https://doi.org/10.17952/38EPS.2026.P543

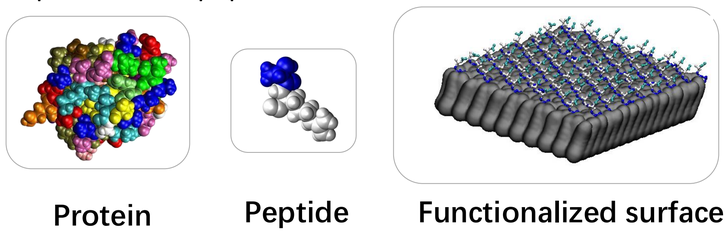
Computational Exploration of Nanoscale Chemical Patterning Using Short Peptides

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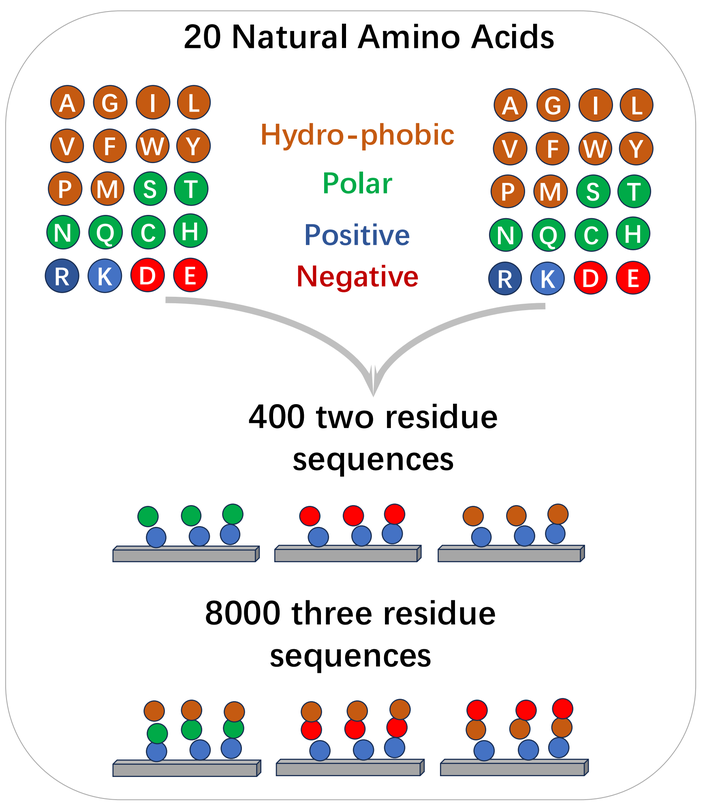
Overview

- Chemically patterned surfaces refers to the surfaces that are chemically and structurally diverse such as proteins and peptides.



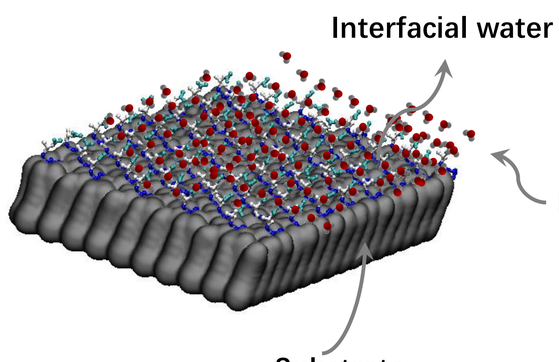
Protein | Peptide | Functionalized surface

- **Applications:** Enable selective nanoparticle binding, antifouling materials, and separation membranes.
- Peptides offer a versatile platform for surface functionalization due to their broad chemical and structural diversity.



- Assuming fixed substrate and grafting density, peptides can efficiently be modeled using computational approaches.

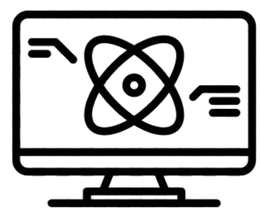
Background



Water at interface controls stickiness, i.e., adsorption property[1]

Polymeric materials such as peptides provide chemical and structural diversity[2]

Substrate mostly controls peptide assembly on surface[3]



This study: Computationally explores a **dipeptide library** at a fixed grafting density for wetting properties using MD simulation and predictive models.

