Electronic Supplementary Material (ESI) for RSC Advances.

Modelling of interactions between A$\beta(25-35)$ peptide and phospholipid bilayers: effects of cholesterol and lipid saturation

Supplementary Information for Reviewers

Inna Ermilova, Alexander P. Lyubartsev

Department of Materials and Environmental Chemistry,
Stockholm University, SE 106 91, Stockholm, Sweden

We have carried out 50 ns molecular dynamics simulations for a single A$\beta(25-35)$ peptide in water using GAFF and Amber-99SB-ILDN force field[1]. All simulation parameters were the same as in other simulations described in this paper. We have computed torsional angle distribution and determined secondary structures. Comparison also made with experimental 1QXC structure solved by D'Ursi et al[2] for peptides in solution with water (80 %) and HFIP (20 %), by the best fit of molecular dynamics simulated structures to NMR data.

Torsion angle distribution

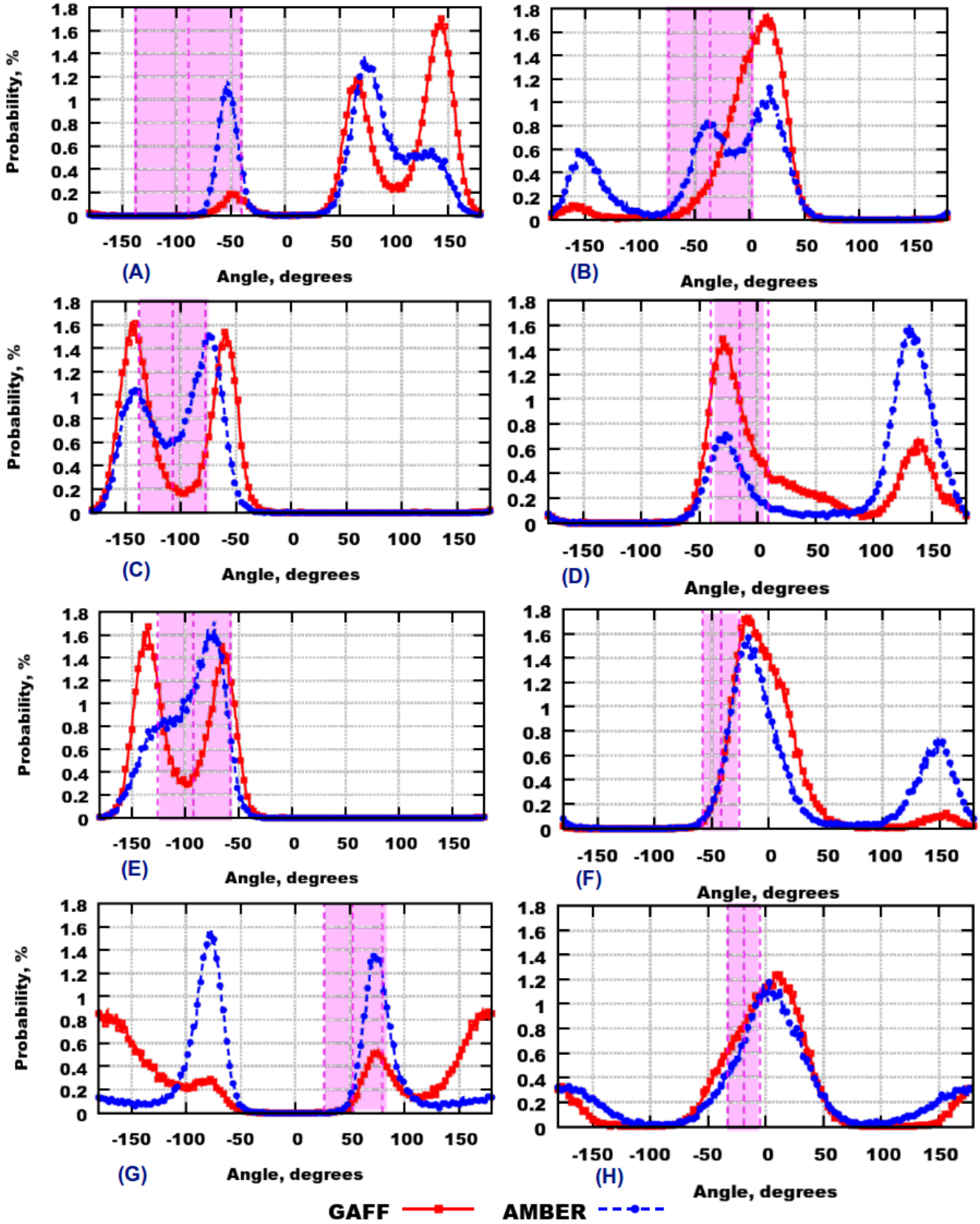

Figure Si1. Distributions of dihedrals ϕ and ψ for residues SER_{26}-GLY_{29} from MD simulations of single peptides in water. (A) SER_{26} (ϕ) (B) SER_{26} (ψ) (C) ASN_{27} (ϕ) (D) ASN_{27} (ψ) (E) LYS_{28} (ϕ) (F) LYS_{28} (ψ) (G) GLY_{29} (ϕ) (H) GLY_{29} (ψ) Vertical magenta bars represent experimental results from the structure 1QXC solved by D'Ursi et al.[2] for peptides in solution with water (80 %) and HFIP (20 %).

