

Supplementary Material.

Modelling bionano interactions and potential health risks for environmental nanoplastics: the case of functionalized polystyrene

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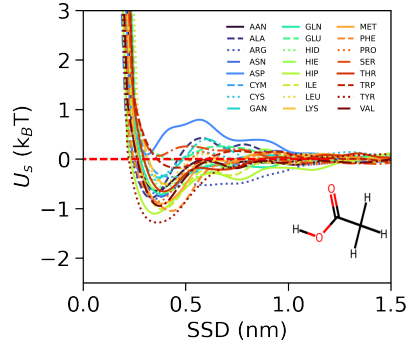
1 Short-range CG potentials for NP-SCA interactions.

The set of calculated surface potentials for all possible pairwise interactions between NP fragments and AA side chains is shown in Figure S1. The adsorption energy minima for all SCAs interacting with the PS fragment were located at 0.2-0.3 nm. This range of distances aligns with typical van der Waals contact distances between interacting coarse-grained sites. This observation confirms that the obtained potentials behave in a physically consistent manner, thereby serving as a validation of the potential parameterization. The integration of obtained potential mean force (PMFs) curves along the SSD distance suggests that AA interaction energy with bare PS bead would range from $-0.10k_B T$ to $-1.91k_B T$. The aromatic Phe and Trp SCAs had the highest binding affinity to PS. Negatively charged SCAs (Cym, Asp and Glu) were predicted to be least attracted to the pristine PS surface. The positively charged SCAs have been shown to have a median binding affinity. This binding pattern can be rationalized in terms of interactions between electron densities of the benzene ring in PS and on SCAs. The non-bonded π -interaction between aromatic rings and various groups (e.g. π - π stacking interactions, CH- π interactions, cation- π interactions, and XH- π interactions, where XH = NH, SH, OH) were studied previously by different authors (Tsuzuki *et al.*, 2000, Zhu *et al.*, 2021). The favorable π - π stacking interaction will lead to stabilization of binding to aromatic fragments, while the repulsive interaction between the negative charge and electrons of the π -system should destabilize PS interaction with negatively charged fragments. However, the interaction between anions and electron-deficient aromatic systems can be favorable and can be further assisted by induced polarization or other factors (Schottel *et al.*, 2008, Frontera *et al.*, 2011). The interaction between positively charged fragments and the π -system of the benzene ring would have a stronger stabilization effect (Mahadevi and Sastry, 2013).

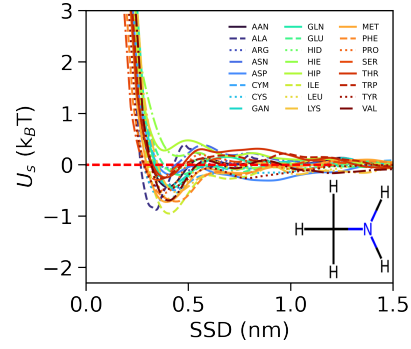
For non-ionized -COOH and -NH₂ beads slightly weaker binding affinity to SCAs was calculated as compared to the PS fragment: the interaction energies E_{ads}^{int} ranged from $-0.01k_B T$ to $-1.28k_B T$. The ionization of -COOH/-NH₂ beads resulted in a weakening of their interactions with neutrally charged SCA beads and a strengthening of their interactions with oppositely charged SCAs due to charge-charge attraction. In case of -NH₃⁺ CG beads, this synergistic effect was even stronger than for -COO⁻ CG beads: the interaction between -NH₃⁺ fragment and negatively charged SCAs, e.g. Glu, was about $E_{ads}^{int} = -1.57k_B T$ and was energetically comparable to the interaction energy with PS fragment. The obtained binding trends for individual amino-acids suggest that pristine PS NPs should have a high affinity for aromatic, aliphatic, and positively charged SCAs. Amino-functionalization of PS NPs should improve the adsorption of proteins with a high content of aromatic and negatively charged AAs exposed to the nanomaterial-accessible surface area at physiological pH. While carboxylated PS NPs should have a preference for binding proteins with high content of positivity charged AAs.

References

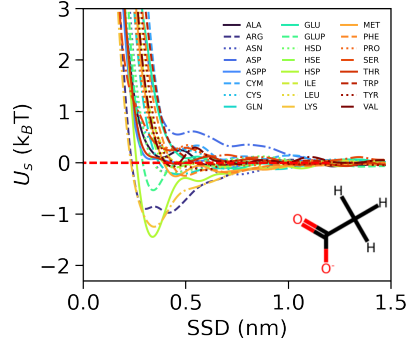
- S. Tsuzuki, K. Honda, T. Uchimaru, M. Mikami and K. Tanabe, *Journal of the American Chemical Society*, 2000, **122**, 11450–11458.
- Y. Zhu, S. Alqahtani and X. Hu, *Molecules*, 2021, **26**, 1776.
- B. L. Schottel, H. T. Chifotides and K. R. Dunbar, *Chemical Society Reviews*, 2008, **37**, 68–83.
- A. Frontera, D. Quinonero and P. M. Deya, *Wiley Interdisciplinary Reviews: Computational Molecular Science*, 2011, **1**, 440–459.
- A. S. Mahadevi and G. N. Sastry, *Chemical reviews*, 2013, **113**, 2100–2138.



