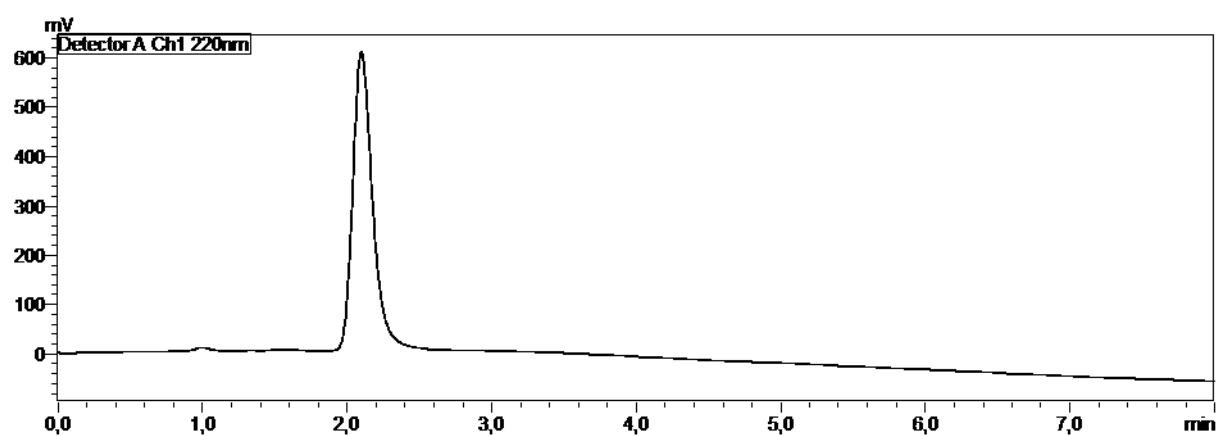
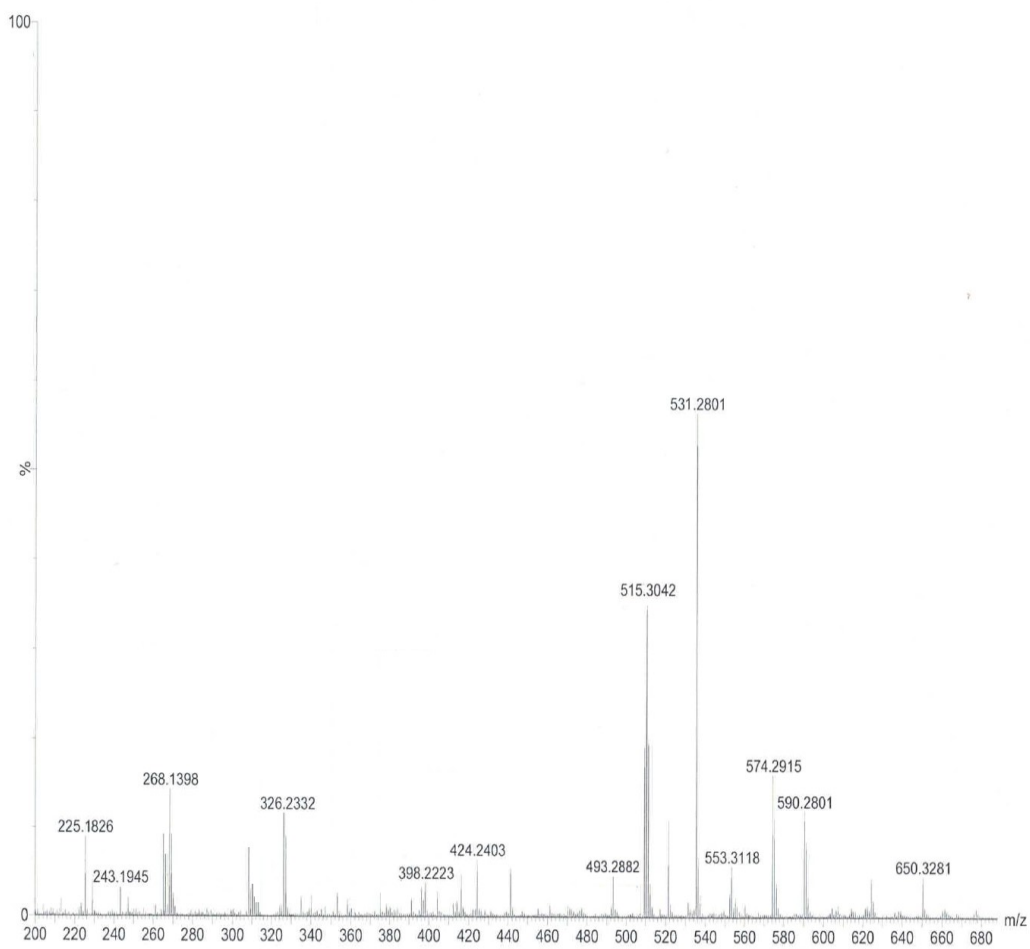