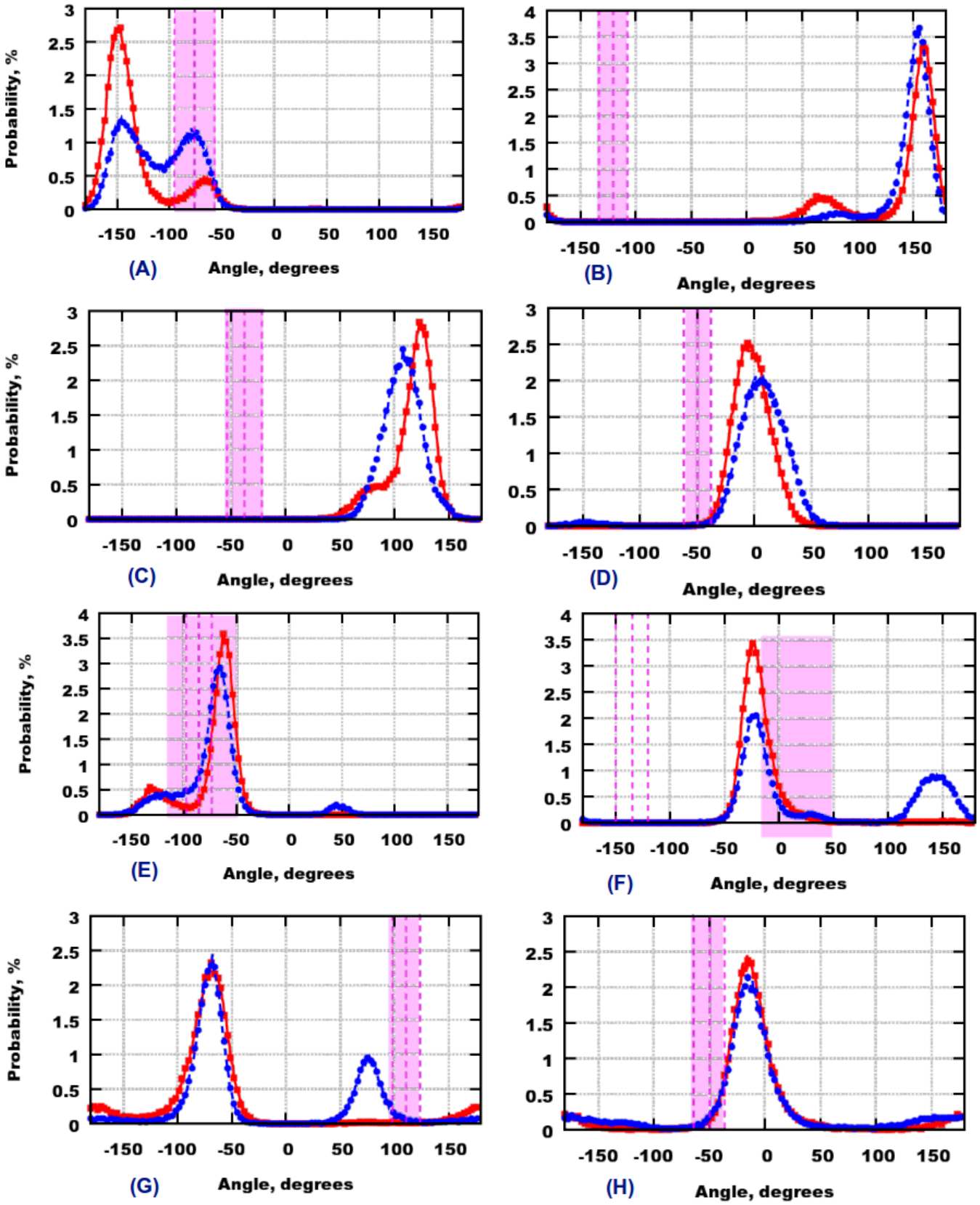

Figure Si2. Distributions of dihedrals ϕ and ψ for residues ALA_{30}-GLY_{33} from MD simulations of single peptides in water. (A) ALA_{30} (ϕ) (B) ALA_{30} (ψ) (C) ILE_{31} (ϕ) (D) ILE_{31} (ψ) (E) ILE_{32} (ϕ) (F) ILE_{32} (ψ) (G) GLY_{33} (ϕ) (H) GLY_{33} (ψ) Vertical magenta bars represent experimental results from the structure 1QXC solved by D'Ursi et al.[2] for peptides in solution with water (80 %) and HFIP (20 %).