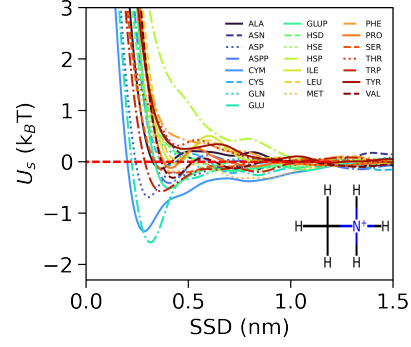
(a) SCA-CH₃COOH PMFs.



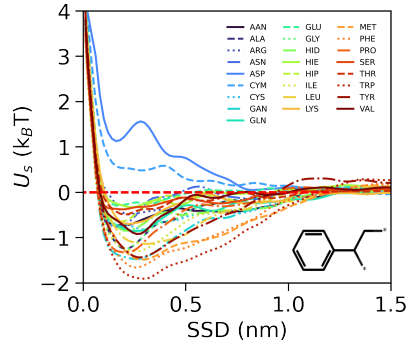
(b) SCA-CH₃NH₂ PMFs.



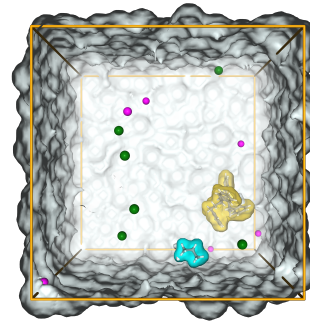
(c) SCA-CH₃COO⁻ PMFs.



(d) SCA-CH₃NH₃⁺ PMFs.

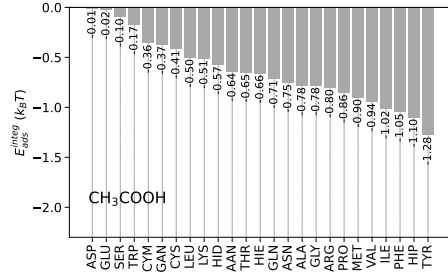


(e) SCA-PS_{tetramer} PMFs.

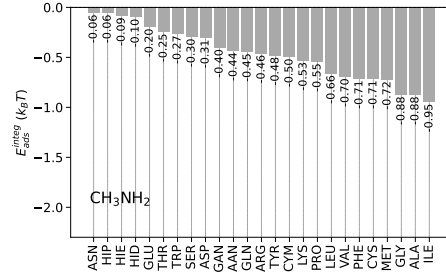


(f) VAL-PS system.

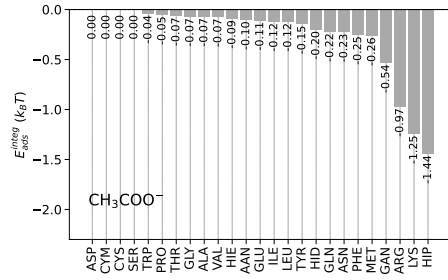
Figure S1 Potential of mean force curves for short-range interactions between SCA fragments and material CG beads ((a)-(e)). The potentials are plotted in $r_{\text{COM-COM}} - r_g$ coordinates. The same potentials in tabulated form are used for calculating the adsorption UA heatmaps. (f) Example of simulation box.



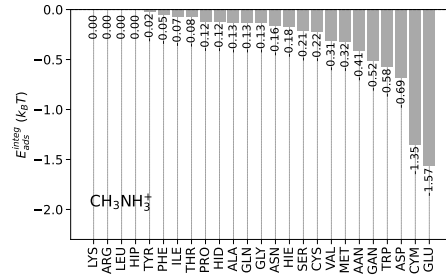
(a) The CH_3COOH fragment.



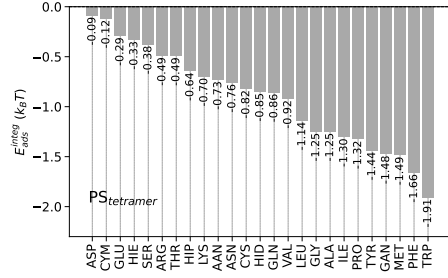
(b) The CH_3NH_2 fragment.



(c) The CH_3COO^- fragment.



(d) The CH_3NH_3^+ fragment.



(e) The $\text{PS}_{\text{tetramer}}$ fragment.

