

Foreword

I am happy to present the Department of Biological Sciences of IISER Mohali in the form of this brochure. Our faculty have interests ranging from biology at the single molecule level to biology at the organismal level.

We participate in all three academic programs of the institute, the BS-MS program, the Int-PhD program and the PhD program and there is a strong sense in the department of maintaining excellence in both teaching and research. As we strive towards this in a spirit of cooperation and collegiality, the hope is to create an exciting, intense and vibrant environment for the exchange and execution of ideas.

I thank all the colleagues in the department for their contributions to this brochure, with a special thanks to Rajesh Ramachandran and Shashi Pandit for putting all of it together, and to Manjari Jain and TR Rao for contributing to the cover page and back page respectively.

25th September 2015



Anand K. Bachhawat
Head of the Department



Kavita Babu

Assistant Professor; Wellcome-DBT Intermediate Fellow

Dr. Kavita Babu did her undergraduate degree in Physics, Chemistry and Mathematics at Bangalore University. She obtained her Ph.D. from National University of Singapore and Kings College, London, UK (1998-2004). She was a Postdoctoral Fellow Massachusetts General Hospital and Harvard University Boston, USA (2005-2011). She joined as Assistant Professor at IISER Mohali in August 2011.

Representative Publications

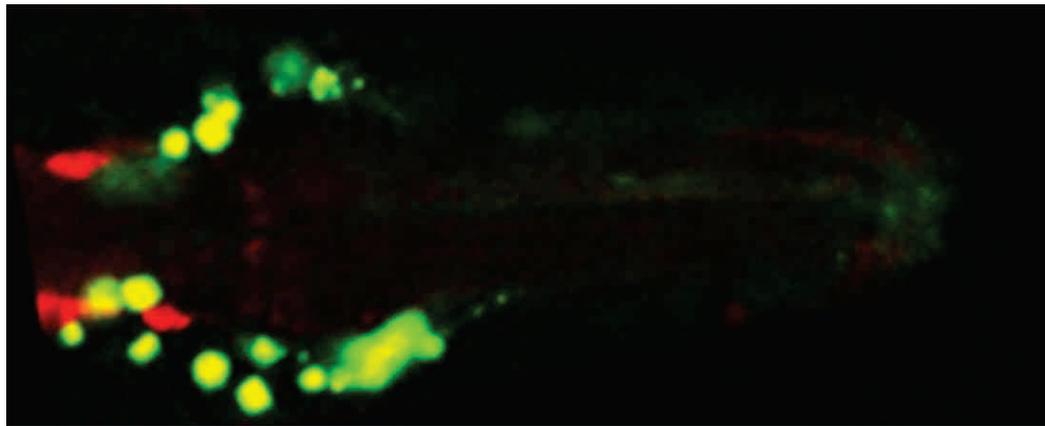
Babu, K., Hu, Z., Chien, S-C., Garriga, G. and Kaplan, J.M. (2011) The Immunoglobulin super family protein RIG-3 prevents synaptic potentiation and regulates Wnt signaling. *Neuron* 2011 Jul 14; 71(1): 103-16.

Hu, Z.* , Pym, E.C.G.* , **Babu, K.***, Vahlishan Murray, A.B.* and Kaplan, J.M. (2011) A neuropeptide-mediated stretch response links muscle contraction to changes in neurotransmitter release. *Neuron* 71:92-102.* Equal contribution

Babu, K., Bahri, S., Alpey, L. and Chia, W. (2005) Bifocal and PP1 interaction regulates targeting of the R-cell growth cone in *Drosophila*. *Developmental Biology* 288: 372-86. Corresponding author

Babu, K., Cai, Y., Bahri, S. and Chia, W. (2004) Roles of Bifocal, Homer and F-actin in anchoring Oskar to the posterior cortex of *Drosophila* oocytes. *Genes and Development*. 18: 138-43.

Helps, N.R.* , Cohen, P.T., Bahri, S.M., Chia, W. and **Babu, K.*** (2001) Interaction with protein phosphatase 1 is essential for bifocal function during the morphogenesis of the *Drosophila* compound eye. *Molecular and Cellular Biology*. 21: 2154-64.* Equal contribution.



Mouth region of *C. elegans* with neurons indicated in yellow

Research Interests & Projects

Synapses are essential for brain functions. Normal functioning of synapses is required for all activities from the generation of movement to learning and memory. Synaptic function requires a co-ordination between pre-synaptic neurotransmitter release and post-synaptic receptor levels. In my lab we use *C. elegans* as a model system to study the development and function of synapses.

Multiple studies have revealed that cell adhesion molecules are required for normal synapse formation and function. My post-doctoral work has shown that the cell adhesion molecules, RIG-3 functions through a receptor tyrosine kinase, CAM-1/Ror to maintain normal post-synaptic receptor levels at the neuromuscular junction. We are interested in understanding the mechanism of RIG-3 function at the synapse.

We are also interested in understanding the role of other cell adhesion molecules at the synapse. Our Laboratory has also recently started trying to understand the molecular basis of learning and memory using *C. elegans* as a model to study the same.

Techniques used in our Laboratory include *C. elegans* genetics, RNA interference and behavioral assays in combination with Molecular Biology, Cell Biology and Biochemistry.

For more information on our Laboratory, Lab members and the projects we work on, please visit www.babulab.org





Anand Bachhawat

Professor; J. C. Bose Fellow

Dr. Anand K Bachhawat did his Masters in Chemistry at IIT Kanpur. He obtained his Ph.D. in Biochemistry from Calcutta University (Bose Institute), India. He did his first post-doctoral research at the MGH Cancer Center, Harvard Medical School, Boston, USA and second one at the Carnegie Mellon University, Pittsburgh, USA. He joined the Institute of Microbial Technology in 1993. He moved to IISER Mohali as Professor in September 2010.

Representative Publications

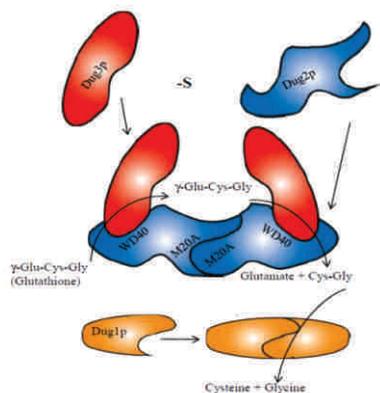
Desai PR, Thakur A, Ganguli D, Paul S, Morschhauser J, **Bachhawat AK*** (2011). Glutathione utilization by *Candida albicans* requires a functional DUG pathway and OPT7, an unusual member of the oligopeptide transporter family. *Journal Biological Chemistry*. 286,41183-41194 2011

Kaur H, Ganguli D, **Bachhawat AK.*** (2012). Glutathione degradation by the alternative pathway (DUG pathway) in *Saccharomyces cerevisiae* is initiated by the (Dug2p-Dug3p)₂ complex, a novel GATase enzyme acting on glutathione. *Journal Biological Chemistry*. 286, 8920-8931.

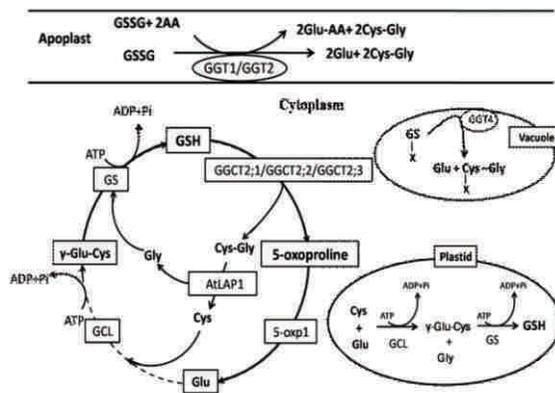
Kumar A, Tikoo S, Maity S, Sengupta S, Sengupta S, Kaur A, **Bachhawat AK.*** (2012) Mammalian proapoptotic factor ChaC1 and its homologues function as γ -glutamyl cyclotransferases acting specifically on glutathione. *EMBO Rep*. 13:1095-101.

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Kumar S, Kaur A, Chattopadhyay B, **Bachhawat AK*** (2015). Defining the Cytosolic Pathway of Glutathione Degradation in *Arabidopsis thaliana*: Role of the ChaC/GCG Family of γ -glutamyl cyclotransferases as Glutathione Degrading Enzymes and AtLAP1 as the Cys-Gly Peptidase. *Biochemical Journal*. 468,73-85.



DUG Pathway' or 'alternative pathway' for glutathione degradation



Plant Glutathione metabolism

Research Interests & Projects

Glutathione, Sulphur and Redox are the key areas around which our lab interests are centred. The major question that we are asking is 'How is glutathione homeostasis maintained in living cells?' Surrounding this major question are several other questions that become important for our understanding. The principal model systems that we use to address these questions are the yeasts *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe*. Glutathione, γ -glutamyl cysteinyl glycine, an unusual thiol containing tripeptide that is present in high concentrations in almost all eukaryotic cells, plays multiple roles including protection from oxidative stress, maintenance of the cellular redox buffer, in mitochondrial iron-sulphur metabolism, in gene regulation, and in metal and drug detoxification. Glutathione metabolism is intimately linked to sulphur metabolism owing to the presence of the key cysteine residue, and we thus also investigate aspects of sulphur metabolism related to glutathione homeostasis. As the focus is on understanding how glutathione levels are maintained in the cell, we are examining different pathways that contribute towards this maintenance. This includes the high affinity plasma membrane transporter of glutathione that was identified in our lab, the classical and two recently discovered non-classical pathways of glutathione degradation (also discovered in our lab) biosynthesis, organellar compartmentalization and utilization of glutathione. We are attempting to not only understand these different pathways and their regulation in detail, but are interested in integrating these pathways and their regulation into a larger picture of glutathione homeostasis in living cells.

We have also an interest in the human lysosomal disorder, cystinosis, that is due to a defect in the lysosomal cystine transporter and we are using yeasts to investigate different aspects of this disease. Very recently, we have also initiated a project on the synthetic biology of commercially important terpenoids.





Samarjit Bhattacharyya

Assistant Professor

Dr. Samarjit Bhattacharyya did his Masters in Biophysics, Molecular Biology and Genetics at University of Calcutta, West Bengal, India (1997-1999). He obtained his Ph.D. from National Centre for Biological Sciences (NCBS), Tata Institute of Fundamental Research (TIFR), Bangalore, India. He did his postdoctoral research at Stanford University, USA (2005-2010). He joined as Assistant Professor at IISER Mohali in June 2010.

Representative Publications

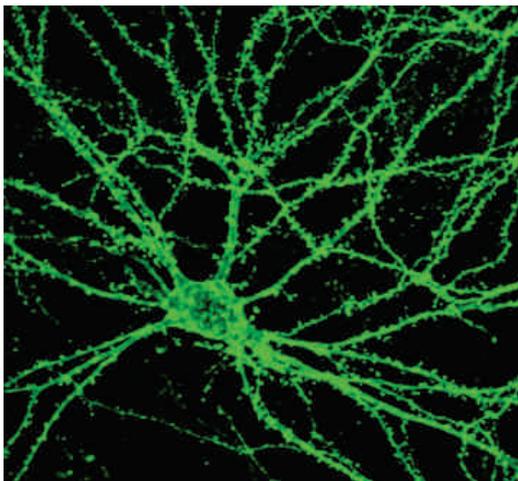
Mahato PK, Pandey S & **Bhattacharyya, S.** (2015) Differential effects of protein phosphatases in the recycling of metabotropic glutamate receptor 5. *Neuroscience*, 306:138-150.

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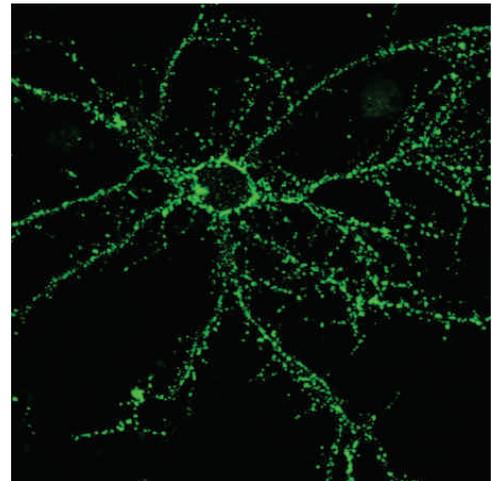
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Bhattacharyya S, Puri S, Miledi R & Panicker MM. (2002) Internalization and recycling of 5-HT_{2A} receptors activated by serotonin and protein kinase C mediated mechanisms. *Proceedings of the National Academy of Sciences, USA*, 99:14470-5.



Primary hippocampal neurons expressing AMPA receptors



Primary hippocampal neurons expressing mGluR1 receptors

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Research Interests & Projects

Cellular and Molecular Mechanisms of Protein Trafficking in the Central Nervous System

An essential requirement for maintenance of homeostasis in any living organism is the ability of cells to sense the external environment and, in the case of multicellular organisms, for cells to communicate with each other via mediators released into the extracellular milieu. In the brain, a variety of neurotransmitters and neuromodulators act on target receptors to activate cellular signaling events which transfer information from one cell to the next. Normal signaling depends on accurate localization of such receptors in specific regions of the cell, and the process of receptor trafficking plays a critical role in controlling this localization. Despite the obvious significance of this process, we still know very little about the protein machineries that mediate trafficking of neurotransmitter receptors in the brain, the regulatory events that control these protein machineries, and the functional consequences of these regulatory events. Our lab's specific interest lies in studying the cellular and molecular mechanisms that regulate the trafficking of neurotransmitter receptors in the central nervous system. Currently, the lab is studying the cellular and molecular mechanisms that regulate the trafficking of **(1) ionotropic glutamate receptors** and **(2) metabotropic glutamate receptors (mGluRs)**. We employ multidisciplinary approaches ranging from biochemistry and molecular biology to cell biology and imaging to address these questions.





Rachna Chaba

Assistant Professor

Dr. Rachna Chaba did her Masters in Biotechnology at Guru Nanak Dev University, Amritsar, India (1996-1998). She obtained her Ph.D from Institute of Microbial Technology, Chandigarh, India (1998-2003). She did her post-doctoral research at University of California, San Francisco, USA (2004-2011). She joined as Assistant Professor at IISER Mohali in January 2012.

Representative Publications

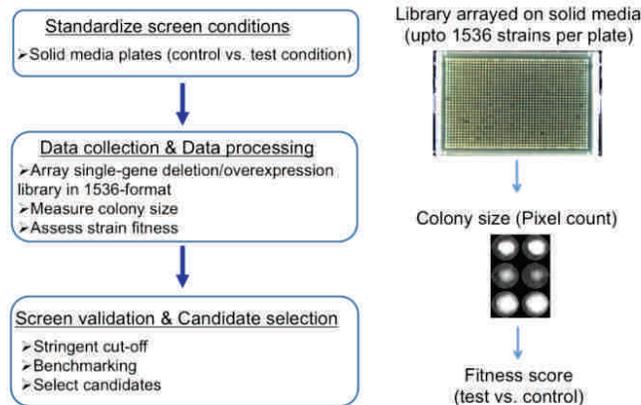
Lima, S., Guo, M. S., **Chaba, R.**, Gross, C. A. and Sauer, R. T. (2013). Dual molecular signals mediate the bacterial response to outer-membrane stress. *Science* 340: 837-841.

