Supplementary Data for "Silica in Silico: A Molecular Dynamics Characterization of the Early Stages of Protein Embedding for Atom Probe Tomography"

Giovanni Novi Inverardi [1,2], Francesco Carnovale[1,2], Lorenzo Petrolli[1,2], Simone Taioli[2,3,4] and Gianluca Lattanzi [1,2,*]

[1] *Department of Physics, University of Trento, via Sommarive, 14 I-38123 Trento, Italy*
[2] *INFN-TIFPA, Trento Institute for Fundamental Physics and Applications, I-38123 Trento, Italy*
[3] *European Centre for Theoretical Studies in Nuclear Physics and Related Areas (ECT*), Bruno Kessler Foundation, Trento, Italy*
[4] *Faculty of Applied Physics and Mathematics, Gdańsk University of Technology, Gdańsk, Poland*

1 Water-silica system

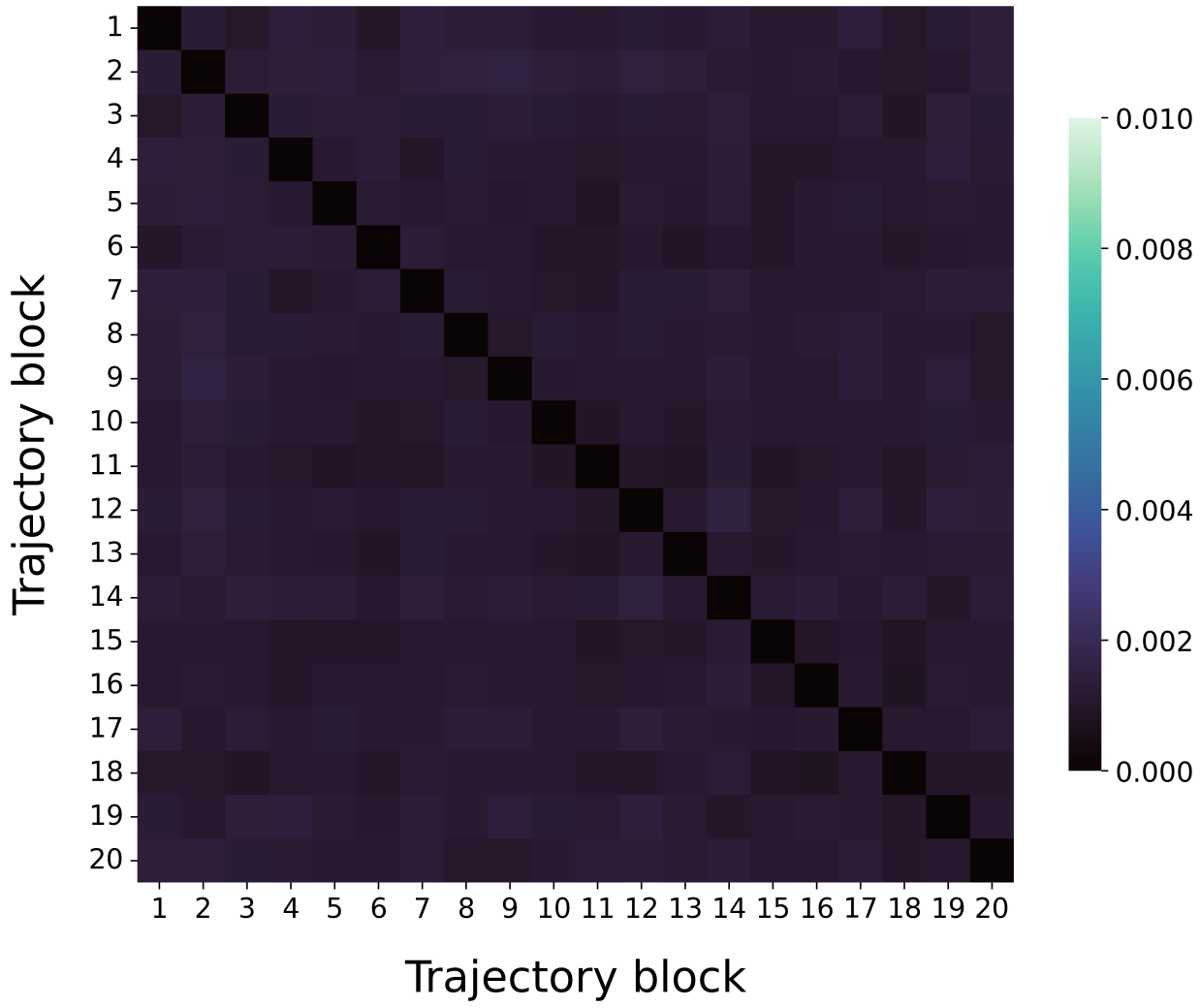

Figure S1: Heatmap of the Jensen-Shannon divergence between the radial distribution functions (RDF) associated with each (25-nanosecond) block of the trajectory of the water-silica system.

2 Ubiquitin systems

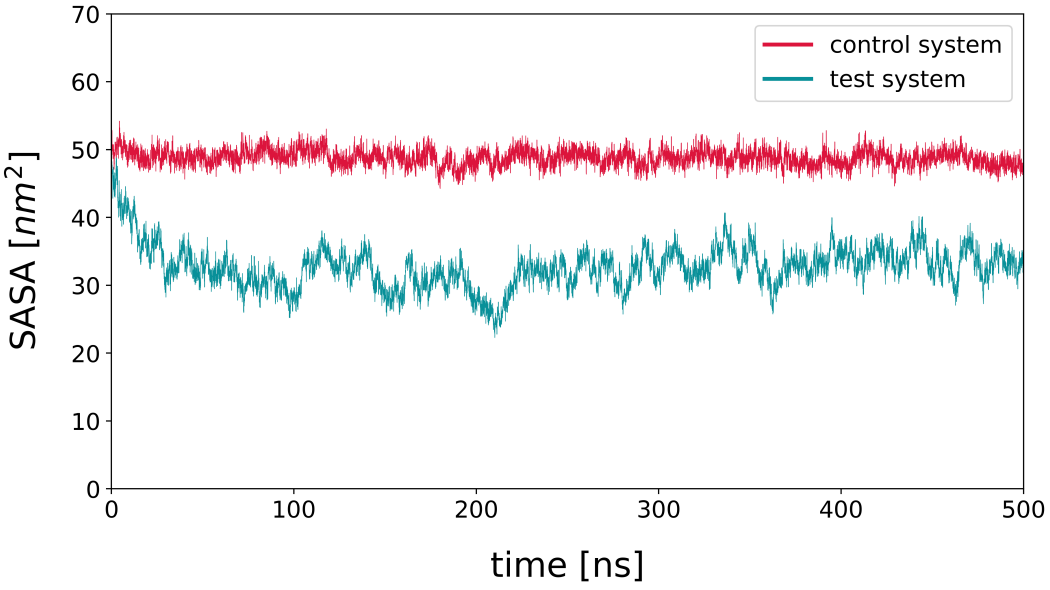

Figure S2: Solvent-accessible surface area (SASA) of ubiquitin in the *control* (red) and *test* (blue) scenarios. The decreasing trend observed in the latter is accounted for by orthosilicic acid partially replacing water molecules on the surface of ubiquitin.

