

# SUPPLEMENTARY INFORMATION

## **Structure-Based Epitope Design: Toward A Greater Antibody-SARS-CoV-2 - RBD Affinity**

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(Supplementary Information)

**Figure S1 to Figure S4:** HPLC Analyses of synthesized peptides

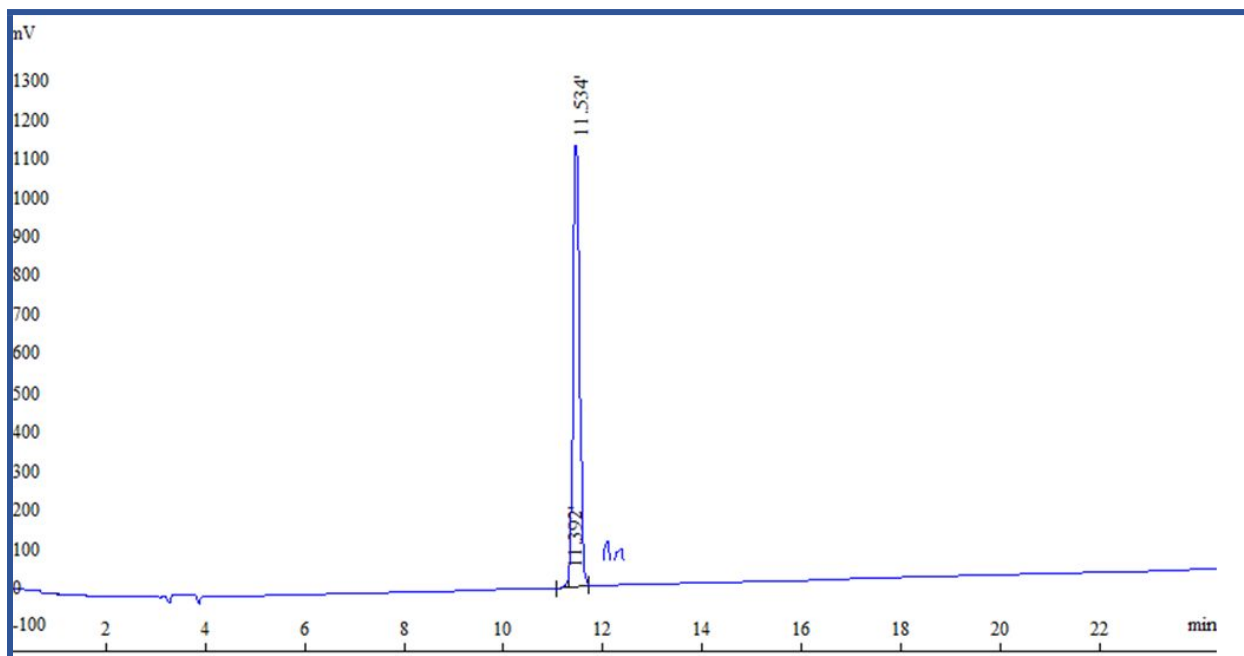
**Figure S5 to Figure S8:** LC-MS Analyses of synthesized peptides

**Figure S9:** Molecular Dynamics (MD) of peptides **(1)**, **(2)** and **(4)** showing the reference peptide and the minimized form after MD

