Jyotirmoy **Das**

PRINCIPAL RESEARCH ENGINEER

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Jyotirmoy-Das-3 | JD2112 | dasjyotirmoy | jyotirmoy21

Highly effective bioinformatician with more than 10+ years work experience focussing on pipeline development and biological data analysis. Research experience in development and implementation of computational tools for multi-omics data analysis, high-throughput image analysis. At present, I am a Principal Research Engineer at the Bioinformatics Core Facility of Faculty of Medicine and Health Sciences in Linkoping University, Sweden. I write bioinformatics pipelines to analyse arrays or sequencing (short and long-read) data (clinical and research samples) from human, bacteria and viruses.

Area Of Expertise

- **Genomics:** Structural and functional genomics, Whole genome analysis.
- **Epigenomics:** DNA Methylation, microRNAs.
- **Transcriptomics:** RNA microarray, sequence analysis, expression analysis, miRNA microarray, Single-cell RNAseq.
- **Metabolomics:** Metabolite expression analysis.
- **Proteomics:** Protein expression and protein-protein interaction networks.
- **Downstream analysis:** GO, Pathways, Networks.

Research Experience

Principal Research Engineer
Linkoping University, Sweden

BIOINFORMATICS, CORE FACILITY, FACILITY OF FACULTY OF MEDICAL AND HEALTH SCIENCES · *Sep. 2020 - present*

- Developing bioinformatics pipeline using Python, R for standardization of different DNA, RNA analyses.
- Developing semi/automated Nextflow workflow to analyze the SARS-CoV-2 whole genome data using Illumina and Nanopore sequencing technologies.
- Developing Shiny based graphical user interface to analyze Illumina array-based DNA methylation and downstream analyses.
- Shiny server setup using CentOS.
- Developing source code on GitHub for general public use.
- Linux system administration, user group maintenance and setup workstation for pipeline development and production.
- User and project investigator on different HPCs (Tetralith on NSC, Rackham on Uppmax and NGP).
- Designed course curriculum and carried out course on Bioinformatics for Microbiology at the Medical Microbiology course (8BKG24) at Linköping University, Sweden.
- Networking with Clinical Genomics Sweden and Genomic Medicine Sweden (GMS) groups.
- Extensive user of contenarized applications (Docker, Singularity, Conda) on multi-OS architectures.
- Support different research groups on their projects bioinformatics application.
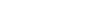- Using Jupyter, Rmarkdown, Quarto for reporting results

Postdoctoral Fellow
Linkoping University, Sweden

DEPARTMENT OF CLINICAL AND EXPERIMENTAL MEDICINE, LINKÖPING UNIVERSITY, SWEDEN · *Jun. 2017 - Aug. 2020*

- Computational analysis of whole genome (WGBS/RRBS)/ array based (450K/850K) DNA methylation analysis from different participants in Sweden and Peru.
- Develop analysis pipelines to identify differential methylation patterns in different groups of dataset. Works in HPC and Linux OS.
- Develop pipelines with unsupervised analyses like Multi-Dimensional Analysis (MDA), Principal Component Analysis (PCA), Component Analysis (CA), Multiple Factor Analysis (MFA) to reduce the dimensionality of data.
- Pipeline development to use supervised machine learning algorithms (LDA, GLMNET, RandomForest) to identify biosignature from the study.
- Develop analysis pipeline for transcriptome data analysis.
- Use of MATLAB image processing to analyze live cell imaging.
- Co-supervising 2 Ph.D. students
- Supervised (main supervisor) two master degree students.

Senior Research Fellow, DST-INSPIRE (Govt. of India)
West Bengal, India

BIOINFORMATICS CENTRE, BOSE INSTITUTE · *Jan. 2014 - Jan. 2017*

- Develop of analysis pipelines to identify different microRNAs (miRNAs) in human diseases and their roles in evolutionary perspective.
- Rendering databases to calculate the evolutionary rates in human and orthologs.
- Linux-based approach to search sequence homology. Linux system maintenance and computation.
- Use of different programming languages like Perl, Python, R to analyze dataset.
- Extensive statistical software analyses with SPSS.

