Supporting Information for

Molecular Mechanism of Robust Macrophage Immune Responses Induced by PEGylated Molybdenum Disulfide

Zonglin Gu^{‡,1}, Serena H. Chen^{‡,2}, Zhaowen Ding³, Wei Song¹, Wei Wei^{3,4}, Shengtang Liu⁵, Guanghui Ma^{*,3,4}, Ruhong Zhou^{*,1,2,6}

¹ Institute of Quantitative Biology, Department of Physics, Zhejiang University, Hangzhou 310027, China; ² Computational Biology Center, IBM Thomas J. Watson Research Center, Yorktown Heights, NY 10598; ³ State Key Laboratory of Biochemical Engineering, Institute of Process Engineering, Chinese Academy of Sciences, Beijing 100190, PR China; ⁴ University of Chinese Academy of Sciences, Beijing 100049, PR China; ⁵ State Key Laboratory of Radiation Medicine and Protection, School of Radiation Medicine and Protection, Collaborative Innovation Center of Radiological Medicine of Jiangsu Higher Education Institutions, Soochow University, Jiangsu 215123, China; ⁶ Department of Chemistry, Columbia University, New York, NY 10027

[‡]*These authors contributed equally to this work.* **Corresponding author: (G.M.) <u>ghma@ipe.ac.cn</u>, (R.Z.) <u>ruhongz@us.ibm.com</u>*



Figure S1. The MoS_2/MoS_2 -PEG nanoflakes used in this study. MoS_2 is shown in a yellow and pink ball-and-stick representation. The two PEG chains are displayed in mauve spheres, one chain at each side of the MoS_2 basal plane.



Figure S2. Initial simulation setups of the one and three small MoS_2 nanoflakes with the macrophage membrane. The lipid carbon atoms are represented in gray, oxygen atoms in red, nitrogen atoms in blue, and phosphorus atoms in purple, respectively. The MoS_2 sulfur atoms are rendered in yellow and molybdenum atoms in pink. The Na⁺ and Cl⁻ ions are displayed in blue and cyan spheres, respectively. The water boundaries are indicated by white surfaces.



Figure S3. Snapshots from the molecular dynamics simulations of sys-1 at 400 K.



Figure S4. Initial simulation setups of the macrophage membrane with the large MoS₂ and MoS₂-PEG nanoflakes placed in corner point-on configurations.



Figure S5. The orientation of PEG relative to the membrane during the insertion process.



Figure S6. Averaged center of mass (CoM) distances between the macrophage membrane and

 MoS_2/MoS_2 -PEG or between MoS_2 and PEG in three parallel simulations of sys-3 and sys-4.



Figure S7. 2D x-y distribution probabilities of each lipid type in outer leaflet.



Figure S8. Initial simulation setups of the macrophage membrane with the large MoS_2 and MoS_2 -PEG nanoflakes placed in face-on configurations.



Figure S9. Decomposed interaction energies in corner point-on and face-on configurations. The energies were averaged from last 10 ns in each trajectory.



Figure S10. Lipid extraction by MoS_2 and MoS_2 -PEG. The extracted lipids are shown in spheres and indicated by red arrows, while the other lipids are depicted in lines.



Figure S11. PMF of a POPC molecule binding to graphene and MoS_2 surface. The x-axis indicates the center of mass (CoM) distance between graphene/MoS₂ and POPC.



Figure S12. Membrane diffusion constants of the MoS_2 /membrane and MoS_2 -PEG/membrane systems. The diffusion constant was computed based on the head group atoms in the outer leaflet of the membrane. The trajectories from face-on configurations were used for the calculations.

	Box size (nm ³)	Number of water	Simulation time
		molecules	(ns)
sys-1	10.00×10.00×12.51	26,232	300
(one small MoS ₂)			
sys-2	10.00×10.00×12.50	26,022	300
(three small MoS ₂)			
sys-3	10.00×10.00×13.93	30,881	150
(one large MoS ₂ , corner			
point-on)			
sys-4	10.00×10.00×13.91	30,548	150
(one large MoS ₂ -PEG,			
corner point-on)			
sys-5 (one large MoS ₂ ,	10.00×10.00×9.59	20,401	1000
face-on)			
sys-6	10.00×10.00×9.47	20,372	1000
(one large MoS ₂ -PEG,			
face-on)			

Table S1. Simulation system details.