Oh, E., Becker, A. H., Sandikci, A., Huber, D., **Chaba, R.**, Gloge, F., Nichols, R. J., Typas, A., Gross, C. A., Kramer, G., Weissman, J. S. and Bukau, B. (2011). Selective ribosome profiling reveals the co-translational chaperone action of trigger factor in vivo. *Cell* 147:1295-1308.

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Chaba, R., Grigorova, I. L., Flynn, J. M., Baker, T. A. and Gross, C. A. (2007). Design principles of the proteolytic cascade governing the ^E-mediated envelope stress response in *Escherichia coli*: keys to graded, buffered, and rapid signal transduction. *Genes and Development*. 21(1): 124-136.

Grigorova, I. L., **Chaba, R.**, Zhong, H. J., Alba, B. M., Rhodius, V., Herman, C. and Gross, C. A. (2004). Fine-tuning of the *Escherichia coli*^E envelope stress response relies on multiple mechanisms to inhibit signal-independent proteolysis of the transmembrane anti-sigma factor, RseA. *Genes and Development*. 18(21): 2686-2697.



Methodology for high-throughput quantitative genetic screen to identify new players in metabolism

Research Interests & Projects

Systems-level analysis and mechanistic dissection of metabolic pathways in bacteria

Metabolism provides energy, creates building blocks, and regulates macromolecular processes. Integrating metabolism with other cellular responses provides the robustness enabling bacterial survival in diverse environments, key to their success as commensals, pathogens and industrial workhorses. Metabolic processes have often been probed by qualitative, non-saturating genetic techniques that may miss players and connections, thereby leading to a focus on the identification/characterization of individual components rather than considering metabolism as a cellular system. Thus despite decades of active research, our knowledge of metabolism even in the well-studied microbe, *E. coli*, is far from complete. A major obstacle impeding systems-level analysis of metabolism has been the lack of a comprehensive, quantitative, functional-genomics approach that provides an entire parts list and hints of connections. In this direction, my lab utilizes high-throughput quantitative genetic screening methodology (response of every gene deletion/overexpression strain to chemical perturbations, ~4000 genes), to identify novel players and networks in metabolism. The information extracted from these genomic approaches is integrated with knowledge from other high-throughput datasets to generate testable hypotheses about the function of novel genes, the process they participate in, and interconnections between pathways. As a complement, we also perform detailed molecular studies of important targets to establish their functional roles. Our research mainly focuses on metabolic processes that govern utilization of carbon sources implicated in pathogenesis and/or are important in biofuel production. Overall, our study intends to identify novel transporters, metabolic enzymes and regulators required for the degradation of carbon sources, and cross-talk between metabolic pathways and stress response pathways important for carbon source utilization. Thus, the combined use of a functional-genomics approach and mechanistic analysis will expand our knowledge of metabolism beyond a mere description of parts and will provide new metabolic information that can be harnessed to design novel antibacterials and create strains for biofuel production.





Kausik Chattopadhyay

Associate Professor; Member, MHRD Centre of Excellence in Protein Science, Design and Engineering

Dr. Kausik Chattopadhyay did his Masters in Biochemistry at Calcutta University, India (1996-1998). He obtained his Ph.D. in Biochemistry from National Institute of Cholera and Enteric Diseases, Kolkata, India (1998-2003). He has done his post-doctoral research at Albert Einstein College of Medicine, New York, USA (2003-2009). He joined as Assistant Professor at IISER Mohali in March 2009, and is presently an Associate Professor, since December 2014.

Representative Publications

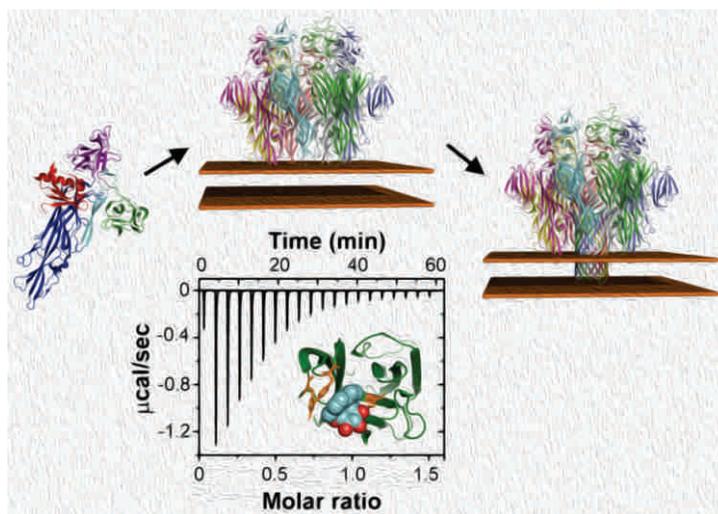
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Lata, K., and **Chattopadhyay, K.** (2015) *Helicobacter pylori* TlyA forms amyloid-like aggregates with potent cytotoxic activity. ***Biochemistry***, 54: 3649-3659.

Khilwani, B., Mukhopadhyaya, A.*, and **Chattopadhyay, K.*** (2015) Transmembrane oligomeric form of *Vibrio cholerae* cytolysin triggers TLR2/TLR6-dependent pro-inflammatory responses in monocytes and macrophages. ***Biochemical Journal***, 466: 147-161. [*Joint Corresponding Authors]

Rai, A. K., and **Chattopadhyay, K.** (2014) Trapping of *Vibrio cholerae* cytolysin in the membrane-bound monomeric state blocks membrane insertion and functional pore formation by the toxin. ***Journal of Biological Chemistry***, 289: 16978-16987.

Rai, A. K.*, Paul, K.*, and **Chattopadhyay, K.** (2013) Functional mapping of the lectin activity site on the b-Prism domain of *Vibrio cholerae* cytolysin: implications for the membrane pore-formation mechanism of the toxin. ***Journal of Biological Chemistry***, 288: 1665-1673. (*These authors contributed equally to this work)



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Research Interests & Projects

Structure-Function Studies on Pore-Forming Protein Toxins

Pore-forming protein toxins (PFTs) represent a special class of membrane damaging cytolytic proteins, and they are found in wide spectrum of organisms ranging from bacteria to humans. They exert their toxic effects by punching 'holes' into target cell membrane, thus destroying the natural permeability barrier function of the cell membrane. PFTs are, in general, synthesized as water-soluble molecules, and in contact with target cell membranes they form membrane-inserted pores. However, in spite of sharing this overall general scheme, PFTs differ significantly from each other in the intricate details of their pore formation mechanisms. A major mechanistic challenge associated with the membrane pore formation process by PFTs is elucidating the folding pathways that ensure thermodynamic compatibility of the water-soluble and the membrane-inserted form of the toxin with aqueous and membrane lipid milieu, respectively. One of the major research interests of my group is focused on studying structure-function relationship of some of the prominent bacterial PFTs. The critical issues we address are:

- Mechanistic details of membrane channel formation by PFTs.
- Mechanism(s) associated with cellular responses triggered by PFTs.





Purnananda Guptasarma

Professor; Director, MHRD Centre of Excellence in Protein Science, Design and Engineering

Dr. Purnananda Guptasarma did his Bachelors' degree in engineering and an integrated Masters' degree in Science, under the dual-degree program of the Birla Institute of Technology & Science, BITS, Pilani, India (1983-1988). He obtained his Ph.D. from the Centre for Cellular and Molecular Biology, Hyderabad, India (1988-1993). He was a research associate of the DBT at CCMB, Hyderabad, India (1993-1994) and an International Research Fellow of the Wellcome Trust at the Department of Biochemistry, University of Cambridge, UK (1994-1996). He joined the Institute of Microbial Technology, Chandigarh, India as a principal investigator in 1996. In 2008, he became an adjunct faculty at IISER Mohali, and left IMTECH and joined as Professor at IISER Mohali in October 2010.

Representative Publications

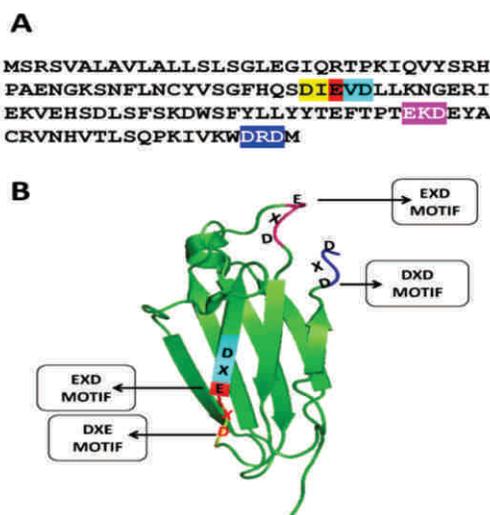
Prakash, S., Sundd, M. & Guptasarma, P (2014). The Key to the Extraordinary Thermal Stability of *P. furiosus* Holo-Rubredoxin: Iron Binding-Guided Packing of a Core Aromatic Cluster Responsible for High Kinetic Stability of the Native Structure. *PLoS ONE* 9(3):e89703. (An explanation)

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Shukla, A., Raje, M. & Guptasarma, P. (2003). A backbone-reversed form of an all- β α -crystallin domain from a small heat-shock protein (retro-HSP12.6) folds and assembles into structured multimers. *Journal of Biological Chemistry* 278: 26505-26510. (An exploration)

Guptasarma, P. (1995). Does replication-induced transcription regulate synthesis of the myriad low copy number proteins of *Escherichia coli*? *BioEssays* 17: 987-997. (A hypothesis)



Potential sites for binding of calcium in the sequence (Panel A) and structure (Panel B) of the HLA light chain protein, beta-2-microglobulin (β_2m). The DXDXD/DXDXE/DXEXD calcium-binding motif is found in microbial primases and topoisomerases. The DXD/DXE/EXD motif is found in glycosyl transferases, and binds to either sugar and metal atom, or metal alone. The presence of potential calcium-binding motifs in beta-2-microglobulin has not been previously noted in the literature.

In a recent discovery reported by us (Kumar et al, 2014, PLOS One, 9, e95725), we showed that β_2m protein at physiological pH binds to calcium, undergoes a rapid conformational change in its beta-sheet structure, and immediately precipitates out of solution. Microaggregation is visible at physiological (serum) concentrations of calcium and β_2m protein. The initially-formed precipitates, constituted of amorphous aggregates, transform into amyloids with time. This discovery offers an explanation for the disease known as dialysis-related amyloidosis (DRA), and suggests a possible cure involving chelator (e.g., EDTA) treatment during blood dialysis of patients with kidney disease.

Research Interests & Projects

My interests lie in proteins : in the regulation of their production within cells; in their folding, misfolding and structural stabilities; in their interactions with other proteins, DNA and small molecules; in their functions as enzymes and transporters; in developing new techniques for their characterization; in studying all sorts of new proteins, in respect of any, or all, of the above; and, in particular, in engineering any or all of the above through the use of predictive ideas and concepts, ideational testing through computational modelling and structural bioinformatics, implementation through the use of recombinant DNA techniques, bio-molecular purification and separation methods, and characterization through a wide variety of spectroscopic, spectrometric and other methods.

Currently, three-fifths of the work in my lab is on ex-vivo studies of protein structure, stability, folding and function, or misfolding and aggregation, using many different experimental systems; mostly hyperthermophile-derived proteins. The remaining two-fifths relate to studies of DNA-protein interactions or gene expression, or cellular responses to protein aggregates.

Amongst highlights from our activity, in recent years, we have discovered a novel fluorescence in proteins (from H-bonded peptide bonds) which has gained prominence; invented a new technique for grafting beta sheet-based active surfaces between proteins, which has also been patented; unraveled the molecular mechanisms of high kinetic stability in hyperthermophile proteins (and used these to engineer proteins, to make them more or less kinetically stable, by design); discovered novel health implications and modes of aggregation of certain medically-relevant proteins; and developed new methods in fluorescence spectroscopy, mass spectrometry, gene expression, microscopy and bioinformatics.





Manjari Jain
Assistant Professor

Dr. Manjari Jain did her Masters in Zoology from University of Calcutta (2001-2003). She obtained her Ph.D. from Indian Institute of Science (IISc), Bangalore, India (2004-2010). She worked as Research associate at IISc Bangalore (2010-2011). She did her post-doctoral research at School of Biological Sciences, University of Bristol, UK (2011) and University of Zurich, Switzerland (2011-2012). She joined as Adjunct Faculty at the National Institute of Advanced Studies, Bangalore in 2013. She joined as Assistant Professor at IISER Mohali in October 2013.

Representative Publications

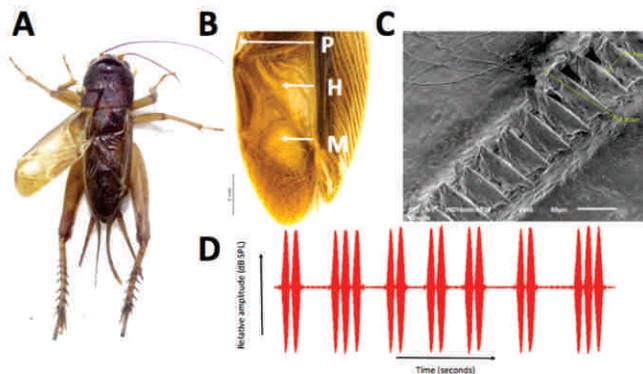
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Jain M, Diwakar S, Bahuleyan J, Deb R and Balakrishnan R (2013). A Rain Forest Dusk Chorus: Cacophony or sounds of silence? *Evolutionary Ecology*, 28: 1-22

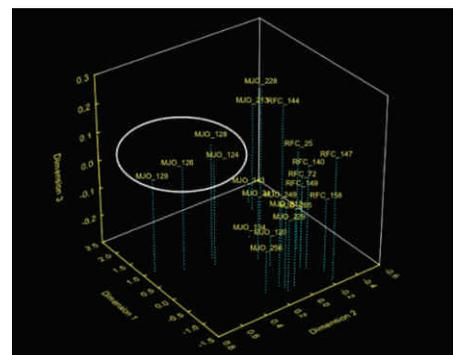
Rajaraman K, Mhatre N, Jain M, Postles M, Balakrishnan R & Robert D (2013). Low pass filters and differential tympanal tuning in a paleotropical bushcricket with an unusually low frequency call. *Journal of Experimental Biology*, 216: 777-787.

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A) *Teleogryllus* sp. male with extended elytra. B) *Teleogryllus* sp. forewing showing structures that are implicated in sound production, Plectrum (P), Harp (H) and Mirror (M). C) SEM image of underside of wing showing row of teeth (file) on the underside of Cubitus 2 vein that borders the Harp region. D) Oscillogram of song of *Teleogryllus* sp. recorded from IISER Mohali campus showing chirps containing 2 or 3 syllables.



Grouping of 22 individuals of *Teleogryllus* sp. (collected from different parts of India) based on song characteristics using Multi-Dimensional Scaling. Circled individuals likely belong to a different species than the rest.

