

Hao Wang

List of Publications by Year in descending order

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31
papers

5,666
citations

304743

22
h-index

414414

32
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35
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35
docs citations

35
times ranked

7832
citing authors

#	ARTICLE	IF	CITATIONS
1	Silencing of STE20-type kinase STK25 in human aortic endothelial and smooth muscle cells is atheroprotective. <i>Communications Biology</i> , 2022, 5, 379.	4.4	4
2	Bayesian genome scale modelling identifies thermal determinants of yeast metabolism. <i>Nature Communications</i> , 2021, 12, 190.	12.8	25
3	Genome-scale insights into the metabolic versatility of <i>Limosilactobacillus reuteri</i> . <i>BMC Biotechnology</i> , 2021, 21, 46.	3.3	8
4	Genome-scale metabolic network reconstruction of model animals as a platform for translational research. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	48
5	Yeast metabolic innovations emerged via expanded metabolic network and gene positive selection. <i>Molecular Systems Biology</i> , 2021, 17, e10427.	7.2	17
6	Optimizing cultivation of <i>Cordyceps militaris</i> for fast growth and cordycepin overproduction using rational design of synthetic media. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1-8.	4.1	31
7	An atlas of human metabolism. <i>Science Signaling</i> , 2020, 13, .	3.6	223
8	The Swinholide Biosynthesis Gene Cluster from a Terrestrial Cyanobacterium, <i>Nostoc</i> sp. Strain UHCC 0450. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	21
9	RAVEN 2.0: A versatile toolbox for metabolic network reconstruction and a case study on <i>Streptomyces coelicolor</i> . <i>PLoS Computational Biology</i> , 2018, 14, e1006541.	3.2	228
10	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	17.5	356
11	Production of High Amounts of Hepatotoxin Nodularin and New Protease Inhibitors Pseudospumigins by the Brazilian Benthic <i>Nostoc</i> sp. CENA543. <i>Frontiers in Microbiology</i> , 2017, 8, 1963.	3.5	35
12	A Unique Tryptophan C ϵ Prenyltransferase from the Kawaguchi-peptin Biosynthetic Pathway. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 3596-3599.	13.8	49
13	Antifungal activity improved by coproduction of cyclodextrins and anabaenolysins in Cyanobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13669-13674.	7.1	27
14	Genomic insights into the distribution, genetic diversity and evolution of polyketide synthases and nonribosomal peptide synthetases. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 79-85.	3.3	33
15	Recurrent Loss of Specific Introns during Angiosperm Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004843.	3.5	26
16	Reply to Sasso et al.: Distribution and phylogeny of nonribosomal peptide and polyketide biosynthetic pathways in eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3947-E3947.	7.1	2
17	Hassallidins, antifungal glycolipopeptides, are widespread among cyanobacteria and are the end-product of a nonribosomal pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1909-17.	7.1	102
18	Atlas of nonribosomal peptide and polyketide biosynthetic pathways reveals common occurrence of nonmodular enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9259-9264.	7.1	310

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19	Global Genomic Diversity of <i>Oryza sativa</i> Varieties Revealed by Comparative Physical Mapping. <i>Genetics</i> , 2014, 196, 937-949.	2.9	10
20	Genome-derived insights into the biology of the hepatotoxic bloom-forming cyanobacterium <i>Anabaena</i> sp. strain 90. <i>BMC Genomics</i> , 2012, 13, 613.	2.8	52
21	Anatoxin-a Synthetase Gene Cluster of the Cyanobacterium <i>Anabaena</i> sp. Strain 37 and Molecular Methods To Detect Potential Producers. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7271-7278.	3.1	166
22	De novo genome sequencing and comparative genomics of date palm (<i>Phoenix dactylifera</i>). <i>Nature Biotechnology</i> , 2011, 29, 521-527.	17.5	356
23	Genome Mining Demonstrates the Widespread Occurrence of Gene Clusters Encoding Bacteriocins in Cyanobacteria. <i>PLoS ONE</i> , 2011, 6, e22384.	2.5	78
24	Recurrent adenylation domain replacement in the microcystin synthetase gene cluster. <i>BMC Evolutionary Biology</i> , 2007, 7, 183.	3.2	97
25	An analysis of the proteomic profile for <i>Thermoanaerobacter tengcongensis</i> under optimal culture conditions. <i>Proteomics</i> , 2004, 4, 136-150.	2.2	39
26	Assessment of Immunoreactive Synthetic Peptides from the Structural Proteins of Severe Acute Respiratory Syndrome Coronavirus. <i>Clinical Chemistry</i> , 2003, 49, 1989-1996.	3.2	71
27	The C-Terminal Portion of the Nucleocapsid Protein Demonstrates SARS-CoV Antigenicity. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 193-197.	6.9	11
28	The Epitope Study on the SARS-CoV Nucleocapsid Protein. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 198-206.	6.9	27
29	A Strategy for Searching Antigenic Regions in the SARS-CoV Spike Protein. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 207-215.	6.9	14
30	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. <i>indica</i>). <i>Science</i> , 2002, 296, 79-92.	12.6	3,146
31	A draft sequence of the rice (<i>Oryza sativa</i> ssp. <i>indica</i>) genome. <i>Science Bulletin</i> , 2001, 46, 1937-1942.	1.7	35