

Gaoyang Li

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

281
citations

1040056

9
h-index

996975

15
g-index

17
all docs

17
docs citations

17
times ranked

403
citing authors

#	ARTICLE	IF	CITATIONS
1	Classifying Breast Cancer Subtypes Using Deep Neural Networks Based on Multi-Omics Data. <i>Genes</i> , 2020, 11, 888.	2.4	52
2	Systems-level understanding of ethanol-induced stresses and adaptation in <i>E. coli</i> . <i>Scientific Reports</i> , 2017, 7, 44150.	3.3	43
3	Nitrogen remobilization and conservation, and underlying senescence-associated gene expression in the perennial switchgrass <i>Panicum virgatum</i> . <i>New Phytologist</i> , 2016, 211, 75-89.	7.3	37
4	The LA-ICP-MS zircons U-Pb ages and geochemistry of the Baihua basic igneous complexes in Tianshui area of West Qinling. <i>Science in China Series D: Earth Sciences</i> , 2007, 50, 264-276.	0.9	35
5	Globally-optimal prediction-based adaptive mutation particle swarm optimization. <i>Information Sciences</i> , 2017, 418-419, 186-217.	6.9	28
6	Direct and Indirect Effects of Penguin Feces on Microbiomes in Antarctic Ornithogenic Soils. <i>Frontiers in Microbiology</i> , 2018, 9, 552.	3.5	20
7	Biodiversity and dynamics of cyanobacterial communities during blooms in temperate lake (Harsha) Tj ETQq1 1 0.784314 rgBT /Overl	4.8	15
8	An Efficient Genetic Algorithm for Optimization Problems with Time-Consuming Fitness Evaluation. <i>International Journal of Computational Methods</i> , 2015, 12, 1350106.	1.3	10
9	Genome-Scale Identification of Cell-Wall-Related Genes in Switchgrass through Comparative Genomics and Computational Analyses of Transcriptomic Data. <i>Bioenergy Research</i> , 2016, 9, 172-180.	3.9	10
10	CapsNet-SSP: multilane capsule network for predicting human saliva-secretory proteins. <i>BMC Bioinformatics</i> , 2020, 21, 237.	2.6	9
11	Geochemical-Compositional-Functional Changes in Arctic Soil Microbiomes Post Land Submergence Revealed by Metagenomics. <i>Microbes and Environments</i> , 2019, 34, 180-190.	1.6	6
12	Structural and functional analyses of microbial metabolic networks reveal novel insights into genome-scale metabolic fluxes. <i>Briefings in Bioinformatics</i> , 2019, 20, 1590-1603.	6.5	6
13	CyanoPATH: a knowledgebase of genome-scale functional repertoire for toxic cyanobacterial blooms. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	4
14	DeepUEP: Prediction of Urine Excretory Proteins Using Deep Learning. <i>IEEE Access</i> , 2020, 8, 100251-100261.	4.2	3
15	DEEPSMP: A deep learning model for predicting the ectodomain shedding events of membrane proteins. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050017.	0.8	3