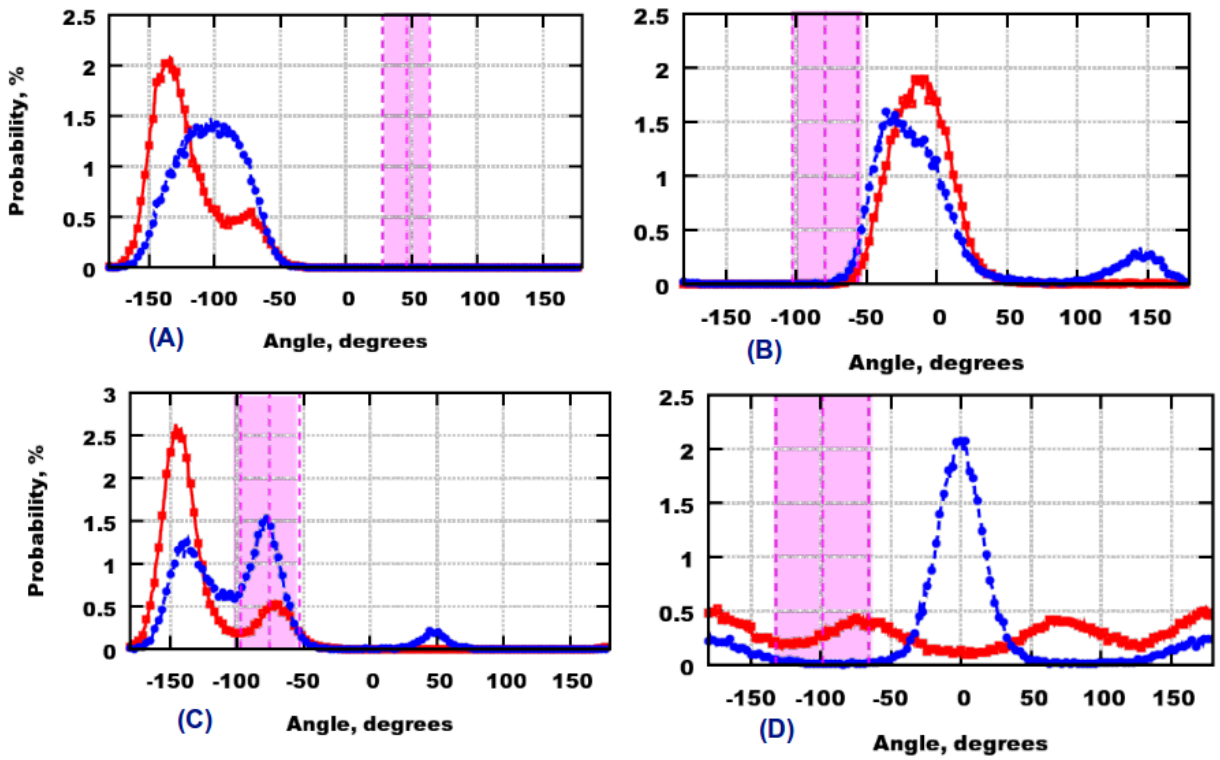

Figure Si3. Distributions of dihedrals ϕ and ψ for other residues from MD simulations of single peptides in water. (A) LEU_{34} (ϕ) (B) LEU_{34} (ψ) (C) MET_{35} (ϕ) (MET_{35} has no ψ here) (D) GLY_{25} (ψ) (GLY_{25} has no ϕ here) Vertical magenta bars represent experimental results from the structure 1QXC solved by D'Ursi et al. [2] for peptides in solution with water (80 %) and HFIP (20 %).

Secondary structures

Secondary structures A$\beta(25-35)$ obtained in 50 ns simulations using GAFF and