Research Interests & Projects

I am a behavioural ecologist and my research interests lie in the interface of ethology, ecology and evolutionary biology. I am primarily interested in understanding the ecology and evolution of acoustic communication in animals. Variation and complexity in acoustic communication, the numerous constraints on communication and how animals deal with these are the main drivers of my curiosity and my research largely revolves around these topics. The approaches used are a combination of field and lab-based experiments, empirical observations and theoretical modeling. My work is question-driven and I work on a range of study systems including insects, birds and mammals.

PROJECTS

- (1) Evolution of signal design: An astonishing variety of signals exist in the animal kingdom. One of the major aims of my research is to understand the structure of signals used by animals, the ecological contexts in which they are used, the constraints under which the animals must communicate and the evolutionary forces driving the communication system.
- (2) Acoustic communication and sociality: Over the course of evolution, non-human social animals have achieved remarkable complexity in the organization of their societies and sophistication in communication. I am interested in understanding the social evolution of acoustic communication. A variety of animal societies, across different taxa, allow us to study this by examining interaction between animals that are mediated by acoustic communication.
- (3) Biodiversity and conservation: Living in the tropics, we are blessed with a rich diversity of habitats, flora and fauna. One cannot turn a blind eye towards the rapid loss of biodiversity and degradation of habitats due to rapid urbanization. Through my research I aim to develop novel, non-invasive and whenever possible, inexpensive techniques to monitor biological diversity in order to concentrate conservation efforts to biodiversity-rich areas.





Lolitika Mandal

Assistant Professor; Wellcome-DBT Intermediate Fellow

Dr. Lolitika Mandal did her Masters in Zoology at Burdwan University West Bengal, India. She obtained her Ph.D from Banaras Hindu University, Varanasi, India. She did her post-doctoral research at Department of Molecular, Cell and Developmental Biology, University of California, Los Angeles, USA. She joined as Assistant Professor at IISER Mohali in July 2009.

Stem and progenitor cell development:
Molecular pathways of hematopoiesis and cardiogenesis

Representative Publications

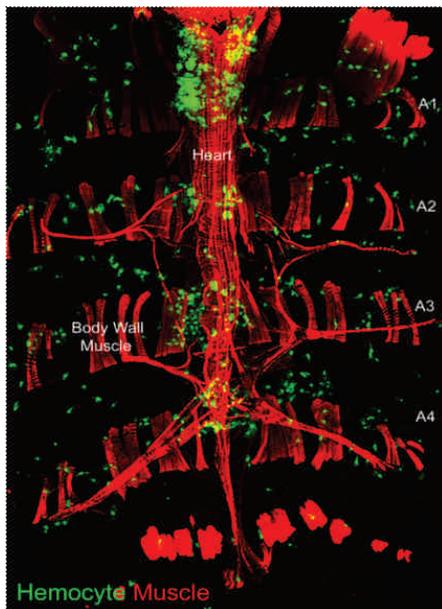
Ghosh S, Singh A, Mandal S, and Mandal L. (2015). Active Hematopoietic Hubs in *Drosophila* Adults Generate Hemocytes and Contribute to Immune Response. *Developmental Cell* 33:478-88.

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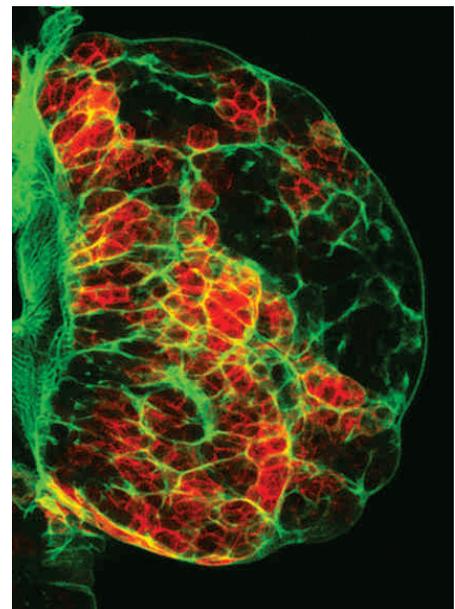
Mukherjee T, Kim WS, Mandal L, and Banerjee U. (2011). Interaction between Notch and Hif-alpha in development and survival of *Drosophila* blood cells. *Science*. 332:1210-3.

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Mandal, L., , Banerjee, U and Hartenstein, V (2004). Evidence for a fruit fly hemangioblast and similarities between lymph-gland hematopoiesis in fruit fly and mammal aorta-gonadal-mesonephros mesoderm. *Nature Genetics*. 36: 1019-23.



Hematopoietic Hub in Adult Fruit fly
Hemocyte are embedded in ECM



The larval hematopoietic organ
in *Drosophila*

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Research Interests & Projects

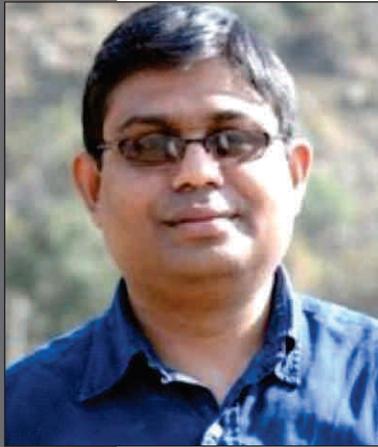
Developmental Genetics Laboratory at IISER (MOHALI) is interested in Hematopoiesis, Cardiogenesis and Molecular pathways in stem and progenitor cell development.

Ongoing Project: Molecular genetic dissection of signaling pathways involved in hematopoietic niche maintenance in *Drosophila*. A proposal funded by WELLCOME DBT Alliance.

Stem cells are the source of virtually all highly differentiated cells that are replenished during the lifetime of an animal. The critical balance between stem and differentiated cell populations is crucial for the long-term maintenance of functional tissue types. A microenvironment that is supportive of stem cells is commonly referred to as a stem cell niche. Although, several signaling molecules emanating from the niche has been identified for regulation of stem cell state and function, the information regarding niche maintenance is still in its infancy. We are interested to know the mechanistic basis of niche maintenance.

Last decade established *Drosophila* as the best invertebrate model system for studying hematopoiesis. Due to the limited access of mammalian hematopoietic niche this amenable system allows us to unravel molecular regulation of stem cell progenitors and its relation with the niche. The power of *Drosophila* as a model organism is very well established, most notably its genetics and developmental biology. Taking advantage of these strengths our group also aims in unraveling novel genes and mechanisms that controls hematopoietic progenitors cell specification and differentiation. Given the high degree of conservation of blood development between *Drosophila* and the vertebrates, we hope that the ability to manipulate the function of such genes in *Drosophila* would aid in understanding function and dysfunction in human hematopoiesis.





Sudip Mandal

Assistant Professor

Dr. Sudip Mandal did his Masters in Zoology at Banaras Hindu University, Varanasi, India. He obtained his Ph.D from Banaras Hindu University, Varanasi, India. He did his post-doctoral research at Department of Molecular, Cell and Developmental Biology, University of California, Los Angeles, USA. He joined as Assistant Professor at IISER Mohali in July 2009.

Representative Publications

Ghosh, S., Singh, A., Mandal, S., Mandal, L. (2015). Active hematopoietic hubs in *Drosophila* adults generate hemocytes and contribute to immune response *Developmental Cell* 26 33: 478-88

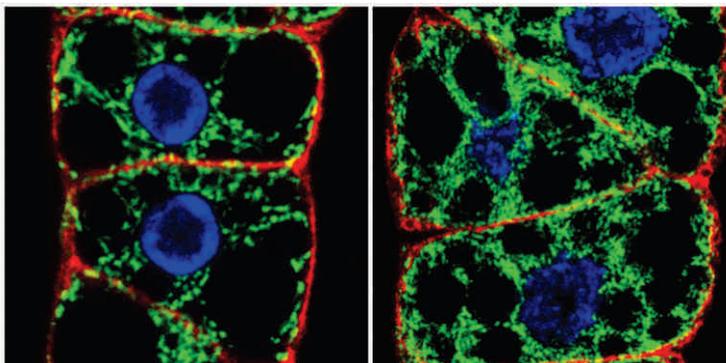
Mandal, S., Lindgren, AG., Srivastava, AS., Clark, AT., Banerjee, U. (2011). Mitochondrial function controls proliferation and early differentiation potential of embryonic stem cells. *Stem Cells*. 29: 486-95.

Mandal, S., Freije, WA., Guptan, P., Banerjee, U. (2010). Metabolic control of G1-S transition: cyclin E degradation by p53-induced activation of the ubiquitin-proteasome system. *Journal of Cell Biology*. 188: 473-79.

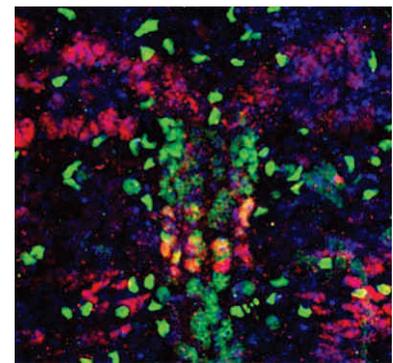
Owusu-Ansah, E, Yavari, A, Mandal, S, Banerjee, U. (2008). Distinct mitochondrial retrograde signals control the G1-S cell cycle checkpoint. *Nature Genetics*. 40: 356-61.

Mandal, S., Guptan, P., Owusu-Ansah, E., Banerjee, U. (2005). Mitochondrial regulation of cell cycle progression during development as revealed by the tenured mutation in *Drosophila*. *Developmental Cell*. 9:843-54.

Molecular Cell & Developmental Biology:
Mitochondrial regulation of cellular function



Drosophila fat body cells expressing mito-GFP



Embryonic cardiogenic mesoderm

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Research Interests & Projects

Mitochondria, as we all studied in our school days, are bean shaped organelles considered as the powerhouse of the cell and the biochemical pathways leading to ATP synthesis within the mitochondria is well understood. However, studies in the recent past have established mitochondria as dynamic polymorphic structures having branched reticulate network interspersed with small bean shaped structures that integrate diverse extra and intra cellular signals to regulate several cellular functions. Mitochondrial biology, therefore, has become a fast growing area in genetics and medicine, linking cell biological processes to metabolic disorders and cancer. We are interested in understanding the role of mitochondrion in controlling cell biological processes like proliferation, growth and differentiation. We use the model organism, *Drosophila melanogaster*, for genetic dissection of retrograde signaling pathways from mitochondria to nucleus that are essential in modulating cellular responses. Taking advantage of the advanced genetic tools available in this model system and using high-end microscopy and molecular genetic approaches we aim to unravel the mechanistic basis of mitochondrial regulation of cellular functions.

The other focus of our research involves embryonic stem cells. Embryonic stem cells, by virtue of their capacity to proliferate indefinitely and to differentiate into almost all types of somatic cells, hold the potential to be used for therapeutic purposes. Current research in this field aims to a) develop means to direct embryonic stem cells to differentiate into specific cell types that can be used for therapy and (b) to reprogram adult somatic cells to form induced pluripotent stem (IPS) cells. In this pursuit scientists are trying to understand the genetic regulations and modifications in the genome that contribute to the processes of reprogramming and differentiation. Although it is equally important to understand how these processes are affected by the cellular metabolic state, very limited studies address this issue. We aim to understand the metabolic control of pluripotency and early lineage specification of ESCs and EpiSCs. To achieve this goal, we employ a combination of microscopic, histological, biochemical, genetic and molecular cell biological approaches.





Shравan Kumar Mishra

Assistant Professor; Head, DST-Max Plank Partner Group; Member, MHRD Centre of Excellence in Protein Science, Design and Engineering

Dr. Shравan Kumar Mishra did his Masters in Biotechnology, M. S. University of Baroda, India (1997-1999). He obtained his Ph.D. from J. W. Goethe University of Frankfurt, Germany (2000-2004) He did his postdoctoral research at Max Planck Institute of Biochemistry, Martinsried/Munich Germany. (2004-2012). He joined as Assistant Professor at IISER Mohali in March 2012.

Representative Publications

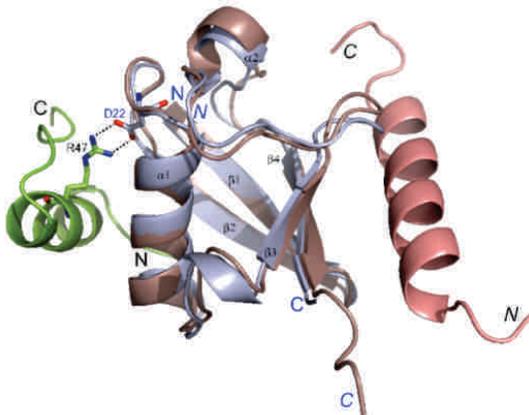
Ammon, T., **Mishra, S.K.**, Kowalska, K., Popowicz, G.M., Holak, T., and Jentsch, S. (2014). The conserved ubiquitin-like protein Hub1 plays a critical role in splicing in human cells. *Journal of Molecular Cell Biology* 6: 312-323.

Mishra, S.K., Ammon, T., Popowicz, G.M., Krajewski, M., Nagel, R.J., Ares, M., Holak, T., and Jentsch, S. (2011). Role of the ubiquitin-like protein Hub1 in splice-site usage and alternative splicing. *Nature* 474: 173-178.

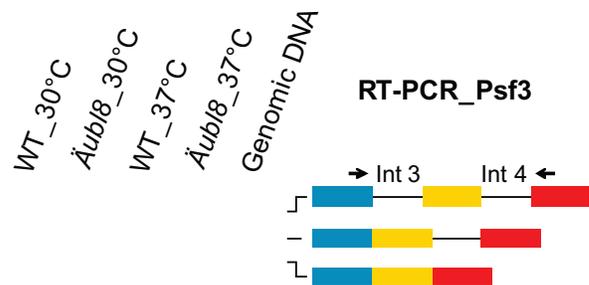
Tripp, J*, **Mishra, S.K.***, and Scharf, K.-D. (2009). Functional dissection of the cytosolic chaperone network in tomato mesophyll protoplasts. *Plant, Cell and Environment* 32: 123-133. (*Co-first authors).

Baniwal, S.K., Bharti, K., Chan, K.Y., Fauth, M., Ganguli, A., Kotak, S., **Mishra, S.K.**, Nover, L., Port, M., Scharf, K.-D., Tripp, J., Zielinski, D., and von Koskull-Doering, P. (2004). Heat stress response in plants: a complex game with chaperones and more than 20 heat stress transcription factors. *Journal of Biosciences* 29: 471–487.

Mishra, S.K., Tripp, J., Winkelhaus, S., Tschiersch, B., Theres, K., Nover, L., and Scharf, K.-D. (2002). In the complex family of heat stress transcription factors, HsfA1 has a unique role as master regulator of thermo tolerance in tomato. *Genes and Development* 16: 1555-1567.