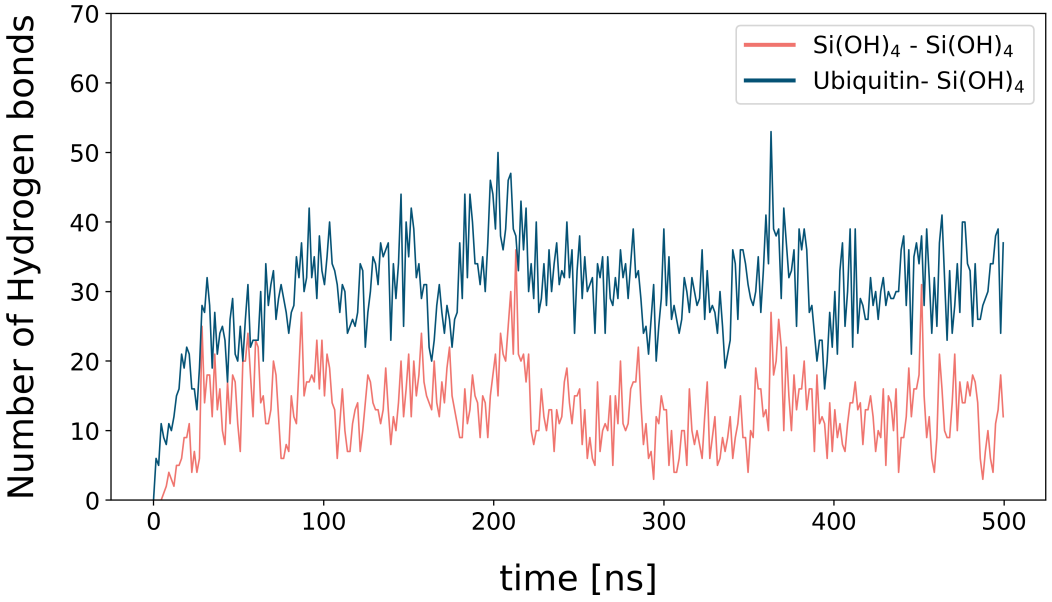

Figure S3: Total amount of hydrogen bonds between ubiquitin and $Si(OH)_4$ molecules (blue), and between $Si(OH)_4$ molecules lying within 5 Å of the protein surface (red).

3 SUMO-1 systems

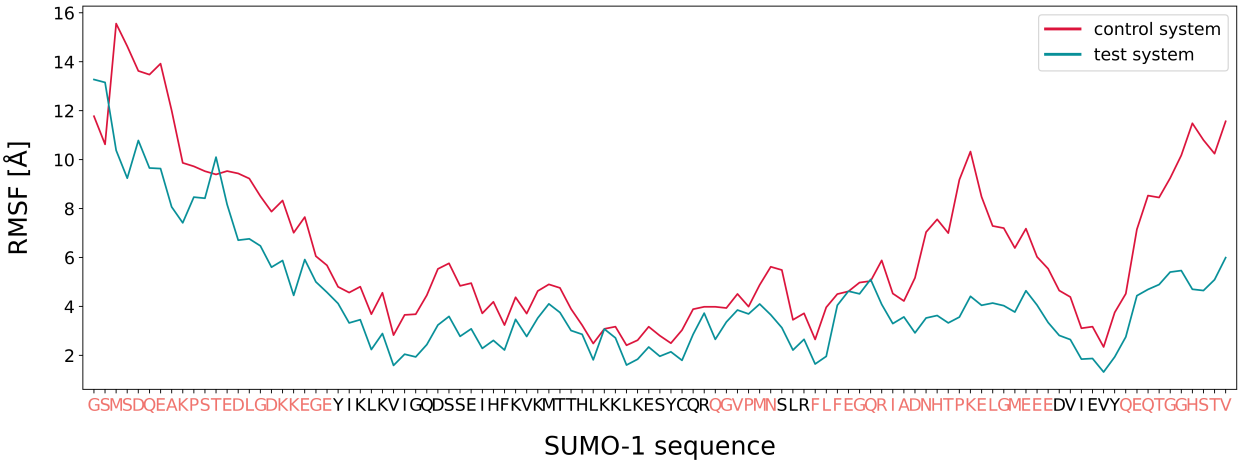

Figure S4: RMSF of SUMO-1, evaluated on the first 325 nanoseconds of the *control* (red) and *test* (blue) trajectory, respectively. Residues belonging to the flexible domains of SUMO-1 are highlighted. These trends match the analysis of the Protein Dispersion Angle (PAD_ω - see the main text), suggesting a tendency of orthosilicic acid to limit the flexibility of the unstructured moieties of SUMO-1.

