Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics.

Supporting Information

Adsorption of amyloid β40 monomer on charged gold nanoparticles and slabs: A molecular dynamics study

Pandurangan Kalipillai and Ethayaraja Mani*

Polymer Engineering and Colloid Science Lab, Department of Chemical Engineering, Indian Institute of Technology Madras, Chennai - 600036, India

E-mail: ethaya@iitm.ac.in

I.Force field validation

To ensure the right choice of force field for the protein and water models for solvent, four different force field were used for simulation of monomer Aβ40 in water. The details of water model, force fields and potential cut-offs for non-bonded parameters are given in Table.1

Table 1: Force field, water models and potential cutoffs for non-bonded interactions.

Force field	**Water model**	$\mathbf{r}_c/\mathbf{r}_{list}$	$\mathbf{r}_{vdw}$
AMBER03	TIP3P	0.8	0.8
CHARMM22 + CMAP	TIP3P	1.2	1.2
OPLS-AA	TIP4P	1.0	1.0
GROMOS96 53A6	SPC	1.0	1.0

Table 2: Average secondary structure distribution (in percentage)

Force field	**Coil**	**β-sheet**	**Bend**	**Turn**	**α-Helix**
AMBER03	27 (29)	0 (0)	7 (13)	27 (19)	39 (39)
CHARMM22 + CMAP	19 (21)	0 (0)	10 (9)	14 (12)	57 (58)
OPLS-AA	34 (31)	6 (16)	27 (23)	23 (18)	10 (12)

The experimentally reported secondary structure of oligomer Aβ40 in water: α-helix 22%, coil 18%, and β sheet + bends + turns 60%.

Table 3: Average secondary structure distribution (in percentage) obtained from GROMOS96 53A6 force field.

MD study	**α-Helix**	**β-sheet**	**Others***
This work	19(±2)	19 (±4)	60 (±4)
Ref[1]	24 (±3)	11 (±2)	65(±5)
Ref[2]	20 (±2)	15(±4)	65(±5)

The standard deviation given in the parenthesis are obtained by averaging three set of independent simulation.

Table 4: $\mathbf{R}_g$

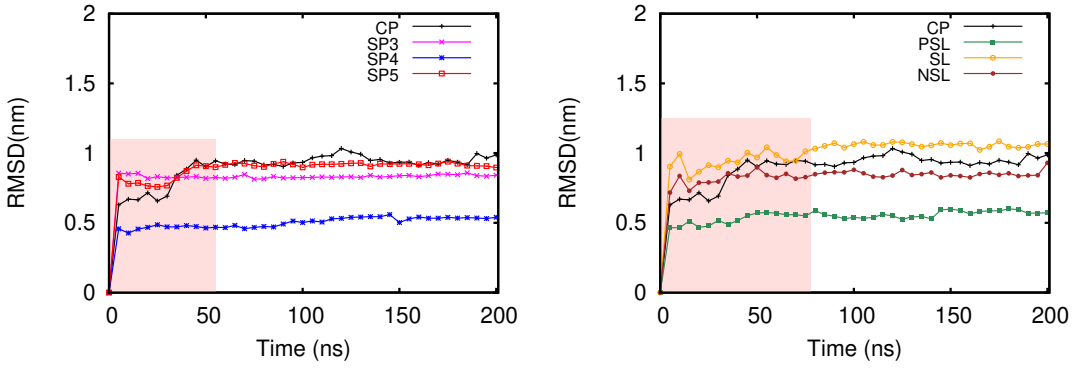
.

Force field	$\mathbf{R}_g$(nm)	$\mathbf{R}_g^{ref1}$(nm)
AMBER03	1.10	1.03
CHARMM22 + CMAP	1.35	1.30
GROMOS96 53A6	0.99	1.05
OPLS-AA	0.96	0.96

The experimentally reported value of R_g for the oligomer Aβ40 in solution is 0.9 (±0.1) nm.