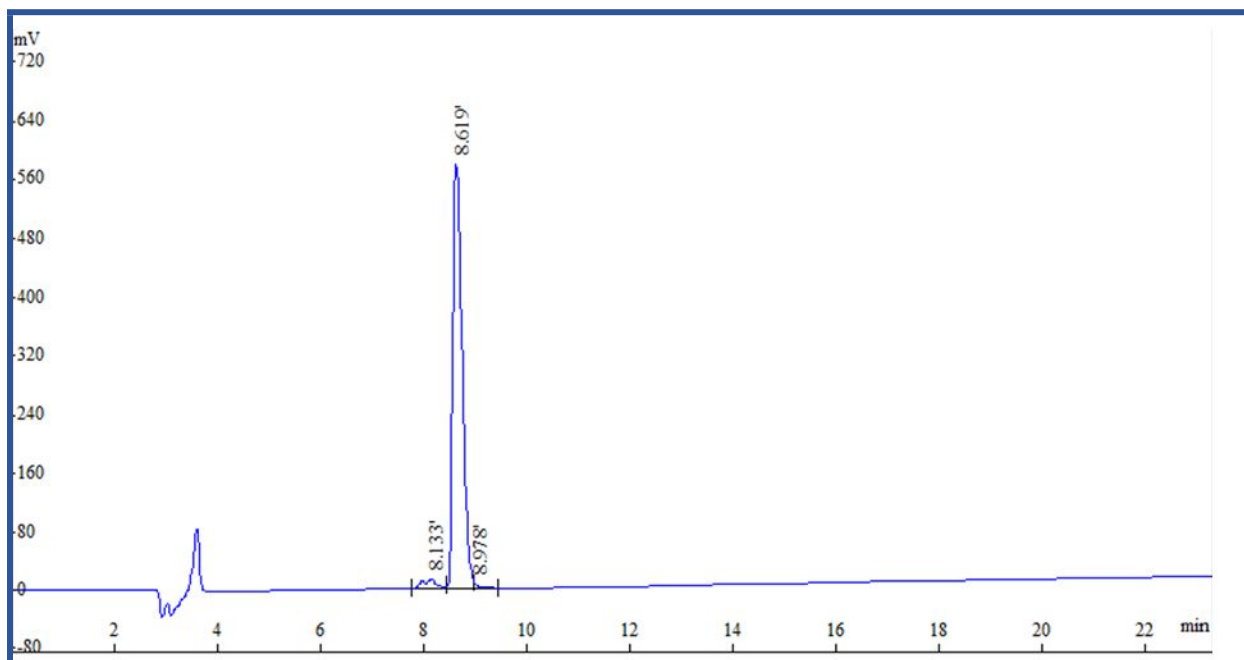
**Figure S10:** ELISA data conducted on the sera of rabbits immunized with epitopes **(1)**, **(2)**, **(3)** and **(4)**

## HPLC Analyses

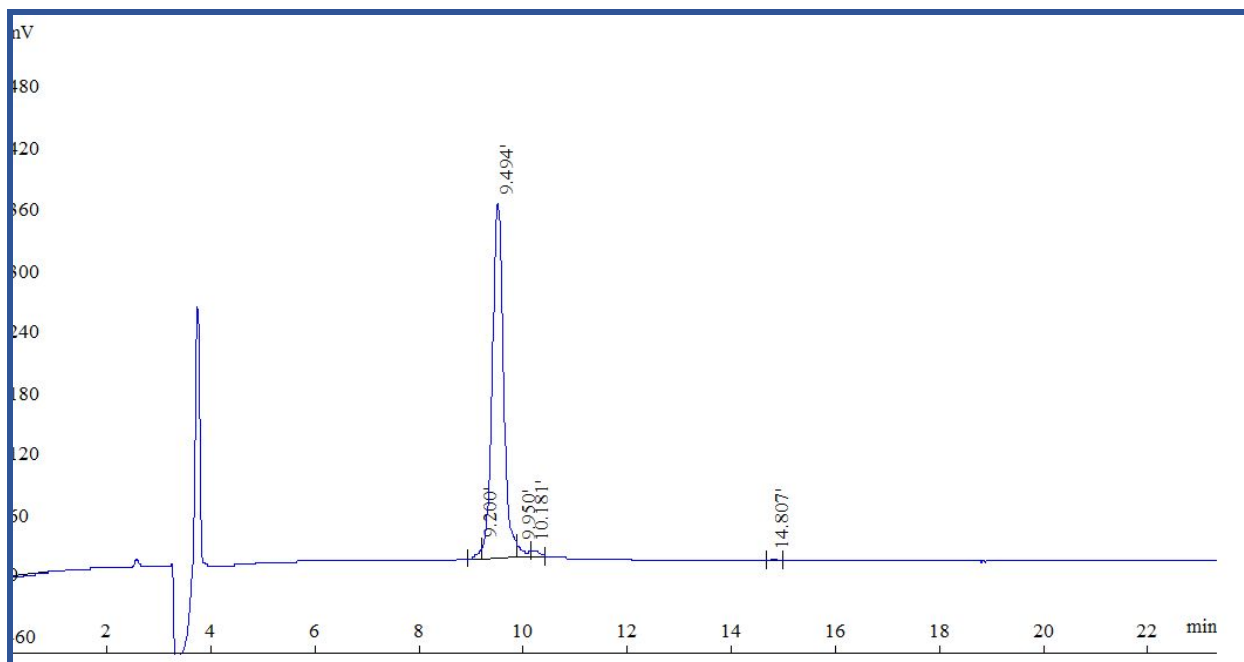
The mobile phase consisted of 0.1% Trifluoroacetic in 100% Acetonitrile and 0.1% Trifluoroacetic in 100% Water with a detection wavelength of 220 nm, Flow rate: 1.0 ml/min and volume: 20  $\mu$ l.



