

# ASHLIN JAMES PORUTHOOR



[ashlinjamesporuthoor@gmail.com](mailto:ashlinjamesporuthoor@gmail.com)

+1(551) 214-4142 ◇ College Park, MD, 20740

## SUMMARY

Post-doctoral fellow skilled in molecular dynamics, modeling, methods development, and computer-aided drug design. Experienced in collaborative industry settings, with multiple internships in discovery chemistry and modeling teams.

## EDUCATION

<b>Doctor of Philosophy, Biophysics</b> , University of Rochester	2018 - 2024
<b>Master of Science, Biophysics</b> , University of Rochester	2018 - 2021
<b>Master of Science, Physics</b> , NIT Calicut	2016 - 2018
<b>Bachelor of Science, Physics (Honors)</b> , St.Stephen's College, University of Delhi	2013 - 2016

## RESEARCH EXPERIENCE

<b>Post Doctoral Fellow</b> University of Maryland Baltimore, <b>MacKerell Lab</b>	July 2024 - Present Baltimore, MD
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- Developed ensemble learning and deep learning models to predict small molecule membrane permeability using physics-based SILCS continuum models with fragment-based 3D mapping of membranes of varying complexity. Feature engineered multiple novel molecular descriptors and assessed their effects on the explainability of models<sup>1</sup>
- Lead optimization and High Throughput Virtual Screening of SCP2 inhibitors: Using Site Identification by Ligand Competitive Saturation (SILCS) platform, I led the fragment-based computational campaign to expand chemical modifications, corresponding SAR analysis on targets and off-targets with experimental collaboration<sup>2</sup>
- In-silico designing of photoaffinity probes for target characterization and identification for the SCP2 campaign
- Developing an *in silico* renal proximal tubule model for ADMET prediction with SILCS whole cell simulation

<b>Graduate Research Student</b> University of Rochester Medical Center, <b>Grossfield Lab</b>	June 2019 - Present Rochester, NY
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- **Developed a computational method** to estimate the free energy landscape of phase separation in the lipid bilayers from molecular dynamics (MD) simulations using **enhanced sampling** protocols<sup>3</sup> ◇ **Analyzed > 100 TB simulation data** ◇ Unsupervised Learning ◇ Coarse Grained MD ◇ **Weighted Ensemble** ◇ GROMACS
- Studied the MD finite-box size effects in constructing free energy landscapes of phase separating lipid bilayers<sup>4</sup>
- Developed statistical mechanics-based analysis schemes to track and visualize ultrafast dynamics of Rhodopsin upon light activation to interpret the XFEL experiments ◇ **Analyzed > 10000 short All-Atom simulations** ◇ NAMD ◇ OpenMM ◇ Cross-functional collaboration ◇ **Membrane-GPCR modeling** ◇ Python

<b>Discovery Chemistry Co-op - Part Time</b> <b>Moderna, Computational Sciences</b>	Jun 2023 - Oct 2023 Cambridge, MA
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- Studied the role of ionizable lipids in lipid nanoparticles (**LNPs**) and their preferential interactions with RNA with NAMD3 All-Atom Molecular Dynamics simulations in AWS<sup>5</sup> ◇ RNA-bilayer Modeling
- Generalized and automated in-house protocol for customized in-silico lipid bilayer model generation

<b>Molecular Engineering and Modeling Co-op - Full Time</b> <b>Moderna, Computational Sciences</b>	January 2022 - June 2022 Cambridge, MA
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- Studied **RNA - small molecule** interaction via **docking** & Molecular Dynamics. Proposed and implemented a python analysis suite for initial validation of **binding pocket interactions** and ligand conformational dynamics

- Benchmarked different alchemical and geometrical routes for RNA-small molecule **binding free energy calculations**. Implemented a test pipeline module that can be extended for an extensive ligand library screening
- Studied **RNA - lipid bilayer** interactions with NAMD All-Atom Molecular Dynamics simulations
- Proposed and initiated an internal pilot project that involved cross-functional teams
  - ◊ Schrödinger Glide, Maestro ◊ BFEE2 ◊ AMBER Antechamber, GAFF2 ◊ Bitbucket ◊ JupyterLab ◊ AWS

