Supplementary Materials for

Potential interference of graphene nanosheet to immune response via

disrupting the recognition of TCR to HLA-presented KK10: A

molecular dynamics simulation study

Rui Ye,^{†,1} Wei Song,^{†,1} Mei Feng,^{1,2} and Ruhong Zhou,^{*,1,3}

¹Institute of Quantitative Biology, Department of Physics, and College of Life Sciences, Zhejiang University, Hangzhou 310027, China

²Lanzhou Center for Theoretical Physics, Key Laboratory of Theoretical Physics of Gansu Province, Lanzhou University, Lanzhou, Gansu 730000, China

³Department of Chemistry, Columbia University, New York, 10027, United States



Fig. S1 Structural view of TCR-KK10-HLA(B*2705) 3-way binding complex. The TCR is colored in pink, the HLA (B*2705) is in ice blue, and the KK10 peptide is in red.



Fig. S2 Illustration of the initial simulation system. TCR-KK10-HLA is in the cartoon representation. The HLA is shown in ice blue, the KK10 peptide is in red, and the TCR is in pink. Water is shown transparently. Sodium and chlorine ions are shown as blue and green spheres, respectively. The graphene nanosheet is placed near the protein complex interface, and is in licorice representation.



Fig. S3 (a) Illustration of a graphene oxide nanosheet (GO) with with 10% oxidation following a previous study (Feng et al. J. Phys. Chem. B 2016, 144, 666-386).¹ Oxygen and hydrogen atoms are displayed by purple and white spheres, respectively. (b) The initial configuration of GO inserting the TCR-pHLA complex from the D1 direction. (c) Several typical snapshots extracted from a simulation trajectory

illustrate the separation process of TCR and pHLA by insertion of GO. (d) Timedependent atom contact numbers for TCR-pHLA, TCR-GO, and pHLA-GO during the insertion process. (e) Time-dependent potential energies (including Coul and vdW energies) between TCR and pHLA, between TCR and GO, and between pHLA and GO.



Fig. S4 Time-dependent contact areas of the TCR-KK10-HLA complex during the insertion of a graphene sheet in four directions. (a) D1. (b) D2. (c) D3. (d) D4. These four directions are shown in Fig. 1.



Fig. S5 Several typical snapshots extracted from a representative simulation trajectory from D4 directions illustrate the separation process of TCR and pHLA by insertion of GRA. Colors for different components are the same as those in **Fig. 1**.



Fig. S6 Time-dependent contact areas of the KK10-HLA binary complex during the insertion of a graphene sheet.



Fig. S7 Time-dependent Coulomb (the purple line) and van der Waals (the gray line) energies between TCR and pHLA.



Fig. S8 Structural comparison of KK10 peptide bound to the HLA-TCR complex. The contact ratio of each residue of HLA (a) and TCR (b) with KK10 peptide. [(c)-(e)] The binding residues and interactions of the N-terminal region (c), the C-terminal region (d), and the middle region (e) of KK10 peptide are rendered with spheres (non-polar interactions) or sticks (polar interactions) (ice blue, HLA; red, peptides; pink, TCR).

Contact ratio and structural binding details.

Fig. S8a and b show the contact ratio of the residues of HLA and TCR with KK10, respectively. A residue of HLA-TCR complex is in contact if any atom of that residue is within 4Å of the KK10. The contact ratio of a residue was obtained by normalizing the number of frames a residue contacts the KK10 over the entire trajectory. Nine hydrophobic residues (Val25, Val34, Phe36, Ile66, Cys67, Ala69, Trp147, Val152 and Leu156) and sixteen hydrophilic residues (Tyr7, His9, Thr24, Arg35, Glu45, Glu63, Thr73, Asp77, Thr80, Tyr99, His114, Thr143, Lys146, Gln155, Tyr159, Glu163) of HLA and five hydrophobic residues (Gly28, Leu27, Pro95, Gly96, Leu97) and two hydrophilic residues (Asp29, Arg94) of TCR hold high contact ratios with KK10 peptide. The rest of the residues have zero or negligible contact ratio.



Fig. S9 Time-dependent center of mass (COM) distance of key residues between HLA and KK10 peptide during the insertion of the graphene nanosheet.

Reference

1. M. Feng, H. S. Kang, Z. X. Yang, B. Q. Luan and R. H. Zhou, *J. Chem. Phys.*, 2016, **144**, 225102.