Non-covalent interactions of ubiquitin-like protein Hub1 and Ubiquitin. Structure of HIND (green) – Hub1 (silver) complex superimposed with structure of Ubiquitin (dark pink)– UIM (pink)



UBL8 as an intron specific-splicing factor:
RT-PCR assay

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Research Interests & Projects

Proteins Related to Ubiquitin as Regulators of RNA Splicing

Ubiquitin and ubiquitin-related proteins (here collectively referred to as UBL) are highly conserved, generally small (around 10 kilo-daltons), which share a typical ubiquitin fold, but with distinct surfaces. Using a set of dedicated enzymes, a canonical UBL attaches and modifies its substrates through covalent linkages. And, substrates/targets of an UBL can be proteins, lipids or RNA, depending of the UBL. The reversible nature of this modification makes UBLs central regulators of a large number of processes in the cell. Most UBLs, however, also interact non-covalently with proteins harboring specific UBL-binding domains. Thus, UBLs not only determine fates of their targets through proteasomal destruction, but also confer functional diversity to their substrates in non-proteolytic ways. Therefore, in processes like DNA repair, recombination, ribosome biogenesis, cellular signaling pathways etc., substrates gain new functions upon modification by various UBLs including the prototype ubiquitin.

Several reports hint towards UBL activities also at the spliceosome (the catalyst that removes non-coding parts – introns and joins protein-coding parts – exons from pre-messenger RNAs by the process of RNA splicing). Several spliceosomal proteins appear to be modified by UBLs, but precise roles of such modifications are not clear. In metazoans, the spliceosome also performs alternative RNA splicing to increase the cellular repertoire of mRNAs, thus to fulfill the demand of a larger proteome from a lower gene number. Although, the composition of spliceosomes core is well studied, but its regulation that ensures constitutive and alternative splicing of almost every gene in humans is not understood. Intriguingly, UBLs, which function as regulators of numerous processes in the cell, are also suited for the control of RNA splicing. Our research group at IISER Mohali is interested in finding new mechanisms of RNA splicing regulation that are acted upon by UBL and UBL-associated proteins. And, since UBLs as well as the process of RNA splicing are conserved from yeast to humans, we are able to use approaches of molecular cell biology, biochemistry and genetics in yeasts *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe* for our studies.

We have previously shown that the UBL Hub1 (also called UBL5) is unique and modifies the spliceosome by its non-covalent associations with HIND (Hub1-interaction domain)-containing splicing factors and plays a crucial role in alternative RNA splicing. More recently we have identified a new UBL as a component of the spliceosome, which functions like an intron-specific splicing factor. This finding indicates that in a pre-messenger RNA all introns are not recognized uniformly by the spliceosome and for some introns the machinery requires additional UBL-like regulatory factors.





Arunika Mukhopadhyaya

Arunika Mukhopadhyaya

Dr. Arunika Mukhopadhyaya did her Masters at University of Burdwan West Bengal, India. She obtained her Ph.D. from National Institute of Cholera and Enteric Diseases, Kolkata, India. She was a research associate at Radiation and Oncology Department, and also at Department of Microbiology and Immunology in Albert Einstein College of Medicine, New York, USA. She joined as Assistant Professor at IISER Mohali in March 2009.

Representative Publications

Sakharwade, SC. and Mukhopadhyaya, A. *Vibrio cholerae* porin OmpU induces LPS tolerance by attenuating TLR-mediated signaling. (2015). *Molecular Immunology* (accepted)

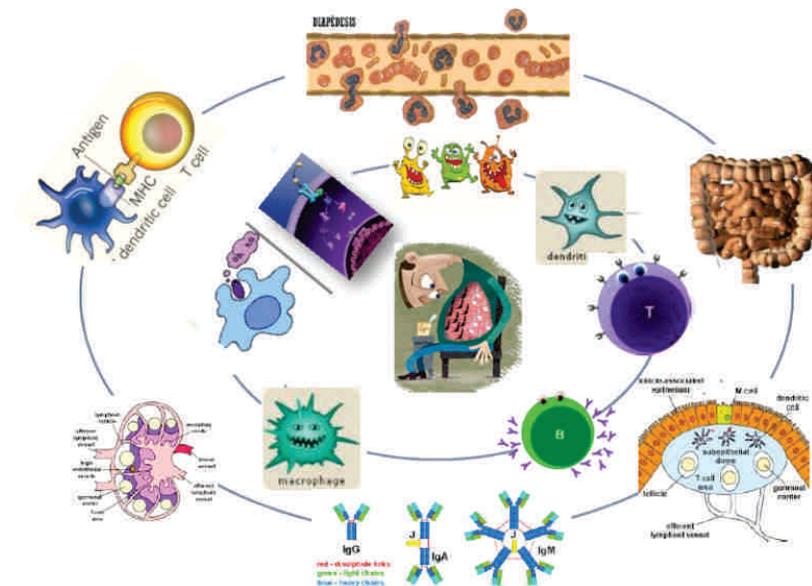
Khan, J, Sharma PK, **Mukhopadhyaya, A.** (2015) *Vibrio cholerae* porin OmpU mediates M1-polarization of macrophages/monocytes via TLR1/TLR2 activation. *Immunobiology.*; 220 :1199-209.

Khilwan, B, **Mukhopadhyaya, A***, Chattopadhyay, K*. (2015) Transmembrane oligomeric form of *Vibrio cholerae* cytolysin triggers TLR2/TLR6-dependent proinflammatory responses in monocytes and macrophages. *Biochemical Journal.* 466:147-61. *Joint corresponding author.

Sakharwade SC, Sharma PK, **Mukhopadhyaya A.** (2013). *Vibrio cholerae* porin OmpU induces pro-inflammatory responses, but down-regulates LPS-mediated effects in RAW 264.7, THP-1 and human PBMCs.. *PLoS One* 8(9):e76583.

Khan, J., Gupta, S., Chattopadhyay, K., **Mukhopadhyaya, A.** (2012). Refolding and functional assembly of the *Vibrio cholerae* porin OmpU recombinantly expressed in the cytoplasm of *Escherichia coli*. *Protein Expression and Purification.* 85:204-10.

Immunology :
Host-microbe interactions



Immunobiology of Host-Pathogen Interaction of Enteric Bacterial Diseases

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My group is interested in characterization of host-immunomodulatory responses by pathogenic gram negative enteric bacteria. Pathogenic enteric bacteria are those which upon entering into the host colonize in the gut region and secrete toxin(s) or invade gut epithelial cells to pathogenize the host. Pathogens carry pathogen associated molecular patterns (PAMPs) which are recognized by the pattern recognition receptor (PRRs) present on the cells such as macrophages, dendritic cells, intestinal epithelial cells. PAMP recognition by PRRs initiate signal transduction cascades resulting in production of an array of cytokines and chemokines which are not only important for innate immune responses also shapes up adaptive immune responses in terms of inflammation and B/T cell effector function and memory generation. Different PAMPs or antigens have the ability to excite or suppress the immune responses. If the antigen is a potent stimulator of the host's immune system, it can be considered for vaccine development. On the other hand if the antigen is an immune suppressor that help us to understand more about the pathogenesis of the bacteria.

Currently we are working on three broad projects:

Project 1: Understanding the host-immunomodulatory role of *Vibrio cholerae* porin

Project 2: Understanding the host-immunomodulatory role of homologous porin from *Vibrio parahaemolyticus*

Project 3: Understanding the host-immunomodulatory role of TypeIII secretion system translocation effector proteins of *Salmonella enterica* serovar Typhimurium.





Samrat Mukhopadhyay

Associate Professor; Member, MHRD Centre of Excellence in Protein Science, Design and Engineering

Dr. Samrat Mukhopadhyay did his Masters at Indian Institute of Science, Bangalore, India (2000). He obtained his Ph.D. from Indian Institute of Science, Bangalore, India (2005). He did his postdoctoral research at Scripps Research Institute, USA (2005-2008). He joined as Assistant Professor at IISER Mohali in December 2008 and is presently an Associate Professor, since September 2013.

Representative Publications

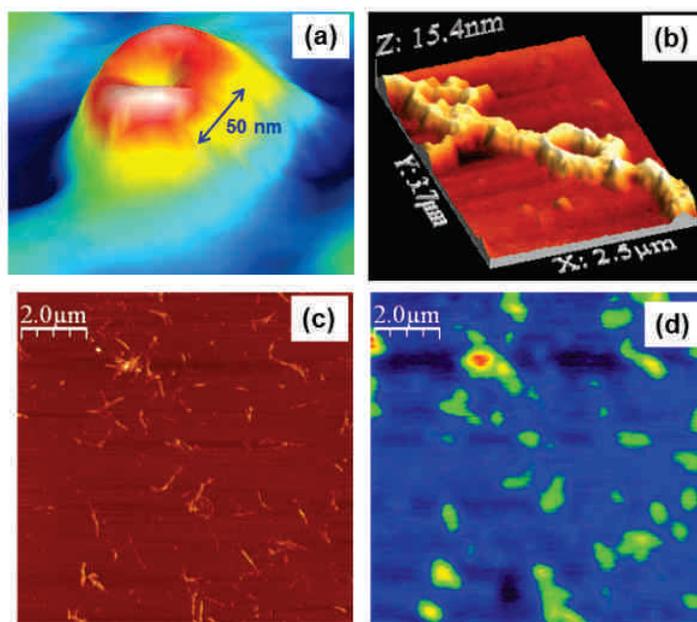
S. Arya, A. Kumari, V. Dalal, M. hattacharya and **S. Mukhopadhyay** (2015). Appearance of Annular Ring-like Intermediates during Amyloid Fibril Formation from Human Serum Albumin". *Physical Chemistry Chemical Physics*. 17, 22862-22871

S. Arya and **S. Mukhopadhyay**. (2014). Ordered Water within the Collapsed Globules of an Amyloidogenic Intrinsically Disordered Protein *Journal of Physical Chemistry B*. 118: 9191–9198.

N. Jain, K. Bhasne, M. Hemaswathi and **S. Mukhopadhyay**. (2013). Structural and Dynamical Insights into the Membrane-bound α -Synuclein *PLoS ONE*, 8(12):e83752.

V. Dalal, M. Bhattacharya, D. Narang, P.K. Sharma and **S. Mukhopadhyay**. (2012). Nanoscale Fluorescence Imaging of Single Amyloid Fibrils. *Journal of Physical Chemistry Letters*, 3: 1783-1787

N. Jain, M. Bhattacharya and **S. Mukhopadhyay**. (2011). Chain Collapse of an Amyloidogenic Intrinsically Disordered Protein. *Biophysical Journal*. 101: 1720-1729.



Atomic force microscopy images of (a) an amyloid pore and (b) human prion protein fibrils. Correlated nanoscale topography (c) and fluorescence (d) images of amyloid fibrils performed using near-field scanning optical microscopy.

Research Interests & Projects

My lab is involved in addressing a variety of intriguing and important molecular and cellular aspects of aberrant protein aggregation resulting in the formation of amyloid fibrils that are linked to devastating neurological disorders such as Alzheimer's, Parkinson's, Huntington's and transmissible prion diseases. Using a diverse array of modern biophysical techniques in combination with other biophysical, biochemical and molecular biology tools, our laboratory has been able to extensively characterize the morphologically-distinct 'obligatory' oligomeric intermediates that serve as the precursors to fibrils and are considered to be the killer species in amyloid disorders. We have utilized a super-resolution nanophotonic methodology, namely the near-field scanning optical microscopy, that combines the capabilities of atomic force microscopy and optical spectroscopy to simultaneously map the nanoscale topography and the underlying molecular structure and packing within the nanoscopic assembly. Our results make an attempt to provide structural underpinnings of diverse amyloid polymorphs that underlie the strain phenomenon in prion and amyloid biology. We have now embarked upon the cell biological aspects of amyloids. Many of the amyloid-forming proteins belong to the unique class of intrinsically disordered proteins (IDPs) that challenge the tenets of traditional sequence-structure-function paradigm. My laboratory is also involved in investigating intriguing conformational attributes such as astonishing structural plasticity, membrane-induced folding, internal chain friction, internal water structure and order-to-disorder transitions of amyloidogenic IDPs that are of significant interest to the understanding of the functional repertoires of IDPs as well as their transition into pathological amyloids.





Shashi Bhushan Pandit

Assistant Professor; Member, MHRD Centre of Excellence in Protein Science, Design and Engineering

Dr. Shashi Bhushan Pandit did his Masters and PhD (Integrated PhD) in Computational Biology from Indian Institute of Science, Bangalore, India (2005). He did his first postdoctoral research at Georgia Institute of Technology, USA and second one at Genoscope, France and Institute of Systems and Synthetic Biology, France. He joined as assistant professor at IISER Mohali in June 2012.

Representative Publications

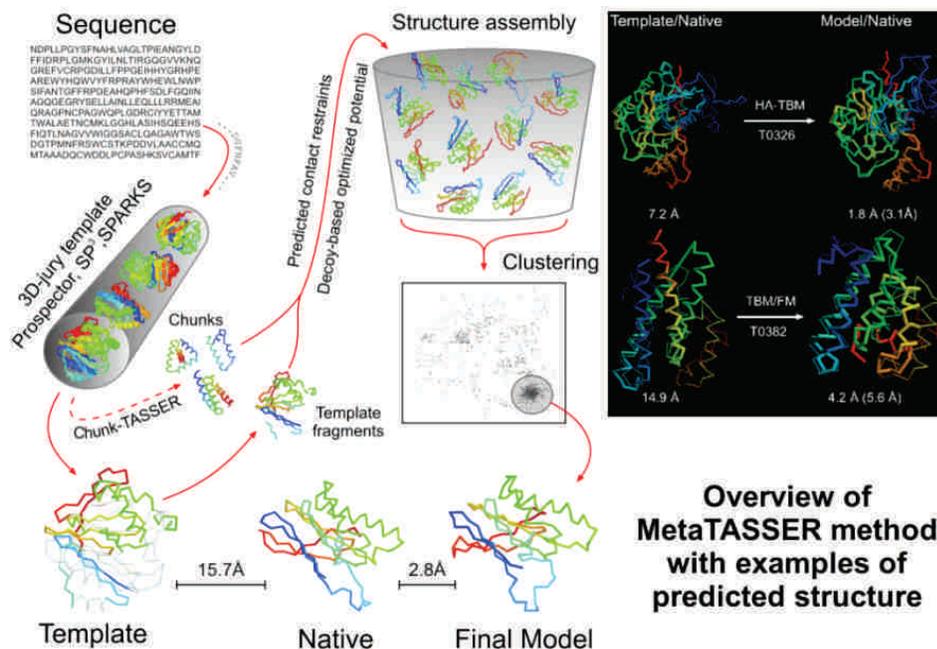
Carbonell P, Parutto P, Herisson J, **Pandit SB**, Faulon JL. (2014). XTMS: pathway design in an eXTended metabolic space. *Nucleic Acids Research* 42 (Web Server issue):W389-94.

S. B. Pandit, Brylinski, M, Gao M, Arakaki, A and J. Skolnick. (2010). PSiFR: An integrated resource for prediction of protein structure and function. *Bioinformatics*, 26: 687-688.

S. B. Pandit and J. Skolnick. (2008). Fr-TM-align : A new protein structural alignment method based on fragment alignments and the TM-score. *BMC Bioinformatics* 9:531 (Highly accessed).

S. B. Pandit, Y. Zhang and J. Skolnick. (2006) TASSER-Lite: An automated tool for protein comparative modeling. *Biophysical Journal* 91: 4180-4190.

