Supplementary Information

Protein-Surface Interactions in Nano-Scale Biosensors for IL-6 Detection Using Functional Monolayers

Serena Giberti[1], Sutapa Dutta[1], Stefano Corni[2], Marco Frasconi[2] Giorgia Brancolini[1*]*

[1] Institute Nanoscience – CNR-NANO, Center S3, via G. Campi 213/A, 41125, Modena, Italy

[2] Department of Chemistry, University of Padova, via Marzolo 1, 35131 Padova, Italy

*: corresponding author: marco.frasconi@unipd.it; giorgia.brancolini@nano.cnr.it

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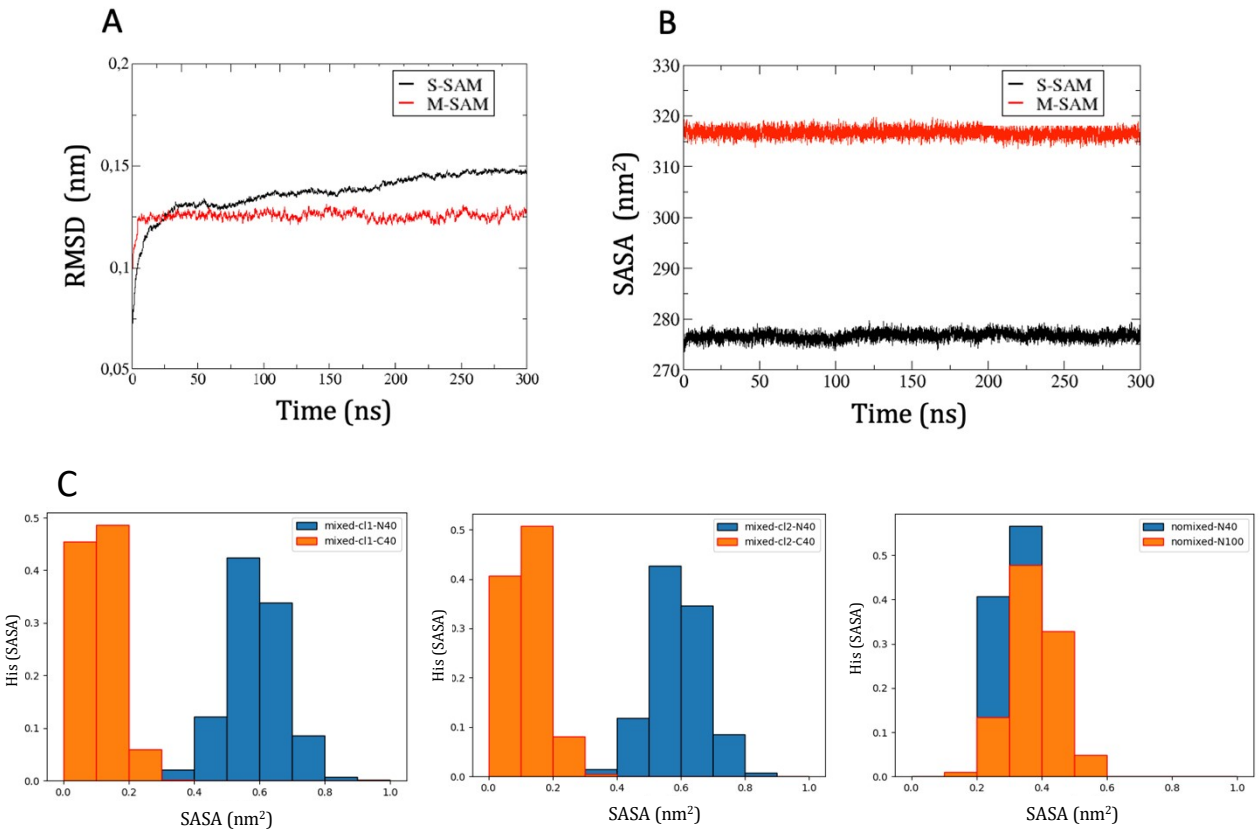


Figure S1. RMSD (panel A) and SASA (panel B) of the 300 ns trajectories collected for M-SAM and S-SAM, using as the reference the first frame. Panel C, SASA computed for individual NH3+ spacers is increased in M-SAM compared to S-SAM. SASA of each N4 (namely N of NH3+ group) are qualitatively classified in three regimes: SASA < 0.4 nm, 0.4 < SASA > 0.5, SASA > 0.5. Since the overall SASA of amino groups in the second and third groups is larger for the mixed-SAM compared to the S-SAM, fully functionalized high-density surfaces are expected to reach saturation earlier than their half-functionalized counterparts.

