ABHISHEK SHARMA

PROFESSIONAL SUMMARY

A computational biologist with 5+ years of research experience in the field of bioinformatics. This includes Molecular dynamics (MD) simulations, virtual screening of small-drug molecules and protein sequence and structure analysis.

CONTACT DETAILS

Email: abhishek.lambloo@gmail.com

Phone: +91-8826357012 Bangalore, India 560097

HOBBIES

Exploring tea-shops to enjoy a nice cupof tea, Sportsperson Certified UrbanPro instructor

PROFESSIONAL CAREER

Integrated PhD (Graduate-Student Batch-2017)

NCBS (TIFR), Bengaluru | July 2017- Present

ACADEMIC BACKGROUND

D.A.V Public School, Hamirpur (H.P)

Matriculate- 2012- 10 CGPA

Vision Convent School, Ghumarwin (H.P) Intermediate-2014, 93.4%

Ram Lal Anand College (D.U) B.Sc (H)-Microbiology, 80%

NCBS (TIFR), Bengaluru Integrated-Ph.D. Life Sciences | GS-2017

PRESENTATIONS

- 1.Poster presentation on "Computational search for potential COVID-19 drugs from FDA-approved drugs and small molecules of natural origin identifies several anti-virals and plant products" in NCBS annual talks 2021 Zooming through Biology
- 2. Poster presentation on "Bioinformatics Analysis of Mutations Sheds Light on the Evolution of Dengue NS1 Protein With Implications in the Identification of Potential Functional and Druggable Sites" in NCBS annual talks 2023.
- 3. 10 minute talk on "Bioinformatics Analysis of Mutations Sheds Light on the Evolution of Dengue NS1 Protein With Implications in the Identification of Potential Functional and Druggable Sites" in ISMB/ECCB-2023 conference at Lyon, France.

PUBLISHED WORK

- 1. Abhishek Sharma, Vikas Tiwari and Ramanathan Sowdhamini Computational search for potential COVID-19 drugs from FDA- approved drugs and small molecules of natural origin identifies several anti-virals and plant products J Biosci (2020) 45:100, DOI:
- 2. **Abhishek Sharma**, Sudhir Krishna, Ramanathan Sowdhamini Bioinformatics Analysis of Mutations Sheds Light on the Evolution of Dengue NS1 Protein With Implications in the Identification of Potential Functional and Druggable Sites, *Molecular Biology and Evolution*, Volume 40, Issue 3, March 2023, msad033, Doi: https://doi.org/10.1093/molbev/msad033

RESEARCH HIGHLIGHTS

1.Exploring the mutational landscape and protein-protein interaction of Dengue and SARS proteins as drug targets for novel anti-viral therapeutics. Ph.D. Thesis at NCBS, Bengaluru: The project aimed to understand how viral protein accumulated mutations and .

- Bioinformatics Analysis of Mutations Sheds Light on the Evolution of Dengue NS1 Protein With Implications in the Identification of Potential Functional and Druggable Sites: The project aimed to understand how antigenic protein of Dengue virus: "NS1 protein" is conserved in nature. This followed by a development of computational pipeline to identify protein-protein interaction and druggable sites on antigenic proteins
- Computational search for potential COVID-19 drugs from FDA-approved drugs and small molecules of natural origin identifies several anti-virals and plant products: This project aimed to identify small molecule inhibitors against SARS-COV2 NSP1 protein. This work was one of the first in world to carried out.

RESEARCH EXPERTISE

Molecular Dynamic Simulations (MD)	Virtual screening of small molecules as potential Inhibitors
Sequence analysis: Sequence alignment (Muscle, MEGA), and Phylogeny	Protein structure analysis: Virtual Mutagenesis, amino-acid network analysis,
	Data Visualisation using Python
Data Analysis: Statistic using R and Python	Deep Learning: Using Tenserflow and Pytorch, Experience with CNN and RNN, Computer Vision and Large language models
Machine Learning: Regression and Classification Models	Experimental Expertise: PCR, Cloning, Antibody Isolation, Bacterial cultures

RESEARCH ACCOMPLISHMENTS

- 1. Winner of NCBS Best poster award (2023) and international traveling grant for presenting "Bioinformatics Analysis of Mutations Sheds Light on the Evolution of Dengue NS1 Protein With Implications in the Identification of Potential Functional and Druggable Sites"
- 2. Winner of ISMB Travel-grant of \$1000 for giving 10 minute talk on "Bioinformatics Analysis of Mutations Sheds Light on the Evolution of Dengue NS1 Protein With Implications in the Identification of Potential Functional and Druggable Sites" in ISMB/ECCB.

REFERENCES