Junior Research Fellow, DST-INSPIRE (Govt. of India)

West Bengal, India

Bioinformatics Centre, Bose Institute

Jan. 2012 - Jan. 2014

- Extensive use of statistical tool, like SPSS, MATLAB. Works on Excel, NCBI databases.
- Use of Perl for data analysis.
- Learn research ethics, FAIR data and data sharing.

Institute Fellow

West Bengal, India

Bioinformatics Centre, Bose Institute

Sep. 2010 - Jan. 2012

- Works on MATLAB and WGCNA network in R.

Research Trainee

New Delhi, India

National Institute of Plant Genome Research, New Delhi

Jul. 2009 - May. 2010

- Develop ILP markers using online bioinformatics tools.

Skills

Programming	R, Python, Perl, Shell, C/C++, HTML, Rstudio, Shiny, DASH.
OS handling	Linux/Unix, MacOS, Windows, HPC, RedHat, amazon and google cloud.
Reproducible Report	Markdown/Rmarkdown, Quarto, R shiny apps, Jupyter Notebook, LaTeX, Pandoc, lua.
Statistical analysis	SPSS, MATLAB, GraphPad, STATA, OriginLab.
Image processing	ImageJ, CellProfiler, Photoshop, GIMP, Inkscape.
Front-End	HTML/CSS/JS, WordPress, Shiny, DASH.
Containers	Conda/Anaconda, Singularity/Apptainer, Docker, Podman.
Wrokflow manager	NextFlow, Snakemake, CWL
Version control	git, bitbucket.
Office tools	Open office, google docs, Microsoft office, pages, keynote, numbers.
Quantitative Research	t-test, within-/between-subjects/Repeated Measures ANOVAs, Regressions, Clustering, HLM, Factor Analysis, Network Analysis, SEM, PCA, MDS, Unsupervised/Supervised Machine Learning
Editors	vim, nano, gedit, VS Code, VS codium, DataSpell, notepad++.
Mixed Research	Text Mining, Explanatory/Exploratory Data Analysis (EDA)

Education

Ph.D. (Technology) in Bioinformatics

West Bengal, India

Maulana Abul Kalam Azad University of Technology, West Bengal (Formerly known as West Bengal University of Technology), India

2017

- Dissertation Title: "In-silico studies of MicroRNA Regulations in higher eukaryotes from the perspective of Molecular Evolution."
- Supervisor: Prof. Tapash C Ghosh, Bose Institute, India.

Master of Technology in Biotechnology

West Bengal, India

West Bengal University of Technology, India

2010

- Title of the Thesis: "Identification and evaluation of Intron Length Polymorphism (ILP) marker in Foxtail millet (Setaria italica) and to study evolutionary relationship between species by cross-species transferability".
- Supervisors: Dr. Manoj Prasad, NIPGR, India. Prof. Nandan Bhattacharyya, Haldia Institute of Technology, India

Master of Science in Biotechnology

Karnataka, India

Bangalore University

2008

Bachelor of Science in Biotechnology

West Bengal, India

University of Kalyani

2006

- Project 1: "Drug Designing: Evaluation of iron chelation through blood in phytic acid treated thalassemia patients".
- Project 2: "Study of Ecological Diversity in Sunderbans, Especially on Kingfishers"
- Supervisors: Prof. Amit Chakravorty, Dr. Sudipa Chakravorty, IGE, India

Certificates

Research Supervision

Linköping University Pedagogy Course

2020

How to Lead a Research Group

Certificate

2019

Becoming a Teacher in Higher Education

Linköping University Pedagogy Course *2019*

Astrobiology and the Search for Extraterrestrial Life The origin and evolution of life and the search for life beyond the Earth.