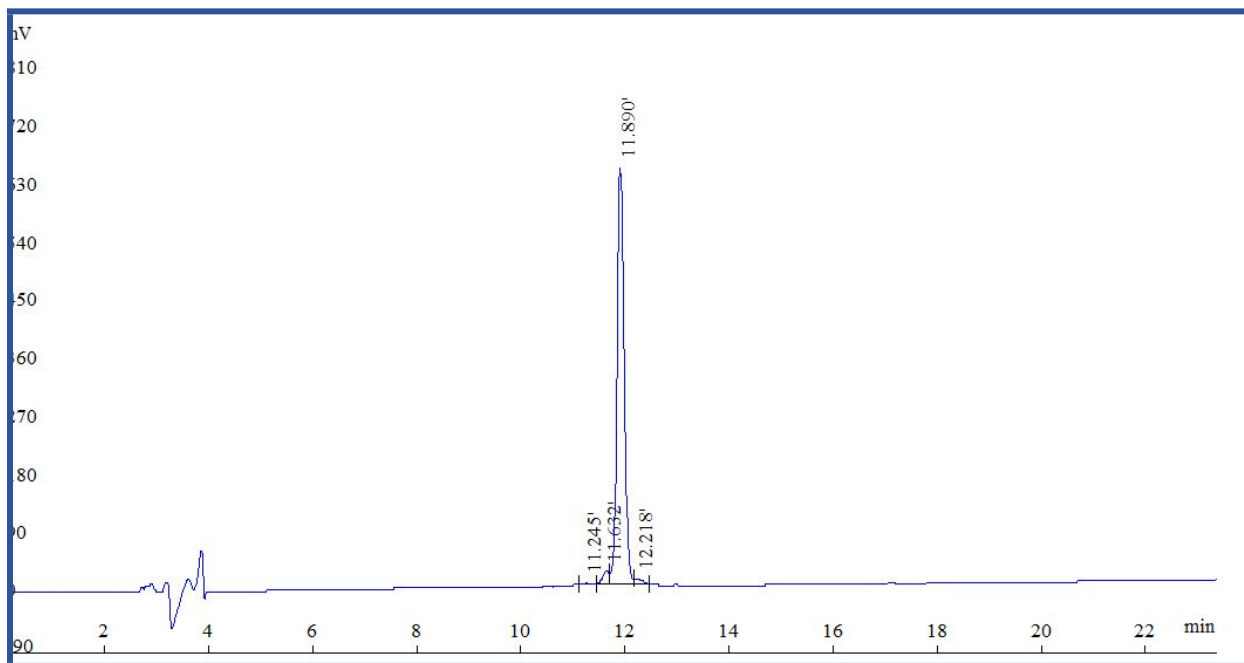
**Figure S 1:** HPLC characterization performed on peptide (1)