S. B. Pandit and N. Srinivasan. (2003) Survey for G-proteins in the prokaryotic genomes: prediction of functional roles based on classification. *Proteins: Structure Function and Genetics* 52, 585-597. (Recommend article in Faculty of 1000 Biology).



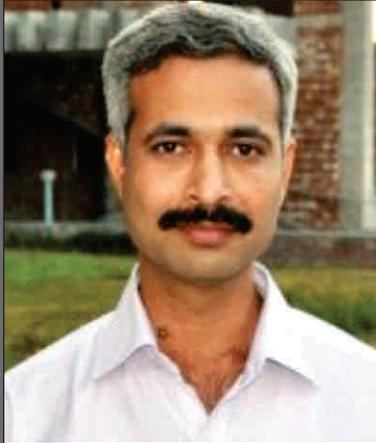
Overview of MetaTASSER method with examples of predicted structure

Research Interests & Projects

Computational structural and systems biology

The main research interest of the group is to understand structural/sequence basis of enzyme promiscuity, ligand-protein interactions and modeling of multi-domain proteins with an aim to develop robust computational prediction methodologies. Microorganisms show remarkable resilience towards deletion of genes involved in metabolic pathways. Usually, this is attributed to enzyme's capability to catalyze alternate substrate/reaction (promiscuous activity). Hence, including these promiscuous reactions in metabolic pathway reconstructions can provide complete metabolic capability of an organism. Recently, using chemoinformatics approach we have developed a method to predict putative promiscuous reactions using molecular reaction signatures. In this approach, we assumed that enzymes would accommodate any substrate and catalyze the same. To evaluate this assumption, we are systematically investigating the structural and sequence properties of enzymes or substrates binding sites, which could confer them promiscuity. Furthermore, we will investigate the mechanistic aspect of enzyme promiscuity and study their evolution. We will study the role of protein dynamics in ligand-protein interactions. Many enzymes are multi-domain proteins. Hence, we are developing methods for tertiary structure prediction of multi-domain proteins using our recently developed method TASSER (Threading ASSEMBly and Refinement).





N. G. Prasad

Associate Professor

Dr. N.G. Prasad did his Masters in Zoology at Bangalore University, India (1995-1997). He worked as Lecturer at Department of Zoology, MES College of Arts, Commerce and Science, Bangalore University, India (1997-1998). He obtained his Ph.D. from Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore, India (1998-2003). He did his postdoctoral research at Department of Biology, Queen's University, Kingston, Canada (2003-2007). He joined as assistant professor at School of Life Sciences, IISER, Kolkata, India in August 2007. In January 2009, he joined as assistant professor at IISER Mohali and presently is an associate professor, since September 2013.

Representative Publications

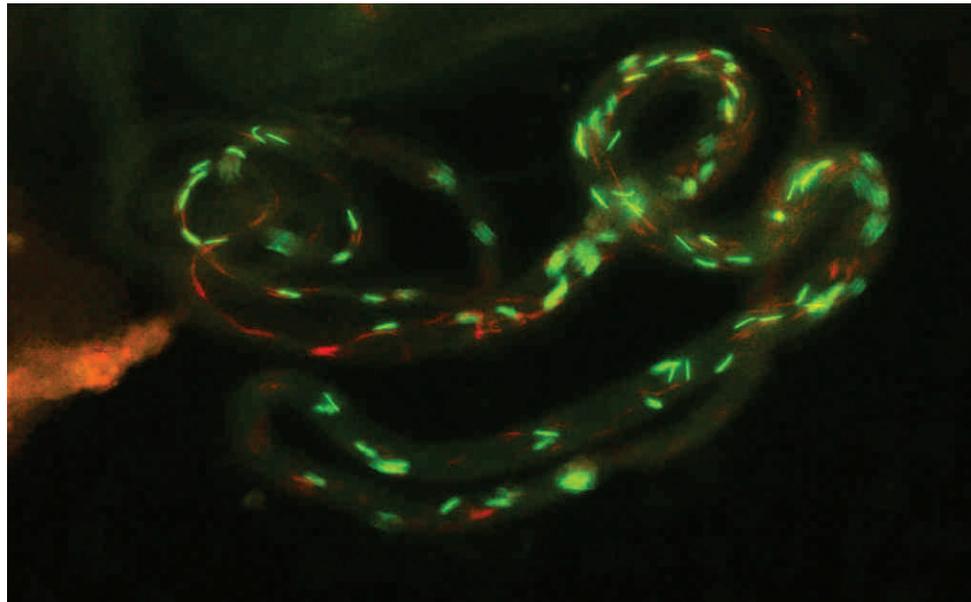
Singh, K., Kochar, E. and **Prasad, N. G.** (2015). Increased egg viability, mating frequency and male mating ability evolve in populations of *Drosophila melanogaster* selected for increased resistance to cold shock. ***PLoS One***. 10(6):e0129992

Gupta, V., Zeeshan, S. A. and **Prasad, N. G.** (2013). Sexual activity increases resistance against *Pseudomonas entomophila* in male *Drosophila melanogaster*. ***BMC Evolutionary Biology*** 13: 185.

Nandy, B., Vanika, G., Udaykumar, N., Samant, M. A., Sen, S. and **Prasad, N.G.** (2013). Experimental evolution of female traits under different levels of intersexual conflict in *Drosophila melanogaster*. ***Evolution*** doi:10.1111/evo.12271.

Nandy, B., Chakraborty, P., Ali, Z.S. and **Prasad, N.G.** (2013). Sperm competitive ability evolves in response to altered operational sex ratio. ***Evolution***. doi:10.1111/evo.12076

Khan, I. and **Prasad N. G.** (2012). The aging of the immune response in *Drosophila melanogaster*. ***Journals of Gerontology: Biological Sciences***. doi:10.1093/Gerona/gls144.



Sperms from two different Drosophila melanogaster males within the seminal receptacle of a female. The sperms have been tagged with GFP and RFP to help visualise sperm competition.

Research Interests & Projects

We work in the broad area of Evolutionary Genetics. Our special interest lies in understanding the co-evolution between males and females of a species. In promiscuous species, the correlation for fitness between males and females is less than one. Thus, males and females can potentially evolve traits that increase their own Darwinian fitness but harm the fitness of the other sex. This leads to open-ended cycles of adaptation and counter adaptation - a form of intra-species Red Queen process - often called Intersexual Conflict. Such antagonistic co-evolution between sexes has been suggested to drive rapid divergence between populations in their life-history and behaviour and act as an engine for speciation. The long term goal of our lab is to understand the interplay between sexual conflict, sexual selection and life-history evolution. Specifically, we are working on Sexual conflict and Sexual Selection, Evolutionary Ecology of immunity and Life-History Evolution.





Rajesh Ramachandran

Assistant Professor; Wellcome-DBT Intermediate Fellow

Dr. Rajesh Ramachandran did his Masters in Marine Biology at Cochin University of Science and Technology, Cochin, India (1997-1999). He obtained his Ph.D. from the Centre for Cellular and Molecular Biology, Hyderabad, India (1999-2005). He did his initial postdoctoral research at CCMB, Hyderabad, India (2005-2007) and moved to the Molecular and Behavioral Neuroscience Institute, University of Michigan, Ann Arbor, USA (2007-2012). He joined as Assistant Professor at IISER Mohali in June 2012.

Representative Publications

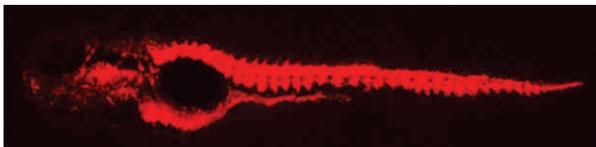
Zhao, X-F., Wan, J., Powell, C., **Ramachandran, R.**, Myers MG Jr, Goldman D. (2014) Leptin and IL-6 family cytokines synergize to stimulate Müller glia reprogramming and retina regeneration. *Cell Reports* 9: 272-284

Ramachandran, R Zhao, X-F., Goldman, D. (2012). Insm1a-mediated gene repression is essential for the formation and differentiation of Müller glia-derived stem cells in the injured retina. *Nature Cell Biology* 14: 1013-1023.

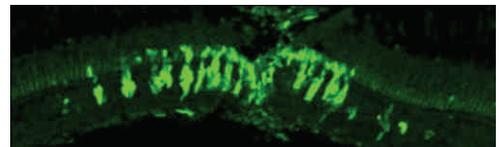
Wan, J., **Ramachandran, R.**, Goldman, D. (2012). HB-EGF Is Necessary and Sufficient for Müller Glia Dedifferentiation and Retina Regeneration. *Developmental Cell* 22: 334-347

Ramachandran, R., Zhao, X-F., Goldman, D. (2011) An Ascl1a/Dkk/ β -Catenin signaling pathway is necessary and glycogen synthase kinase-3 β inhibition is sufficient for zebrafish retina regeneration. *Proceedings of the National Academy of Sciences, USA* 108: 15858-15863

Ramachandran, R., Fausett, B and Goldman, D. (2010). Ascl1a regulates Müller glia dedifferentiation and retina regeneration via a Lin28-dependent, let-7 miRNA signaling pathway. *Nature Cell Biology* 12: 1101-1107



Confocal image of Sonic hedgehog (*shh*) signaling reporter transgenic zebrafish line generated at IISER, Mohali. The red fluorescence indicate expression of mCherry protein because of active *shh* signaling in neurons and muscle fibers in a 7day old zebrafish embryo.



Confocal image showing the proliferating cell nuclear antigen (PCNA)-immuno-fluorescence, seen as green cells in a 4 day post injured zebrafish retina section. Asterisk indicates the injury spot on retina.

Research Interests & Projects

Retinal damage is one of the most common causes of blindness in the modern world. The possible solution to this problem is to harness the regenerative potential of the retinal stem cells. However, this is not possible unless we understand the mechanism of retinal regeneration. The piscine model zebrafish offers the maximum potential in unraveling the mystery of retinal regeneration compared to mammalian and avian counterparts. Towards this goal, we are working on signaling pathways like *wnt*, *notch* and *hedgehog* to assess their impact on fish retina regeneration. We are also working on a few selected candidate genes like pluripotency inducing factors like *sox2*, *oct4*, *nanog*, *klf4*, *cMyc* and *lin28* involved in retina regeneration. Currently the major research projects we carry out are

- (1) An investigation on the role of transcription factors *Ascl1a*, *FoxN4*, *Zic2b* and tumor suppressor *Pten* in retina regeneration and functional analysis of pluripotency factors in retinal stem cells, funded by Wellcome Trust-DBT India Alliance and
- (2) Understanding the molecular mechanisms of epigenetically regulated genes during Muller glia dedifferentiation and retina regeneration in zebrafish, funded by DBT India.
- (3) Understanding the role of hedgehog signaling in the regenerating retina.





Rhitoban Ray Choudhury

Assistant Professor

Dr. Rhitoban Ray Choudhury did his Masters in Zoology at Calcutta University, India (2001), MS in ecology and evolution at University of Rochester (2005). He obtained his Ph.D. in evolutionary genetics from University of Rochester (2010). He did his postdoctoral research at Purdue University. He joined as Assistant Professor at IISER Mohali in December 2013.

Representative Publications

Raychoudhury R, Baldo L, Oliveira DCSG, Werren JH (2009). Modes of acquisition of *Wolbachia*: Horizontal transfer, hybrid introgression and co-divergence in the *Nasonia* species complex. *Evolution*, **63**(1): 165-183 (DOI:10.1111/j.1558-5646.2008.00533.x)

Raychoudhury R, Grillenberger BK, Gadau J, Bijlsma R, van de zande L, Werren JH, Beukeboom LW (2010). Phylogeography of *Nasonia vitripennis* (Hymenoptera) indicates a mitochondrial sweep in North America. *Heredity*, 104:318-326. (DOI:10.1038/hdy.2009.160)

Raychoudhury R, Desajrdins CA, Buellsbach J, Loehlin DW, Grillenberger BK, Beukeboom L, Schmitt T, Werren JH (2010). Behavioral and genetic characteristics of a new species of *Nasonia*. *Heredity*, 104:278-288. (DOI: 10.1038/hdy.2009.147).

Raychoudhury R and Werren JH (2012). Host genotype changes bi-directional to uni-directional cytoplasmic incompatibility in *Nasonia longicornis*. *Heredity*, 108: 105-114. (DOI: 10.1038/hdy.2011.53)

Sen R, **Raychoudhury R**, Cai Y, Sun Y, Ulrike-Lietz V, Boucias DG and Scharf ME. Differential impacts of juvenile hormone, soldier head extract and alternate caste phenotypes on host and symbiont transcriptome composition in the gut of the termite *Reticulitermes flavipes* and its symbionts. *BMC Genomics*, 2013, **14**(1): p 1-18. (DOI: 10.1186/10.1186/1471-2164-14-491).



Nasonia male and female

Research Interests & Projects

I am an evolutionary geneticist by training but my interests range from molecular ecology to functional genomics. I am particularly interested in **i)** the evolution of arthropod-endosymbiont interactions with a special emphasis on *Wolbachia*, *Cardinium* and *Arsenophonus*, **ii)** evolutionary genetics with the parasitic wasp *Nasonia* as the model system and **iii)** molecular evolution and functional genomics of arthropod-bacterial symbiosis; **iv)** I am also interested in phylogeography with particular emphasis on Indian taxa. The biological questions that I seek to answer often involves the use of various techniques ranging from field work to genomic tools. Presently the two broad research areas are:

Symbiosis: *Wolbachia* is one of the most abundant endosymbionts of the world and infects majority of terrestrial arthropods. They also cause various reproductive alterations in their hosts like cytoplasmic incompatibility, feminization, male-killing and parthenogenesis. I am interested in various aspects of *Wolbachia* biology like its abundance in Indian insects, the genetic basis of these reproductive alterations, evolutionary history of host-bacterial symbiosis, etc. We are now trying to figure out the genetic and genomic basis of how *Wolbachia* produces the many reproductive alterations of its arthropod hosts using the parasitoid wasp *Nasonia*.

Evolutionary Genetics and Genomics: The parasitic wasp *Nasonia* is an excellent model system for the genetic dissection of complex traits. These four species are relatively easy to interbreed and also have a wealth of molecular markers along with sequenced genomes. I am interested in investigating the genetic basis of various biological traits using *Nasonia* as a model system.





Kuljeet Sandhu

Assistant Professor

Dr. Kuljeet Sandhu did his Masters at Institute of Bioinformatics and Applied Biotechnology, Bangalore, India (2002-2004). He obtained his Ph.D. from Karolinska Institute, Stockholm, Sweden. He has done his post-doctoral research at Genome Institute of Singapore. He joined as Assistant Professor at IISER Mohali in July 2012.