Coursera e-learning *2015*

Programming for Everybody (Getting Started with Python)

Coursera e-learning *2015*

Grants

- "Travel Grant awarded of 9920 SEK to attend 4th International Conference on Innate Immune Memory, Nijmegen, the Netherlands. 31 October- 1 November", Primary awardee, Oct 2019.

- "Proof-of-Concept Grant from Swedish Research Council (VR) with a funding of 2 MSEK.", Participant Researcher, Dec. 2022 - Dec. 2024.

Publications

∗: Shared first-author publication (sorted by **year** - descending)

Refereed Journal Papers

1. Shahin, H., Belcastro, L., **Das, J.**, Perdiki Grigoriadi, M., Saager, R. B., Steinvall, I., Sjöberg, F., Olofsson, P., Elmasry, M., & El-Serafi, A. T. (2024). MicroRNA-155 mediates multiple gene regulations pertinent to the role of human adipose-derived mesenchymal stem cells in skin regeneration. In *Frontiers in Bioengineering and Biotechnology* (Vol. 12). `https://doi.org/10.3389/fbioe.2024.1328504`

2. Braian, C., Karlsson, L., **Das, J.**, & Lerm, M. (2023). Selected beta-glucans act as immune-training agents by improving anti-mycobacterial activity in human macrophages-a pilot study. In *Journal of Innate Immunity*.

3. Lundquist, H., Andersson, H., Chew, M. S., **Das, J.**, Turkina, M. V., & Welin, A. (2023). The olfactomedin-4-defined human neutrophil subsets differ in proteomic profile in healthy individuals and patients with septic shock. *Journal of Innate Immunity*, *15*(1), 351–364.

4. Shahin, H., Abdallah, S., **Das, J.**, He, W., El-Serafi, I., Steinvall, I., Sjoberg, F., Elmasry, M., & El-Serafi, A. T. (2023). miRNome and proteome profiling of human keratinocytes and adipose derived stem cells proposed miRNA-mediated regulations of epidermal growth factor and interleukin 1-alpha. *International Journal of Molecular Sciences*, *24*(5), 4956.

5. Verma, D., Kasic, N.-K., Jeppsson, F., Eding, C. B., Lysiak, M., Fekri, S. Z., **Das, J.**, & Enerback, C. (2023). 815 altered methylation of microRNA in the psoriatic epidermis highlights the wnt pathway. *Journal of Investigative Dermatology*, *143*(5), S140.

6. Verma, D., Kasic, N.-K., Jeppsson, F., Eding, C. B., Lysiak, M., Fekri, S. Z., **Das, J.**, & Enerback, C. (2023). Differential DNA methylation of miRNA-encoding genes in psoriatic epidermis highlights the wnt pathway. *The Journal of Investigative Dermatology*, S0022–202X.

7. Volpe, M., & **Das, J.** (2023). methylR: A graphical interface for comprehensive DNA methylation array data analysis. *Bioinformatics*, *39*(4), btad184.

8. Huoman, J., Sayyab, S., Apostolou, E., Karlsson, L., Porcile, L., Rizwan, M., Sharma, S., **Das, J.**, Rosen, A., & Lerm, M. (2022). Epigenetic rewiring of pathways related to odour perception in immune cells exposed to SARS-CoV-2 in vivo and in vitro. *Epigenetics*, *17*(13), 1875–1891.

9. Lundquist, H., Andersson, H., Chew, M. S., **Das, J.**, Turkina, M. V., & Welin, A. (2022). The Olfm4-defined human neutrophil subsets differ in proteomic profile in septic shock. *bioRxiv*.

10. Lysiak, M., **Das, J.**, Malmstrom, A., & Soderkvist, P. (2022). Methylation associated with long-or short-term survival in glioblastoma patients from the nordic phase 3 trial. *Frontiers in Genetics*, *13*, 934519.

