

# NIKHIL YENGALA REDDY

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## OBJECTIVE

Highly skilled and collaborative Bioinformatics Scientist with a strong background in interdisciplinary research and a passion for driving innovation in developing and supporting effective data analysis and machine learning workflows. Skilled in overseeing the development and maintenance of complex databases to support research projects. Capable of investigating and solving intricate problems with puzzling data.

## EDUCATION

<b>MS in Bioinformatics</b> <i>Johns Hopkins University, Maryland</i>	08/2021-05/2023
<b>BS in Molecular Biology, Minor Chemistry</b> <i>San Jose State University, California</i>	08/2018-05/2021

## RELEVANT EXPERIENCE AND PROJECTS

**Thermo Fisher Scientific | Associate Scientist | Madison, WI** 2024-Current

Maintaining electronic laboratory notebook, performing sample preparation and analysis, SOPs, regulatory guidelines, and completion of documentation.

**Github Project | [rnikhil10.github.io](https://github.com/rnikhil10) | Personal Project** 2023-2024

A meticulously curated showcase of my interdisciplinary expertise at the intersection of bioinformatics, data science, and UI/UX design, my portfolio demonstrates a deep commitment to leveraging technology for solving complex biological problems and enhancing user experience in scientific applications. It reflects my proficiency in a range of technical skills, from advanced data analysis to intuitive web design, underpinned by a solid educational foundation in bioinformatics from Johns Hopkins University.

**Research | Department of Microbiology and Bioinformatics | San Jose State University** 2020-2020

Worked on Multidrug Resistance (MDR) genes to identify species from which they originate and to further understand the structure and mechanism through which it functions. The genes belonged to a family of proteins known as the major facilitator superfamily (MFS). Used Biopython to obtain large genomic data from PDB. The tools, such as MABL and UNIPROT, were used to understand the gene's origination through multiple sequence alignment with related species and then constructed a phylogenetic tree. Another tool such as Pymol was used to analyze the structure of MDR proteins.

**Bioinformatics Academic Project | Department of Bioinformatics | San Jose State University** 2019-2019

Identified and analyzed conserved regions in the Rhodopsin protein sequence among the various species. Performed series of data collection through the NCBI data bank. The tools, such as Galaxy and UCSC Genome Browser, was used to perform for NGS data analysis. In addition, the tool, WEBLOGO3, was used to make motif sequence to find highly conserved regions.

## VOLUNTEER EXPERIENCE

**Sinai Hospital | Baltimore, Maryland** 2022-2023

- Collaborated with healthcare staff to ensure smooth patient flow and efficient operations.
- Demonstrated strong communication skills while interacting with diverse patient populations.

## INVOLVEMENT

**BSA Advisory Board Chair and Student Member** 2019-2021  
*Biological Student Association (BSA), San Jose State University, San Jose, CA*

- BSA Advisory Board is a program run by junior and senior students designed to advise students majoring in biology
- Chair of BSA Advisory Board and served as a mentor to new and fellow students

## SKILLS

Python (Pandas, Spark, Jupyter), Java, HTML, CSS, JS, SQL, R (ggplot), Linux/UNIX, NGS, UCSC Genome, Tableau, Github, Clustal, Galaxy, Bioconductor, NCBI, Conda, Docker