**Figure S 2:** HPLC characterization performed on peptide (2)



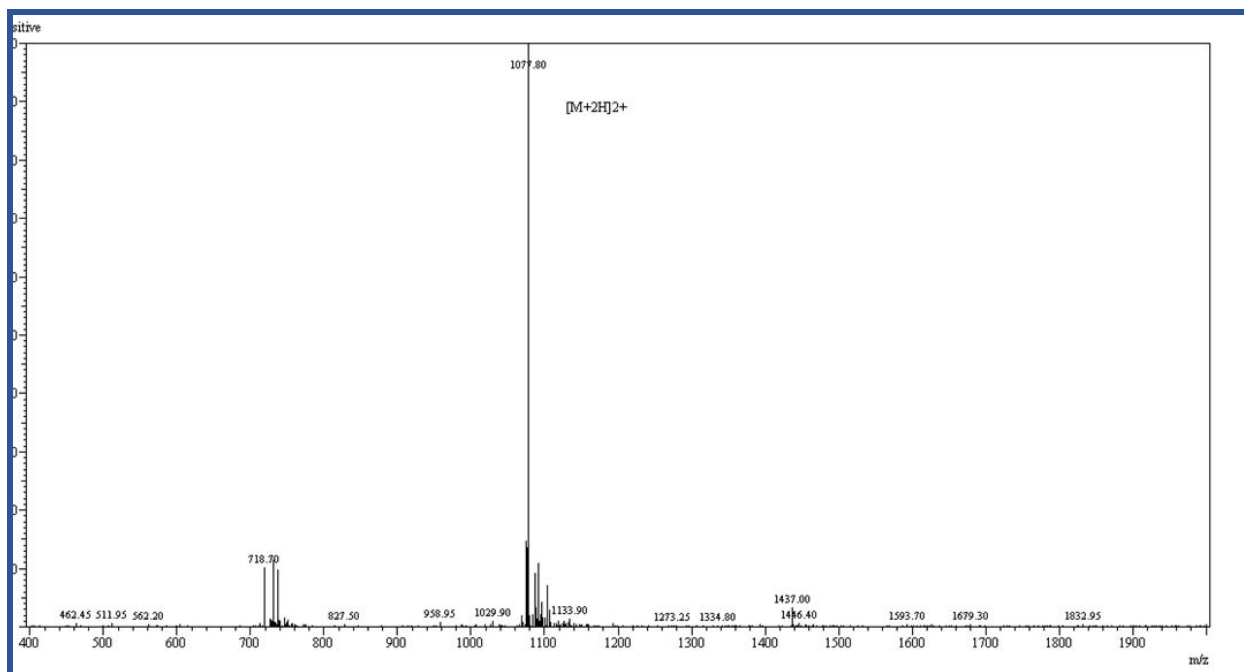
**Figure S 3:** HPLC characterization performed on peptide (3)



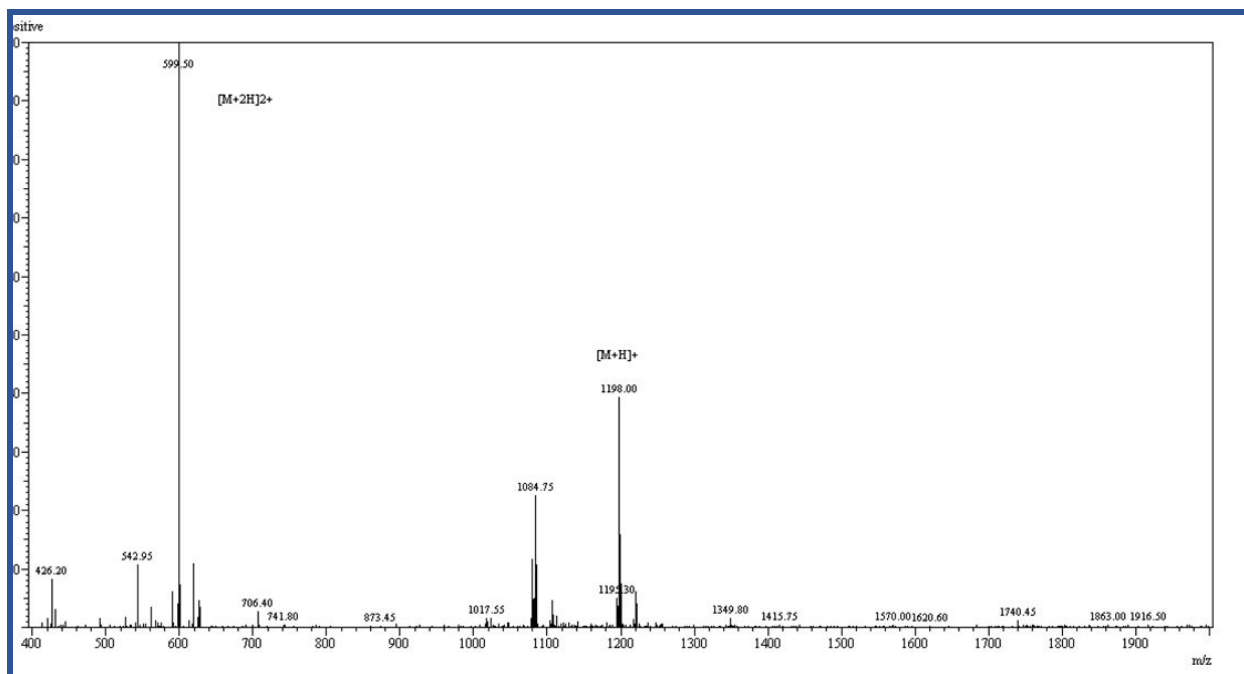
**Figure S 4:** HPLC characterization performed on peptide (4)