Figure S2 Energy values obtained from integration of potential of mean force curves for short-range interactions between SCA fragments and decorative material CG beads ((a)-(e)). Composite trapezoidal rule was applied (via *numpy.trapz* Python library).

2 CG models of polystyrene NPs.

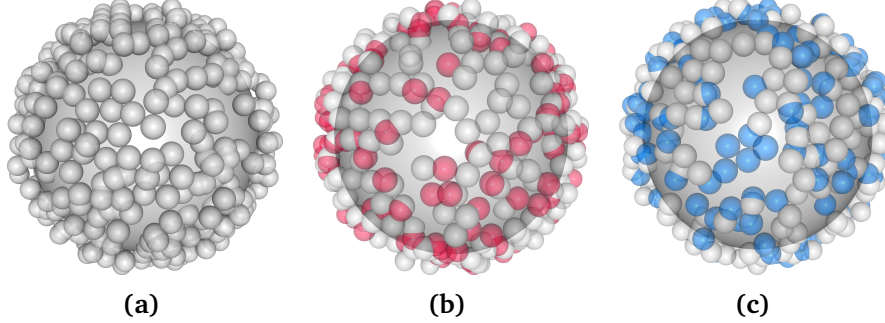


Figure S3 CG models of 10 nm PS NPs in used in calculations: from left to right: PS (a), PS-COOH (b), PS-NH₂ (c) NPs. The grey coloured beads represent PS, the red colored beads represent ionised COO⁻ fragment, the blue coloured beads represent ionised NH₃⁺ fragment

3 Close contacts for protein-NP interaction.

Table S1 UA docking poses, their rotational coordinates, corresponding adsorption energy, and a list of close contacts within 0.5 nm from the PS NP surface.

NP	Protein	$\phi, ^\circ$	$\theta, ^\circ$	$E_{ads}, k_B T$	Nearby residues (residue number : chain ID)
PS	IGH	330.0	35.0	-24.6	ARG18:C, ARG24:C, ARG29:C, SER67:C, THR69:C, ASP70:C
		345.0	115.0	-13.7	ILE266:B, LEU328:B, GLN330:B, LYS336:B
		60.0	45.0	-27.1	GLU542:A, ALA546:A, ALA553:A, LYS557:A, GLU571:A, LYS574:A, LEU575:A, ALA578:A
	HSA	145.0	30.0	-17.5	GLU570:A, LYS573:A, LYS574:A, ALA577:A, GLN580:A
		305.0	95.0	-28.9	GLU16:A, GLU17:A, HSD128:A, GLU131:A, LYS162:A, THR166:A, GLN170:A
		20.0	60.0	-25.8	LYS402:A, LYS439:A, GLU556:A, LYS560:A, ASP562:A
	FG	345.0	165.0	-19.2	GLU227:A, LYS313:A, ASP314:A, LYS317:A
		55.0	105.0	-20.7	SER304:A, ASP375:A, LYS378:A, GLU382:A, LYS389:A, GLU442:A
		205.0	75.0	-23.9	PHE74:J, GLU75:J, LYS78:J, LYS81:J
	APOAI	345.0	30.0	-19.5	LYS273:L, ASP318:L, ASN319:L, PHE322:L, GLU323:L, GLY324:L
		30.0	105.0	-20.7	LYS78:G, LYS81:G, ASN89:G, ILE93:G
		30.0	25.0	-9.7	LYS173:L, ASN175:L, PRO269:L, ALA271:L
PS-COOH	FG	210.0	150.0	-12.1	PRO307:H, LEU172:I, LYS173:I, ASN175:I, PRO269:I, ALA271:I
		115.0	130.0	-20.8	ARG124:G, LYS125:G, ARG108:I, GLU112:I
		95.0	110.0	-43.4	GLN41:A, LYS45:A, LEU46:A, LEU47:A
	APOAI	195.0	155.0	-34.9	ASP51:A, LYS59:A, SER201:B, GLU205:B, LYS206:B, LYS208:B, LEU211:B, ARG215:B, ASN241:B
		340.0	100.0	-29.9	PRO121:A, GLU125:A, GLU139:B, LEU163:B
		340.0	85.0	-25.2	LYS663:B, LYS700:B, ASP704:B, TYR708:B, GLU711:B, ARG714:B, GLN715:B, ARG718:B
	C3	140.0	110.0	-22.4	ASN1271:B, ASP1273:B, THR1286:B, ARG1288:B, HSD1290:B
		230.0	150.0	-16.7	GLN1625:B, GLU1632:B, VAL1636:B, PHE1637:B
		60.0	85.0	-18.7	THR1148:B, ASP1152:B, GLU1155:B, LYS1181:B
	C3	195.0	90.0	-16.9	SER548:A, GLN558:A, LEU768:B, ASN770:B, PHE898:B

Table S2 UA docking poses, their rotational coordinates, corresponding adsorption energy, and a list of close contacts within 0.5 nm from the PS-COOH NP surface.