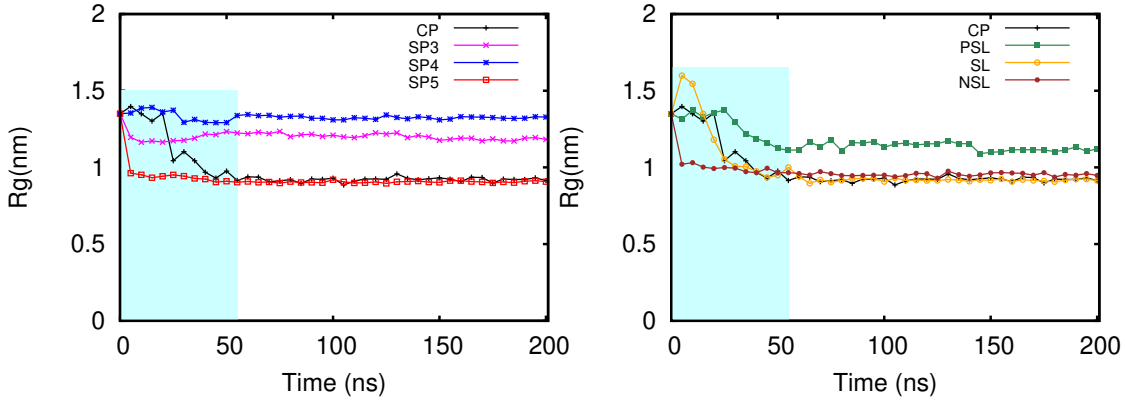
II. Convergence check

The structural properties such as RMSD and Rg values are plotted as a function of simulation time and shown in Figures S1 and S2 to assess the attainment of equilibration. After 50 ns, both quantities show steady values without any drift indicating that the system has reached equilibration. Of the total 200 ns trajectory, the last 100 ns trajectory is used to calculate average properties.



(a) (b)

Figure S1: Time evolution of the root mean square deviation (RMSD) of Aβ40 (CP) with (a) SP3, SP4 and SP5. (b) PSL, SL and NSL.



(a) (b)

Figure S2: Time evolution of the radius of gyration (Rg) of Aβ40: (a)CP, SP3, SP4 and SP5. (b) PSL, SL and NSL.

Table 5: Parameters used in binding free energy calculation.[3]

Parameters(P)	**P notation in code**	**Values**
Solute dielectric constant	pdie	2.0
Solvent dielectric constant	sdie	80
Vacuum dielectric constant	vdie	1.0
Surface tension(kJ/mol A^2)	gamma	0.022678
Probe radius (A^o)	sasrad	1.40
Offset constant (kJ/mol)	sasaconstant	3.84982
Temperature (K)	APtemp	300

III.Binding free energy calculation

To assess the strength of adsorption, binding free energy between amyloid protein and substate (gold nanoparticle and slab) is calculated using Molecular Mechanics - Poisson Boltzmann Solvent Area (MM-PBSA) method.[3] In this method, the binding free energy (ΔG_{bind}) is decomposed into two parts: molecular mechanics and solvation free energy.

$\Delta G_{bind} = \Delta E_{MM} + \Delta G_{Solv}$

where, $\Delta E_{MM} = \Delta E_{vdW} + \Delta E_{elect}$ and

$\Delta G_{Solv} = \Delta G_{polar} + \Delta G_{apolar}$.

The parameters used in calculation of binding free energy are shown in Table 5. The MM-PBSA binding free energy values are reported in Table. 6. These values suggest that binding free energy is more negative for SP3 and SP4 systems, yet the van der Waal interaction contributes more to the overall binding energy.

Table 6: Binding Free Energy of Aβ40 with different AuNP surfaces

Energy (kJ/mol)	**SP3**	**SP4**	**SP5**	**PSL**	**SL**	**NSL**
ΔE_{vdW}	-284.4(0.3)	-269.2(1.0)	-77.3(0.2)	-98.9(1.2)	-39.5(0.1)	-37.2(0.1)
ΔE_{elect}	24.4(0.0)	35.5(0.0)	45.6(0.10)	-19.2(0.09)	0.0 (0.0)	17.4(.04)
ΔG_{polar}	28.9(0.22)	23.0(0.2)	4.8(0.01)	16.2(0.24)	-1.0(0.0)	3.1(1.0)
ΔG_{apolar}	-5.0(0.14)	-5.1(0.16)	-2.3(0.01)	-1.9(0.61)	-0.8(0.03)	-0.8(0.26)
ΔG_{bind}	-236.1(0.7)	-216(0.8)	-29.2(0.4)	-104(1.15)	-42(0.23)	-17.5(0.20)

References

(1) Xu, Y.; Shen, J.; Luo, X.; Zhu, W.; Chen, K.; Ma, J.; Jiang, H. Conformational transition of amyloid β-peptide. *Proceedings of the National Academy of Sciences* **2005**, *102*, 5403–5407.

(2) Olubiyi, O. O.; Strodel, B. Structures of the amyloid β-peptides Aβ1–40 and Aβ1–42 as influenced by pH and a D-peptide. *The Journal of Physical Chemistry B* **2012**, *116*, 3280–3291.

(3) Kumari, R.; Kumar, R.; Consortium, O. S. D. D.; Lynn, A. g_mmpbsa A GROMACS tool for high-throughput MM-PBSA calculations. *Journal of chemical information and modeling* **2014**, *54*, 1951–1962.