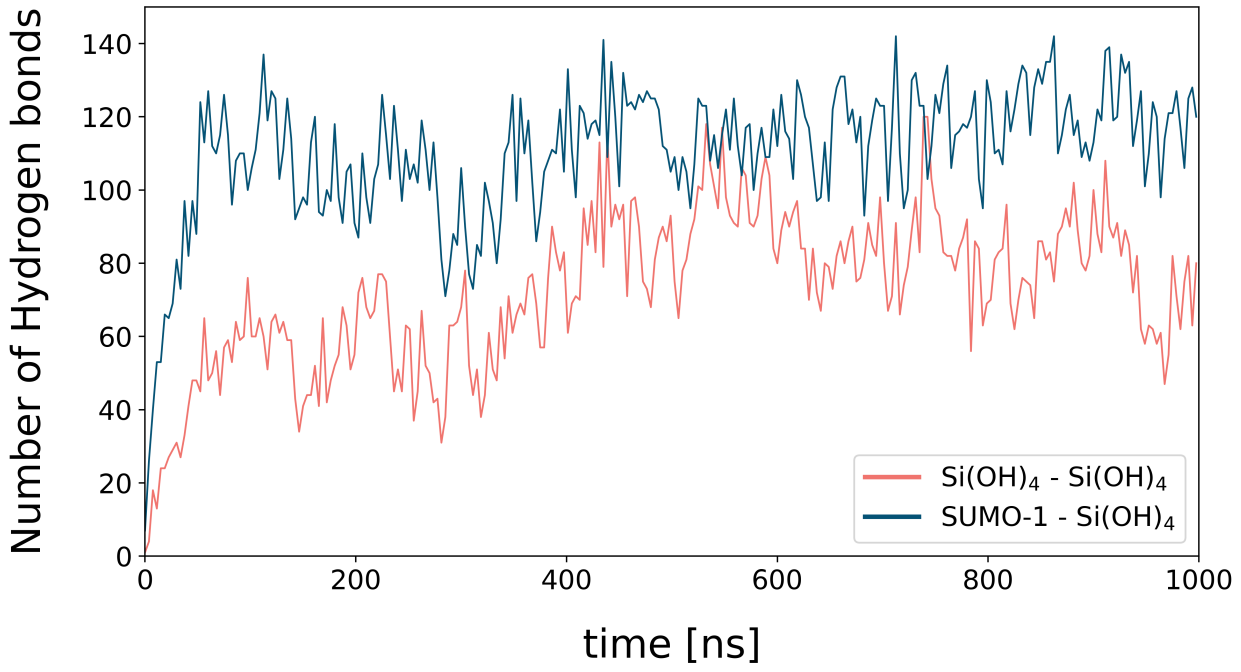

Figure S5: In blue, the total amount of hydrogen bonds between SUMO-1 and $Si(OH)_4$ molecules. In red, the total amount of hydrogen bonds between $Si(OH)_4$ molecules belonging to the embedding shell, i.e. lying within 5 Å of the protein surface.