Representative Publications

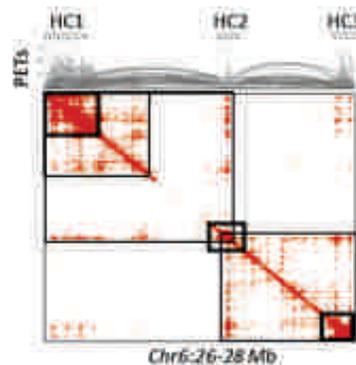
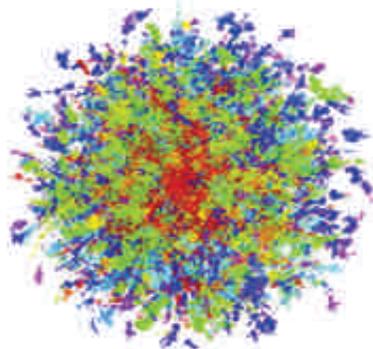
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Sandhu KS*, Guoliang Li, Huay Mei Poh, Yu Ling Kelly Quek, Yee Yen Sia, Su Qin Peh, Fabianus Hendriyan Mulawadi, Mile Sikic, Francesca Menghi, Anbupalam Thalamuthu, Wing Kin Sung, Xiaoan Ruan, Melissa Jane Fullwood, Edison Liu, Peter Csermely, Yijun Ruan[†] (2012). Large scale functional organization of long-range chromatin interaction networks. *Cell Reports*. 2: 1207-19.

Li G[#], Ruan X[#], Auerbach R[#], **Sandhu KS[#]** et al (2012). Extensive promoter centered chromatin interactions provide a architectural basis for transcription regulation in eukaryotes. *Cell*. 148: 84-98 (#co-first author)

Sandhu KS, Shi C, Sjolinder M, Zhao Z, Gondor A, Liu L, Tiwari VK, Guibert S, Emilsson L, Imreh MP, Ohlsson R* (2009). Nonallelic transvection of multiple imprinted loci is organized by the H19 imprinting control region during germline development. *Genes and Development*. 23: 2592-2597.

Zhao Z, Tavoosidana G, Sjölander M, Göndör A, Mariano P, Wang S, Kanduri C, Lezcano M, **Sandhu KS**, Singh U, Pant V, Tiwari V, Kurukuti S, Ohlsson R* (2006). Circular chromosome conformation capture (4C) uncovers extensive networks of epigenetically regulated intra- and interchromosomal interactions. *Nature Genetics*. 38:1341-7.



Hierarchical architecture of long-range Chromatin Interaction Network (CHIN)

sandhuks@iisermohali.ac.in

Research Interests & Projects

Kuljeet is a computational biologist and primarily interested in questions pertaining to genome organization and function. Some of the questions that his group is presently working on are as following:

- (1) What are the evolutionary constraints governing non-random linear and 3-dimensional organization of eukaryotic genome?
- (2) What explains the global disconnect between location and effect of chromatin factors.
- (3) What governs clonally inherited random mono-allelic expression of genes?
- (4) What are the major determinants of transcriptional noise in the eukaryotic genome?
- (5) Why do neighbouring genes exhibit ripple like effect upon transcriptional induction ?
- (6) How do epigenetic errors radiate across different networks in the cell?





Sharvan Sehrawat

Assistant Professor

Dr. Sharvan Sehrawat did his Masters at Veterinary Science and Veterinary Immunology at CCS Haryana Agricultural University, Hisar, India (2001-2004). He obtained his Ph.D. from University of Tennessee, Knoxville, TN, USA (2005-2008). He did his first postdoctoral research at Department of Pathobiology, The University of Tennessee, Knoxville, TN, USA (2008-2009) and second one at Whitehead Institute for Biomedical Research of MIT, Cambridge, MA, USA (2009-2013). He joined as Assistant Professor at IISER Mohali in November 2013.

Representative Publications

Veiga-Parga, T., **Sehrawat, S** and Rouse, BT. (2014) Regulatory T cell function in anti-viral immunity. *Immunological Reviews* 255: 185-196

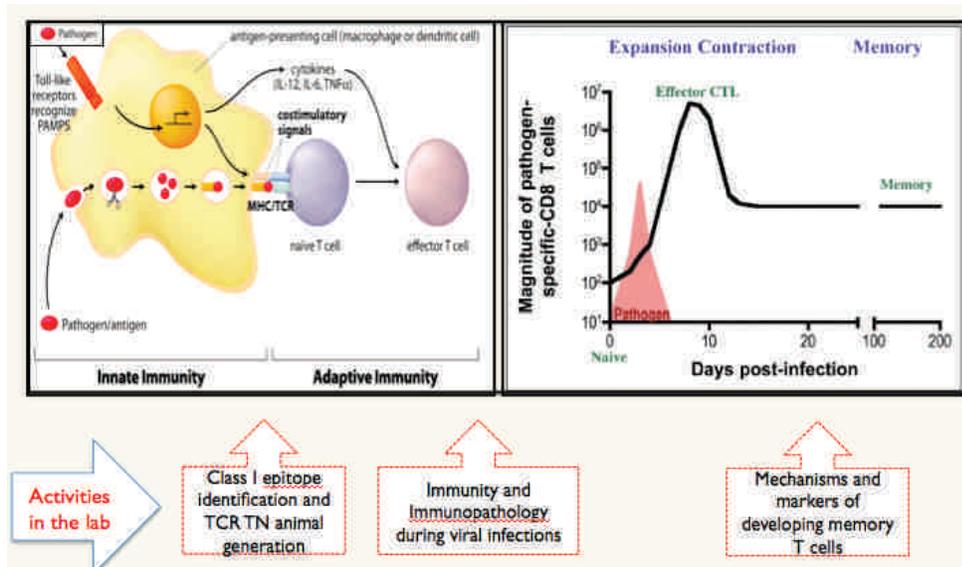
Sehrawat S, Koenig, PA, Kirak O, Schlieker C and Ploegh HL (2013) A catalytically inactive mutant of deubiquitylase YOD-1 enhances the antigen cross presentation. *Blood* 121(7):1145-56

Sehrawat S, Kirak O, Koenig PA, Issacson MK, Marques S, Bozkurt G, Simas JP, Jaenisch R and Ploegh HL (2012). CD8+ T cells from mice transnuclear for a TCR that recognizes a single H-2Kb- restricted MHV68 epitope derived from gB (ORF8) help control the infection. *Cell Reports* 1: 461-471.

Sehrawat S, Reddy PB, Rajasagi N, Suryawanshi A, Hirashima M, Rouse BT (2010) Galectin-9/TIM-3 interaction regulates virus-specific primary and memory CD8 T cell response. *PLoS Pathogens*. 6 (5): e1000882

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Immunology and Immunopathology



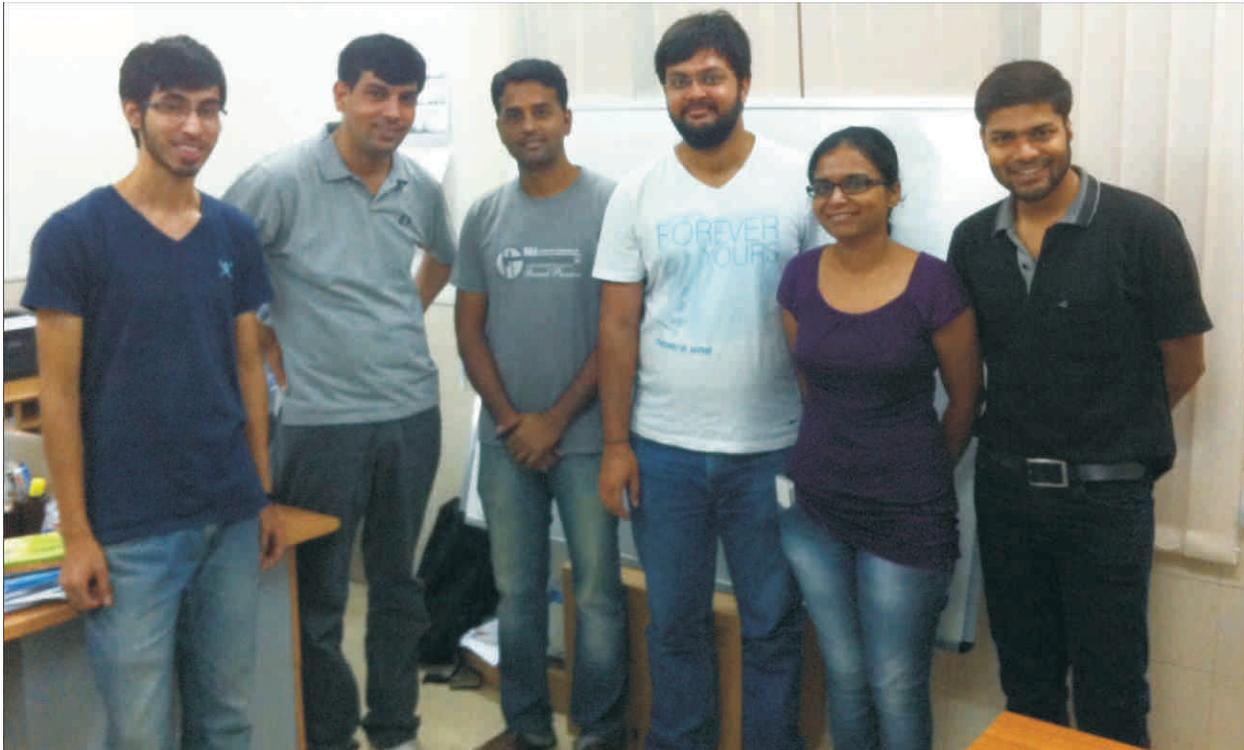
Research are of our laboratory at a glance

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Research Interests & Projects

Area: Infectious Immunology and Immunopathology

In a quest to clear infections of various kinds, the host responds to the insults and induces activation of cells of innate and adaptive immune system that eradicate invading pathogens. At the same time regulatory mechanisms also operate to curtail excessive inflammatory responses. The timely induction of an adaptive immune response and its maintenance in the memory phase forms the basis of lasting protective immunity against infectious diseases and provides clue for successful vaccination. After receiving help from CD4 T cells, pathogen-specific CD8 T cells are appropriately activated to control the spread of intracellular pathogens such as viruses. Animal models are used to investigate host-pathogen interaction. For studying the function and differentiation of adaptive T and B cells, one has to secure sufficient number of antigen-specific cells in naïve state but in a normal host the frequency of T cells specific to any given antigen is very low and frustrates attempts at isolating such cells in meaningful numbers. In our laboratory we aim to understand the function and differentiation of CD8 T cells during infection with endemic pathogens such as dengue virus, Chikungunya virus and protozoan parasites such as Plasmodium in addition to herpes viruses, the latter being the most successful pathogen. Employing various molecular and immunological approaches, we try to understand the host-pathogen interaction. We are also putting efforts in developing novel animal models to study immunity and immunopathology during viral infections. We welcome creative colleagues who are interested in learning and contributing to the advancement of immunology to join our group.





Mahak Sharma

Assistant Professor; Wellcome-DBT Intermediate Fellow

Dr. Mahak Sharma did her B.Tech. degree in Biotechnology from Guru Gobind Singh Indraprastha University, Delhi, India (2000-2004). She obtained her Ph.D. from Department of Biochemistry and Molecular Biology, University of Nebraska Medical Center, Omaha, Nebraska, USA (2005-2009). She did her post-doctoral research at Department of Rheumatology, Immunology and Allergy, Brigham and Women's Hospital/Harvard Medical School, Boston, USA (2009-2011). She joined as assistant professor at IISER Mohali in October 2011.

Representative Publications

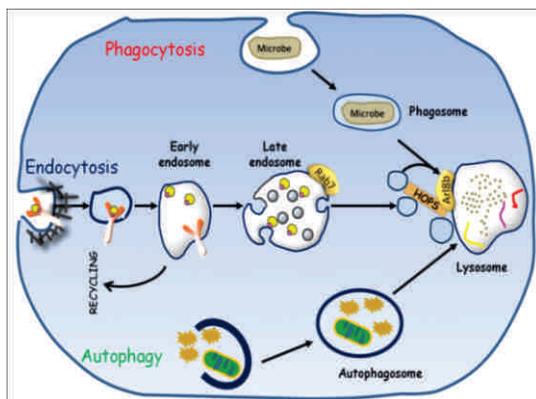
Divya Khatter*, Aastha Sindhwani* and **Mahak Sharma**[#]. (2015). Arf-like GTPase Arl8: Moving from the periphery to the center of lysosomal biology. *Equal contribution. [#]corresponding author. *Cellular Logistics* (accepted).

Divya Khatter, Vivek B. Raina, Devashish Dwivedi, Aastha, Sindhwani, Surbhi Bahl and **Mahak Sharma*** (2015). The small GTPase Arl8b regulates assembly of the mammalian HOPS complex to lysosomes. *corresponding author. *Journal of Cell Science.*, 128:1746-1761.

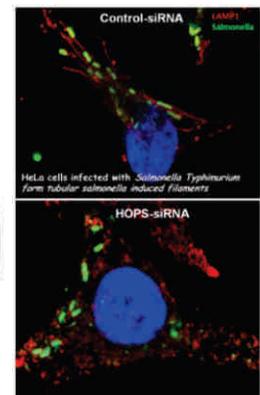
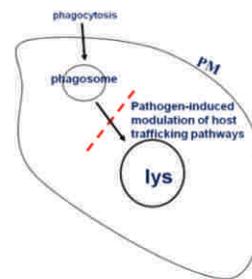
Salil Garg*, **Mahak Sharma***, Cindy Ung, Amit Tuli, Duarte C. Barral, David L. Hava, Natacha Veerapen, Gurdyal S. Besra, Nir Hacohen and Michael B. Brenner. (2011). Lysosomal trafficking, antigen presentation, and microbial killing are controlled by the Arf-like GTPase Arl8b. *Equal contribution. *Immunity*, 35:182-193.

Fabien Kieken*, **Mahak Sharma***, Marko Jovic*, Sai Srinivas Panapakkam Giridharan, Naava Naslavsky, Steve Caplan and Paul Sorgen. (2010). Mechanism for the selective interaction of C-terminal EH-domain proteins with specific NPF-containing partners. *Equal contribution. *Journal of Biological Chemistry*, 285:8687-8694.

Mahak Sharma, Sai Srinivas Panapakkam Giridharan, Juliati Rahajeng, Naava Naslavsky and Steve Caplan. (2009). MICAL-L1 links EHD1 to tubular recycling endosomes and regulates receptor recycling. *Molecular Biology of the Cell*, 20:5181-5194.



Membrane trafficking towards lysosomes Lysosomes receive extracellular cargo from endocytic and phagocytic route and intracellular cargo via autophagic pathways. Small GTP-binding proteins of the Rab, Arf and Arf-like (Arl) family localize to distinct intracellular membranes and recruit their effectors including tethering factors to mediate cargo trafficking and vesicular fusion.



Interaction of host trafficking machinery and intracellular pathogens: *Salmonella typhimurium* is an intracellular pathogen that establishes its replicative niche inside the host cell by acquiring membrane from the endo-lysosomal pathway. *Salmonella* forms characteristic membranous filaments known as *Salmonella*-induced filaments (Sifs) that are detected by lysosomal marker LAMP1. Transient depletion of HOPS subunits impairs Sif formation and consequently, intracellular *Salmonella* replication.