#### Summer Research Fellow

April 2018 - June 2018

JNCASR, Theoretical Sciences Unit

Bangalore, India

- Studied the sensitivity of population dynamics of bacteria towards the nutrient environment using modeling and numerical simulation. Modeled quorum sensing and chemotaxis behaviors and emulated racing conditions

#### Summer Research Fellow

May 2017 - July 2017

JNCASR, Theoretical Sciences Unit

Bangalore, India

- Conducted metabolic network reconstructions and flux balance analyses on constraint-based *in silico* yeast models. Studied the effect of various metabolites on the yeast growth rates upon network perturbations
- Integrated transcriptomic data into *in silico* models of *Plasmodium falciparum* to emulate multiple malaria variants in southeast Asia to understand the rise of drug resistance using cross-functional efforts

### OTHER RELEVANT EXPERIENCE

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**Software Contributions (2024 - Present)** **SILCS**: Created protocols for handling complex user-input custom membranes for SILCS-Membrane tool that eliminated early runtime termination. Bug fixes, and beta-testing.

**URBEST Trainee (2021 - 2024)** University of Rochester initiative to **Broaden Experiences in Scientific Training** for early career scientists. Training on leadership and management skills for scientists via coursework, panel discussions, informational interviews, career stories, mentoring, and other personalized programs

**Teaching Assistant, BPH509 - Molecular Biophysics (2020)** Instructed students in theoretical, experimental, and computational methods to study macromolecules. Topics include statistical mechanics, optical melting experiments, dynamic programming algorithms, molecular dynamics, protein folding, and isothermal titration calorimetry

**Open-source Contributions (2020 - 2023)** **LOOS** : A lightweight object-oriented structure analysis library for MD simulations. **WESTPA** : The Weighted Ensemble Simulation Toolkit with Parallelization and Analysis. FLOPSS 2.0 : pipeline to compute **Free energy Landscape Of Phase Separating Systems** - to be released soon ([Early version](#))

### RELEVANT PUBLICATIONS

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1. Elizabeth S. Liedhegner, Caitlin Bauer, Nathalia Rocha Lainetti, **Ashlin Poruthoor**, Alexander MacKerell, Christopher Cunningham, Cecilia Hillard. Sterol Carrier Protein 2 (SCP-2), trafficker of endocannabinoids, interacts with the phytocannabinoids, cannabidiol (CBD) and cannabigerol (CBG). GRC Cannabinoid Function in the CNS, New Hampshire, August 2025 [Poster]
2. **Ashlin Poruthoor**, Alexander MacKerell Jr. Lessons learned from predicting drug permeability by bridging physics and machine learning using the SILCS methodology. ACS Fall Meeting 2025, Washington, D.C. [Poster]
3. **Ashlin Poruthoor**, Akshara Sharma, Alan Grossfield. (2023). Understanding the Free Energy Landscape of Phase Separation in Lipid Bilayers using Molecular Dynamics. Biophysical Journal. 122. 10.1016/j.bpj.2023.09.012.
4. **Ashlin Poruthoor**, Jack Stallone, Megan Miaro, Akshara Sharma, Alan Grossfield (2024). System size effects on the free energy landscapes from molecular dynamics of phase-separating bilayers. J. Chem. Phys. 161, 145101
5. **Ashlin Poruthoor**, Sepehr Dehghanighahnaviyeh, Semiha Bali, Mehtap Isik, Sreyoshi Sur. (2024). Interactions between ionizable amino lipids and a short RNA hairpin: Insights from molecular dynamics simulations for lipid nanoparticle optimization. Biophysical Journal. 123. 97a. 10.1016/j.bpj.2023.11.699. [Poster]