Anirban Dutta

List of Publications by Year
in descending order

24 papers	**594** citations	567281 **15** h-index	642732 **23** g-index
30 all docs	**30** docs citations	**30** times ranked	**832** citing authors

#	Article	IF	Citations
1	Sensing Host Health: Insights from Sensory Protein Signature of the Metagenome. Applied and Environmental Microbiology, 2022, 88, .	3.1	3
2	Trans-ethnic gut microbial signatures of prediabetic subjects from India and Denmark. Genome Medicine, 2021, 13, 36.	8.2	31
3	Trans-ethnic gut microbiota signatures of type 2 diabetes in Denmark and India. Genome Medicine, 2021, 13, 37.	8.2	34
4	Chaperonin Abundance Enhances Bacterial Fitness. Frontiers in Molecular Biosciences, 2021, 8, 669996.	3.5	2
5	Antibiotic Stewardship in Premature Infants: A Systematic Review. Neonatology, 2020, 117, 673-686.	2.0	23
6	Can Targeting Non-Contiguous V-Regions With Paired-End Sequencing Improve 16S rRNA-Based Taxonomic Resolution of Microbiomes?: An In Silico Evaluation. Frontiers in Genetics, 2019, 10, 653.	2.3	7
7	Rewiring of Metabolic Network in Mycobacterium tuberculosis During Adaptation to Different Stresses. Frontiers in Microbiology, 2019, 10, 2417.	3.5	30
8	OTUX: V-region specific OTU database for improved 16S rRNA OTU picking and efficient cross-study taxonomic comparison of microbiomes. DNA Research, 2019, 26, 147-156.	3.4	18
9	Alterations in the gut bacterial microbiome in fungal Keratitis patients. PLoS ONE, 2018, 13, e0199640.	2.5	65
10	Understanding the role of interactions between host and Mycobacterium tuberculosis under hypoxic condition: an in silico approach. BMC Genomics, 2018, 19, 555.	2.8	13
11	First-trimester vaginal microbiome diversity: A potential indicator of preterm delivery risk. Scientific Reports, 2017, 7, 16145.	3.3	63
12	CompNet: a GUI based tool for comparison of multiple biological interaction networks. BMC Bioinformatics, 2016, 17, 185.	2.6	38
13	CS-SCORE: Rapid identification and removal of human genome contaminants from metagenomic datasets. Genomics, 2015, 106, 116-121.	2.9	18
14	FQC: A novel approach for efficient compression, archival, and dissemination of fastq datasets. Journal of Bioinformatics and Computational Biology, 2015, 13, 1541003.	0.8	16
15	FASTR: A novel data format for concomitant representation of RNA sequence and secondary structure information. Journal of Biosciences, 2015, 40, 571-577.	1.1	1
16	Binpairs: Utilization of Illumina Paired-End Information for Improving Efficiency of Taxonomic Binning of Metagenomic Sequences. PLoS ONE, 2014, 9, e114814.	2.5	16
17	Understanding the sequential activation of Type III and Type VI Secretion Systems in Salmonella typhimurium using Boolean modeling. Gut Pathogens, 2013, 5, 28.	3.4	12
18	DELIMINATEâ€"a fast and efficient method for loss-less compression of genomic sequences. Bioinformatics, 2012, 28, 2527-2529.	4.1	47

#	Article	IF	Citations
19	BIND â€" An algorithm for loss-less compression of nucleotide sequence data. Journal of Biosciences, 2012, 37, 785-789.	1.1	25
20	Indian genetic disease database. Nucleic Acids Research, 2011, 39, D933-D938.	14.5	26
21	Distinct, ecotype-specific genome and proteome signatures in the marine cyanobacteria Prochlorococcus. BMC Genomics, 2010, 11, 103.	2.8	31
22	GCâ€'rich intraâ€'operonic spacers in prokaryotes: Possible relation to gene order conservation. FEBS Letters, 2010, 584, 4633-4638.	2.8	1
23	In silico identification of potential therapeutic targets in the human pathogen Helicobacter pylori. In Silico Biology, 2006, 6, 43-7.	0.9	70
24	Towards Engineering an Ecosystem: A Review of Computational Approaches to Explore and Exploit the Human Microbiome for Healthcare. , 0, , 1.		0