Figure S11. HR-ESI-MS of Peptide 13 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.



Datafile Name: Peptide 14

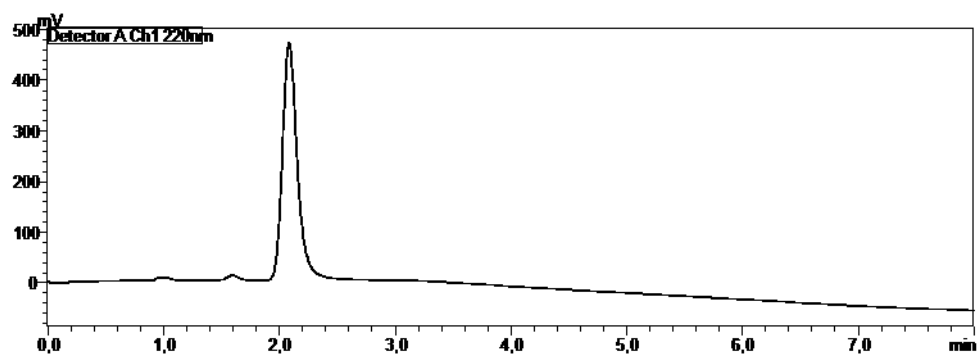


Figure S12. HR-ESI-MS of Peptide 14 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.

