

Ying Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1801111/publications.pdf>

Version: 2024-02-01

25
papers

1,467
citations

623734

14
h-index

552781

26
g-index

31
all docs

31
docs citations

31
times ranked

2415
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple integrated metabolic strategies allow foraminiferan protists to thrive in anoxic marine sediments. <i>Science Advances</i> , 2021, 7, .	10.3	20
2	Microbiome Analysis Reveals Diversity and Function of <i>Mollicutes</i> Associated with the Eastern Oyster, <i>Crassostrea virginica</i> . <i>MSphere</i> , 2021, 6, .	2.9	21
3	Genome-Scale Metabolic Model of <i>Caldicellulosiruptor bescii</i> Reveals Optimal Metabolic Engineering Strategies for Bio-based Chemical Production. <i>MSystems</i> , 2021, 6, e0135120.	3.8	6
4	Transcriptional Regulation of Plant Biomass Degradation and Carbohydrate Utilization Genes in the Extreme Thermophile <i>Caldicellulosiruptor bescii</i> . <i>MSystems</i> , 2021, 6, e0134520.	3.8	10
5	Durable changes in the gut microbiome in survivors of childhood acute lymphoblastic leukemia. <i>Pediatric Blood and Cancer</i> , 2021, 68, e29308.	1.5	4
6	Leave no stone unturned: individually adapted xerotolerant Thaumarchaeota sheltered below the boulders of the Atacama Desert hyperarid core. <i>Microbiome</i> , 2021, 9, 234.	11.1	18
7	FARCI: Fast and Robust Connectome Inference. <i>Brain Sciences</i> , 2021, 11, 1556.	2.3	3
8	The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. <i>BMC Biology</i> , 2020, 18, 90.	3.8	40
9	From the raw bar to the bench: Bivalves as models for human health. <i>Developmental and Comparative Immunology</i> , 2019, 92, 260-282.	2.3	48
10	Variation in genome content and predatory phenotypes between <i>Bdellovibrio</i> sp. NC01 isolated from soil and <i>B. bacteriovorus</i> type strain HD100. <i>Microbiology (United Kingdom)</i> , 2019, 165, 1315-1330.	1.8	11
11	Using PSAMM for the Curation and Analysis of Genome-Scale Metabolic Models. <i>Methods in Molecular Biology</i> , 2018, 1716, 131-150.	0.9	8
12	Evolution of the Natural Transformation Protein, ComEC, in Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 2980.	3.5	42
13	A Simple <i>In Vitro</i> Gut Model for Studying the Interaction between <i>Escherichia coli</i> and the Intestinal Commensal Microbiota in Cecal Mucus. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	6
14	FindPrimaryPairs: An efficient algorithm for predicting element-transferring reactant/product pairs in metabolic networks. <i>PLoS ONE</i> , 2018, 13, e0192891.	2.5	0
15	A Genome-Scale Model of <i>Shewanella piezotolerans</i> Simulates Mechanisms of Metabolic Diversity and Energy Conservation. <i>MSystems</i> , 2017, 2, .	3.8	14
16	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017, 8, 682.	3.5	409
17	PSAMM: A Portable System for the Analysis of Metabolic Models. <i>PLoS Computational Biology</i> , 2016, 12, e1004732.	3.2	35
18	Pan-genome analyses identify lineage- and niche-specific markers of evolution and adaptation in Epsilonproteobacteria. <i>Frontiers in Microbiology</i> , 2014, 5, 110.	3.5	63

#	ARTICLE	IF	CITATIONS
19	Structural Determinants of Limited Proteolysis. <i>Journal of Proteome Research</i> , 2011, 10, 3642-3651.	3.7	68
20	The FGGY Carbohydrate Kinase Family: Insights into the Evolution of Functional Specificities. <i>PLoS Computational Biology</i> , 2011, 7, e1002318.	3.2	48
21	PMAP: databases for analyzing proteolytic events and pathways. <i>Nucleic Acids Research</i> , 2009, 37, D611-D618.	14.5	57
22	Global distribution of conformational states derived from redundant models in the PDB points to non-uniqueness of the protein structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10505-10510.	7.1	73
23	Three-Dimensional Structural View of the Central Metabolic Network of <i>Thermotoga maritima</i> . <i>Science</i> , 2009, 325, 1544-1549.	12.6	176
24	CutDB: a proteolytic event database. <i>Nucleic Acids Research</i> , 2007, 35, D546-D549.	14.5	119
25	Between Order and Disorder in Protein Structures: Analysis of "Dual Personality" Fragments in Proteins. <i>Structure</i> , 2007, 15, 1141-1147.	3.3	72