

Vineet K Sharma

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

1,234
citations

471061

17
h-index

476904

29
g-index

33
all docs

33
docs citations

33
times ranked

1894
citing authors

#	ARTICLE	IF	CITATIONS
1	The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches. <i>GigaScience</i> , 2019, 8, .	3.3	143
2	Gut Microbial Dysbiosis in Indian Children with Autism Spectrum Disorders. <i>Microbial Ecology</i> , 2018, 76, 1102-1114.	1.4	130
3	Gut microbiome contributes to impairment of immunity in pulmonary tuberculosis patients by alteration of butyrate and propionate producers. <i>Environmental Microbiology</i> , 2018, 20, 402-419.	1.8	120
4	MP3: A Software Tool for the Prediction of Pathogenic Proteins in Genomic and Metagenomic Data. <i>PLoS ONE</i> , 2014, 9, e93907.	1.1	112
5	Association of <i>Flavonifractor plautii</i> , a Flavonoid-Degrading Bacterium, with the Gut Microbiome of Colorectal Cancer Patients in India. <i>MSystems</i> , 2019, 4, .	1.7	109
6	Prediction of anti-inflammatory proteins/peptides: an insilico approach. <i>Journal of Translational Medicine</i> , 2017, 15, 7.	1.8	91
7	16S Classifier: A Tool for Fast and Accurate Taxonomic Classification of 16S rRNA Hypervariable Regions in Metagenomic Datasets. <i>PLoS ONE</i> , 2015, 10, e0116106.	1.1	71
8	ProlInflam: a webserver for the prediction of proinflammatory antigenicity of peptides and proteins. <i>Journal of Translational Medicine</i> , 2016, 14, 178.	1.8	52
9	ToxiM: A Toxicity Prediction Tool for Small Molecules Developed Using Machine Learning and Chemoinformatics Approaches. <i>Frontiers in Pharmacology</i> , 2017, 8, 880.	1.6	48
10	IL17eScan: A Tool for the Identification of Peptides Inducing IL-17 Response. <i>Frontiers in Immunology</i> , 2017, 8, 1430.	2.2	36
11	Woods: A fast and accurate functional annotator and classifier of genomic and metagenomic sequences. <i>Genomics</i> , 2015, 106, 1-6.	1.3	34
12	The genome sequence of <i>Aloe vera</i> reveals adaptive evolution of drought tolerance mechanisms. <i>IScience</i> , 2021, 24, 102079.	1.9	29
13	Western and non-western gut microbiomes reveal new roles of <i>Prevotella</i> in carbohydrate metabolism and mouth-gut axis. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 77.	2.9	28
14	Fast and Accurate Taxonomic Assignments of Metagenomic Sequences Using MetaBin. <i>PLoS ONE</i> , 2012, 7, e34030.	1.1	27
15	Comparative analysis of corrected tiger genome provides clues to its neuronal evolution. <i>Scientific Reports</i> , 2019, 9, 18459.	1.6	24
16	Abundance of dinucleotide repeats and gene expression are inversely correlated: a role for gene function in addition to intron length. <i>Physiological Genomics</i> , 2007, 31, 96-103.	1.0	23
17	Genome sequencing of turmeric provides evolutionary insights into its medicinal properties. <i>Communications Biology</i> , 2021, 4, 1193.	2.0	23
18	Mechanistic and structural insight into promiscuity based metabolism of cardiac drug digoxin by gut microbial enzyme. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 5287-5296.	1.2	20

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19	(TG/CA) _n Repeats in Human Housekeeping Genes. Journal of Biomolecular Structure and Dynamics, 2003, 21, 303-310.	2.0	15
20	Using the taxon-specific genes for the taxonomic classification of bacterial genomes. BMC Genomics, 2015, 16, 396.	1.2	15
21	Molib: A machine learning based classification tool for the prediction of biofilm inhibitory molecules. Genomics, 2020, 112, 2823-2832.	1.3	15
22	Genome-scale metabolic reconstruction and metabolic versatility of an obligate methanotroph <i>Methylococcus capsulatus</i> . Bath. PeerJ, 2019, 7, e6685.	0.9	13
23	SkinBug: an artificial intelligence approach to predict human skin microbiome-mediated metabolism of biotics and xenobiotics. IScience, 2021, 24, 101925.	1.9	9
24	BioFuelDB: a database and prediction server of enzymes involved in biofuels production. PeerJ, 2017, 5, e3497.	0.9	9
25	Draft Genome Sequence of Tepidimonas taiwanensis Strain MB2, a Chemolithotrophic Thermophile Isolated from a Hot Spring in Central India. Genome Announcements, 2016, 4, .	0.8	8
26	Draft Genome Sequence of Anoxybacillus mongoliensis Strain MB4, a Sulfur-Utilizing Aerobic Thermophile Isolated from a Hot Spring in Tattapani, Central India. Genome Announcements, 2017, 5, .	0.8	7
27	Draft Genome Sequence of Gulbenkiania mobilis Strain MB1, a Sulfur-Metabolizing Thermophile Isolated from a Hot Spring in Central India. Genome Announcements, 2015, 3, .	0.8	6
28	Draft Genome Sequence of Pseudomonas hussainii Strain MB3, a Denitrifying Aerobic Bacterium Isolated from the Rhizospheric Region of Mangrove Trees in the Andaman Islands, India. Genome Announcements, 2017, 5, .	0.8	4
29	Mechanistic elucidation of amphetamine metabolism by tyramine oxidase from human gut microbiota using molecular dynamics simulations. Journal of Cellular Biochemistry, 2019, 120, 11206-11215.	1.2	4