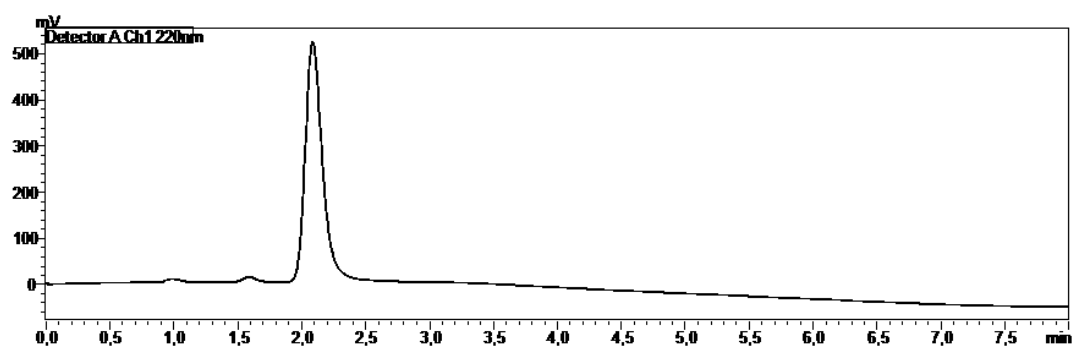
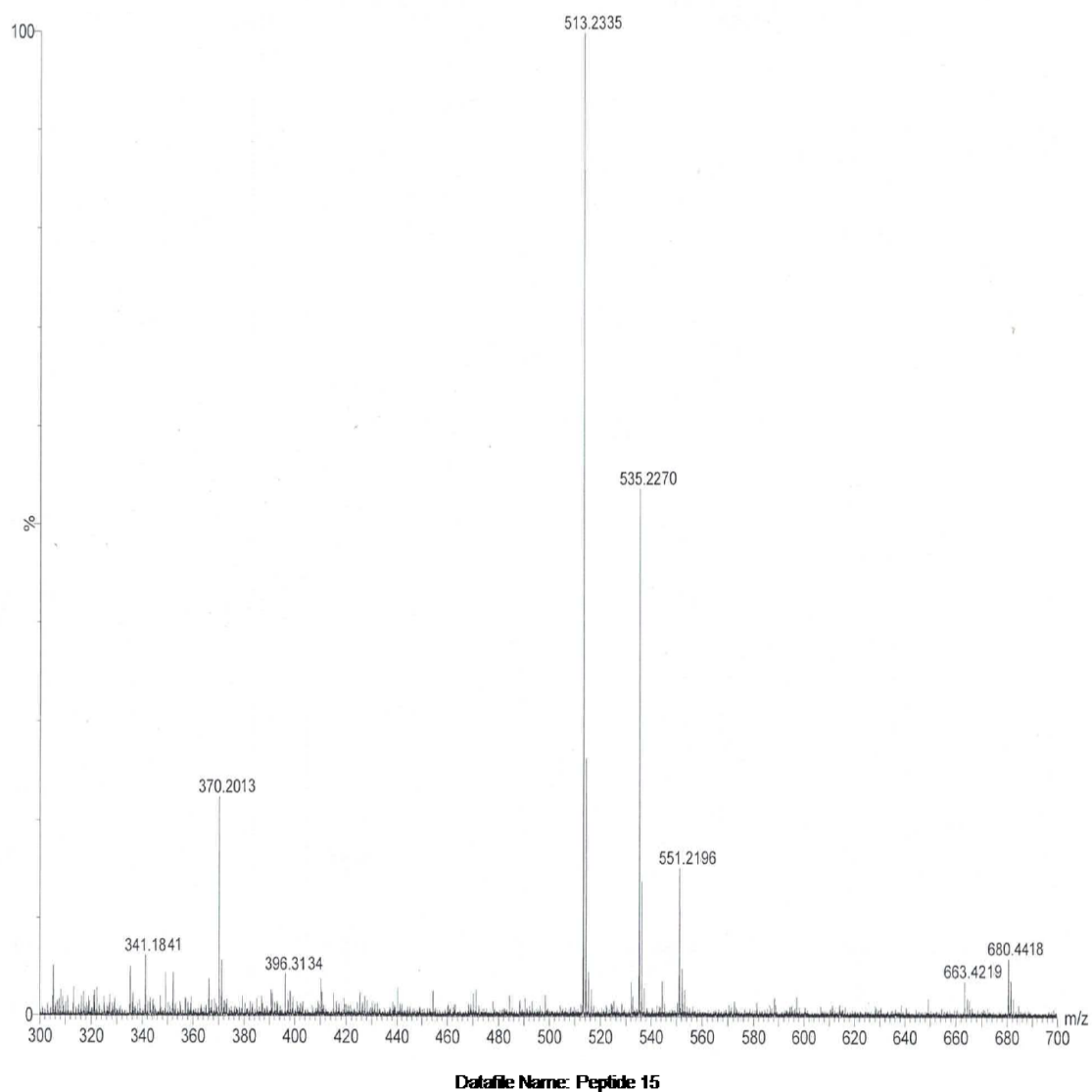


Figure S13. HR-ESI-MS of Peptide 15 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.

