SUDIP KUNDU, M.Sc., Ph D., FNASc

Date of Birth: 30.07.1971   **Telephone:** 033-23508386 (Ext: 322), 9433428324, 8617272767

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Employment and Education

2014-present	University of Calcutta	Professor, Department of Biophysics, Molecular Biology and Bioinformatics
2011-2014	University of Calcutta	Associate Professor, Department of Biophysics, Molecular Biology and Bioinformatics
2008 -2011	University of Calcutta	Reader, Department of Biophysics, Molecular Biology and Bioinformatics
2001-2008	University of Calcutta	Lecturer, Department of Biophysics, Molecular Biology and Bioinformatics
1999-2001	Uluberia College	Lecturer, Physics Department
1994-1999	University of Calcutta	Ph.D. in Biophysics, entitled "Studies on DNA Polymorphism"
1991-1993	University of Calcutta	M.Sc. in Physics (High Energy Physics)
1988-1991	University of Calcutta	B.Sc. in Physics (Honours)

Academic awards, Prizes, Achievements and Fellowships

- DBT-Crest Award (2011-12)- Govt of India - to work in Prof. David Fell's laboratory, Oxford Brookes University; duration: 5 months
- BBSRC-India UK Partnering Award (2009-13) – with Prof. David Fell, Oxford Brookes University and Prof. Swapan Datta, University of Calcutta
- Visiting Fellow, Academic Visitor (July-Sept, 2008) – Oxford Brookes University, UK
- DAAD-DST Fellow (2003) – Institute for Informatics, Germany
- National Merit Scholarship (1985) – Government of India
- Rural Merit Scholarship (1983) – Government of West Bengal
- Deputy Coordinator – UGC-CAS Programme
- Joint Investigator (2013-) – COE on Systems Biology and Biomedical Engineering
- Coordinator – Distributed Information Center, DBT, GOI

Teaching

- Systems Biology (CU)
- Biomolecules: Sequence, Structure and Interaction (Theory at CU)
- Bioinformatics : Sequence , Structure and Functional Analysis (Theory at CU)
- Computational Systems Biology (Theory and Practical at CU)
- Linux Fundamental and Programming Language (Practical at CU)
- Bioinformatics Techniques (Practical at CU)
- Biomathematics (Basic Theory at Bose Institute)

Brief summary of our works:
My research aim is to understand the design principle of different biological systems (from the architecture, self-assembly and degradation of cellular nano-machines to cellular networks) and to put these findings in the biological context. Some of the important observations from my group are:

(i) To extract the evolutionary signal imprinted in sequence space that can relate the thermodynamics, kinetics and functional interactions of self-assembly pathway of macromolecular complex (**NAR, 2015, Proteins, 2017, Genome Biology and Evolution, 2017**, etc.) and proteins (**Febs Letters, 2015, 2017, Biophysics J, 2005**, etc.).

(ii) To show that native topology and monomeric proteins and sequestration of oligomeric proteins into macromolecular complexes influence their half-lives in the cell and during evolution presumably by ubiquitinoylation sites and disorder segments (**Structure, 2018**)

(iii) To show for the first time (at residue level) translational regulation drives characteristic residue-level epistasis-not only between a protein and its own mRNA but also between a protein and the mRNA of an entirely different protein. (**Proteins, 2018**)

(iv) A systematic understanding of the synergistic interactions of different cellular networks (e.g., metabolic, transcriptional, post-transcriptional etc.) at normal and varying conditions not only provides a comprehensive understanding of cellular dynamics, but also provides useful information for geneticists and biotechnologists to develop efficient, stress-tolerant and high yield rice cultivars. Aiming towards this goal, the group has constructed the first genome scale metabolic model of rice leaf that systematically explains the metabolic readjustments at varying light intensities and CO2/O2 ratios (**Frontiers Plant Sci 2017, Plant Physiol 2013**), during chlorosis and ammonia accumulation in GS2 mutant plant leaf at higher oxygenic condition (**Sci Rep 2015**) and so on. We have also identified the transcriptional and post-transcriptional combinatorial regulations and cross-talks among different biological processes like hormone biosynthesis pathway within rice cell (**Molecular Biosystems 2015; Frontiers Plant Sci 2016**), the biomolecular interactions that link rice cellular physiology to phenotypic changes under stresses (**Plant and Cell physiology, 2018**). We have also provided a formal demonstration that photorespiration itself does not impact on the CO2:O2 ratio (assimilation quotient), except in those modes associated with concomitant nitrate reduction (**Plant J, 2018**) The current efforts include integration of different levels of cellular networks.

