Nanoscale *in-silico* classification of ligand functionalised surfaces for protein adsorption resistance

*Matthew Penna†‡ and Irene Yarovsky†‡*

† School of Engineering, RMIT University, Melbourne, VIC, Australia, 3000

‡ ARC Research Hub for Australian Steel Manufacturing, Wollongong, NSW, 2522
Fig. S1: Average RMSFs of heavy atoms along the ligand chain (from left to right C₁, C₂, C₃, O, C₄, C₅, C₁₀) against the height above the substrate for (a) GPS, (b) CF₃, (c) GPS:sNH₂, and (d) GPS:sCF₃ systems.
Fig. S2: Relative density maps for 2 equilibrated water droplets on the (a) GPS, (b) CF₃, (c) GPS:sNH₂, and (d) GPS:sCF₃ systems in-vacuum with colorbar showing relative atomic density compared to bulk TIP3P water and contact angle estimates shown.
Fig. S3: Relative density maps of water droplet immersed in cyclooctane for the time from 10 to 5 ns before run termination; droplet fitted circle, droplet base height and tangent at the cross over point are shown in black, water contact angle estimates, $\theta_{\text{cyc}}$, are shown for each system.
Fig. S4: Magnified PSCA data for exemplar trajectory.
Fig. S5: Protein-surface contact area as a function of run time (black); time evolution of whether the protein is in contact (C) or not in contact (N) with the surface by the PAE definition (blue); PSCA for defining a PAE (horizontal red); force release point (vertical black dotted) for the protein at (a) GPS from the bound release point; (b) GPS from the transition release point; and (c) GPS from the association release point.
Fig. S6: Protein-surface contact area as a function of run time (black); time evolution of whether the protein is in contact (C) or not in contact (N) with the surface by the PAE definition (blue); PSCA for defining a PAE (horizontal red); force release point (vertical black dotted) for the protein at (a) CF$_3$ from the bound release point; (b) CF$_3$ from the transition release point; and (c) CF$_3$ from the association release point.
Fig. S7: Protein-surface contact area as a function of run time (black); time evolution of whether the protein is in contact (C) or not in contact (N) with the surface by the PAE definition (blue); PSCA for defining a PAE (horizontal red); force release point (vertical black dotted) for the protein at (a) GPS::sNH₂ from the bound release point; (b) GPS::sNH₂ from the transition release point; and (c) GPS::sNH₂ from the association release point.
Fig. S8: Protein-surface contact area as a function of run time (black); time evolution of whether the protein is in contact (C) or not in contact (N) with the surface by the PAE definition (blue); PSCA for defining a PAE (horizontal red); force release point (vertical black dotted) for the protein at (a) GPS:sCF₃ from the bound release point; (b) GPS:sCF₃ from the transition release point; and (c) GPS:sCF₃ from the association release point.
**Fig. S9:** Temporal evolution of the centre of mass of the protein from the exemplar trajectory presented in Fig 4, colorbar showing time in ns.

**Fig. S10:** Minimum height of protein from exemplar trajectory presented in Fig 4, average height of ligand $C_T$ atoms (horizontal dot-dash), force release time (vertical dot line).
Fig. S11: Aligned RMSD trajectories for ubiquitin in (a and c) bulk water averaged from 20 x 20 ns blocks from the 400 ns bulk solvent simulation and (b and d) from bound release point runs for the GPS:sNH$_2$ system averaged from 20 runs performed. The shaded region shows 1 standard deviation for all systems. (a and b) RMSD based on C$_\alpha$ atoms, (c and d) RMSD based on all heavy backbone atoms calculated over all residues (blue) and excluding C-terminal residues 72-76 (red).

Fig. S12: Total number of PDEs with different threshold for defining contact.
**Table S1**: Interfacial hydration data; the count of interfacial water molecules, \(I(H_2O)\); the count of embedded water molecules, \(E(H_2O)\); the total number of ligand associated water molecules, \(T(H_2O)\); and the maximum of the relative atomic density profile of embedded and interfacial water, \((\rho_I+\rho_E)_{\text{max}}\).

<table>
<thead>
<tr>
<th>System</th>
<th>(I(H_2O)) molecules per Å(^2)</th>
<th>(E(H_2O)) molecules per Å(^2)</th>
<th>(T(H_2O)) molecules per Å(^2)</th>
<th>((\rho_I+\rho_E)_{\text{max}})</th>
</tr>
</thead>
<tbody>
<tr>
<td>GPS</td>
<td>0.096</td>
<td>0.034</td>
<td>0.130</td>
<td>0.67</td>
</tr>
<tr>
<td>CF3</td>
<td>0.093</td>
<td>0.026</td>
<td>0.119</td>
<td>0.69</td>
</tr>
<tr>
<td>GPS:sNH(_2)</td>
<td>0.102</td>
<td>0.032</td>
<td>0.133</td>
<td>0.59</td>
</tr>
<tr>
<td>GPS:sCF(_3)</td>
<td>0.098</td>
<td>0.030</td>
<td>0.128</td>
<td>0.64</td>
</tr>
</tbody>
</table>