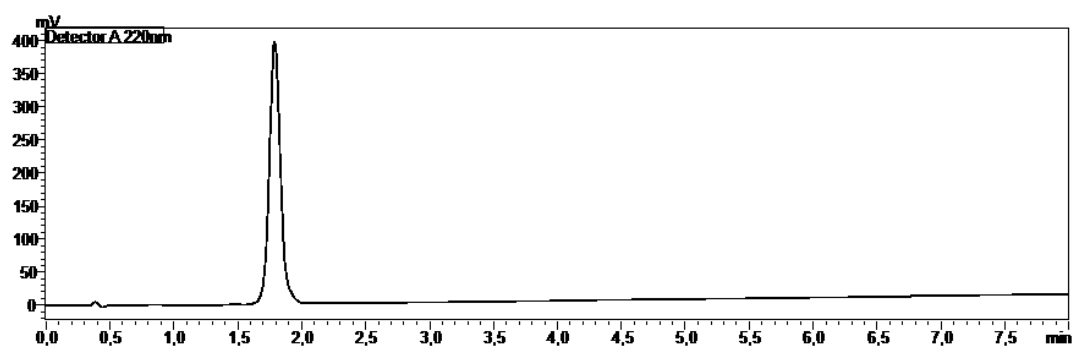
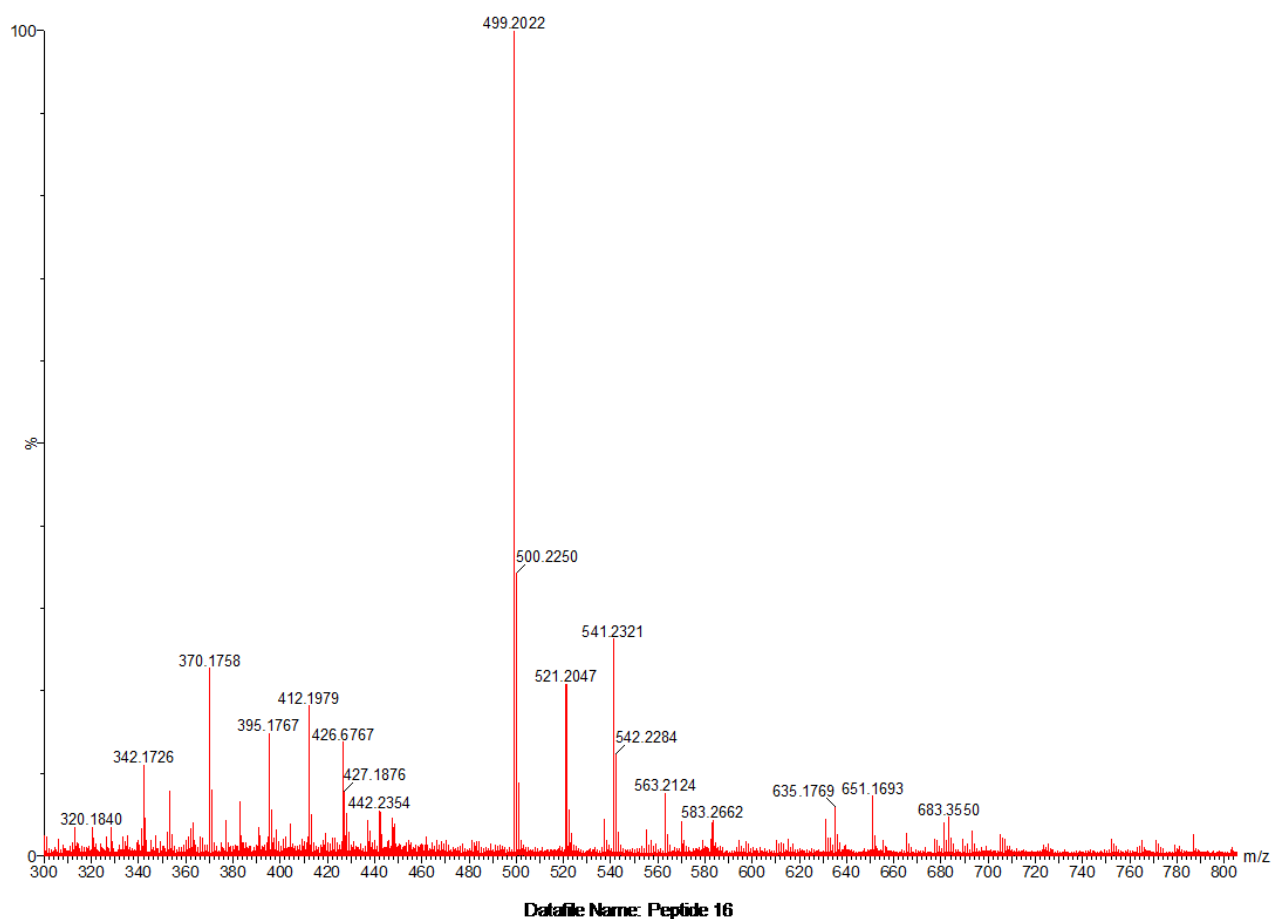


Figure S14. HR-ESI-MS of Peptide 16 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.