## LC-MS Analyses

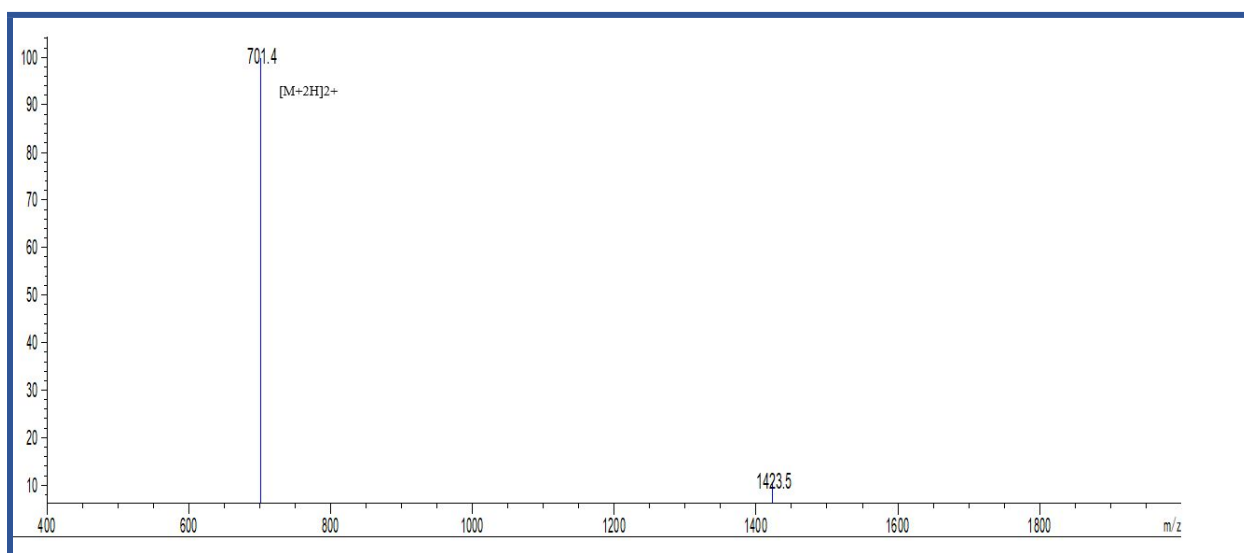
The analyses were conducted using Agilent 6125B (ESI) LC/MS. The detection was monitored out by an MS equipped with a V electrospray ionization (ESI) source, with the application of the following parameters: Nebulizer Gas Flow: 1.5L/min ; CDL: -20.0 v CDL Probe Bias: +4.5kv Detector: 1.5 kv and Flow rate: 0.2 ml/min. The separation of samples was achieved by isocratic elution on a reverse-phase Gemini-NX 5 $\mu$  C- 18 110A, 4.6\*250 mm column, using a mobile phase consisting of 50 % H<sub>2</sub>O / 50 % acetonitrile. Agilent Open LAB CDS software was used to control the MS data acquisition and analysis.