NP	Protein	$\phi, ^\circ$	$\theta, ^\circ$	$E_{ads}, k_B T$	Nearby residues (residue number : chain ID)
PS-COOH	IGH	85.0	75.0	-35.0	LYS13:B, PRO14:B, GLY15:B, ALA16:B, SER113:B, SER115:B
		330.0	35.0	-45.9	ARG18:C, ARG24:C, ARG29:C, SER67:C, THR69:C, ASP70:C
		135.0	55.0	-23.3	LYS19:A, THR70:A, ASP72:A, SER74:A, GLU81:A
	HSA	125.0	55.0	-17.3	GLU501:A, LYS538:A, GLN580:A, ALA581:A
		70.0	50.0	-12.5	GLU542:A, GLN543:A, ALA546:A, ALA581:A
		80.0	10.0	-23.9	ALA241:L, ILE242:L, PRO243:L, ASN390:L, THR393:L, ILE394:L
	FG	30.0	20.0	-24.6	LYS173:L, ALA241:L, PRO269:L, ALA271:L
		210.0	155.0	-28.2	LEU172:I, LYS173:I, ASN175:I, SER240:I, ALA241:I, PRO269:I, ALA271:I, ASP272:I
		155.0	165.0	-23.3	SER240:I, ALA241:I, ILE242:I, PRO243:I, ASN390:I, THR393:I, ILE394:I
	APOAI	170.0	20.0	-19.9	LYS162:L, GLY186:L, SER187:L, ILE394:L, GLY395:L
		95.0	150.0	-14.3	LYS159:I, GLY160:I, LYS162:I, GLY186:I, SER187:I
		90.0	115.0	-48.7	GLN41:A, LEU42:A, ASN43:A, LEU44:A, LYS45:A, LEU46:A
PS-COOH	C3	70.0	15.0	-28.0	HIS193:A, THR197:A, LEU200:A, SER204:A, ALA207:A, LYS208:A
		345.0	95.0	-41.2	GLU711:B, ARG714:B, GLN715:B, ARG718:B

Table S3 UA docking poses, their rotational coordinates, corresponding adsorption energy, and a list of close contacts within 0.5 nm from the PS-NH₂ NP surface.

NP	Protein	$\phi, ^\circ$	$\theta, ^\circ$	$E_{ads}, k_B T$	Nearby residues (residue number : chain ID)
PS-NH ₂	IGH	345.0	110.0	-2.6	ILE266:B, LEU328:B, GLN330:B, ASN334:B, LYS336:B
		305.0	100.0	-50.9	GLU17:A, LYS162:A, GLN170:A, PRO282:A
	HSA	345.0	165.0	-42.4	GLU227:A, LYS313:A, ASP314:A, LYS317:A
		270.0	150.0	-40.1	LYS262:A, TYR263:A, GLU266:A, ASN267:A
		270.0	75.0	-37.9	ASN44:A, GLU48:A, LYS51:A, THR52:A, ALA55:A
		215.0	115.0	-37.7	SER58:A, GLU60:A, ASN61:A, ASP63:A, LYS64:A, GLN94:A
		305.0	55.0	-29.6	ASP121:A, THR125:A, HSD128:A, ASP129:A, GLN170:A, ALA172:A, LYS174:A
		260.0	35.0	-27.4	GLU119:A, VAL122:A, THR125:A, ASP129:A, LYS564:A, GLU565:A
		60.0	110.0	-24.6	SER304:A, GLU311:A, ASP375:A, LYS378:A
		45.0	65.0	-36.3	SER37:J, ASP38:J, GLU39:J, LYS38:L
		185.0	115.0	-33.5	ASP38:G, GLU39:G, ARG199:G, LYS127:H
		225.0	110.0	-22.4	SER31:G, PHE35:G, SER37:G, ALA68:K
	FG	200.0	85.0	-40.8	PHE35:G, SER37:G, ASP38:G, GLU39:G, ASP40:G
		340.0	80.0	-19.7	LEU66:H, SER31:J, PRO34:J, PHE35:J
	APOAI	170.0	85.0	-25.9	GLN69:B, GLU76:B, GLU80:B, ARG83:B
		145.0	60.0	-25.0	ASP73:B, GLU76:B, LYS77:B, GLU80:B, ARG83:B
		215.0	120.0	-23.7	ASP73:A, GLU80:A, ARG83:A, GLN84:A
		195.0	105.0	-22.1	GLN69:A, TRP72:A, GLU76:A, GLU80:A, ARG83:A
		310.0	55.0	-23.7	LYS226:A, VAL227:A, LEU230:A, GLU234:A
		325.0	165.0	-19.6	LEU219:B, LEU222:B, GLU223:B, LYS226:B, VAL227:B, PHE229:B, TYR236:B
		295.0	140.0	-16.1	ASP1:A, GLU2:A, ASP9:A, ARG10:A, GLU234:B, TYR236:B
	C3	260.0	40.0	-11.2	PRO220:A, GLU223:A, VAL227:A, ARG27:B, SER31:B, GLN32:B
		245.0	155.0	-65.6	GLN1616:B, GLN1621:B, GLN1625:B, GLU1632:B, PHE1637:B
		295.0	140.0	-42.5	ASP1613:B, GLN1616:B, ASP1617:B, GLU1618:B, GLN1621:B
		125.0	90.0	-39.6	GLU1013:B, HSD1267:B, GLU1269:B, GLU1292:B

