Curriculum vitae

Name: Debarun Acharya



Contact Information: Residential Address 2/54, Netaji Nagar

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Academic Degrees:

2018: Ph.D. (Sc.) from Bioinformatics Centre, Bose Institute, affiliated to

University of Calcutta.

2011: M.Sc. Zoology (with specialization in Cytogenetics) from Maulana Azad

College, affiliated to University of Calcutta.

2009: B.Sc. Zoology (Hons.) from Vijaygarh Jyotish Ray College, affiliated to

University of Calcutta.

Present Status:

Visiting Faculty, Department of Zoology, Ramakrishna Mission Vidyamandira, Belur Math, Howrah, West Bengal.

Research Experience:

- **2018-2021: Research Associate**, Department of Microbiology, Bose Institute, Kolkata (Funded by Department of Science and Technology)
- 2012-2018: Ph.D. Scholar, Centre of Excellence in Bioinformatics, Bose Institute, Kolkata

Details of Ph.D.:

PhD supervisor

Prof. Tapash Chandra Ghosh, Bioinformatics Centre, Bose Institute, Kolkata, West Bengal, India

Thesis title:

"The importance of human duplicated genes: insights from evolutionary perspective".

Research Publications in International Peer-reviewed Journals:

As First Author:

- 1. **Debarun Acharya**, Dola Mukherjee, Soumita Podder, Tapash Chandra Ghosh* (2015) Investigating different duplication pattern of essential genes in mouse and human. **PLoS ONE** 03/2015; 10(3). DOI:10.1371/journal.pone.0120784.
- 2. **Debarun Acharya**, Tapash Chandra Ghosh* (2016) Global analysis of human duplicated genes reveals the relative importance of whole-genome duplicates originated in the early vertebrate evolution. **BMC Genomics** 12/2016; 17(1). DOI:10.1186/s12864-016- 2392-0.
- 3. **Debarun Acharya** and Tapan K. Dutta (2021) Elucidating the network features and evolutionary attributes of intra- and interspecific protein–protein interactions between human and pathogenic bacteria. **Scientific Reports** 11, DOI:10.1038/s41598-020-80549-x.

As Corresponding Author:

- 4. Arup Panda, **Debarun Acharya***, Tapash Chandra Ghosh* (2017) Insights into human intrinsically disordered proteins from their gene expression profile. **Molecular BioSystems** 13(12) 2521-2530; DOI: 10.1039/C7MB00311K.
- 5. Manish Prakash Victor, **Debarun Acharya***, Tina Begum, Tapash Chandra Ghosh* (2019) The optimization of mRNA expression level by its intrinsic properties insights from codon usage pattern and structural stability of mRNA. **Genomics** 111(6)/2019:1292-1297.
- 6. Manish Prakash Victor, **Debarun Acharya***, Sandip Chakraborty, Tapash Chandra Ghosh* (2020) The combined influence of codon composition and tRNA copy number regulates translational efficiency by influencing synonymous nucleotide substitution. **Gene** 745 (2020): 144640. DOI:10.1016/j.gene.2020.144640.

As Co-Author:

- 7. Kakali Biswas, **Debarun Acharya**, Soumita Podder, Tapash Chandra Ghosh (2018) Evolutionary rate heterogeneity between multi- and single-interface hubs across human housekeeping and tissue-specific protein interaction network: insights from proteins' and its partners' properties. **Genomics** 110(5)/2018: 283-290.
- 8. Dola Mukherjee, Deeya Saha, **Debarun Acharya**, Ashutosh Mukherjee, Sandip Chakraborty, Tapash Chandra Ghosh (2018) The role of introns in the conservation of the metabolic genes of Arabidopsis thaliana. **Genomics** 110/2018: 310-317.
- Manish Prakash Victor, Debarun Acharya, Sandip Chakraborty*, Tapash Chandra Ghosh* (2020) Chaperone client proteins evolve slower than non-client proteins. Functional & Integrative Genomics 20: 621–631(2020). DOI: https://doi.org/10.1007/s10142-020-00740-1.

Skills:

(a) Computational Expertise:

• Software Packages used:

CodonW, BLAST, ClustalW, MSOffice, QiiME, PICRUSt, SPSS (ver20), Photoshop.

Bio-databases:

Biobase, Ensembl, UCSC Genome Browser, Uniprot, Gene Ontology database, Human protein interaction database (HPRD), Expression database (BioGPS, Human Protein Atlas, EBI- Expression Atlas, RNAseq Atlas), Pseudogene database (pseudogene.org), Gene Essentiality Database (SGD, MGI, OGEE, DEG), Whole-Genome duplication database (ohnologs DB), Disease gene database (HGMD, GAD), Functional enrichment analysis webservers (DAVID, GOrilla, EnrichR, IntermineR etc.).

Microbiome analysis databases (QiiME, Mg-RASTetc.) and many more.

• Programming with PERL,R.

• Operating System:

Linux, WindowsXP/7/10

(b) Wet-labExperience:

- Hands-on experience on different techniques in molecular biology like Gel electrophoresis (SDS-PAGE, Native PAGE and Agarose Gel Electrophoresis), Chromatography, Nuclear and Mitochondrial DNA isolation, Polymerase Chain Reaction (PCR) etc.
- Hands-on usage of Sonicator machine, Autoclave, Gel Documentation Instrument, UV-Vis spectrophotometer, centrifuge, PCR & Electrophoretic units.
- Hands-on knowledge of different types of bacterial staining techniques; bacterial culture techniques (such as Streak plate, pour plate, spread plate, and serial dilution), and many types of selective culture techniques.

Other Extracurricular Activities:

Birdwatching, Photography

Personal Contact Information

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700092, West Bengal.

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Declaration:

I hereby declare that all the information furnished in this document is free of errors to the best of my knowledge.

Debarun Acharya

Kolkata

24/07/2021