11. Lysiak, M., **Das, J.**, Soderkvist, P., & Malmstrom, A. (2022). Methylome analysis of short versus long-term GBM survivors from the nordic randomised, phase 3 trial. *Brain Tumor Research and Treatment*, *10*(Suppl).

12. Pehrson, I., Sayyab, S., **Das, J.**, Idh, N., Paues, J., Mendez-Aranda, M., Ugarte-Gil, C., & Lerm, M. (2022). *DNA methylomes derived from alveolar macrophages and alveolar t cells display distinct patterns in tuberculosis–a future precision tool for TB status determination?*

13. Pehrson, I., Sayyab, S., **Das, J.**, Idh, N., Paues, J., Mendez-Aranda, M., Ugarte-Gil, C., & Lerm, M. (2022). The spectrum of tuberculosis described as differential DNA methylation patterns in alveolar macrophages and alveolar t cells. *Clinical Epigenetics*, *14*(1), 1–12.

14. **Das, J.**, Idh, N., Sikkeland, L. I. B., Paues, J., & Lerm, M. (2021). DNA methylome-based validation of induced sputum as an effective protocol to study lung immunity: Construction of a classifier of pulmonary cell types. *Epigenetics*, 1–12.

15. Huoman, J., Sayyab, S., Apostolou, E., Karlsson, L., Porcile, L., Rizwan, M., Sharma, S., **Das, J.**, Rosen, A., & Lerm, M. (2021). *Epigenome-wide DNA methylation profiling of healthy COVID-19 recoverees reveals a unique signature in circulating immune cells*.

16. Huoman, J., Sayyab, S., Apostolou, E., Karlsson, L., Porcile, L., Rizwan, M., Sharma, S., **Das, J.**, Rosen, A., & Lerm, M. (2021). Mild SARS-CoV-2 infection modifies DNA methylation of peripheral blood mononuclear cells from COVID-19 convalescents. *medRxiv*, 2021–2007.

17. Kalsum, S., Andersson, B., **Das, J.**, Schon, T., & Lerm, M. (2021). A high-throughput screening assay based on automated microscopy for monitoring antibiotic susceptibility of mycobacterium tuberculosis phenotypes. *BMC Microbiology*, *21*(1), 1–14.

18.[*] Karlsson, L., **Das, J.**, Nilsson, M., Tyren, A., Pehrson, I., Idh, N., Sayyab, S., Paues, J., Gil, C. U., Aranda, M. M., & Lerm, M. (2021). A differential DNA methylome signature of pulmonary immune cells from individuals converting to latent tuberculosis infection. *Scientific Reports*, *11*(1), 19418.

19. Pehrson, I., Braian, C., Karlsson, L., Idh, N., Danielsson, E. K., Andersson, B., Paues, J., **Das, J.**, & Lerm, M. (2021). DNA methylation profiling of immune cells from tuberculosis-exposed individuals overlaps with BCG-induced epigenetic changes and correlates with the emergence of anti-mycobacterial "corralling cells." *medRxiv*, 2021–2009.

20. Zhu, G. H., Azharuddin, M., Islam, R., Rahmoune, H., Deb, S., Kanji, U., **Das, J.**, Osterrieth, J., Aulakh, P., Ibrahim-Hashi, H., Manchanda, R., Nilsson, P. H., Mollnes, T. E., Bhattacharyya, M., Islam, M. M., Hinkula, J., Slater, N. K., & Patra, H. K. (2021). Innate immune invisible ultrasmall gold nanoparticles—framework for synthesis and evaluation. *ACS Applied Materials & Interfaces*, *13*(20), 23410–23422.

21. **Das, J.**, Verma, D., Gustafsson, M., & Lerm, M. (2019). Identification of DNA methylation patterns predisposing for an efficient response to BCG vaccination in healthy BCG-naive subjects. *Epigenetics*, *14*(6), 589–601.