Publications:
* indicate Corresponding Author, Highlighted with bold: research students from SK's group.
2020
1) Francisco-Velilla, R., Embarc-Buh, A., Rangel-Guerrero, S., **Basu, S.**, **Kundu, S**., & Martinez-Salas, E. (**2020**). RNA-protein coevolution study of Gemin5 uncovers the role of the PXSS motif of RBS1 domain for RNA binding. RNA Biology, 1-11.
2) **Sudipto Basu, Saurav Mallik, Suman Hait and Sudip Kundu*** (**2020**). Genome-scale molecular principles of mRNA half-life regulation in yeast. The FEBS Journal.
2019
1) **Suman Hait, Saurav Mallik, Sudipto Basu and Sudip Kundu*** (**2019**). Finding the generalized molecular principles of protein thermal stability. Proteins: Structure, Function, and Bioinformatics, 88(6), 788-808

2018:
1) **Benazir Huma, Sudip Kundu*,** MG Poolman, NJ Kruger, DA Fell (**2018**) Stoichiometric analysis of the energetics and metabolic impact of photorespiration in C3 plants. The Plant Journal, 96, 1228-1241
2) **R.K. Grewal, S Saraf, A, Deb and S. Kundu* (2018)** Differentially Expressed microRNAs Link Cellular Physiology to Phenotypic Changes in Rice under Stress Conditions. Plant and Cell Physiology. 59, 2143-2154
3) **S Mallik and S Kundu*,** Topology and Oligomerization of Mono- and Oligomeric Proteins Regulate Their Half-Lives in the Cell, *Structure* (2018), https://doi.org/10.1016/j.str.2018.04.015

4) **Saurav Mallik, Sudipto Basu, Suman Hait, Sudip Kundu*** (2018) Translational regulation of ribosomal protein S15 drives characteristic patterns of protein-mRNA epistasis *Proteins: Structure, Function, and Bioinformatics* **https://doi.org/10.1002/prot.25518**

5) C Mal, M Aftabuddin and **S. Kundu** (2018) IIKmTA: Inter and Intra Kingdom miRNA-Target Analyzer *Interdisciplinary Sciences: Computational Life Sciences*, 1-6

2017:

6) **A Chatterjee, B Huma, R Shaw, S. Kundu*** (2017) Reconstruction of Oryza sativa indica genome scale metabolic model and its responses to varying RubisCO activity, light intensity and enzymatic cost conditions. *Frontiers in Plant Science* 8, 2060.

7) **S Mallik,** T Ray and **S. Kundu*** (2017) Transiently disordered tails accelerate folding of globular proteins. *FEBS letters* 10.1002/1873-3468.12725

8) **S Mallik, S Kundu*** (2017) Modular organization of residue-level contacts shape the selection pressure on individual amino acid sites of ribosomal proteins. *Genome Biology and Evolution* 9 (4), 916-931.

9) **S Mallik, S Kundu*** (2017) Co-evolutionary constraints in the sequence-space of macromolecular complexes reflect their self-assembly pathways. *Proteins: Structure, Function, and Bioinformatic*s, DOI: 10.1002/prot.25292.

2016

10) **Deb A, Grewal RK, and Sudip Kundu*** (2016) Regulatory cross-talks and cascades in rice hormone biosynthesis pathways contribute to stress signaling. *Frontiers in Plant Science* 7, 1303.

11) **Mallik S, Das S and Sudip Kundu* (**2016) "Predicting protein folding rate change upon point mutation using residue level co evolutionary information" *Proteins: Structure, Function, and Bioinformatics*, 84(1), 3-8.

12) SK Mondal, **S Kundu**, R Das, S Roy (2016) Analysis of phylogeny and codon usage bias and relationship of GC content, amino acid composition with expression of the structural nif genes *Journal of Biomolecular Structure and Dynamics* 34 (8) 1649-1666

2015

13) **Chatterjee Ankita and Sudip Kundu*** (2015) "Revisiting the chlorophyll biosynthesis pathway using genome scale metabolic model of *Oryza sativa japonica" Scientific Reports* 5, 14975. doi: 10.1038/srep14975

14) **Deb Arindam and Sudip Kundu*** (2015) "Deciphering Cis-Regulatory Element Mediated Combinatorial Regulation in Rice under Blast Infected Condition" *PLoS One 10 (9), e0137295*

15) **Shaw Rahul and Sudip Kundu*** (2015) "Flux Balance Analysis of Genome Scale Metabolic Model of Rice (*Oryza sativa*): Aiming to Increase Biomass" *Journal of Biosciences 40 (4), 819-828*

16) **Mallik, Saurav, and Sudip Kundu*** (2015) "Co-evolutionary constraints of globular proteins correlate with their folding rates." *FEBS letters* 589.17 : 2179-2185 [**F1000 recommnded**].

