AKASH

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PROFESSIONAL SUMMARY

Computational biologist and bioinformatics researcher with expertise in protein engineering, structural biology, molecular simulation, and biotech software development. Proficient in Python, Linux, molecular dynamics, and full-stack development. Proven track record of publishing peer-reviewed research (Proteins journal) while architecting production biotech platforms serving 18+ pharmaceutical clients. Experience with PyMOL, AlphaFold, Rosetta, Next.js, React, Node.js, SQL, REST APIs, and Git.

WORK EXPERIENCE

Development Engineer, Merck Life Science, Bangalore

January 2024 – July 2025

- Engineered Bio4C Process Pad—an analytics platform serving 18+ biotech clients (Lotte, Syngene), enabling bioprocess monitoring through data-driven decision making systems.
- Designed h-index clustering algorithm with elbow curve optimization, improving protein classification accuracy and reducing computational overhead by 35%.
- Developed REST API integrations with SQL-based analytics backend for real-time process insights.
- Tech stack: JavaScript, React, Next.js, Node.js, SQL, Python

Research Intern (Student Researcher), Indian Institute of Science (IISc), Molecular Biophysics Department

June 2023 – December 2024

- Conducted in silico saturation mutagenesis of CCDB protein using computational methods to predict variant effects and protein stability.
- Leveraged PyMOL for structural visualization, AlphaFold for protein folding prediction, and Rosetta suite for molecular modeling and energy calculations.
- Published research in Proteins: Structure, Function, and Bioinformatics journal, demonstrating novel protein engineering strategies.
- Used Linux bash scripting for bioinformatics workflow automation.

Program Coordinator (Web Developer), Abhyudaya (NGO)

August 2025 – Present

- Developing responsive web applications for nonprofit using HTML, CSS, JavaScript and Laravel backend.
- Implementing CakePHP-based backend systems for organizational management tools.
- Version control with Git/GitHub.

PROJECTS

In Silico Saturation Mutagenesis of CCDB

Computational protein engineering study on CCDB protein variants with full structural and functional analysis using molecular dynamics.

Tech: PyMOL, AlphaFold, Rosetta, Protein Engineering, Molecular Simulation

AI-Assisted Bioreactor Analytics (Concept)

Tool-calling agent framework for intelligent bioreactor parameter optimization and predictive analytics.

Tech: AI, Analytics, Bioreactor, Python, Agentic AI

SKILLS

Python, Structural Biology, Protein Folding, Molecular Simulation, PyMOL, AlphaFold, Linux/Bash, R, SQL, Git

EDUCATION

Masters in Molecular & Cellular Biology / Life Sciences

MS Ramaiah University | 2024

Published research on protein variant analysis

Bachelors in Biotechnology

Dayananda Sagar University | 2023

State Government Scholarship recipient

PUBLICATIONS

In Silico Saturation Mutagenesis of CCDB, Proteins: Structure, Function, and Bioinformatics (2024)

AWARDS & RECOGNITION

• 1st Place Poster Competition (Dayananda Sagar University)

• State Government Scholarship

• 3rd Place Hackathon (Merck)

LANGUAGES

English (Fluent), Hindi (Native), Kannada (Native), German (Basic)

CERTIFICATIONS

• JavaScript Mastery (Udemy)

• Data Analysis & Analytics (Coursera)