Research Interests & Projects

Overview

Membrane trafficking is a fundamental process that mediates the directed movement of proteins and membranes to different cellular locations, critical for the proper functioning of all eukaryotic cells. The primary research interests of my laboratory focus on studying the molecular mechanisms regulating the trafficking towards late endosomes and lysosomes. We are studying the function of small GTPases and tethering factor complexes that are present on lysosomes and regulate endocytic, phagocytic and autophagic traffic towards lysosomes. The importance of these proteins is reflected by the fact that pathogens such as *Mycobacterium* or *Salmonella* evade killing in the host lysosome by targeting these protein complexes. Our findings will contribute to a better understanding of the mechanisms by which the endocytic regulatory proteins including small GTPases and tethering factors regulates lysosomal trafficking, proper functioning of which is critical for cellular homeostasis and defense against pathogens.

Scientific Questions that we are interested in:

To characterize function of HOPS complex in regulating trafficking towards lysosomes:

HOPS (HOmotypic fusion and Protein Sorting) is an evolutionarily conserved protein complex that regulates cargo trafficking to the lysosome. Unlike yeast where the mechanism of HOPS action is well characterized in vesicle tethering and fusion, not much is understood about mammalian HOPS complex and the mechanism of their action. In this regard, recent work from our laboratory suggests that Arf-like GTPase Arl8b directly binds to and regulates recruitment of human HOPS complex to lysosomal membranes (Khatter et al., *Journal of Cell Science* 2015).

Several intracellular pathogens such as *Mycobacterium*, *Coxiella* and *Salmonella* hijack the endocytic machinery of the cell for their advantage to establish a replicative niche inside the host cells. We are currently exploring the mechanisms by which HOPS complex regulates intracellular survival of *Salmonella*, further we aim to identify *Salmonella* effectors that interact with HOPS subunits to modulate their function.

Understanding the role of mammalian Hook proteins as dyenin adaptors:

Hook proteins were first discovered in *Drosophila* and are regarded as linkers between organelles and microtubule cytoskeleton and/or motor proteins. However, thus far the role of mammalian Hooks in regulating organelle distribution/motility and association with motor proteins has not been explored. We are currently investigating the function of Hook proteins and their interaction with microtubule motors.





Somdatta Sinha

Professor; J. C. Bose Fellow; Member, MHRD Centre of Excellence in Protein Science, Design and Engineering

Dr. Somdatta Sinha did her Masters in Physics at Visva Bharati University, Santiniketan, West Bengal, India. She obtained her M.Phil. and Ph.D from the School of Theoretical and Environmental Sciences, Jawaharlal Nehru University at New Delhi, India. She worked as Scientist at the Centre for Cellular and Molecular Biology (CCMB), Hyderabad Andhra Pradesh, India (1983-2011). She joined as Professor at IISER Mohali in November 2011.

Representative Publications

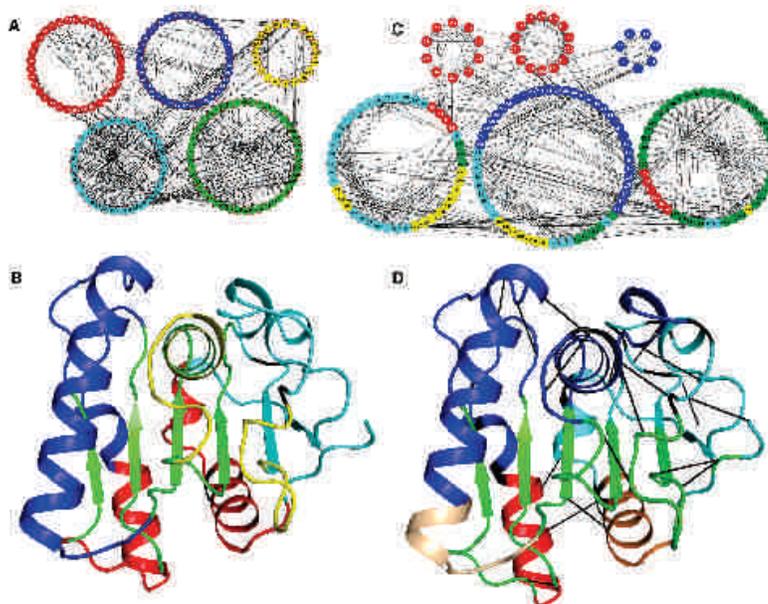
A Srivastava, **Sinha, S.** (2014). Thermostability of In Vitro Evolved *Bacillus subtilis* Lipase A: A Network and Dynamics Perspective.. *PLoS ONE*, 9: e102856. doi:10.1371

Mandal, S., **Sinha, S** and Sarkar, RR. (2013). A Realistic Host-Vector Transmission Model for Describing Malaria Prevalence Pattern. *Bulletin of Mathematical Biology*. 75: 2499-528

Bagler, G and **Sinha, S.** (2007). Assortative Mixing in Protein Contact Networks and Protein Folding Kinetics. *Bioinformatics*, 23: 1760-1767

Parekh, N., Parthasarathy, S and **Sinha, S.** (1998). Global and Local Control of Spatiotemporal Chaos in Coupled Map Lattices. *Physical Review Letters*. 81: 1401-1404

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Reorganisation of communities in the wild-type (WT) and its thermostable (6B) mutant protein networks from *Bacillus subtilis* Lipase A. A) Five communities in WT. B) Five communities mapped on the tertiary structure of WT. C) Six communities in 6B. D) Six communities mapped on the tertiary structure of 6B. The Black lines represent the new contacts made in the 6B as compared to WT. The Root Mean Square Deviation (RMSD) between the two structure is 0.39.

Research Interests & Projects

Sinha group's scientific interests are in the areas of Theoretical Biology, Nonlinear Dynamics and Complex Systems, with a view to understand the logic and design of biological processes at multiple scales - from genetic to ecological. Her early work on circadian rhythms showed that the experimental phase-response curves could well be explained using both limit cycle and structurally unstable oscillator models. Using both experimental tissue transplantation studies and mathematical modelling, she elaborated the interaction of the activator-inhibitor morphogen system in pattern-formation during regeneration of Hydra.

Sinha group used a variety of mathematical and computational approaches to study different biological processes. They used graph theory to model protein structures as protein contact networks, and elucidated the property of assortativity and its association to the protein's folding rate. They also employed graph theory and molecular dynamics simulations to study the small allosteric contact changes in protein structures, that may induce large changes in their function. A combination of phylogenetics, reaction network and flux balance analysis of biochemical pathways is used in their group to study changes in the network properties at multiple scales and pathway evolution. They have studied the collective spatiotemporal behaviour and pattern-formation in coupled cell systems that are models of tissues and organelles. Modelling single and meta-population dynamics in ecology and epidemiology of malaria, and whole genome analysis to study HIV-1 evolution are the two approaches for their infectious disease research. They have developed alignment-free methods, based on Chaos Game Representation and multi-fractal analysis, for classification of closely related genomes. Sinha group also proposed a simple "pinning" method for controlling spatiotemporal dynamics in coupled map lattices for single and coupled discrete systems and continuous dynamical systems. Her current research involves mathematically modelling and analysing epidemiological data of infectious diseases, such as Malaria in India, and study host-pathogen evolution using whole genome sequence data and computational modelling.





Ram K. Yadav

Assistant Professor; Ramalingaswami Fellow

Dr. Ram K Yadav did his Masters in Animal Biotechnology at NDRI, Karnal (2001). He obtained his Ph.D. in Plant Developmental Genetics, from Technical University of Munich, Germany (2007). He did his postdoctoral research at University of California, Riverside, USA (2007-2011). He was assistant professor at South Asian University, New Delhi, India (2011-2012). He joined as assistant professor at IISER Mohali in March 2012.

Representative Publications

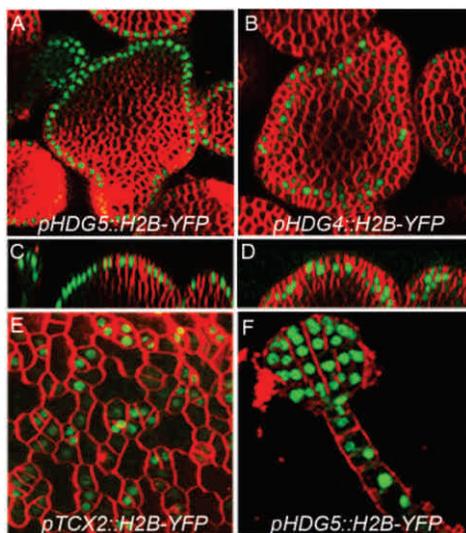
Yadav, R.K.[†], Tavakkoli, M., Girke, T., & Reddy, G.V.[†] (2014). A high-resolution gene expression map of the Arabidopsis shoot apical meristem stem cell niche. *Development* 141: 2735-2744. (†Co-corresponding author)

Yadav, R.K.[#], Perales, M.[#], Gruel, G.[#], Ohno, C., Heisler, M., Grike, T., Jönsson, H., and Reddy, G.V. (2013) Plant stem cell maintenance involves direct transcriptional repression of differentiation program. *Molecular Systems Biology* 9: 654 (#co-first author)

Yadav, R.K.[#], Perales M.[#], Girke, T., & Reddy, G.V., (2011) WUSCHEL protein movement mediates stem cell homeostasis. *Genes and Development* 25: 2025-2030. (#co-first author)

Yadav, R.K., Girke, T., Pasala, S., Xie, M. & Reddy, G.V. (2009). Gene expression map of the Arabidopsis shoot apical meristem stem cell niche. *Proceedings of the National Academy of Sciences, USA* 106: 4941-4946.

Fulton, L., Batoux, M., Vaddepalli, P., **Yadav, R.K.**, Busch, W., Andersen, S.U., Jeong, S., Lohmann, J.U. & Schneitz, K. (2009). DETORQUEO, QUIRKY, and ZERZAUST represent novel components involved in organ development mediated by the receptor-like kinase STRUBBELIG in Arabidopsis thaliana. *PLoS Genetics* 5: e1000355.



Cell type specific transcription factors show spatio-temporal expression pattern during plant development. HDG5 expresses in the epidermal cell layer of shoot as shown in (A and C), while HDG4 expression is restricted to sub-epidermal cell layer as displayed in (B and D). The TCX2 promoter is active in the early stomatal cell lineage of developing leaf epidermis (E). In the globular stage of embryo, HDG5 expresses both in embryo proper and suspensor (F)

Plants are exceptional organisms. They form organs post-embryonically, which allows us to study their development as it proceeds. In addition, being a sessile organism they are always rooted at one place, therefore, they seek intrinsic and extrinsic cues to do well in diverse habitats and to complete their life cycle. In our group, we study cell fate specification in the shoot apical meristem (SAM) of *Arabidopsis thaliana*. In plants, meristematic tissues are considered equivalent to the stem cells niches where pluripotent stem cells reside. One of the goal of our group is to understand how the stem cells are specified and how do they give rise to the stem cells progenitors as they differentiates. In a previous study, role of *WUSCHEL* (*WUS*), a homeodomain transcription factor, has been established in SAM stem cell fate specification. From microarray studies, it was discovered that *WUS* represses a large number of genes including key transcription factors, which are expressed in the differentiating cell types. Currently, we are studying role of *WUS* in mediating repression of auxin biosynthesis in stem cell niche cell types. Ectopic expression of auxin biosynthesis genes leads to termination of shoot. Since, auxin signalling depends directly on the concentration of this phytohormone and plays an important role in cell differentiation. Studies are underway to understand the regulation of auxin biosynthesis.

In multicellular organisms, exquisite cell fate specification of stem cell progenitors in to distinct cell types is immanent to form the body. How do stem cell progenitors acquire precise cell fate in to various tissue types? It largely depends upon their state of gene expression and cell-cell signalling while they differentiate. To decode, the spatio-temporal regulation of gene expression among the SAM cell types, we have identified cell type specific transcription factors (TFs). Currently, we are mapping the interaction between the promoters and TF proteins using Yeast-one-hybrid approach. We are also trying to understand the *in vivo* regulation of these TFs by making promoter reporter fusions.





Centre for Protein Science, Design and Engineering

Director: Purnananda Guptasarma

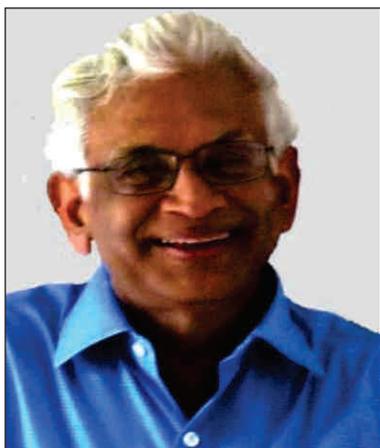
Members: Kausik Chattopadhyay, Samrat Mukhopadhyay,
Shashi Bhushan Pandit, Shravan Kumar Mishra, Somdatta Sinha,
Sabyasachi Rakshit (Chemical Sciences)

The Department of Biological Sciences (DBS) at IISER Mohali, with involvement of the Department of Chemical Sciences (DCS), hosts a Centre of Excellence (CoE) in Frontier Areas of Science & Technology (FAST), under a grant from the Ministry of Human Resource Development (MHRD), Government of India. The centre is known as the Centre for Protein Science, Design and Engineering (CPSDE).

Along with basic research, the centre exists to carry out studies in protein science and engineering with relevance either to the area of human health (bacterial pore-forming toxin-mediated intestinal diseases, neurodegenerative and amyloidogenic disorders, hearing-related disorders, metabolic disorders, and therapeutic proteins and engineered antibodies), or to the area of the new energy biosciences (thermostable hydrolase enzymes relevant to development of biological fuels).

Amongst other goals, the CPSDE also trains Postdoctoral, Doctoral and Masters' level researchers in the above-mentioned research areas, and intends to carry out workshops and meetings that disseminate expertise in protein science and engineering.

Visiting Faculty



Dr. T.R. Rao,
Former Professor & Head
Deptt. of Zoology, University of Delhi

Adjunct Faculty



Dr. Paramvir Singh Ahuja
Former Director General CSIR

Dr. Jayant Udgaonkar, Senior Professor NCBS, Bangalore.