System and Simulation

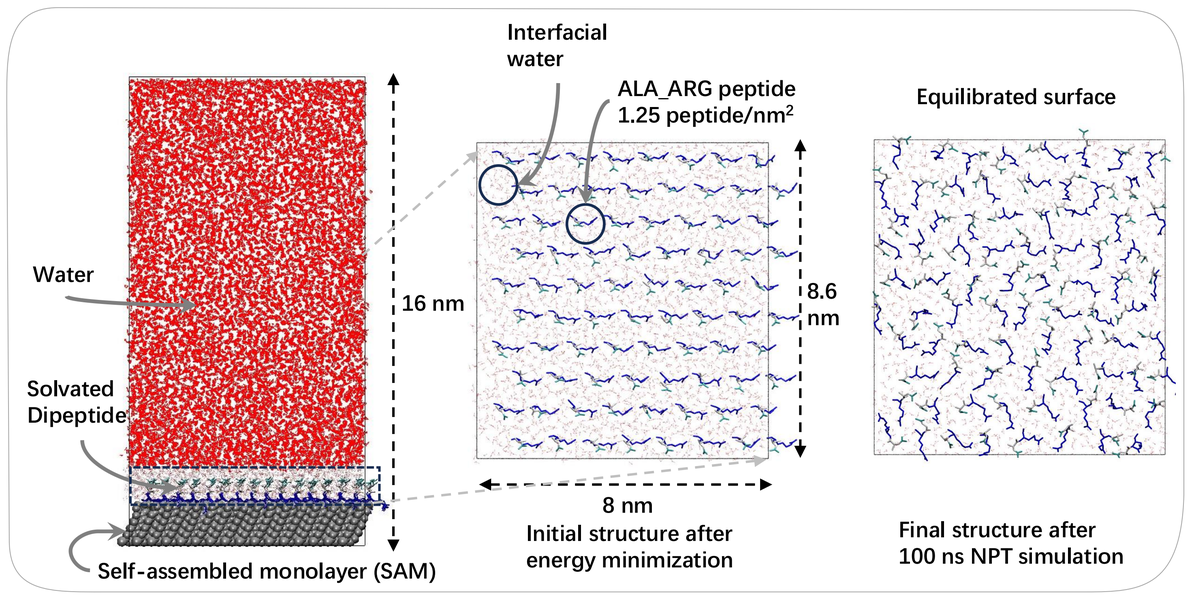
Step 1: *Avorgadro* — Create Single SAM strand and Functionalized SAM strand

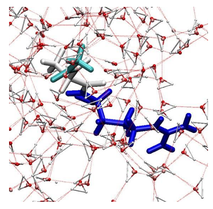
Step 2: *Python* — Build peptide-functionalized surface by repeating strands in xy plane to match 1.25 peptide/nm^2

Step 3: *AMBER* — Force field parameters SAM: GAFF2 Peptides: FF19SB Water Model: OPC (4 point)

Step 4: *VMD* — Visualize using visual molecular dynamics (VMD)

MD Simulation of 289 Dipeptides (Cys, Met, Pro excluded) Immobilized on SAM Surfaces to Probe Peptide–Water Interface Hydrophobicity



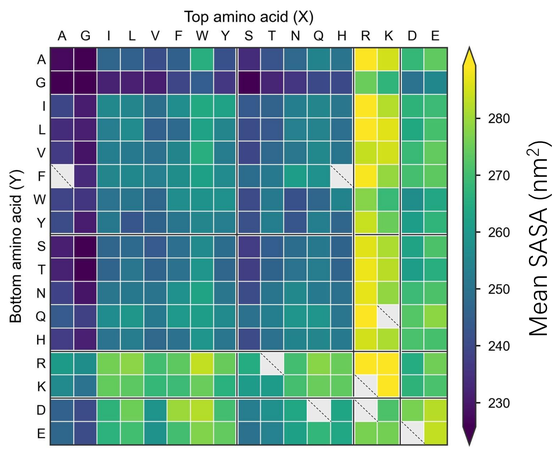


Surface Properties

- **SASA: Solvent accessible surface area**
  Calculated by rolling 0.14 nm probe sphere across the Van der Waals surface of the molecule
- **Peptide-water hydrogen bond:** calculated by Luzar-Chandler[4] geometric criteria
- **Mean Free OH fraction:** Calculated by defining hydration shell around 0.6 nm of peptide heavy atoms and getting the fraction that does not contribute to any hydrogen bond

Results

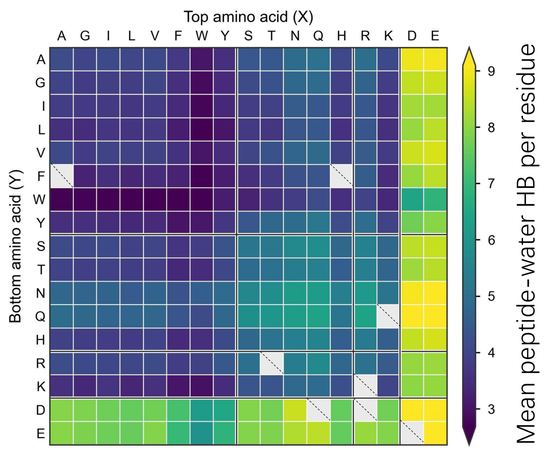
Solvent Accessible Surface Area (SASA)