4 Docking poses for proteins adsorbed at the PS NPs.

4.1 The C3 protein.

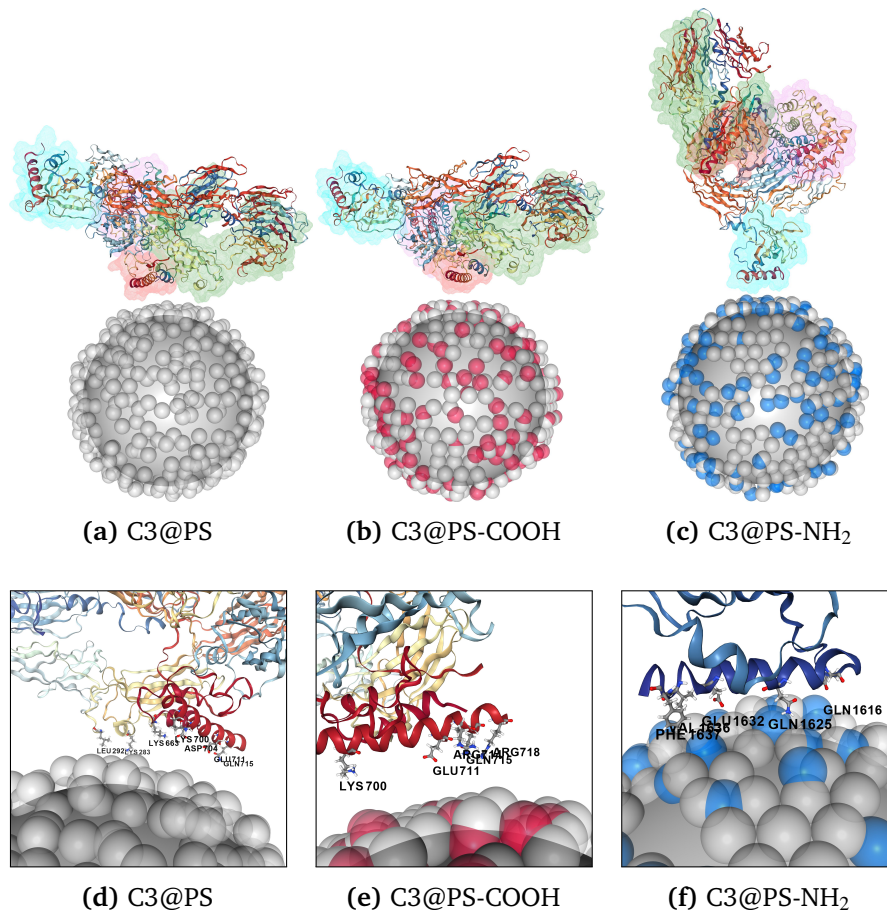


Figure S4 The lowest energy configurations of C3 protein bound to various PS NPs as predicted by the *UA* modelling (a-c). The compstatin site is shown in green, the ANA fragment is coloured in red, the TED unit is shown in violet and C345C is highlighted in cyan colour. . Sub-figures (d-f): snapshots for contact residues. The residues found in 5.0 Å cut-off near the surface are visualised in hyperball style. The full list of closest contacts found within 5 Å cut-off from NP surface for all docking poses can be found in Tables S1, S2, S3.