17) **Shaw, Rahul, and Sudip Kundu*** (2015) "Metabolic Plasticity and Inter-Compartmental Interactions in Rice Metabolism: An Analysis from Reaction Deletion Study." *PLoS One* 10(7) : e0133899.

18) **Mallik, Saurav,** Hiroshi Akashi, and **Sudip Kundu***. (2015) "Assembly constraints drive co-evolution among ribosomal constituents." *Nucleic Acids Research* 43 (11): 5352-5363.

19) **Mal, Chittabrata, Deb A, Aftabuddin Md and Sudip Kundu*** (2015) "A network analysis of miRNA mediated gene regulation of rice: crosstalk among biological processes." *Molecular BioSystems* , 11, 2273-2280

20) **Mallik, Saurav, and Sudip Kundu*** (2015) "Molecular interactions within the halophilic, thermophilic, and mesophilic prokaryotic ribosomal complexes: clues to environmental adaptation." Journal of Biomolecular Structure and Dynamics, 33(3): 639-656.

21) **Mondal S K**, RN Das, **S Kundu**, J Kim, G Grover, SA Ansari (2015) "Mean variance relationships of genome size and GC content" *Annual Research & Review in Biology* 7, 206-221

22) **Bhattacherjee, Amrita, Saurav Mallik, and Sudip Kundu*. (**2015) "Compensatory Mutations Occur Within the Electrostatic Interaction Range of Deleterious Mutations in Protein Structure." *Journal of molecular evolution* 80(1): 10-12.

2014

23) **Mal, Chittabrata, Md Aftabudddin, and Sudip Kundu*.** (2014) "No3CoGP: non-conserved and conserved coexpressed gene pairs." *BMC research notes* 7.1 : 886.

24) **Aftabuddin, Md, Mal C, Deb A and Sudip Kundu* (**2014) "C2Analyzer: Co-target–Co-function Analyzer."*Genomics, proteomics & bioinformatics* 12.3 : 133-136.

25) Ghosh, Somen, Ajay Ghosh, and **Sudip Kundu**. (2014) "Estimating malaria parasitaemia in images of thin smear of human blood." *CSI transactions on ICT*2.1 : 43-48.

26) **Bhattacherjee, Amrita**, Rahul Shubhra Mandal, Santasabuj Das, and **Sudip Kundu***.(2014) "Sequence and 3D structure based analysis of TNT degrading proteins in Arabidopsis thaliana." *Journal of molecular modelling* 20.3 : 1-9.

27) Poolman, Mark G., **Sudip Kundu, Rahul Shaw,** and David A. Fell.(2014) "Metabolic trade-offs between biomass synthesis and photosynthate export at different light intensities in a genome–scale metabolic model of rice." *Frontiers in plant science* 5: 656.

28) Hui, Subhra Prakash, **Dhriti Sengupta**, Serene Gek Ping Lee, Triparna Sen, **Sudip Kundu,** Sinnakaruppan Mathavan, and Sukla Ghosh. (2014) "Genome wide expression profiling during spinal cord regeneration identifies comprehensive cellular responses in zebrafish." *PloS one* 9(1): e84212

2013

29) Roy, Puspita Das, **Dhriti Sengupta,** Anjan Kr Dasgupta, **Sudip Kundu**, Utpal Chaudhuri, Indranil Thakur, Pradipta Guha, Mousumi Majumder, Roshni Roy, and Bidyut Roy. (2013) "Single Nucleotide Polymorphism Network: A Combinatorial Paradigm for Risk Prediction." *PloS one* 8(9):e74607

30) **Mallik, Saurav, and Sudip Kundu*.** (2013) "A comparison of structural and evolutionary attributes of Escherichia coli and Thermus thermophilus small ribosomal subunits: signatures of thermal adaptation." *PloS one* 8(8) : e69898.

31) **Biswas, S. and Kundu, S.** (2013)**.** Does a protein coevolve with its multiple interacting partners? A case study. *Journal of Computational Biology*, *5*(2), 23-43.

