

Pratham Lotia

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About

Graduate student at Carnegie Mellon University interested in **Molecular Dynamics and Simulations** for Proteins and therapeutic molecules. Working on designing a super-glue for Triose Phosphate Isomerase E104D mutation in **Koes group** at University of Pittsburgh. Subjects of interests: Chemistry, Chemical Biology, Computational Chemistry, Drug Discovery, Chemical Engineering, Genome Editing, Biological Modelling and Simulation.

Education

Carnegie Mellon University: M.S. Biotechnology & Pharmaceutical Engineering Aug 2023 – Present

- Current GPA: 3.6/4.0
- **Coursework:** Genome Editing Biotechnology, Mathematical Modeling of Chemical Engineering Processes, Molecular Techniques for Bio-processing, Laboratory Methods for Automated Biology I, Computational Methods for Biological Modeling and Simulation

Institute of Chemical Technology: B.Tech. Pharmaceuticals Chemistry & Technology Aug 2019 – May 2023

- Cumulative GPA: 3.85/4.0
- **Coursework:** Pharmaceutical Chemistry, Pharmaceutical Formulation Technology, Pharmacognosy, Retro-synthesis, Physiology and Pharmacology, Medicinal Chemistry, Biochemistry, Chemical Reaction Engineering, Chemical Engineering Operations, Spectroscopy

Experience

Graduate Researcher, University of Pittsburgh – Pittsburgh, PA Aug 2024 – Present

- Using **VMD & AMBER** to simulate Triose Phosphate Isomerase E104D mutation enzyme under the guidance of Dr. David Koes, Computational Systems and Biology Dept, and the wild type for understanding changes in the water network structure
- Designing a superglue to homo - dimerize E104D mutation

Teaching Assistant, Carnegie Mellon University – Pittsburgh, PA Aug 2024 – Present

- Assisted in an introductory laboratory course (Quantitative Cell & Molecular Biology Lab) under Department of Computational Biology on quantitative biological research, focusing on experimental design, DNA sequencing, PCR, cell culture, microscopy, and data analysis.

Graduate Researcher, Carnegie Mellon University – Pittsburgh, PA Jun 2024 – Aug 2024

- Collected data on shear stress vs shear rate using **Rheometer** under the guidance of Dr. Tagbo Niepa, Dept of Chemical Engineering, to identify changes in Biofilms upon application of various efflux pump inhibitors to verify their biofilm disruption activity

Graduate Researcher, Carnegie Mellon University – Pittsburgh, PA Jan 2024 – Jun 2024

- Worked under Dr. Danith Ly, Dept of Chemistry, in groundbreaking research for synthesizing **Janus Bases** and work on identifying their applications in curing Myotonic Dystrophy (**MD1**) by base pairing of Janus Bases to shRNA

Publications

Peptidomimetics: A Synthetic Tool to Treat Alzheimer's Disease | Bombay Technologist Nov 2022

Shubham Patil, **Pratham Lotia**

10.36664/bt/2022/v69i1/172472

AYURVEDIC REMEDIES FOR NOSOCOMIAL BACTERIAL INFECTIONS | Academic Decipher Press May 2022

Dr. Prashant Kharkar, Rahul Lakhani, Darshan Kothari, Yash Dansingani, **Pratham Lotia**, Dr. Shreerang Joshi
AYURVEDIC REMEDIES FOR DISEASES OF MICROBIAL ORIGIN, VOLUME - II, CHAPTER 17

Projects

Snake venom antidote discovery

github.com/plotia/antidote_discovery

- Investigated toxicity of snake venom of Indian Cobra over mice NT3K3 cells using Automated biology as snake venom is highly lethal
- Generated a treatment plate containing a gradient concentration of the venom in alternating directions of gradient for each row of 96 well plate to avoid direction bias using Cybio Felix and transferred that treatment to another 96 well plate containing cell biofilms. Kept positive control as saponin.
- Performed pictorial data analysis over concentration gradient of venom over mice cells to identify amount of live and dead cells
- Will investigate which genes are over expressed and/or under expressed due to venom for discovering the antidote
- Tools Used: Cybio felix, Opentrons OT-2, 96 well Spectro - photometer

Laplace transformation Project

github.com/plotia/laplace

- Developed a program on Python using Sympy to evaluate mixed nth order differential and mth order integral equation simultaneously by Laplace transformation
- Applications of evaluating mixed nth order differential and mth order integral equations include control theory, signal processing, fluid dynamics, population modeling, structural analysis, finance, and numerical analysis.
- Tools Used: Python and python packages, Sympy, Numpy

Docking Studies

github.com/plotia/docking

- Conducted molecular docking of trimethoprim and related compounds on dihydrofolate reductase (DHFR) using Flaire, calculating Gibbs free energy to assess binding affinities
- Developed expertise in creating docking grids on protein structures, optimizing target sites for accurate molecular interactions
- Tools Used: Flaire, Autodock, py3dmol

Technologies

Languages: C++, C, CSS, JavaScript, Python, py3dmol, bash, html, LaTeX

Technologies: Flaire, Autodock, Amber, Jupyter, VS code, Secure Shell, LINDO, ChemBio Draw, Fusion 360, Autodesk

Analysis: GC (Gas Chromatography), HPLC, TLC, Column Chromatography, Flash Chromatography, IR, FTIR, H1 NMR, C13 NMR, Mass Spectroscopy, UV - Vis Spectroscopy, Electrophoresis, Western Blot, Northern Bolt, Southern Blot, PCR, ChIP Seq, ATAC Seq, mRNA Seq