



# NEWSLETTER

**Department of Biotechnology  
Bhupat & Jyoti Mehta  
School of Biosciences**

**ISSUE 3**

**(Sep-Dec 2024)**



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**Department of Biotechnology  
Bhupat and Jyoti Mehta School of Biosciences  
Indian Institute of Technology Madras,  
Chennai 600036, India.**

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### MESSAGE FROM THE EDITORIAL DESK >>>>>

The Department is delighted to publish the third issue of our newsletter. In this edition, we are pleased to introduce Dr. Mamata Bangera, who joined our department as a faculty last year. We are excited to highlight the new sophisticated instrumentation facility that will greatly enhance cutting-edge research pursued in the department. This issue also highlights the research journey of one of our younger faculty members, Dr. Richa Karmakar. Starting with this issue, we are introducing a section to showcase our graduate students' research published in internationally renowned journals. Finally, we are happy to spotlight a startup venture founded by Prof. Srinivasa Chakravarthy from our department. We invite you to explore this issue, and we hope you find it enjoyable to read as we did when putting it together.

### FACULTY ACHIEVEMENTS >>>>>

Prof. Sathanarayana Gummadi received the BHU Centennial Award from the Biotech Research Society of India.



Prof. M. Michael Gromiha has been appointed as an Editorial Board Member for "Methods" and Associate Editor for "Bioinformatics and Biology Insights".

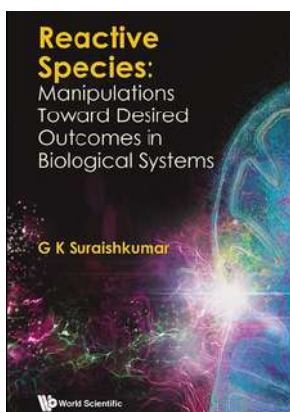


### STAFF ACHIEVEMENTS >>>>>

Sneha Sathapathi and Roshini Unnikrishnan were selected for the India Bioimaging Meeting held in IISER Pune for facility management and microscopy training.



### BOOKS PUBLISHED >>>>>

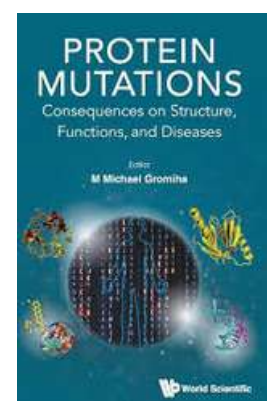


Reactive Species: Manipulations Toward Desired Outcomes in Biological Systems

G. K. Suraishkumar  
World Scientific, Singapore

Protein Mutations: Consequences on Structure, Functions, and Diseases

M. Michael Gromiha  
World Scientific, Singapore



### NEW FACULTY >>>>>

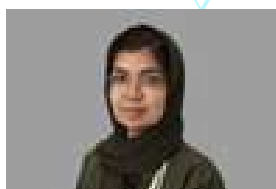
**Dr. Mamata Bangera**, Assistant Professor

**Areas of interest and expertise:**

- Cellular framework in growth, motility and stress
- Cytoskeleton of animals and plants
- Filament assembly and dynamics
- Crosslinking between filaments
- Cryo-electron microscopy and tomography



### STUDENT AWARDS >>>>>



Fathima Ridha (Prof. M. Michael Gromiha Lab) received a travel fellowship award from SERB to deliver a talk at the 1st Asia & Pacific Bioinformatics Joint Conference (APBJC 2024) held in Japan.

Diksha Mall, Anwita Sarkar and Neha Rani Das (Dr. Richa Karmakar lab) received the Best Poster Award at CompFLU, 2024, held at the Indian Institute of Technology, Hyderabad.



Tarun Shyam Mohan (Dr. Greeshma Thrivikraman lab) received BD Biosciences Best Poster Presentation Award in Molecular Medicine at the Pan-IIT Meeting and Conference on Engineering in Medicine held at IIT Kanpur on Dec 6-8, 2024.

Dr. Poovitha Sundar (DST Women Scientist) received the Best Oral Presentation Award in the International Conference on "Biotechnology - the way forward"



#### RESEARCH EXCELLENCE AWARD

- Sowmya Krishnan (Guide: M. Michael Gromiha)
- Pratyay Sengupta (Guide: Karthik Raman)

### START-UP SPOTLIGHT >>>>>

#### Neurogati Pvt Ltd

Neurogati is founded by Dr. V. Srinivasa Chakravarthy (Bioechnology/MST) and Dr. Indira Chaturvedi (Pediatrician). It aims to develop affordable diagnostics and optimal therapeutic interventions for Parkinson's Disease (PD). The QUADIS-PD system developed by Neurogati records from the patient parameters related to gait, handwriting, speech, decision making etc and helps to create a quantitative profile of the severity of the disease.



