Ying Zhang

List of Publications by Year
in descending order

		623734	552781
25	1,467	14	26
papers	citations	h-index	g-index
31	31	31	2415
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). Frontiers in Microbiology, 2017, 8, 682.	3.5	409
2	Three-Dimensional Structural View of the Central Metabolic Network of *Thermotoga maritima*. Science, 2009, 325, 1544-1549.	12.6	176
3	CutDB: a proteolytic event database. Nucleic Acids Research, 2007, 35, D546-D549.	14.5	119
4	Global distribution of conformational states derived from redundant models in the PDB points to non-uniqueness of the protein structure. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10505-10510.	7.1	73
5	Between Order and Disorder in Protein Structures: Analysis of â€œDual Personalityâ€•Fragments in Proteins. Structure, 2007, 15, 1141-1147.	3.3	72
6	Structural Determinants of Limited Proteolysis. Journal of Proteome Research, 2011, 10, 3642-3651.	3.7	68
7	Pan-genome analyses identify lineage- and niche-specific markers of evolution and adaptation in Epsilonproteobacteria. Frontiers in Microbiology, 2014, 5, 110.	3.5	63
8	PMAP: databases for analyzing proteolytic events and pathways. Nucleic Acids Research, 2009, 37, D611-D618.	14.5	57
9	The FGGY Carbohydrate Kinase Family: Insights into the Evolution of Functional Specificities. PLoS Computational Biology, 2011, 7, e1002318.	3.2	48
10	From the raw bar to the bench: Bivalves as models for human health. Developmental and Comparative Immunology, 2019, 92, 260-282.	2.3	48
11	Evolution of the Natural Transformation Protein, ComEC, in Bacteria. Frontiers in Microbiology, 2018, 9, 2980.	3.5	42
12	The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. BMC Biology, 2020, 18, 90.	3.8	40
13	PSAMM: A Portable System for the Analysis of Metabolic Models. PLoS Computational Biology, 2016, 12, e1004732.	3.2	35
14	Microbiome Analysis Reveals Diversity and Function of *Mollicutes* Associated with the Eastern Oyster, *Crassostrea virginica*. MSphere, 2021, 6, .	2.9	21
15	Multiple integrated metabolic strategies allow foraminiferan protists to thrive in anoxic marine sediments. Science Advances, 2021, 7, .	10.3	20
16	Leave no stone unturned: individually adapted xerotolerant Thaumarchaeota sheltered below the boulders of the Atacama Desert hyperarid core. Microbiome, 2021, 9, 234.	11.1	18
17	A Genome-Scale Model of *Shewanella piezotolerans* Simulates Mechanisms of Metabolic Diversity and Energy Conservation. MSystems, 2017, 2, .	3.8	14
18	Variation in genome content and predatory phenotypes between Bdellovibrio sp. NC01 isolated from soil and B. bacteriovorus type strain HD100. Microbiology (United Kingdom), 2019, 165, 1315-1330.	1.8	11

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19	Transcriptional Regulation of Plant Biomass Degradation and Carbohydrate Utilization Genes in the Extreme Thermophile *Caldicellulosiruptor bescii*. MSystems, 2021, 6, e0134520.	3.8	10
20	Using PSAMM for the Curation and Analysis of Genome-Scale Metabolic Models. Methods in Molecular Biology, 2018, 1716, 131-150.	0.9	8
21	A Simple *In Vitro* Gut Model for Studying the Interaction between Escherichia coli and the Intestinal Commensal Microbiota in Cecal Mucus. Applied and Environmental Microbiology, 2018, 84, .	3.1	6
22	Genome-Scale Metabolic Model of *Caldicellulosiruptor bescii* Reveals Optimal Metabolic Engineering Strategies for Bio-based Chemical Production. MSystems, 2021, 6, e0135120.	3.8	6
23	Durable changes in the gut microbiome in survivors of childhood acute lymphoblastic leukemia. Pediatric Blood and Cancer, 2021, 68, e29308.	1.5	4
24	FARCI: Fast and Robust Connectome Inference. Brain Sciences, 2021, 11, 1556.	2.3	3
25	FindPrimaryPairs: An efficient algorithm for predicting element-transferring reactant/product pairs in metabolic networks. PLoS ONE, 2018, 13, e0192891.	2.5	0