Vineet K Sharma

List of Publications by Year
in descending order

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 genome sequence of Aloe vera reveals adaptive evolution of drought tolerance mechanisms. IScience, 2021, 24, 102079.	1.9	29
2	SkinBug: an artificial intelligence approach to predict human skin microbiome-mediated metabolism of biotics and xenobiotics. IScience, 2021, 24, 101925.	1.9	9
3	Genome sequencing of turmeric provides evolutionary insights into its medicinal properties. Communications Biology, 2021, 4, 1193.	2.0	23
4	Western and non-western gut microbiomes reveal new roles of Prevotella in carbohydrate metabolism and mouthâ€"gut axis. Npj Biofilms and Microbiomes, 2021, 7, 77.	2.9	28
5	Molib: A machine learning based classification tool for the prediction of biofilm inhibitory molecules. Genomics, 2020, 112, 2823-2832.	1.3	15
6	The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches. GigaScience, 2019, 8, .	3.3	143
7	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
8	Comparative analysis of corrected tiger genome provides clues to its neuronal evolution. Scientific Reports, 2019, 9, 18459.	1.6	24
9	Association of Flavonifractor plautii, a Flavonoid-Degrading Bacterium, with the Gut Microbiome of Colorectal Cancer Patients in India. MSystems, 2019, 4, .	1.7	109
10	Genome-scale metabolic reconstruction and metabolic versatility of an obligate methanotroph *Methylococcus capsulatus* str. Bath. PeerJ, 2019, 7, e6685.	0.9	13
11	Mechanistic and structural insight into promiscuity based metabolism of cardiac drug digoxin by gut microbial enzyme. Journal of Cellular Biochemistry, 2018, 119, 5287-5296.	1.2	20
12	Gut microbiome contributes to impairment of immunity in pulmonary tuberculosis patients by alteration of butyrate and propionate producers. Environmental Microbiology, 2018, 20, 402-419.	1.8	120
13	Gut Microbial Dysbiosis in Indian Children with Autism Spectrum Disorders. Microbial Ecology, 2018, 76, 1102-1114.	1.4	130
14	Prediction of anti-inflammatory proteins/peptides: an insilico approach. Journal of Translational Medicine, 2017, 15, 7.	1.8	91
15	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
16	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
17	ToxiM: A Toxicity Prediction Tool for Small Molecules Developed Using Machine Learning and Chemoinformatics Approaches. Frontiers in Pharmacology, 2017, 8, 880.	1.6	48
18	IL17eScan: A Tool for the Identification of Peptides Inducing IL-17 Response. Frontiers in Immunology, 2017, 8, 1430.	2.2	36

#	Article	IF	Citations
19	BioFuelDB: a database and prediction server of enzymes involved in biofuels production. PeerJ, 2017, 5, e3497.	0.9	9
20	ProInflam: a webserver for the prediction of proinflammatory antigenicity of peptides and proteins. Journal of Translational Medicine, 2016, 14, 178.	1.8	52
21	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
22	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
23	16S Classifier: A Tool for Fast and Accurate Taxonomic Classification of 16S rRNA Hypervariable Regions in Metagenomic Datasets. PLoS ONE, 2015, 10, e0116106.	1.1	71
24	Woods: A fast and accurate functional annotator and classifier of genomic and metagenomic sequences. Genomics, 2015, 106, 1-6.	1.3	34
25	Using the taxon-specific genes for the taxonomic classification of bacterial genomes. BMC Genomics, 2015, 16, 396.	1.2	15
26	MP3: A Software Tool for the Prediction of Pathogenic Proteins in Genomic and Metagenomic Data. PLoS ONE, 2014, 9, e93907.	1.1	112
27	Fast and Accurate Taxonomic Assignments of Metagenomic Sequences Using MetaBin. PLoS ONE, 2012, 7, e34030.	1.1	27
28	Abundance of dinucleotide repeats and gene expression are inversely correlated: a role for gene function in addition to intron length. Physiological Genomics, 2007, 31, 96-103.	1.0	23
29	(TG/CA)$_n$Repeats in Human Housekeeping Genes. Journal of Biomolecular Structure and Dynamics, 2003, 21, 303-310.	2.0	15