### STUDENT RESEARCH HIGHLIGHTS >>>>>

**Title:** Electroencephalogram (EEG) classification using a bio-inspired deep oscillatory neural network

**Authors:** S. Ghosh, V. Chandrasekaran, N.R Rohan, **V.S. Chakravarthy**

**Reference:** Biomedical Signal Processing and Control 103: 107379 (2024)

**Doi:** <https://doi.org/10.1016/j.bspc.2024.107379>

**Summary:**

- Unlike traditional neural networks, these models utilize oscillatory neurons to process EEG data, enabling them to capture rich dynamics such as phase locking and synchronization across frequency bands like alpha, beta, and gamma.
- The proposed models outperform existing EEG classification methods in terms of accuracy while requiring significantly fewer parameters. This model is able to produce synthetic EEG data which can be useful for further medical research purposes.
- This efficiency opens pathways for energy-efficient hardware implementations, making these models well suited for portable and real-time applications in healthcare and brain-computer interface.



Sayan Ghosh



Fathima Ridha

**Title:** MPA-MutPred: a novel strategy for accurately predicting the binding affinity change upon mutation in membrane protein complexes

**Authors:** F. Ridha, **M.M. Gromiha**

**Reference:** Briefings in Bioinformatics 25(6):bbae598 (2024)

**DOI:** <https://doi.org/10.1093/bib/bbae598>

**Summary:**

- Mutations at the interface of membrane protein complexes significantly contribute to a broad spectrum of human diseases by altering the binding affinities.
- Our novel approach combines the strengths of both linear and nonlinear machine-learning algorithms.
- Utilized sequence and structure based features of membrane protein complexes.
- It is the first method to predict mutation-induced affinity changes in membrane protein-protein complexes.
- We developed a user-friendly web server (<https://web.iitm.ac.in/bioinfo2/MPA-MutPred/>) that enables large-scale analysis.

**Title:** Protein Structure Prediction with High Degrees of Freedom in a Gate-Based Quantum Computer

**Authors:** J.V. Pamidimukkala, S.Bopardikar, A.Dakshinamoorthy, A.Kannan, K.Dasgupta, **S. Senapati**

**Reference:** Journal of Chemical Theory and Computation, 20, 10223–10234 (2024)

**Doi:** <https://doi.org/10.1021/acs.jctc.4c00848>

**Summary:**

- Protein folding, which traces the protein's three-dimensional (3D) structure from its amino acid sequence, is a half-a-century-old problem in biology.
- While recent AI-based methods have shown significant success in protein structure prediction, their accuracy diminishes with proteins of low sequence similarity.
- We developed a novel turn-based encoding algorithm to predict the structure of proteins irrespective of their sequence similarity (based on extensive sampling) with more significant degrees of freedom that successfully runs on a gate-based quantum computer utilizing up to 114 qubits (IBM hardware).



J.V. Pamidimukkala

### RESEARCH HIGHLIGHT >>>>>

Dr. Richa Karmakar is an Assistant Professor in the Department of Biotechnology at IIT Madras. She finished her Ph.D. at IIT Bombay and pursued her postdoctoral training at the University of California San Diego, USA. She is a recipient of the DBT-India Alliance Wellcome Trust Early Career Fellowship. Her lab focuses on understanding the biophysical aspects of Prokaryotic and Eukaryotic chemotaxis and developing disease diagnosis methods using microfluidics.



Dr. Richa Karmakar

1. *What first sparked your interest in your field of research? Was there a specific event or person that inspired you?*

For me, cellular migration and live cell imaging are the most fascinating. During my M.Tech., I watched a video from Prof. Howard Berg, Harvard University, on bacterial motility. The bacterial dynamics, such as run and tumble motion, are wonderful. Also, I was curious about how pathogens exploit host cell migration and how microenvironments influence cell behaviour. So, I decided to work on cellular chemotaxis. Focusing on cell migration allows me to tackle pressing biomedical challenges while contributing to fundamental biology and advancing interdisciplinary technologies.

2. *Can you describe your current research for those who may not be familiar with your field? What excites you most about it?*

My lab investigates the biophysical mechanisms underlying chemotaxis in Prokaryotic and Eukaryotic cells, focusing on how cells sense and respond to chemical gradients. The research employs cutting-edge microfluidics to recreate dynamic microenvironments, enabling precise control and observation of cellular behaviors. This work advances our understanding of cell motility, signalling pathways, and interactions within complex systems.



Simultaneously, my lab develops microfluidic-based disease diagnostic devices that are efficient, cost-effective, and suitable for resource-constrained settings. These Lab-on-a-chip platforms aim to revolutionize healthcare by providing rapid, accurate detection methods for clinical and point-of-care applications, bridging fundamental science and translational innovation. Additionally, I lead a project on microbial CO<sub>2</sub> sequestration and metal utilization for sustainable industrial waste reduction, funded by the Energy Consortium at IIT Madras.