*Gray boxes refer to missing data

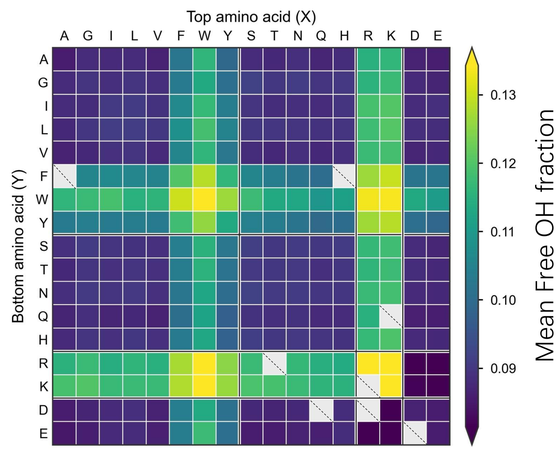
Long, flexible basic residues (R, K) consistently maximize total SASA (~ 280−311 nm^2)

Peptide-water hydrogen bonding

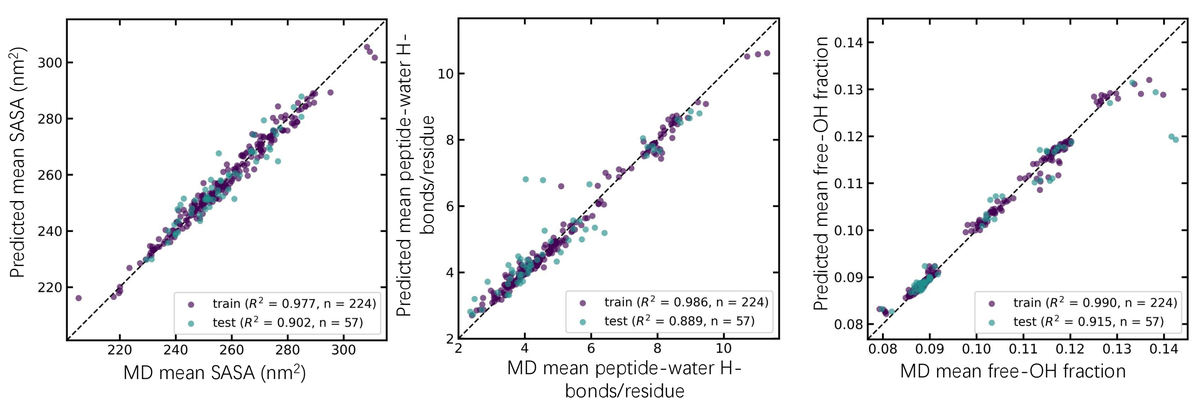


Anionic carboxylates (D, E) dominate hydrogen bonding across all sequences, reaching up to ~11.3 H-bonds per dipeptide

Local water network disruption



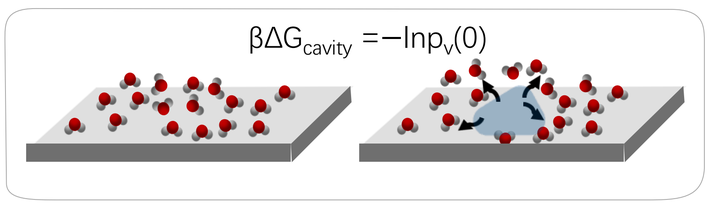
Pairing basic residues (R, K) with aromatic residues (W, F) produces the highest free-OH fraction (~0.13-0.143)



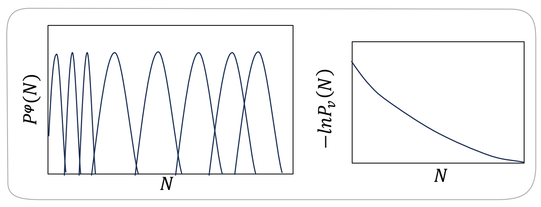
- The models provide a rapid and reasonable approximation of interfacial properties, making them useful for initial screening
- While the models capture general trends well, some scatter in the test data suggests they are approximations rather than exact replacements for detailed MD simulations

Future work

Prepare hydrophobicity dataset

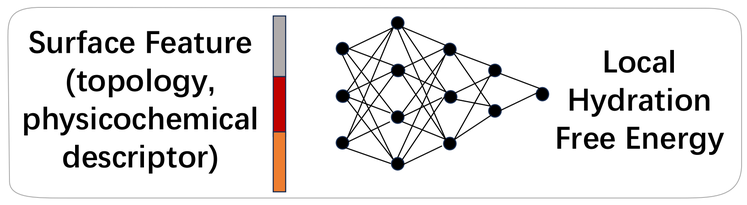


- **Free energy** of cavity formation at interface provides direct quantification of hydrophobicity at molecular scale



- **INDUS** (Indirect Umbrella sampling) quantifies the free energy

Generate Surface Feature and model to predict



- We expect to build a model that predicts local hydrophobicity of peptide functionalized surfaces at nanoscale

Acknowledgements

NSF | Research Computing | BG

References

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2. Fang, Z.; Chen, J.; Zhu, Y.; Hu, G.; Xin, H.; Guo, K.; Li, Q.; Xie, L.; Wang, L.; Shi, X.; et al. High-throughput screening and rational design of biofunctionalized surfaces with optimized biocompatibility and antimicrobial activity. *Nat. Commun.* **2021**, *12* (1), 3757.
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