

Anirban Dutta

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6323795/publications.pdf>

Version: 2024-02-01

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	In silico identification of potential therapeutic targets in the human pathogen <i>Helicobacter pylori</i> . In <i>Silico Biology</i> , 2006, 6, 43-7.	0.9	70
2	Alterations in the gut bacterial microbiome in fungal Keratitis patients. <i>PLoS ONE</i> , 2018, 13, e0199640.	2.5	65
3	First-trimester vaginal microbiome diversity: A potential indicator of preterm delivery risk. <i>Scientific Reports</i> , 2017, 7, 16145.	3.3	63
4	DELIMINATEâ€”a fast and efficient method for loss-less compression of genomic sequences. <i>Bioinformatics</i> , 2012, 28, 2527-2529.	4.1	47
5	CompNet: a GUI based tool for comparison of multiple biological interaction networks. <i>BMC Bioinformatics</i> , 2016, 17, 185.	2.6	38
6	Trans-ethnic gut microbiota signatures of type 2 diabetes in Denmark and India. <i>Genome Medicine</i> , 2021, 13, 37.	8.2	34
7	Distinct, ecotype-specific genome and proteome signatures in the marine cyanobacteria <i>Prochlorococcus</i> . <i>BMC Genomics</i> , 2010, 11, 103.	2.8	31
8	Trans-ethnic gut microbial signatures of prediabetic subjects from India and Denmark. <i>Genome Medicine</i> , 2021, 13, 36.	8.2	31
9	Rewiring of Metabolic Network in <i>Mycobacterium tuberculosis</i> During Adaptation to Different Stresses. <i>Frontiers in Microbiology</i> , 2019, 10, 2417.	3.5	30
10	Indian genetic disease database. <i>Nucleic Acids Research</i> , 2011, 39, D933-D938.	14.5	26
11	BIND â€” An algorithm for loss-less compression of nucleotide sequence data. <i>Journal of Biosciences</i> , 2012, 37, 785-789.	1.1	25
12	Antibiotic Stewardship in Premature Infants: A Systematic Review. <i>Neonatology</i> , 2020, 117, 673-686.	2.0	23
13	CS-SCORE: Rapid identification and removal of human genome contaminants from metagenomic datasets. <i>Genomics</i> , 2015, 106, 116-121.	2.9	18
14	OTUX: V-region specific OTU database for improved 16S rRNA OTU picking and efficient cross-study taxonomic comparison of microbiomes. <i>DNA Research</i> , 2019, 26, 147-156.	3.4	18
15	Binpairs: Utilization of Illumina Paired-End Information for Improving Efficiency of Taxonomic Binning of Metagenomic Sequences. <i>PLoS ONE</i> , 2014, 9, e114814.	2.5	16
16	FQC: A novel approach for efficient compression, archival, and dissemination of fastq datasets. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1541003.	0.8	16
17	Understanding the role of interactions between host and <i>Mycobacterium tuberculosis</i> under hypoxic condition: an in silico approach. <i>BMC Genomics</i> , 2018, 19, 555.	2.8	13
18	Understanding the sequential activation of Type III and Type VI Secretion Systems in <i>Salmonella typhimurium</i> using Boolean modeling. <i>Gut Pathogens</i> , 2013, 5, 28.	3.4	12

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19	Can Targeting Non-Contiguous V-Regions With Paired-End Sequencing Improve 16S rRNA-Based Taxonomic Resolution of Microbiomes?: An In Silico Evaluation. <i>Frontiers in Genetics</i> , 2019, 10, 653.	2.3	7
20	Sensing Host Health: Insights from Sensory Protein Signature of the Metagenome. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	3.1	3
21	Chaperonin Abundance Enhances Bacterial Fitness. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 669996.	3.5	2
22	GC-rich intra-operonic spacers in prokaryotes: Possible relation to gene order conservation. <i>FEBS Letters</i> , 2010, 584, 4633-4638.	2.8	1
23	FASTR: A novel data format for concomitant representation of RNA sequence and secondary structure information. <i>Journal of Biosciences</i> , 2015, 40, 571-577.	1.1	1
24	Towards Engineering an Ecosystem: A Review of Computational Approaches to Explore and Exploit the Human Microbiome for Healthcare. , 0, , 1.		0