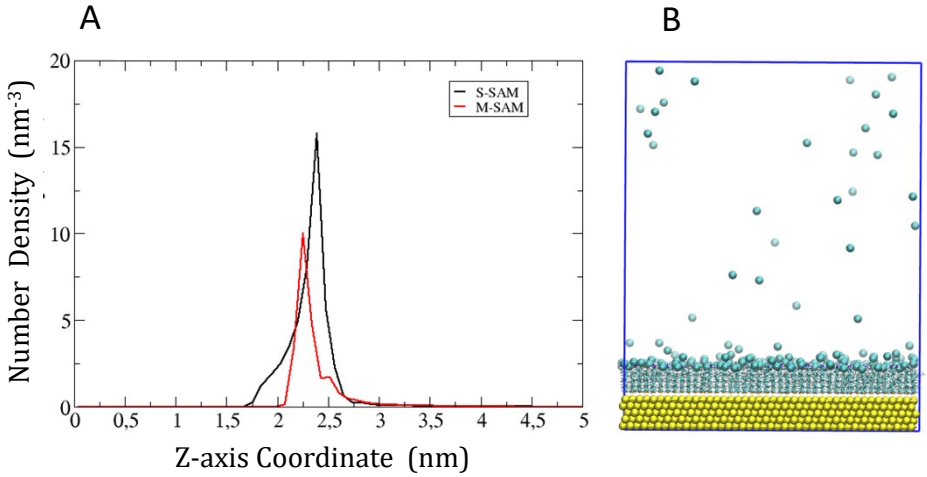


Figure S2. Illustration of the density of Cl^- ions condensed near the SAM surfaces. Panel A shows the calculation of the number density of particles by dividing the box into slices and calculating the temporal average over time. Panel B shows a snapshot of the surface with the total number of Cl^- counterions. A layer of 217 Cl^- ions formed near the ligands of the M-SAM, and 432 formed near the S-SAM.

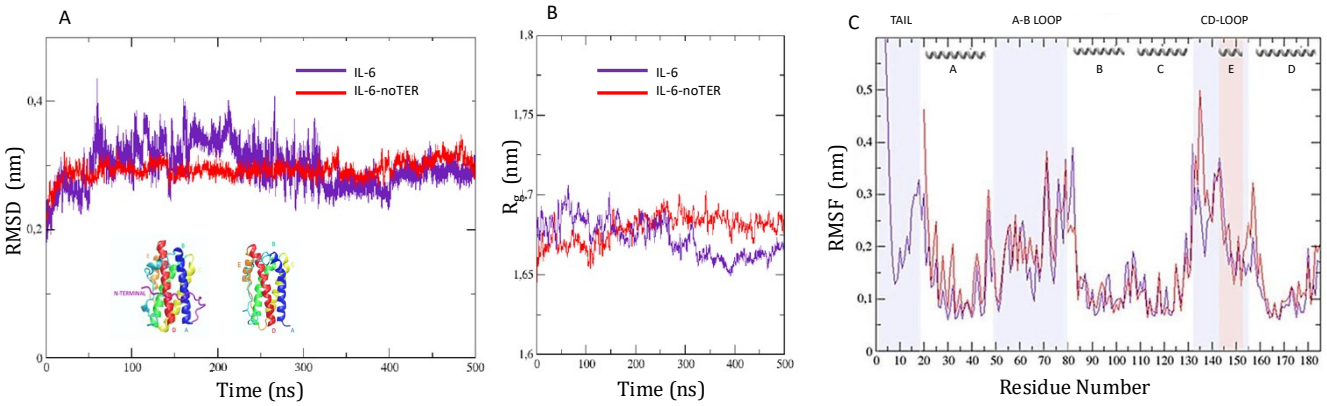


Figure S3. RMSD, Radius of gyration and RMSF of IL-6 and IL-6-noTER.

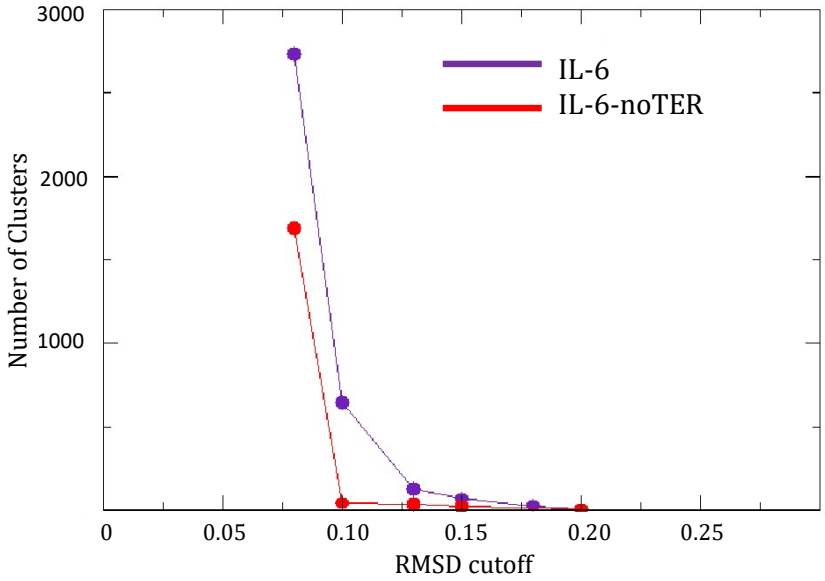


Figure S4. Curve obtained during clustering procedure over protein's trajectories. The cut off= 0.13 nm was choosen for IL-6-noTER and cut off = 0.18 nm was choosen for IL-6.