32) Poolman, Mark G., **Sudip Kundu**, **Rahul Shaw**, and David A. Fell. (2013) "Responses to light intensity in   a genome-scale model of rice metabolism." *Plant Physiology*162(2) : 1060-1072.

33) Mondal, Sunil Kanti, Subhadeep Shit, and **Sudip Kundu*** (2013) "A comparative computational study of the'rbcL' gene in plants and in the three prokaryotic families--Archaea, cyanobacteria and proteobacteria." *Indian Journal of Biotechnology* 12(1) : 58-66.

2012

34) **Shaw, Rahul,** Suma Debsarma, and **Sudip Kundu*** (2012) "An algorithm for removing stoichiometric discrepancies in biochemical reaction databases." *Current Science(Bangalore)* 103(11) : 1328-1334.

35) **Sengupta, Dhriti, and Sudip Kundu*** (2012) "Do topological parameters of amino acids within protein contact networks depend on their physico-chemical properties?."*Physica A: Statistical Mechanics and its Applications* 391(17) : 4266-4278.

36) **Sengupta, Dhriti, and Sudip Kundu*** (2012) "Role of long-and short-range hydrophobic, hydrophilic and charged residues contact network in protein's structural organization." *BMC bioinformatics* 13(1) : 142.

2005-10

37) **Aftabuddin, Md, and Sudip Kundu* (**2010) "AMINONET-a tool to construct and visualize amino acid networks, and to calculate topological parameters."*Journal of Applied Crystallography* 43(2) : 367-369.

38) **Aftabuddin, Md, and S. Kundu*** (2007) "Hydrophobic, hydrophilic, and charged amino acid networks within protein." *Biophysical journal* 93(1) : 225-231.

39) **Aftabuddin, Md, and Sudip Kundu*.** (2006) "Weighted and unweighted network of amino acids within protein." *Physica A: Statistical Mechanics and its Applications* 369(2) : 895-904.

40) **Kundu, Sudip.*** "Amino acid network within protein." (2005) *Physica A: Statistical Mechanics and its Applications* 346(1): 104-109.

Before 2005

41) Betal S, Chowdhury, **Kundu S a**nd Raychaudhuri SS* (2004) "Estimation of genetic variability of Vigna radiata cultivars by RAPD analysis" *Biologia Plantarum* 48 (2), 205-209

42) **Kundu, Sudip**, Debashis Bandyopadhyay, and Ashoke Ranjan Thakur.* (2001) "Sequence-based structural signatures of genome evolution." Indian Journal of Biochemistry and Biophysics, 38(1/2) : 104-106.

43) **Kundu, Sudip**, Dhananjay Bhattacharya, Ashoke Ranjan Thakur*, and Rabi Majumdar (2001). "Nucleosomal positioning and genetic divergence study based on DNA flexibility map." *Journal of Biomolecular Structure and Dynamics* 18(4) : 527-533.

44) Bhattacharyya, Dhananjay, **Sudip Kundu**, Ashoke R. Thakur, and Rabi Majumdar* (1999). "Sequence directed flexibility of DNA and the role of cross-strand hydrogen bonds." *Journal of Biomolecular Structure and Dynamics* 17(2) : 289-300.

45) **Kundu, Sudip,** Ansuman Lahiri, and Ashoke Ranjan Thakur*. (1998) "Denaturation of supercoiled DNA: a Monte Carlo study." *Biophysical chemistry* 75(3): 177-186.

Lab members:

Current members:

Ph. D students	Post-doctoral fellow
Soumya Kundu	Dr. Deeya Saha
Suman Hait	
Sudipto Basu	

Alumni:

Thesis submitted Ph. D students	Degree Awarded Ph. D students	Research Associates
Benazir Huma	Dr. Md. Aftabuddin	Dr. Rumdeep Grewal
	Dr. Subinoy Biswas	
	Dr. Dhriti Sengupta	
	Dr. Amrita Bhattacharaya	
	Dr. Chittabrata Mal	
	Dr. Rahul Shaw	
	Dr. Sunil Kanti Mondal	
	Dr. Ankita Chatterjee	
	Dr. Arindam Deb	
	Dr. Shradha Saraf	
	Dr. Saurav Mallik	

Present Research Collaborators:
- Prof. David Fell, Oxford Brookes University, UK
- Prof. Hiroshi Akashi, National Institute of Genetics, Japan