

Dr. Rachana Banerjee

Email: rachanahere@gmail.com

Dr. Rachana Banerjee has completed her PhD in Bioinformatics from the Department of Biophysics, Molecular Biology and Bioinformatics at University of Calcutta, Kolkata, India. During PhD, her major goal of research was to decipher molecular signature features in microbial genomes, signifying their evolutionary and adaptation strategies, employing comparative genomics, evolutionary genomics and phylogenetics based in-silico approaches. She has proficiency in the analysis of pathogenomic features in bacteria and viruses, as well as the genomic and proteomic signature features of the extremophilic organisms. After PhD, she has carried out her post-doctoral research as DBT-Research Associate in CSIR-Indian Institute of Chemical Biology (structural Biology and Bioinformatics Division). During her post-doctoral studies, she was involved in comparative genome analysis of human microbial components and metagenomic sequence data analysis for human microbiome. She has published 14 manuscripts in peer-reviewed journals. With nearly 10 years of experience in research, she has joined as an assistant professor in JIS Institute of Advanced Studies and Research, Kolkata.

Current Research Interests:

1. Interpreting molecular signatures in microbial genomes responsible for hospital-acquired infection or nosocomial infection, signifying their evolutionary and adaptation strategies. Some of these microbes fail to infect healthy individuals; rather they require immuno-compromised individuals to induce disease. She is interested to explore new horizons related to genomic diversities, speciation as well as host resistance features in these groups of microbial genomes, with restricted pathogenic ability or can be termed as “opportunistic pathogens”. She aspires to develop effective strategies to prevent infections as well as to predict the type of infections caused by the opportunistic pathogens in an immune-compromised host, through studying the evolutionary pattern of drug resistance, disease progression and host adaptation in chronically infected patients.

2. Determining the functional attributes of the human microbiome (collective genetic material of microbiota), essential to infer their role in host metabolism and disease. She aspires to identify molecular biomarkers to accurately classify a particular disease, by correlating the taxonomic and metabolomic profile variation of the microbiome for both diseased and healthy state.

Google scholar link: <https://scholar.google.co.in/citations?user=CBsU258AAAAJ&hl=en>