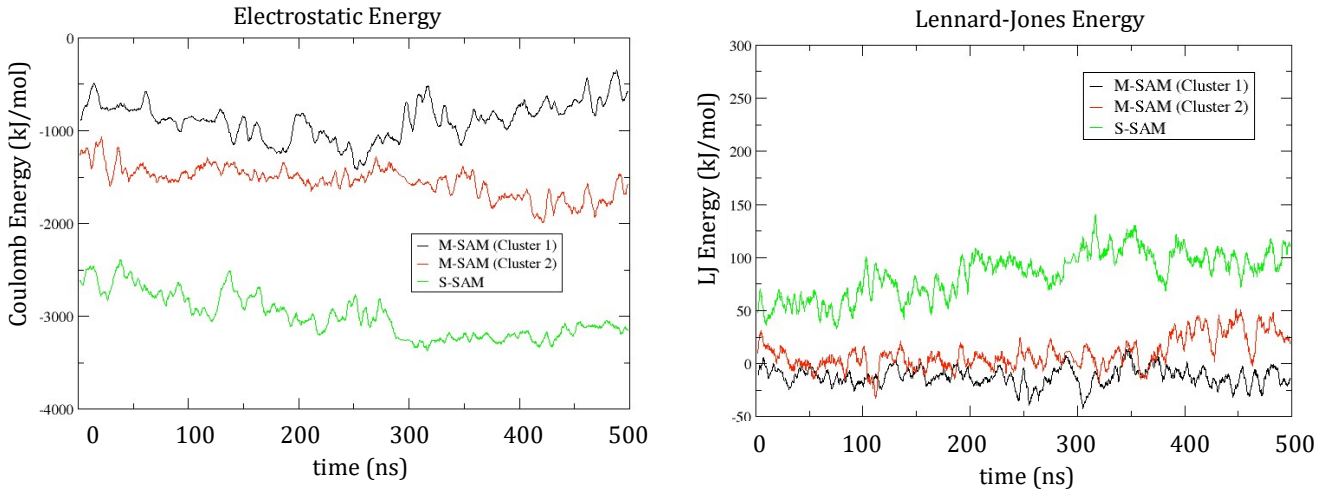
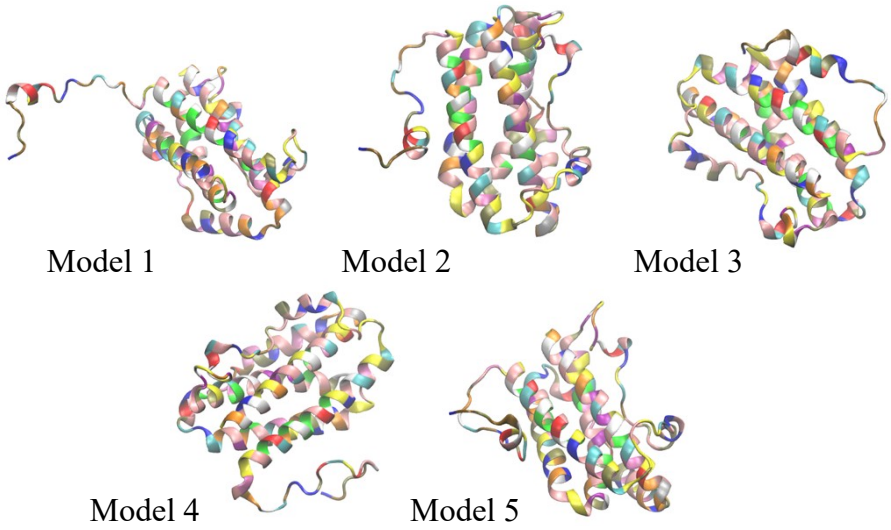


Figure S5. Computed Adsorption Energies along 500 ns trajectories: Coulomb (left panel) and Lennard Jones (right panel) contributions for M-SAM and S-SAM



IL-6 model predicted with AI	RMSD (nm)
Model 2	0.6612
Model 3	0.5811
Model 4	0.7490
Model 5	0.6996

Figure S6. Top. IL-6 models predicted with AI from the primary sequence. Bottom. RMSD with respect to Protein backbone. Model 3 has been used in simulation.