22. Sen, K., Bhattacharyya, D., Sarkar, A., **Das, J.**, Maji, N., Basu, M., Ghosh, Z., & Ghosh, T. C. (2018). Exploring the major cross-talking edges of competitive endogenous RNA networks in human chronic and acute myeloid leukemia. *Biochimica Et Biophysica Acta (BBA)-General Subjects*, *1862*(9), 1883–1892.

23. **Das, J.**, Podder, S., & Ghosh, T. C. (2014). Insights into the miRNA regulations in human disease genes. *BMC Genomics*, *15*(1), 1–7.

24. **Das, J.**, Chakraborty, S., Podder, S., & Ghosh, T. C. (2013). Complex-forming proteins escape the robust regulations of miRNA in human. *FEBS Letters*, *587*(14), 2284–2287.

25. Gupta, S., Kumari, K., **Das, J.**, Lata, C., Puranik, S., & Prasad, M. (2011). Development and utilization of novel intron length polymorphic markers in foxtail millet (setaria italica (l.) p. beauv.). *Genome*, *54*(7), 586–602.

Conference abstract/Papers

1. Shahin, H., Abdallah, S., **Das, J.**, Steinvall, I., Sjöberg, F., Elmasry, M., & El-Serafi, A. T. (2023). Mirnome and proteome profiling of human keratinocytes and adipose-derived stem cells proposed mirna-mediated regulations pertaining to stem cell differentiation and wound healing. *Journal of Plastic, Reconstructive & Aesthetic Surgery*, *87*, S18–S19. https://doi.org/`https://doi.org/10.1016/j.bjps.2023.10.040`. *Abstracts from the 11th EURAPS Research Council Meeting in Stockholm, May 2023*.

2. Lysiak, M., **Das, J.**, Soderkvist, P., & Malmstrom, A. (2022). Methylome analysis of short versus long-term GBM survivors from the nordic randomised, phase 3 trial. *Brain Tumor Res Treat*, *10*(Suppl). `https://doi.org/10.14791/btrt.2022.10.F-1329`

Manuscript sumitted/in preparation

1. Volpe, M., Miralto, M., & **Das, J.** (2024). methylRv2: An EPICv2 user interface solution to DNA methylation array data analysis. In *GigaScience*.

2. Volpe, M., Miralto, M., & **Das, J.** (2024). TranscriptR: GUI for transcriptome data analysis. In *GigaScience*.

Patents

1. Lerm, M., & **Das, J.** (2022). *Biomarker for detection of mycobacterial exposure and infection*. `https://patents.google.com/patent/WO2022169394A1`. *WO Patent WO2022169394A1*.

2. Lerm, M., **Das, J.**, & Sayyab, S. (2022). *Method for determining sars-cov-2 exposure with or without remaining symptoms*. *WO Patent WO2022119495A1*.

Poster Presentations and Invited Talks

- including others

Das, J. (2024, March). *Whole-Genome DNA Methylation data analysis pipeline.* Oral presentation at the Clinical Genomics Linköping Webinar Series.

Das, J. (2024, February). *Twist NGS DNA Methylation data analysis pipeline.* Oral presentation at the Clinical Genomics Linköping Workshop.

Das, J.* (2023, October). *methylR: a graphical interface for comprehensive DNA methylation array data analysis.* Poster presented at the Scilifelab day, Linköping.

Das, J.* (2023, May). *methylR: a graphical interface for comprehensive DNA methylation array data analysis.* EMBL-SciLifeLab Data Science workshop, Uppsala, Sweden, May 15-16. Selected for poster presentation.

Das, J.* (2023, May). *methylR: a graphical interface for comprehensive DNA methylation array data analysis.* Workshop oral presentation organized by Clinical Genomics Linköping.

Das, J.* (2023, September). *GMS-Artic: A containerized NextFlow pipeline for detecting Pangolin Typing by analysing SARS-CoV-2 whole genome from short and long sequence reads.* Poster presentation at JIM Symposium Precision medicine in Europe 2022.

Das, J. (2022, October). *gms-artic: features and applications.* oral presentation talk at the GMS-Micro workshop in Karolinska Institute, Sweden.