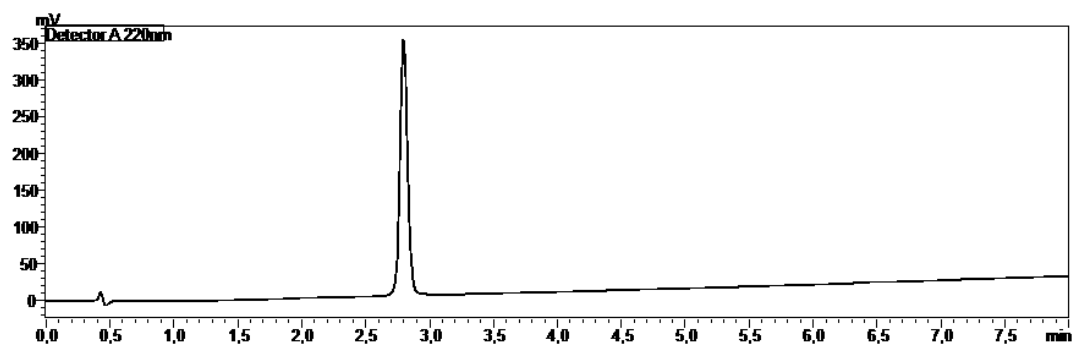
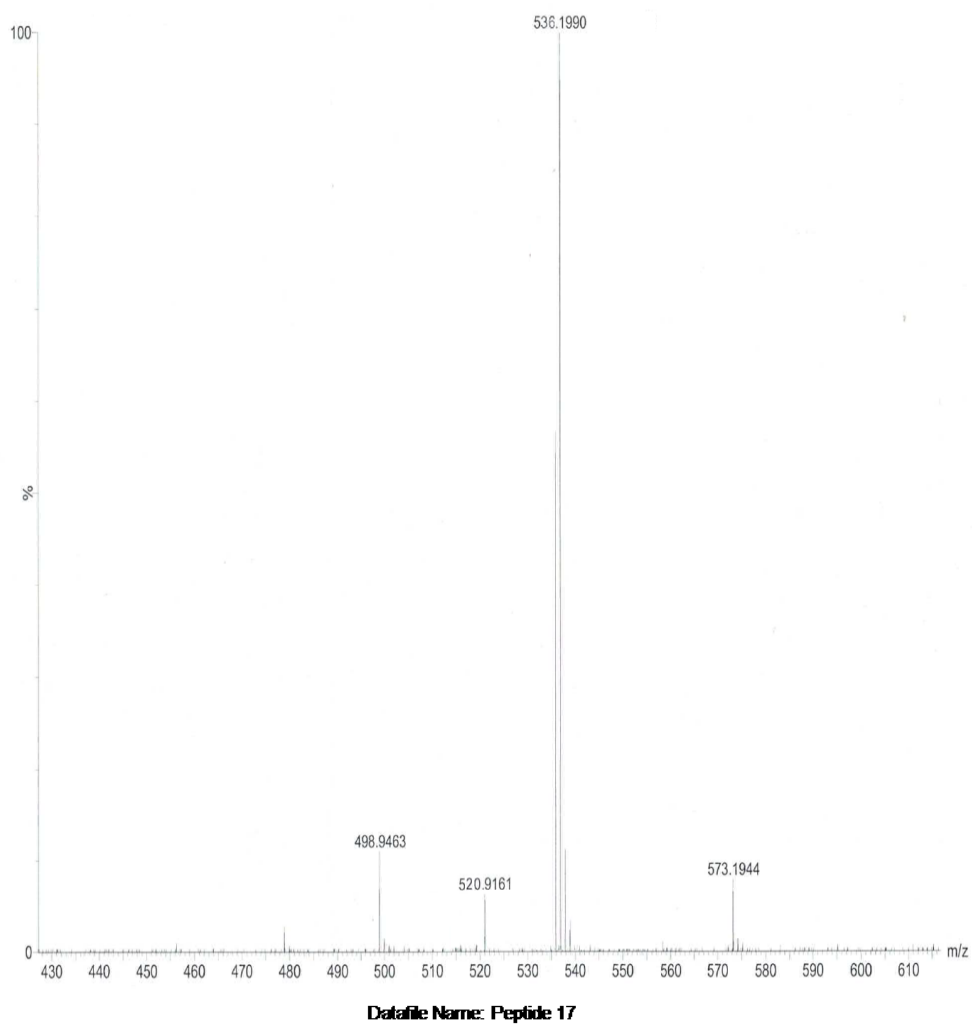


Figure S15. HR-ESI-MS of Peptide 17 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.