Dr. Amitabha Chattopadhyay, Outstanding Scientist
(Director level), CCMB, Hyderabad

Honorary Faculty

Dr. Raghvendra Gadagkar
Indian Institute of Science, Bangalore

Department of Biological Sciences
Veterinarian, Scientific and Technical Staff



Dr. Chander Shekar
M.V.Sc
Veterinarian
Date of joining:26-2-2015

Mr. Rakesh Kumar
M.Sc. Microbiology
M.Phil. Microbiology
Technical Scientific Assistant
Date of joining: 27-4-2009



Mr. Anupam Pandey
Lab Technician
M.Sc. Biotechnology
Date of joining:8-1-2013

Ms. Shikha Gupta
MSc. Microbiology
Lab Technician
Date of joining: 7-2-2013



Mr. Bhavin R. Kansara
M.Sc. Biochemistry
Scientific Assistant
Date of joining:14-3-2013

Mr. Avtar Singh
Technical Assistant
M.Sc., PhD Biotechnology
Date of joining:26-8-2015

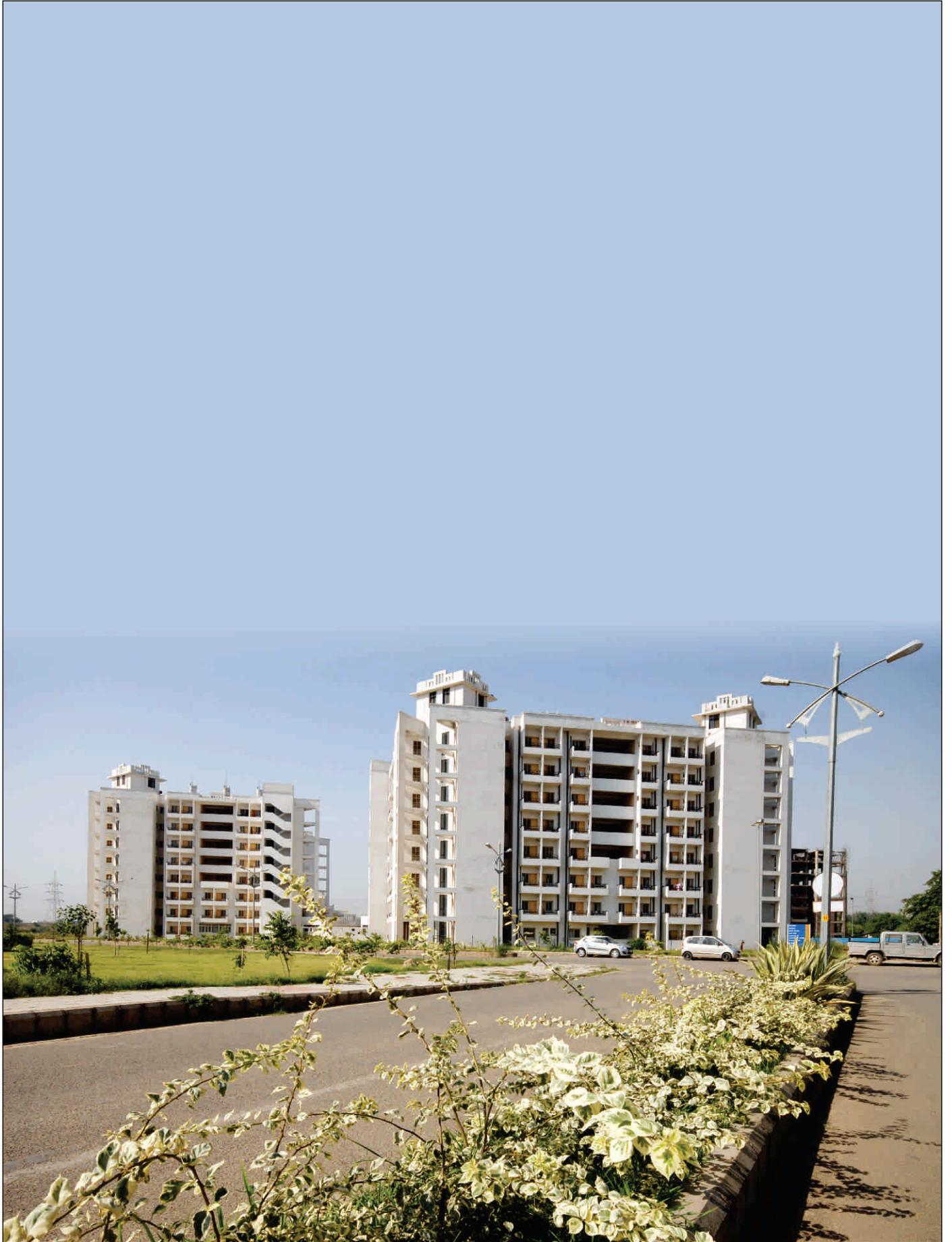


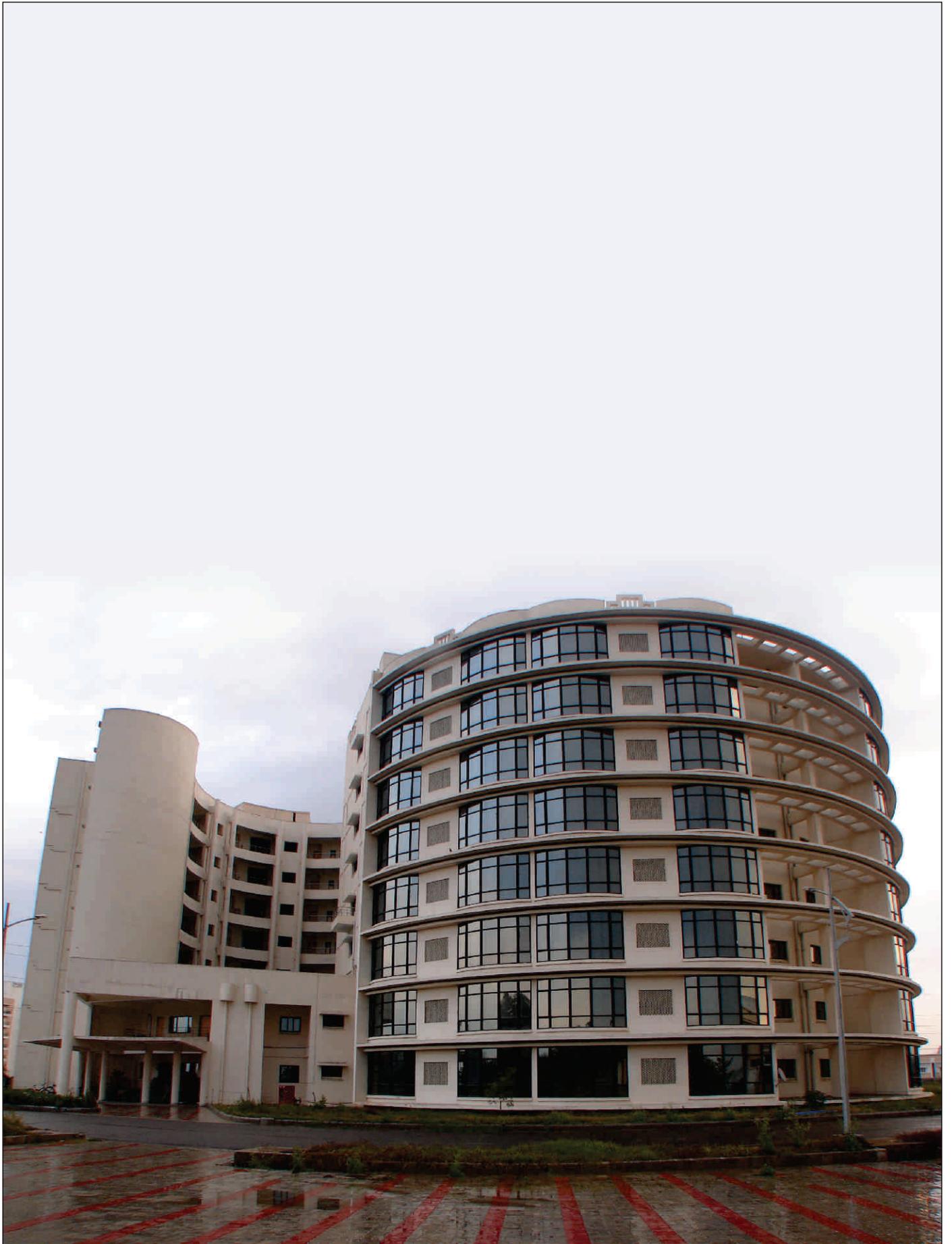
Temporary Support Staff

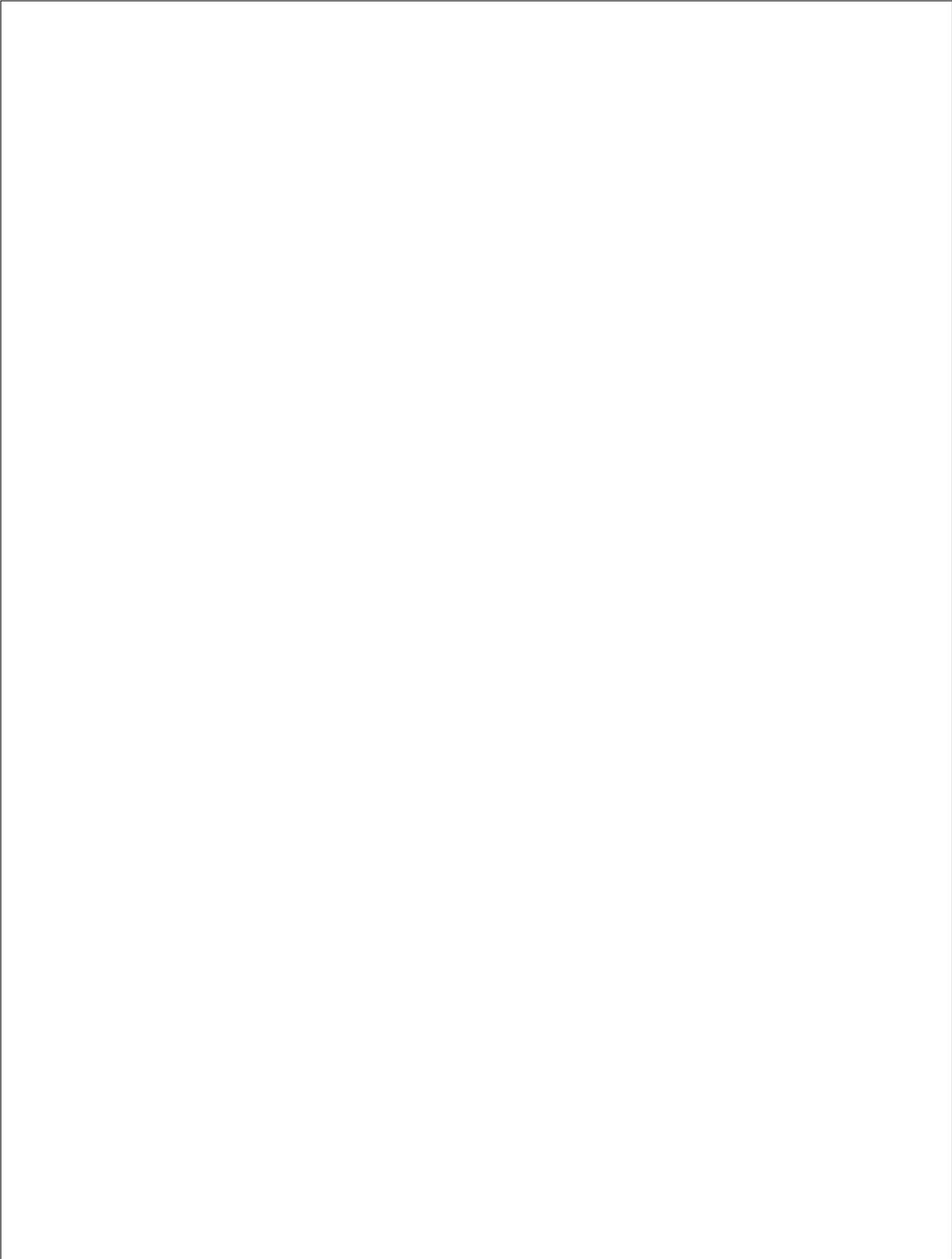
Deepak- Lab Attendant
Negi- Lab Attendant

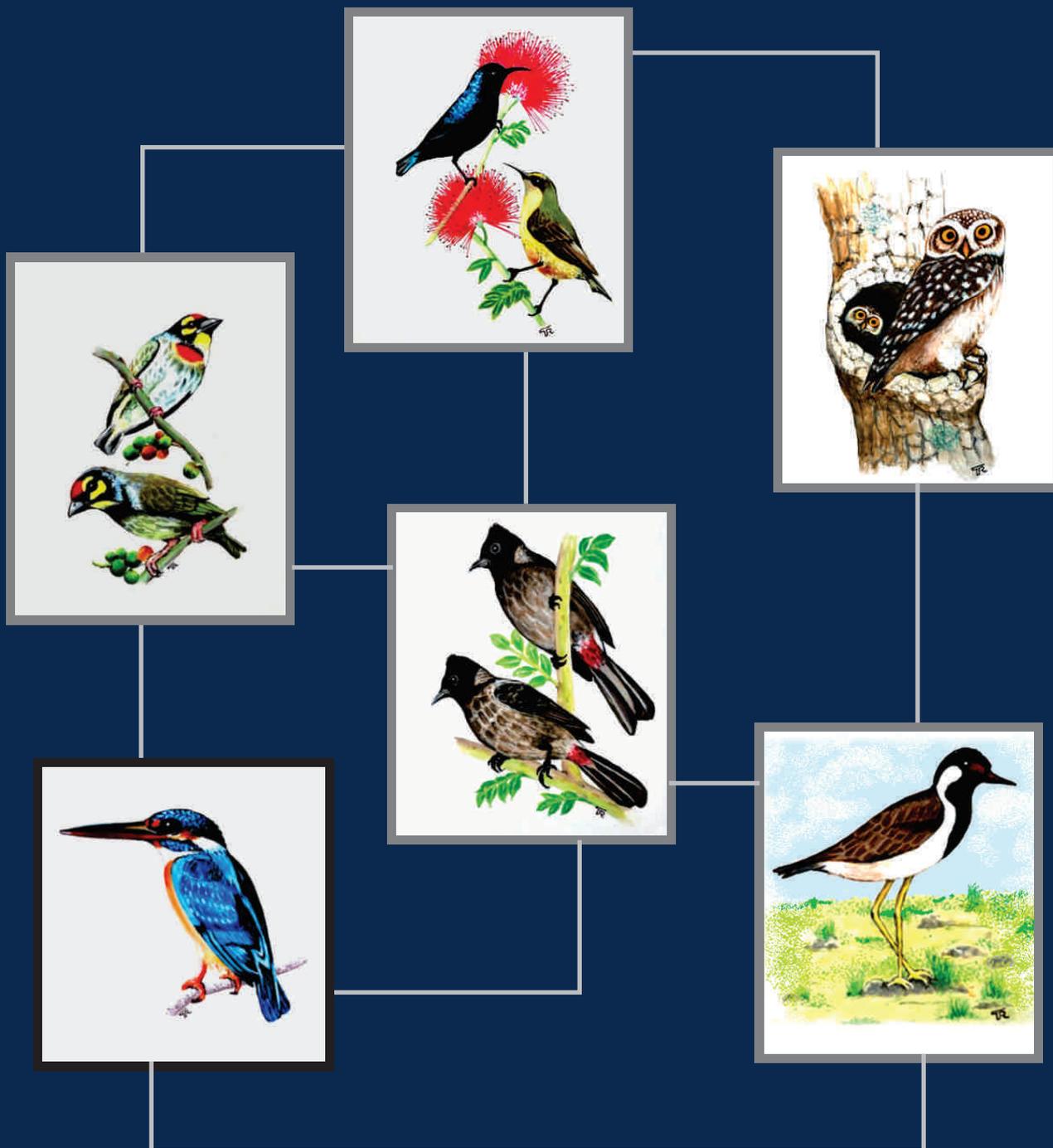
Office Staff

Amanpreet Kaur
Anuj Kumar









"Our feathered friends on the IISER Mohali Campus: paintings by Prof TR Rao."