Amber-99SB-ILDN force field[1] were computed by the VMD software. Comparison also made with experimental structures found in the PDB database .

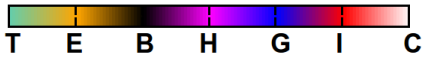

Figure Si4. Palettes for secondary structure codes used in this work. "T" - turn, "E" - extended conformation, "B" - isolated bridge, "H" - alpha helix, "G" - 3-10 helix, "I" - π-helix, "C" - coil.

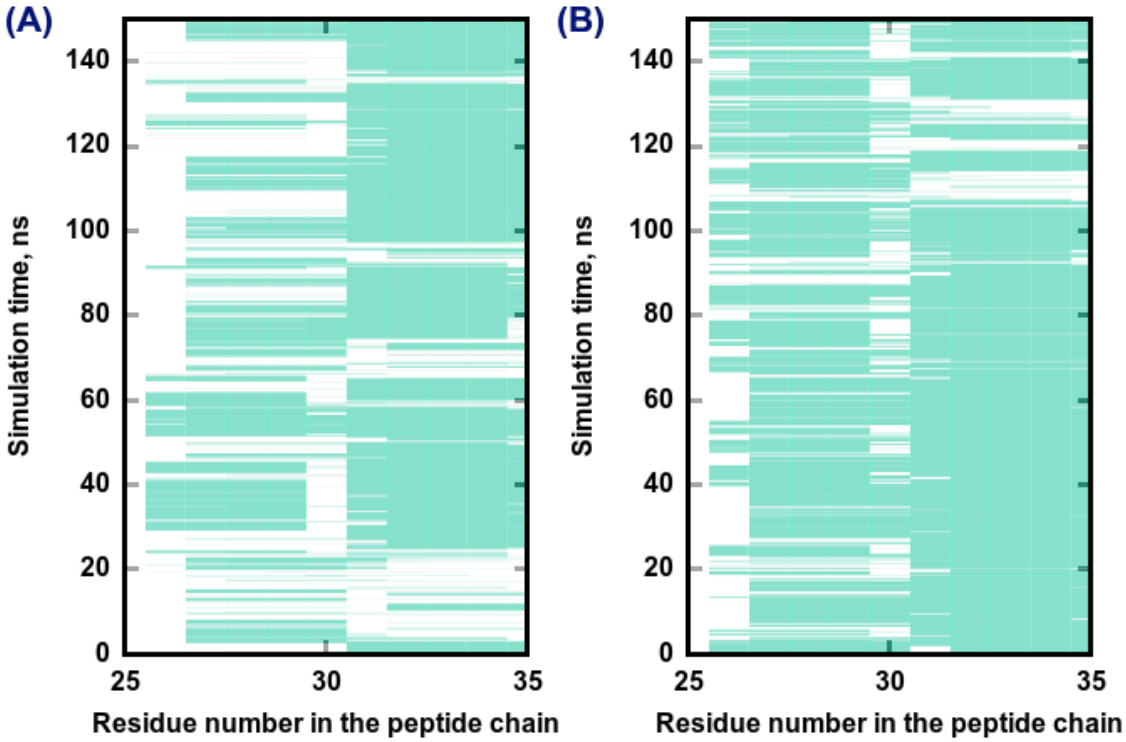

Figure Si5. Secondary structures computed from MD simulations of single peptides in water. (A) Amber-FF99SB-ILDN (B) GAFF