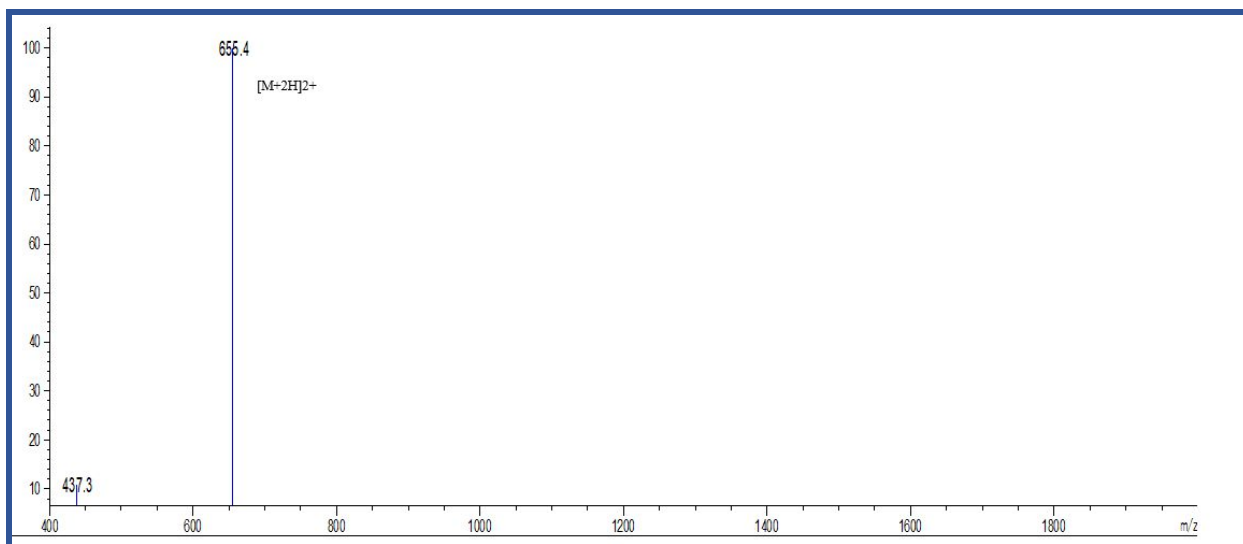
**Figure S 5:** LC-MS characterization performed on linear peptide **(1)**. Sequence of peptide: H-CZYFPLQSYGFQPTNGVGY-NH<sub>2</sub>. Calculated MW : [M+2H]<sup>2+</sup> = 1077.7 ; Obtained : [M+2H]<sup>2+</sup> = 1077.8 gmol<sup>-1</sup>.



**Figure S 6:** LC-MS characterization performed on linear peptide (**2**). Sequence of peptide: H-CZFQPTNGVGY-NH<sub>2</sub>. Calculated MW : [M+H]<sup>+</sup> = 1198.3 ; Obtained : [M+H]<sup>+</sup> = 1198.3 gmol<sup>-1</sup>