Das, J. (2021, October) *Visualization, front-end solution.* lightening-fast oral presentation of group discussion in Clinical Genomics Platform retreat at Sigtuna, Sweden.

Das, J. (2021, September). *gms-artic: the pipeline.* Workshop presentation organized by Genomic Medicine Sweden.

Das, J. (2021, June). *How to run a pipeline on NGP server: with a demonstration of gms-artic.* Workshop oral presentation organized by Genomic Medicine Sweden.

Das, J.* (2019, October). *Identification of DNA methylation patterns predisposing for an efficient response to BCG vaccination in healthy BCG-naïve subjects.* Poster presentation at 4th International Conference on Innate Immune Memory organized by Roudbound University, the Netherlands.

Das, J.* (2019, May). *Altered methylation of microRNA (miRNA) in the psoriatic epidermis* Poster presentation in Society for Investigative Dermatology (SID), Chicago, USA.

Das, J. (2019, April). *Epigenetic patterns predicting the response to tuberculosis vaccination.* One-minute presentation to market your research organized by Mucosal Infection and Inflammation Center (MIIC), Linköping University. *Best Presenter Award.*

Das, J. (2018, November). *Advanced image analysis with MATLAB.* Oral presentation organized by NDPIA and Linköping University.

Das, J.* (2018, October). *Identification of DNA methylation patterns predisposing for a trained immunity response to BCG vaccination in healthy BCG-naïve subjects.* Poster presentation on TB research seminar organized by Centre for Tuberculosis Research, Karolinska Institute.

Das, J.* (2017, August). *High-content screening of live-cell imaging and analysis of Mycobacterium marinum-infected Dictyostellim discoideum.* Poster presentation on International TB conference in Stockholm.

Software Developments

- including others

OPEN-SOURCE PROJECT ON GITHUB

methNext: A NextFlow pipeline to analyse DNA methylation data from different sequencing platforms, Illumina, Twist, Nanopore, PacBio   *https://github.com/JD2112/methNext*

NEXTFLOW, R, PYTHON, SINGULARITY, DOCKER, CONDA   *2024-2025*
- Developer of the application

TranscriptR: shiny-based transcriptome analysis and visualisation*

https://github.com/JD2112/transcriptr

SHINY, R, SNAKEMAKE, DOCKER, SINGULARITY

2023 - 2024

- Developer of the application

MethylR: a single shiny solution from sequencer data to pathway analysis*

https://github.com/JD2112/methylr

SHINY, R, DOCKER, SINGULARITY

2022- 2023

- Developer of the application

ComplexPCA: a ggplot PCA with complex annotation

https://github.com/JD2112/ComplexPCA

R, RSTUDIO

2020 - 2021

- Developer of the application

Alveolar-Cell-Type-Deconvolution: DNA methylome-based validation of induced sputum as an effective protocol to study lung immunity: construction of a classifier of pulmonary cell types

https://github.com/JD2112/Alveolar-Cell-Type-Deconvolution

R, RSTUDIO

2019 - 2020

- Developer of the application

Image-Processing-MATLAB: Acquired time lapse images from the IncuCyte® and processed with MATLAB to create a time-lapse video of one particular aggregate of bacteria

https://github.com/JD2112/Image-Processing-MATLAB

MATLAB

2019 - 2020

- Developer of the application

JASEN: Epitypification pipeline for clinical NGS data. Written in NextFlow, Python & Bash.*

https://github.com/JD2112/JASEN

NEXTFLOW, PYTHON, CONDA, DOCKER, SINGULARITY, BASH

2020 - 2023

- Co-developer

gms-artic: A Nextflow pipeline for running the ARTIC network's fieldbioinformatics tools.*

https://github.com/JD2112/gms-artic

NEXTFLOW, PYTHON, CONDA, DOCKER, SINGULARITY, BASH, R

2020 - 2023

- Co-developer

Teaching Experience

Bioinformatics for Microbiology Course (8BKG24)