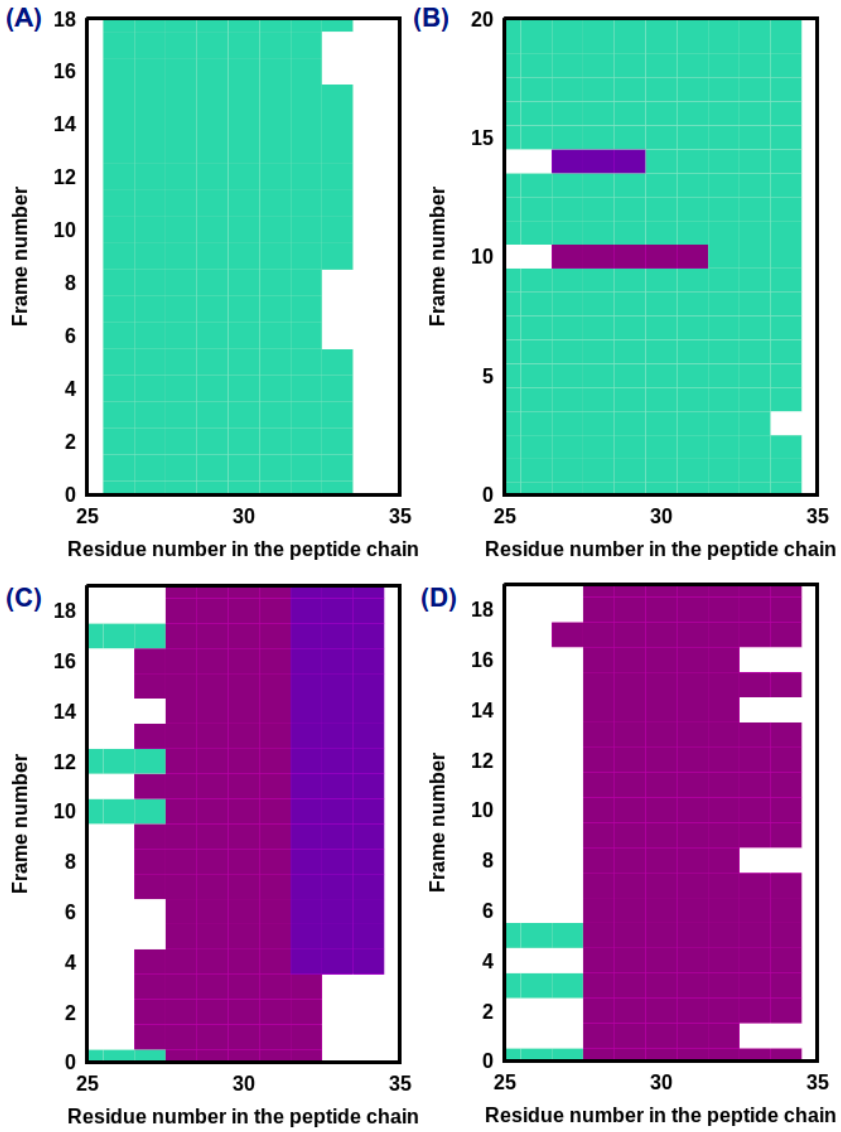

Figure Si6. Secondary structures computed from *pdb*-trajectories published in PDB-database for the following structures. (A) 1QXC (20% of HFIP and 80% of water v/v) from D'Ursi et al.[2], best frames from PDB-databank (B) 1QYT peptides in 100 mM of SDS aqueous solution from D'Ursi et al.[2], best frames from PDB-databank (C) 1QWP (80% of HFIP and 20% of water v/v) from D'Ursi et al.[2], best frames from PDB-databank (D) 1QCM peptides in Deuterated sodium dodecyl sulfate. Note that cases A,B correspond to water-rich solvents which are more similar to our simulation conditions than cases C,D.

References

[1] K. Lindorff-Larsen, S. Piana, K. Palmo, P. Maragakis, J. L. Klepeis, R. O. Dror and D. E. Shaw, *Proteins*, 2010, **78**, 1950 – 1958.

[2] A.M.D'Ursi, M.R.Armenante, R.Guerrini, S.Salvadori, G.Sorrentino and D.Picone, *J. Med. Chem.*, 2004, **47**, 4231 – 4238.