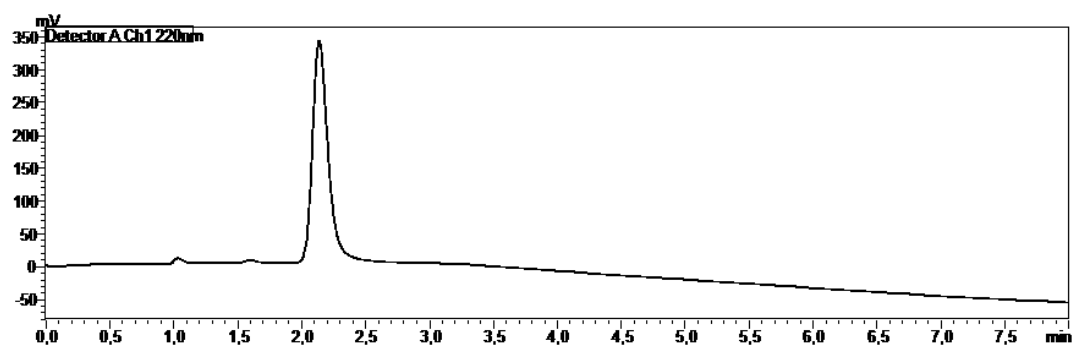
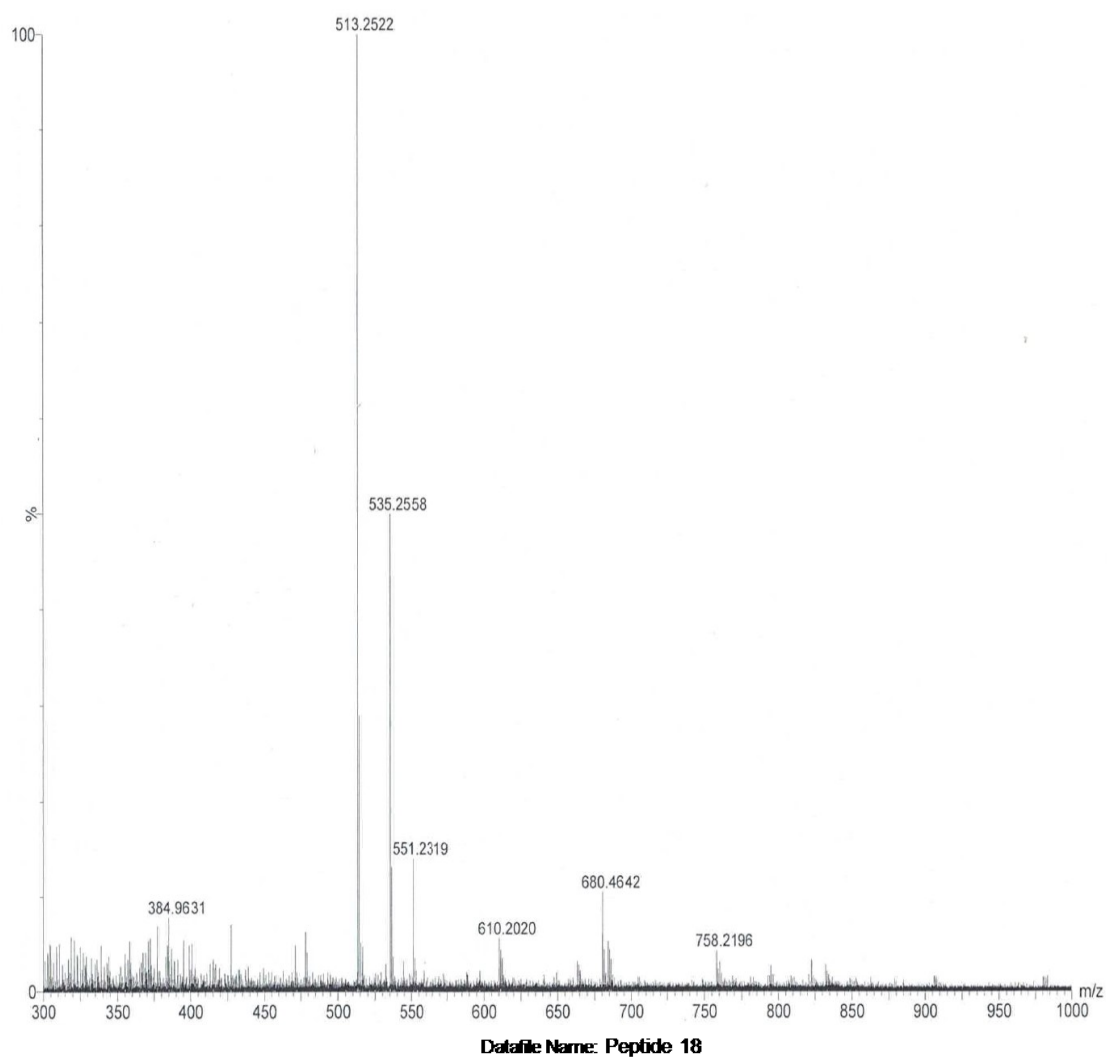


Figure S16. HR-ESI-MS of Peptide 18 ion $[M+H]^+$ and analytical HPLC trace at 220 nm.