Linköping University, Sweden

COURSE LECTURE

2021 - 2023

- Teaching (with designing the curriculum, examination) Bioinformatics for Microbiology to the course Medical Microbiology, Linköping University, Sweden

3 weeks R workshop for PhD students

Linköping University, Sweden

R WORKSHOP

Sep. 2019

- Organise the R fundamental workshop for the PhD students (total 18 participants) to understand the data analysis, management, statistical analysis and graphical representation of multi-variate data in R in 3 weekly sessions. The workshop is supported by Forum Scientium, LiU

Random Forest model to biomarker identification

Linköping University, Sweden

LECTURE

May. 2019

- One lecture to visiting undergraduate students from Purdue University, USA.

Live imaging of intracellular infections

Linköping University, Sweden

NDPIA WORKSHOP

Dec. 2018

- Mentoring and co-working with a group of students at NDPIA one week's workshop at Department of Clinical and Experimental Medicine.

Expert reviewer of master thesis

Linköping University, Sweden

EXAMINER

May. 2018

- Interactome link between Alzheimer's disease and diabetes mellitus type II

Supervise two masters' projects in Bioinformatics

Linköping University, Sweden

SUPERVISOR

2018 - 2019

- to guide two master's theses on the bioinformatics part with DNA methylation analysis in R and fundamental of Linux.

Co-supervise one master's project on Image Analysis   *Linköping University, Sweden*

2018
- guide one master's thesis with image analysis and statistical calculations with live imaging techniques.

Bioinformatics for Microbiology   *Bidhannagar Govt. College, WB,*
                                                                                   India

TEACHING   *Jan. 2015 - May. 2015*
- One semester Bioinformatics course curriculum design, deliver lectures and set examination for a group of masters (microbiology) students.

Supervision

Main supervisor: master degrees project student *Linköping University, Sweden*
SUPERVISOR *Jan. 2019 - Jun. 2019*
- Total number of students - 2

Co-supervisor: master degrees project student *Linköping University, Sweden*
CO-SUPERVISOR *2019 - 2020*
- Total number of students - 9

Co-supervisor: doctoral degrees student *Linköping University, Sweden*
CO-SUPERVISOR *2020 - 2024*
- Total number of students - 2

Awards and Honors

Research Grant Award *Bose Institute, Kolkata*
DOCTORAL FELLOWSHIP *Jan. 2012 - Jan. 2017*
- Awarded by DST-INSPIRE, Government of India for pursuing doctoral research

Institute Scholarship *Bose Institute, Kolkata*
DOCTORAL FELLOWSHIP *Sep. 2010 - Jan. 2012*
- National Scholarship awarded to pursue PhD program by Bose Institute, Kolkata - an autonomous body undertaken by Govt of India.

University Gold Medal *MAKAUT, WB*
UNIVERSITY AWARD *2010*
- Awarded University Gold Medal for the topper of the batch, M.Tech (BT), 2010.

Graduate Aptitude Test in Engineering (GATE) *HIT, WB*
MASTER FELLOWSHIP *2008 - 2010*
- Awarded by Ministry of Human Resources Development, Govt Of India to pursue Master of Technology (Biotechnology).

Invited Reviewer

() indicates number of articles reviewed.

Bioinformatics; Oxford (1)
Frontiers in Genetics; Frontiers (1)
Scientific Reports; Nature Portfolio (1)
Cancer management and research; MDPI (2)
Computational biology and chemistry; Elsevier (3)
Genes & genomics; Springer(1)
Genomics; Elsevier (2)
International journal of environmental research and public health; MDPI (1)
International journal of molecular sciences; MDPI (4)
Journal of clinical medicine; MDPI(1)
Nutrients; MDPI(1)
PeerJ; O'Reilly (1)

Data Deposition

1. GSE104287, Article Link
2. GSE182215, Article Link
3. GSE188586, Article Link