4.2 The IGH protein.

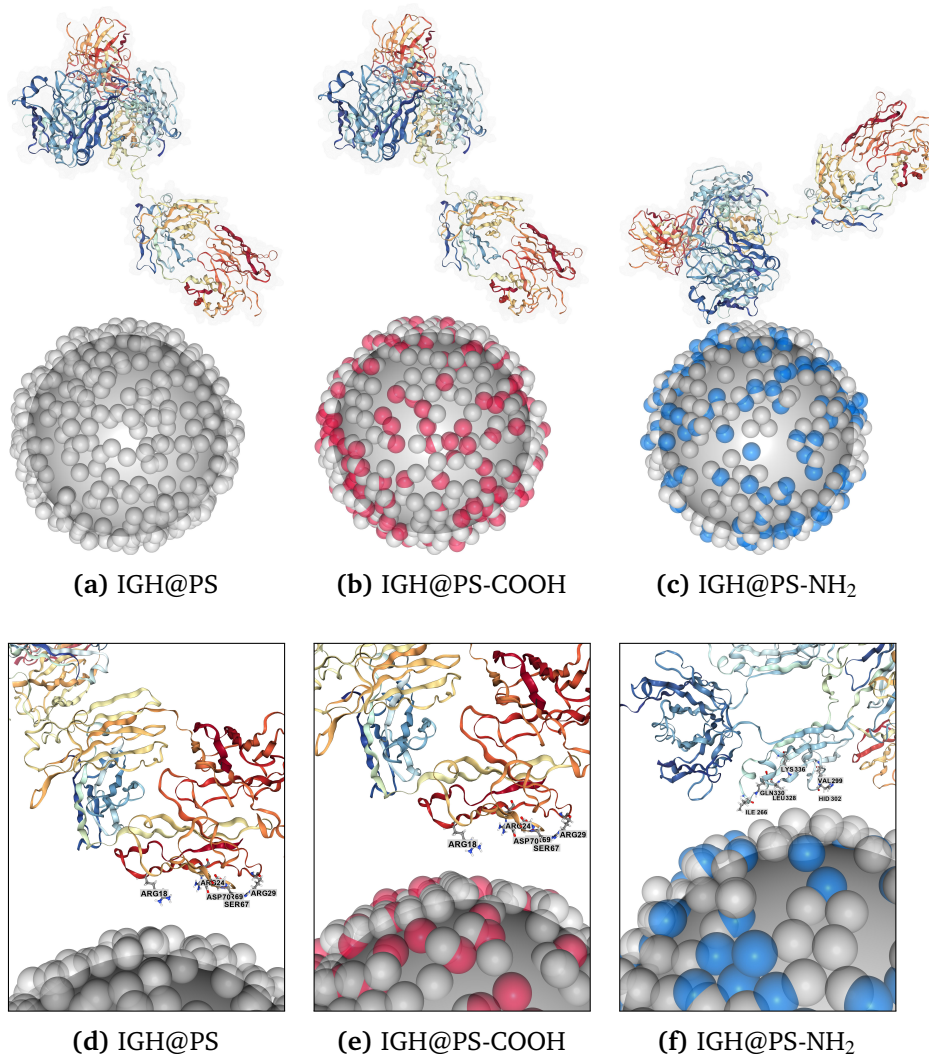


Figure S5 The lowest energy configurations of IGH protein bound to various PS NPs as predicted by the *UA* modelling (a-c). Sub-figures (d-f): snapshots for contact residues. The residues found in 5.0 Å cut-off near the surface are visualised in hyperball style. The full list of closest contacts found within 5 Å cut-off from NP surface for all docking poses can be found in Tables S1, S2, S3.