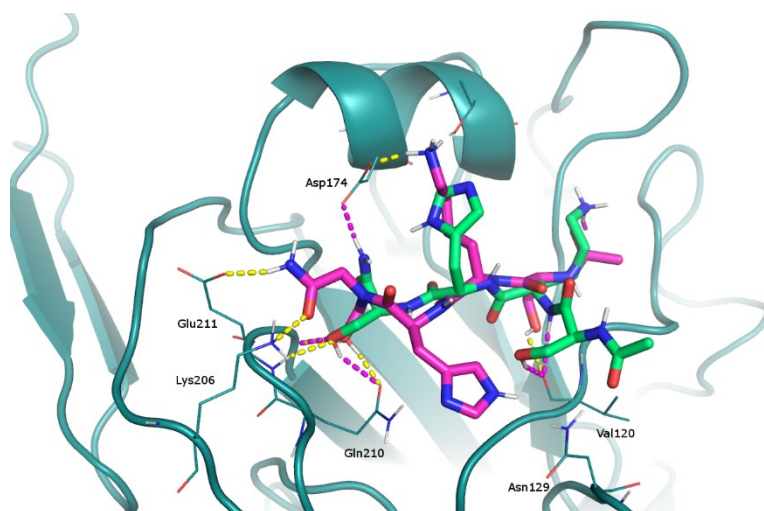


Figure S17. Superimposition of the docked poses of peptoid **18** and reference tetrapeptide **2** represented as sticks (magenta and green C atoms, respectively) in the RBS of A/Parma/24/09 H1N1 (deep-cyan cartoon). Just the HA residues that interact with the ligands are shown as lines for clarity's sake. H-bonds are represented as yellow dashed lines for ligand **18** and magenta for ligand **2**.

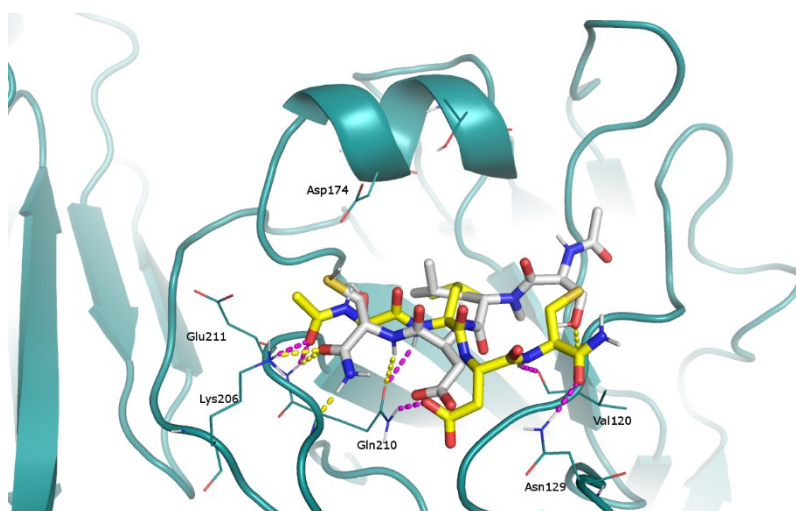


Figure S18. Superimposition of the docked poses of N-methyl peptides **4** and reference tetrapeptide **1** represented as sticks (white and yellow C atoms, respectively) in the RBS of A/Parma/24/09 H1N1 (deep-cyan cartoon). Just the HA residues that interact with the ligands are shown as lines for clarity's sake. H-bonds are represented as yellow dashed lines for ligand **4** and magenta for ligand **1**.

To assess the validity of the docking protocol, the X-ray ligand 6'-sialyl-N-acetylglucosamine was redocked in the receptor binding site of the H1 HA (PDB ID: 3UBN, Proc. Natl. Acad. Sci. USA **2018**, 115, 4240–4245).