4 IL22Rα1 systems

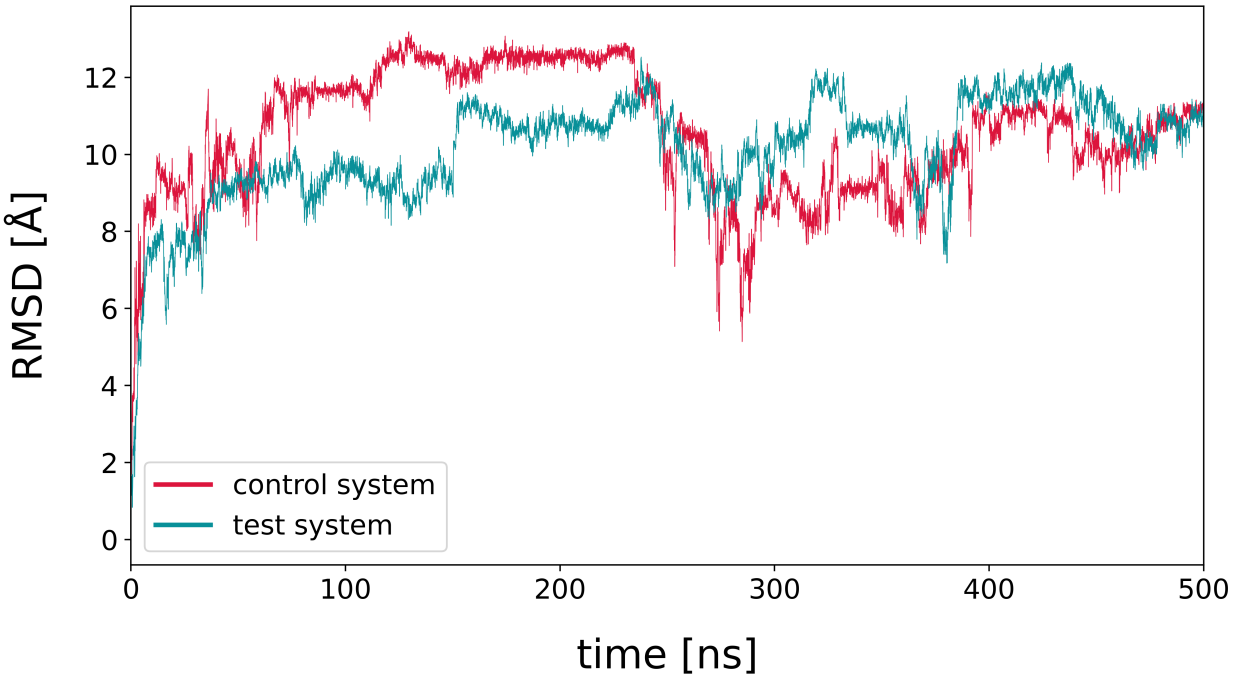

Figure S6: RMSD of the *control* (red) and *test* (blue) trajectories of the transmembrane domain of IL22Rα1.

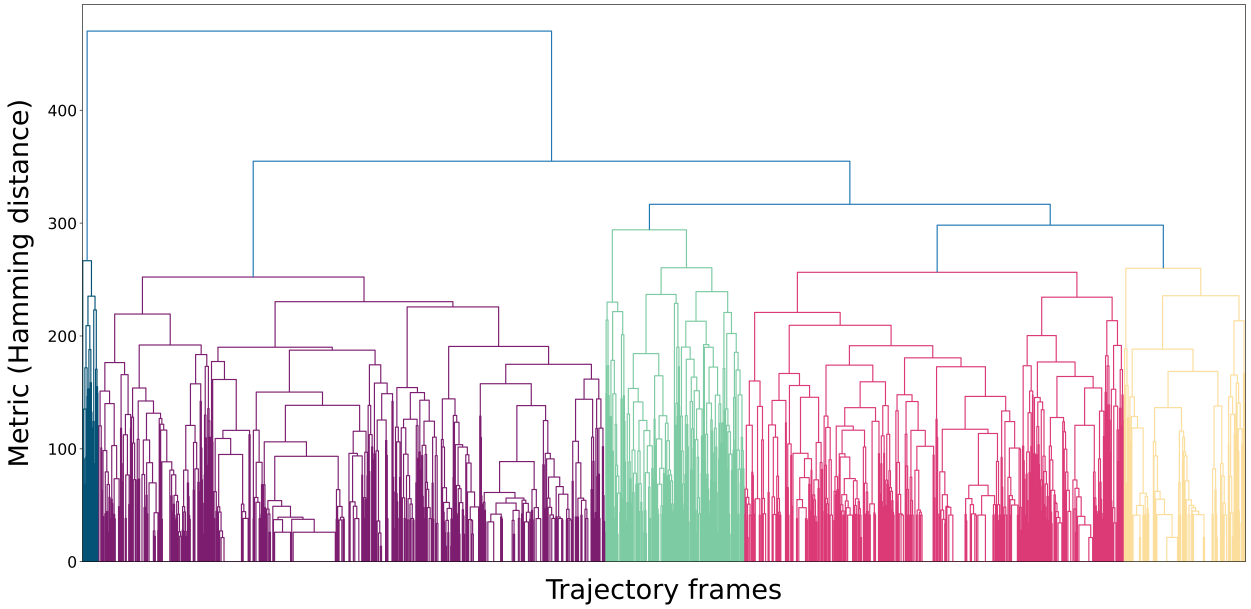

Figure S7: Dendrogram of the hierarchical clustering analysis on the merged (*control*, *test*) trajectory of the transmembrane helix of IL22Rα1, whereby five clusters were isolated based on the dynamical evolution of the secondary structure elements.