4.3 The FG protein.

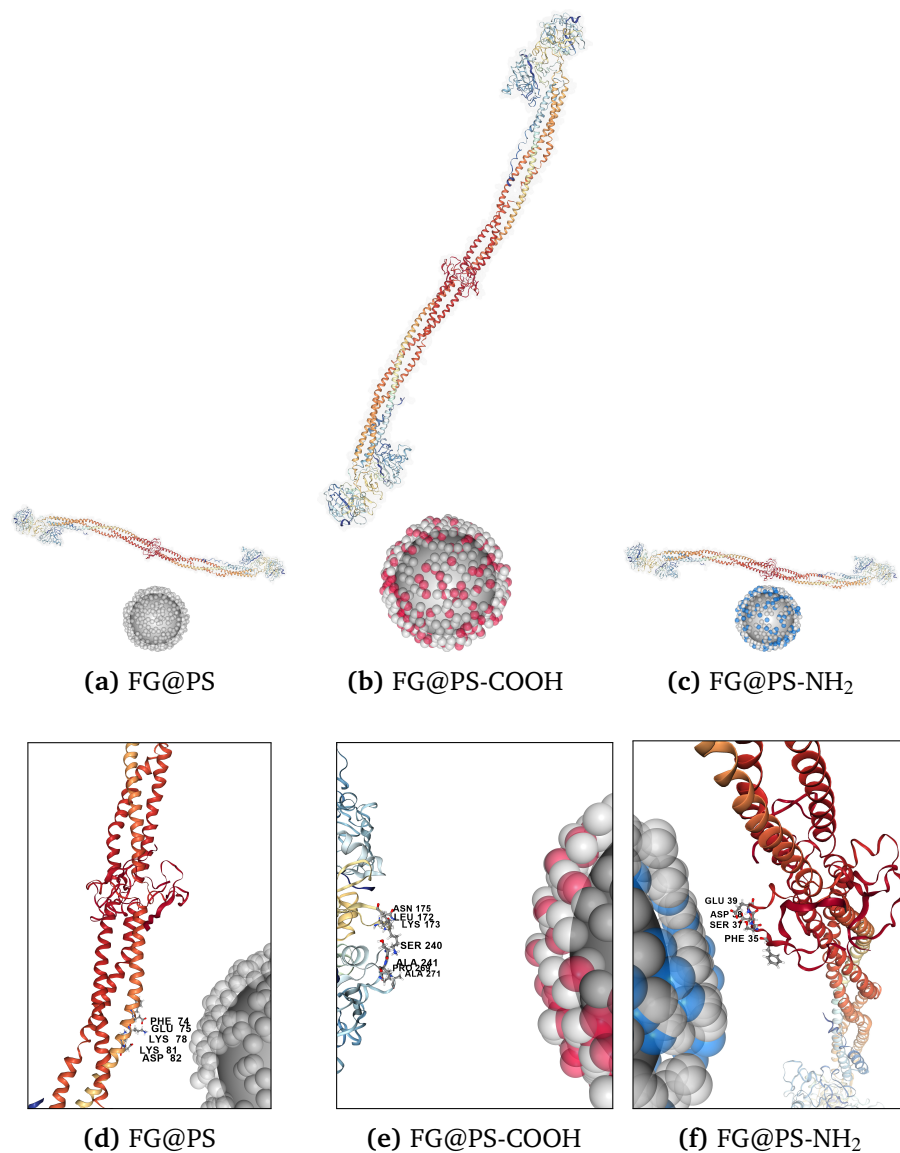


Figure S6 The lowest energy configurations of FG protein bound to various PS NPs as predicted by the UA modelling (a-c). Sub-figures (d-f): snapshots for contact residues. The residues found in 5.0 Å cut-off near the surface are visualised in hyperball style. The full list of closest contacts found within 5 Å cut-off from NP surface for all docking poses can be found in Tables S1, S2, S3.

4.4 The APO-AI protein.

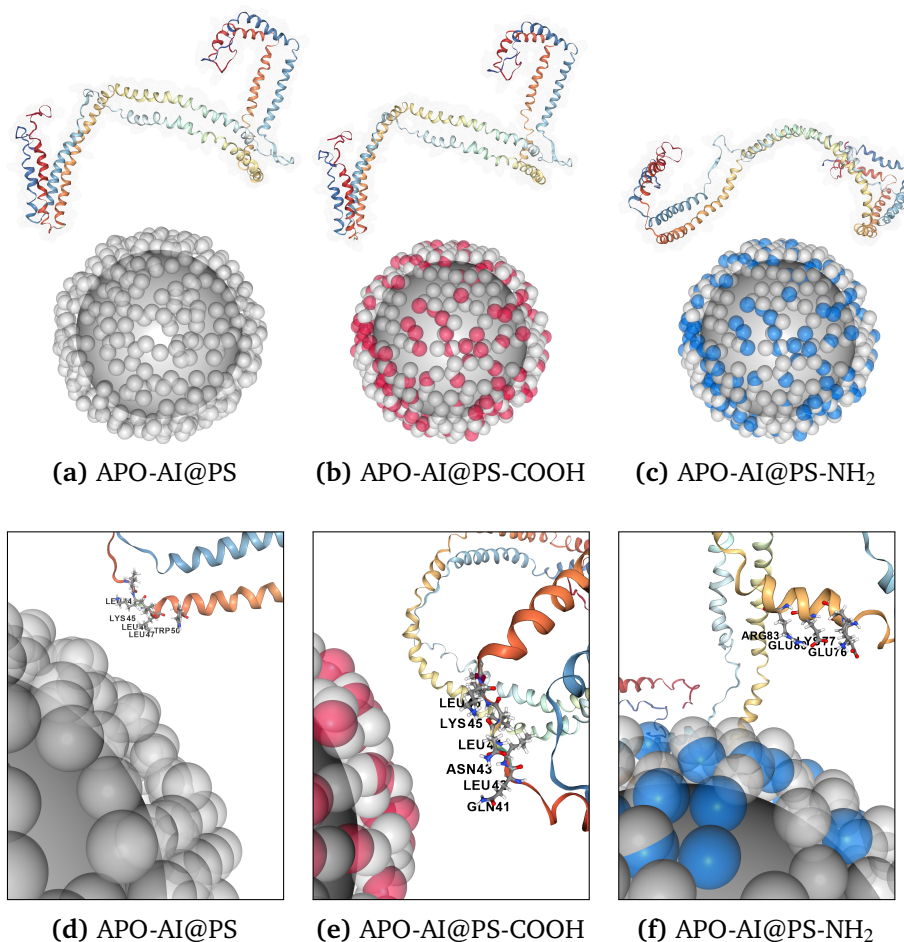


Figure S7 The lowest energy configurations of APO-AI protein bound to various PS NPs as predicted by the *UA* modelling (a-c). Sub-figures (d-f): snapshots for contact residues. The residues found in 5.0 Å cut-off near the surface are visualised in hyperball style. The full list of closest contacts found within 5 Å cut-off from NP surface for all docking poses can be found in Tables S1, S2, S3.