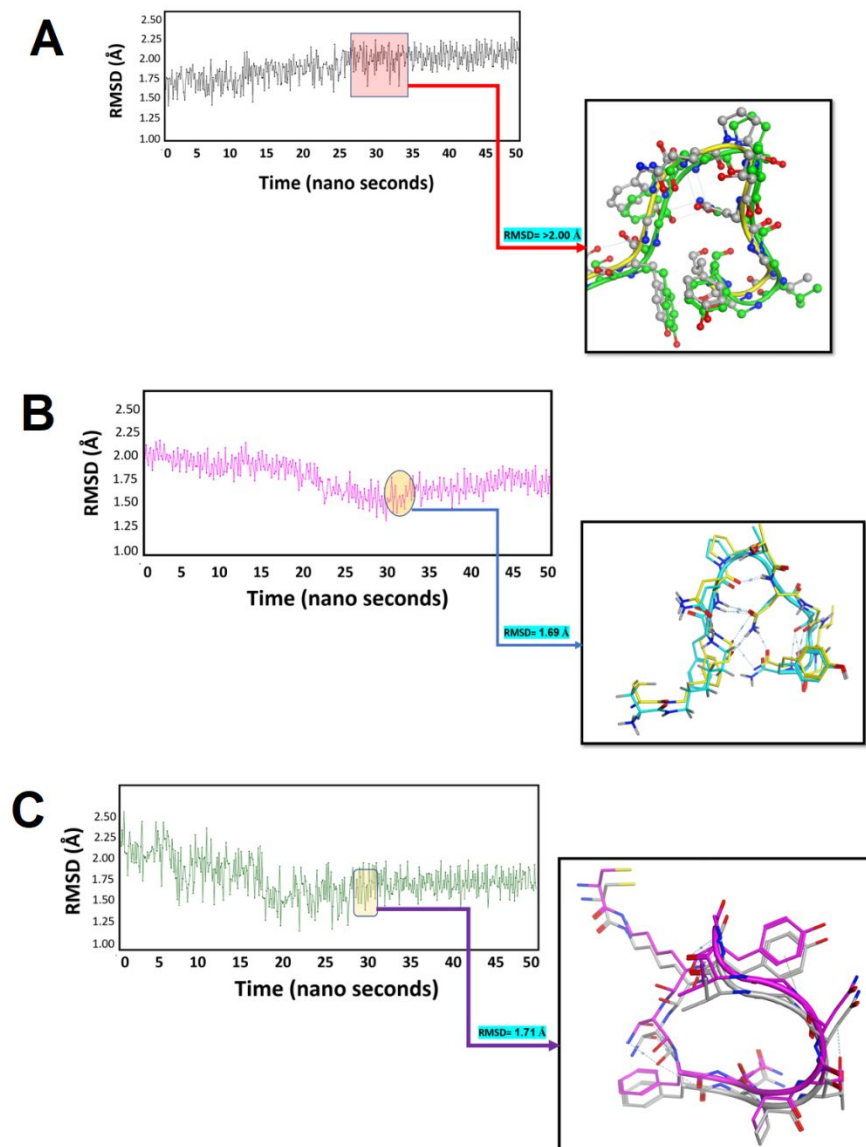


**Figure S 7:** LC-MS characterization performed on macrocyclic peptide (**3**). Sequence of peptide: H-CZ-[CFQPTNGVGYC]-NH<sub>2</sub>. Calculated MW : [M+2H]<sup>2+</sup> = 701.8 ; Obtained : [M+2H]<sup>2+</sup> = 701.4 gmol<sup>-1</sup>

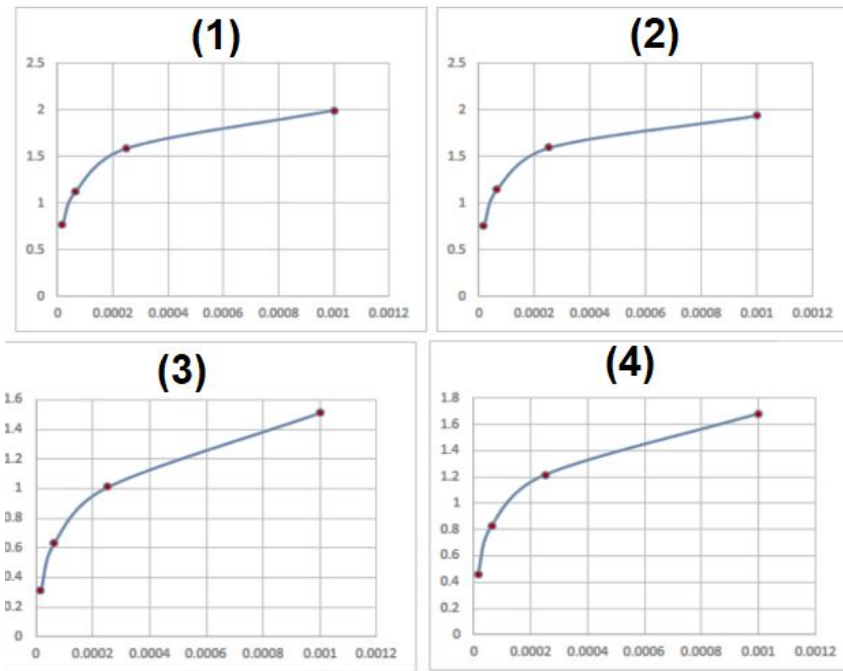


**Figure S 8:** LC-MS characterization performed on macrocyclic peptide (**4**). Sequence of peptide: [FQPTNGVGYK(C)N]-NH<sub>2</sub>. Calculated MW :  $[M+2H]^{2+} = 655.2$  ; Obtained :  $[M+2H]^{2+} = 655.4 \text{ gmol}^{-1}$ .

## Molecular Dynamics



**Figure S9:** A) MD of peptide (1) showing the reference peptide (green) and the minimized form after MD (yellow) B) MD of peptide (2) showing the reference peptide (yellow) and the minimized form after MD (cyan) C) MD of peptide (4) showing the reference peptide (magenta) and the minimized form after MD (grey), over 50 ns and showing the RMSD at equilibrium region.



**Figure S 4:** ELISA data conducted on the sera of rabbits immunized with epitopes (1), (2), (3) and (4)