Both Glide SP-peptide and Glide SP docking protocols were applied obtaining comparable results. The RMSD calculated superimposing the crystallographic and docked poses are 0.86 and 0.81, and obtained docking score values are -6.597 and -6.673 with Glide SP-peptide and Glide SP, respectively. (Figure S19)

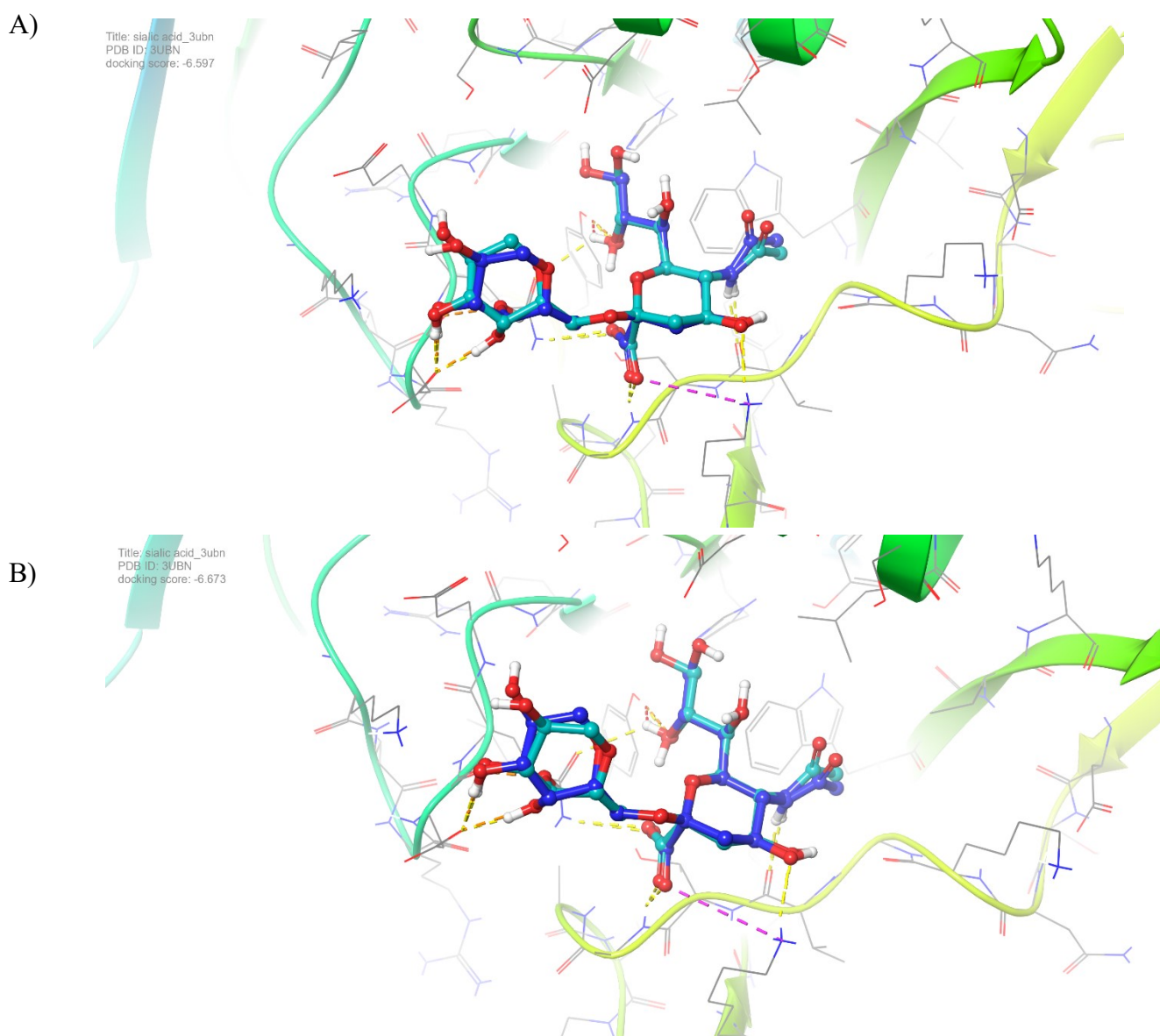


Figure S19. 6'-sialyl-N-acetylglucosamine in its X-ray geometry (blue C atoms), superimposed to its best docked pose (cyan C atoms) obtained with the Glide SP-peptide (panel A) and Glide SP docking protocol (panel B). H-bonds and ionic contacts are represented respectively as yellow and purple dashed lines; the docking score value is reported in the high left corner.