4.5 KMC: individual curves.

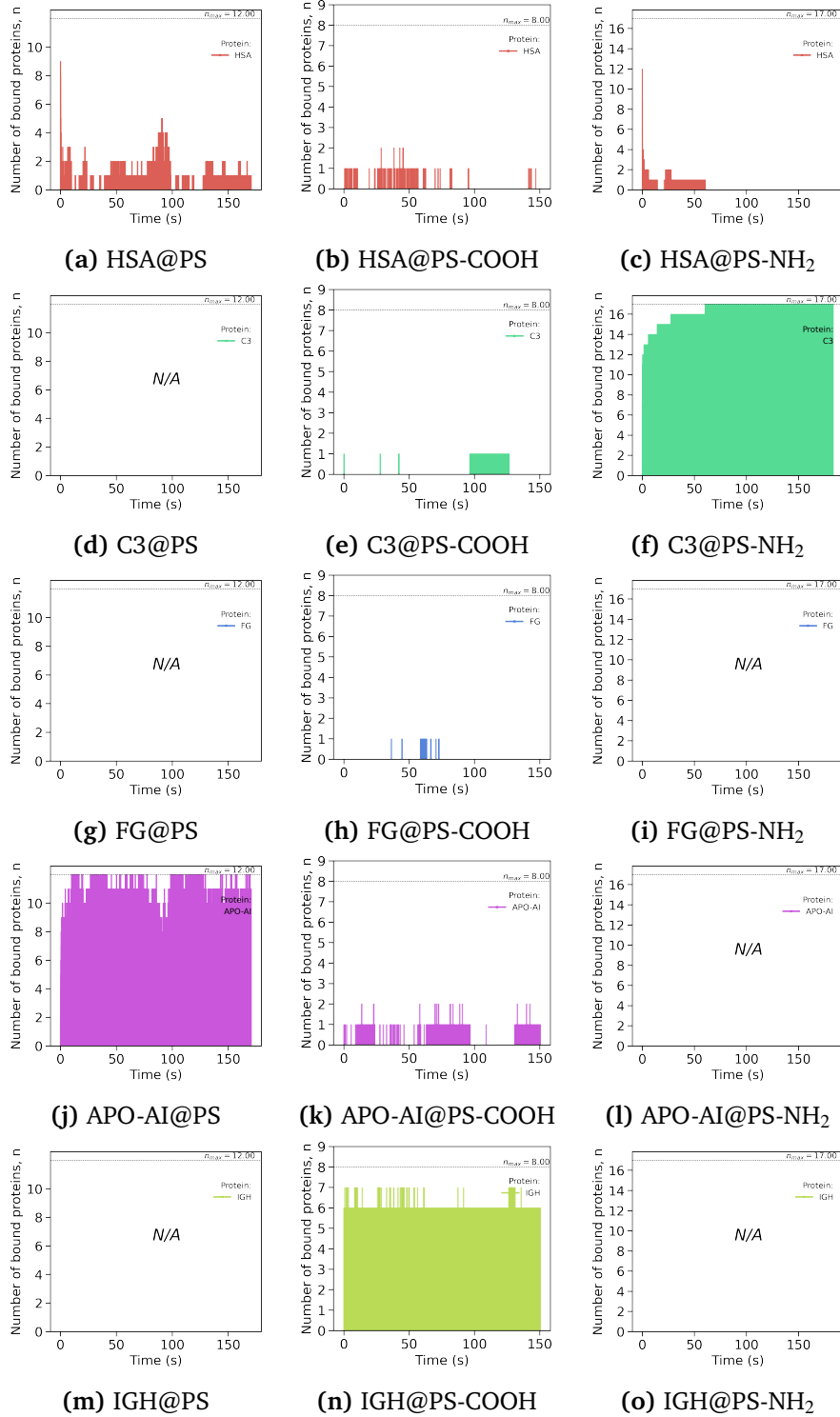


Figure S8 Breakdown of KMC adsorption curves for individual proteins: serum albumin (HSA), fibrinogen (FG), immunoglobulin (IGH), complement component 3 (C3), and apolipoprotein A1 (APO-AI). The absence of plots suggests that this protein was not present on the corona.