3. *What are some real-world applications of your research, and how do you see it impacting society in the future?*

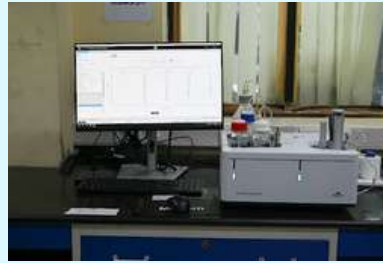
The real-world applications of my research span several critical areas with the potential to create a profound societal impact, such as Point-of-Care disease diagnosis, disease microenvironments for research, microbial CO<sub>2</sub> sequestration and sustainable industrial practices. We have already developed a microfluidics-based electrochemical sensor for detecting Antibiotic Susceptibility Testing. Looking ahead, I see my work driving innovation in healthcare, environmental sustainability, and fundamental biological research.

4. *What do you do outside of research to stay creative and motivated?*

Apart from reading scientific papers, I read lots of story books. I do painting and singing.

### BIO-SAIF INAUGURATION >>>>>

The grand inauguration of our department's cutting-edge Bio-SAIF facility was officiated by the Director, Prof. V. Kamakoti. This facility features a comprehensive array of imaging, spectroscopic, and analytical instruments, designed for the detailed characterization of biological samples, from small biomolecules to cells and tissues. Among the latest additions to this facility are the High-resolution LC-MS, BD FACS Discover™ S8 Cell Sorter, Seahorse Real-Time Cell Metabolic Analysis, Fourier Transform Infrared Spectroscopy, Dynamic Light Scattering, Zetasizer and MicroCal PEAQ-Isothermal Titration Calorimeter.



### BIOPROCESSING INDIA 2024 >>>>>

Bioprocessing India 2024, a 3 day international conference under the theme of "Sustainable Biomanufacturing" was organized by Profs. Guhan Jayaraman and Meiyappan Lakshmanan. It brought together more than 350 local and 30 international attendees from leading universities, research institutions, and biotechnology industries. The conference featured 3 plenary lectures, one special lecture from DBT, GoI representative on recently launched BioE3 policy, 90 invited speakers across 19 technical sessions and one panel discussion on "Navigating the techno-commercial space in Bioprocessing".



### HIGHLIGHTS >>>>>

52



**Publications**

16



**Patents  
Applied/Granted**

2



**Consultancy  
projects**

5



**Sponsored  
Projects**

198.54  
lakhs



**Grant  
Amount**

### DEPARTMENTAL GATHERING >>>>>

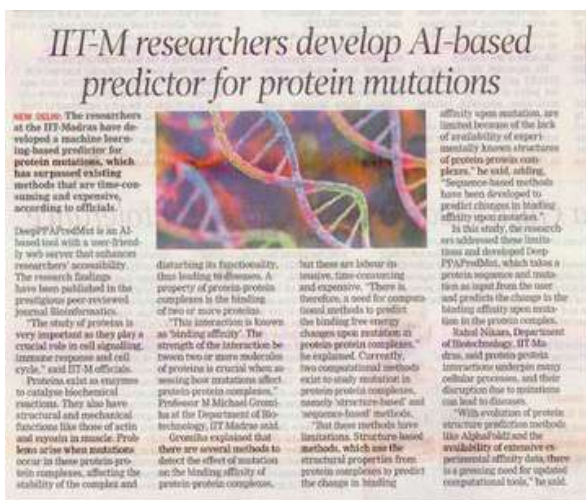


Once a month, our department hosts “Happy Hour” event for the undergraduate students, research scholars, staff, and faculty colleagues to come together for a fun-filled evening.

### VISITS BY DISTINGUISHED SCIENTISTS >>>>>

- Prof. Darren Player (University College London, UK)
- Dr.-Ing. Iris Krupke (Dresden University of Technology, Germany)
- Prof. Anil K. Chauhan (University of Iowa, USA)
- Prof. Rishikesh Narayanan (Indian Institute of Science, Bangalore)
- Dr. Sriram Varahan (Centre for Cellular & Molecular Biology, Hyderabad)
- Dr. Benjamin Krupke (Technical University of Dresden, Germany)
- Prof. Dileep Vasudevan (BRIC-RGCB, Thiruvananthapuram)
- Dr. Kumar Somasundaram (Indian Institute of Science, Bangalore)

### MEDIA OUTREACH >>>>>



Prof. M. Michael Gromiha’s lab developed an AI-based tool for detecting crucial mutations in protein-protein complexes. Specifically, his team (Rahul Nikam and Sherlyn Jemimah) developed a robust, deep ensemble model that can predict the change in binding affinity in protein-protein complexes due to mutations, which exhibited remarkable predictive performance.

<https://www.deccanherald.com/science/iit-madras-researchers-develop-machine-learning-based-predictor-for-protein-mutations-3298986>

#### Newsletter Committee:

Prof. M. Michael Gromiha, Prof. Himanshu Sinha, Prof. Greeshma Thrivikraman, Prof. Santhosh Sethuramanujam & Mr. A.S.Sasitharan