

Zheng Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

673
citations

623734

14
h-index

642732

23
g-index

40
all docs

40
docs citations

40
times ranked

735
citing authors

#	ARTICLE	IF	CITATIONS
1	Docking-guided rational engineering of a macrolide glycosyltransferase glycodiversifies epothilone B. <i>Communications Biology</i> , 2022, 5, 100.	4.4	6
2	Novel furimazine derivatives for nanoluciferase bioluminescence with various C-6 and C-8 substituents. <i>Organic and Biomolecular Chemistry</i> , 2021, 19, 7930-7936.	2.8	9
3	Two PAAR Proteins with Different C-Terminal Extended Domains Have Distinct Ecological Functions in <i>Myxococcus xanthus</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	11
4	Bioinformatic and Functional Characterization of Hsp70s in <i>Myxococcus xanthus</i> . <i>MSphere</i> , 2021, 6, .	2.9	4
5	Global Geographic Diversity and Distribution of the Myxobacteria. <i>Microbiology Spectrum</i> , 2021, 9, e0001221.	3.0	15
6	Diagnostic Techniques for COVID-19: A Mini-review of Early Diagnostic Methods. <i>Journal of Analysis and Testing</i> , 2021, 5, 314-326.	5.1	12
7	Expanded analyses of the functional correlations within structural classifications of glycoside hydrolases. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5931-5942.	4.1	9
8	The Second Chromosome Promotes the Adaptation of the Genus <i>Flammeovirga</i> to Complex Environments. <i>Microbiology Spectrum</i> , 2021, 9, e0098021.	3.0	3
9	PAAR Proteins Are Versatile Clips That Enrich the Antimicrobial Weapon Arsenals of Prokaryotes. <i>MSystems</i> , 2021, 6, e0095321.	3.8	10
10	Insights into the persistence and phenotypic effects of the endogenous and cryptic plasmid pMF1 in its host strain <i>Myxococcus fulvus</i> 124B02. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	3
11	Estimate of the sequenced proportion of the global prokaryotic genome. <i>Microbiome</i> , 2020, 8, 134.	11.1	58
12	Identification of type VI secretion system toxic effectors using adaptors as markers. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3723-3733.	4.1	10
13	Shifts in the Bacterial Population and Ecosystem Functions in Response to Vegetation in the Yellow River Delta Wetlands. <i>MSystems</i> , 2020, 5, .	3.8	19
14	Glycosyltransferase GT1 family: Phylogenetic distribution, substrates coverage, and representative structural features. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1383-1390.	4.1	59
15	Phylogeny-guided characterization of glycosyltransferases for epothilone glycosylation. <i>Microbial Biotechnology</i> , 2019, 12, 763-774.	4.2	12
16	Structural and evolutionary characteristics of dynamin-related GTPase OPA1. <i>PeerJ</i> , 2019, 7, e7285.	2.0	13
17	Effects of transcriptional mode on promoter substitution and tandem engineering for the production of epothilones in <i>Myxococcus xanthus</i> . <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5599-5610.	3.6	13
18	Contributions of substitutions and indels to the structural variations in ancient protein superfamilies. <i>BMC Genomics</i> , 2018, 19, 771.	2.8	8

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19	CIRCE element evolved for the coordinated transcriptional regulation of bacterial duplicate groELs. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 928-937.	1.9	5
20	A Post-segregational Killing Mechanism for Maintaining Plasmid PMF1 in Its <i>Myxococcus fulvus</i> Host. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 274.	3.9	9
21	A nuclease toxin and immunity system for kin discrimination in <i>Myxococcus xanthus</i> . <i>Environmental Microbiology</i> , 2018, 20, 2552-2567.	3.8	20
22	Competitive Interactions Between Incompatible Mutants of the Social Bacterium <i>Myxococcus xanthus</i> DK1622. <i>Frontiers in Microbiology</i> , 2018, 9, 1200.	3.5	10
23	A Newly Determined Member of the <i>meso</i> -Diaminopimelate Dehydrogenase Family with a Broad Substrate Spectrum. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	18
24	Dynamic Interplay of the Myxobacterial Chaperonins. <i>Heat Shock Proteins</i> , 2017, , 53-65.	0.2	0
25	A bacterial negative transcription regulator binding on an inverted repeat in the promoter for epothilone biosynthesis. <i>Microbial Cell Factories</i> , 2017, 16, 92.	4.0	8
26	Error-prone DnaE2 Balances the Genome Mutation Rates in <i>Myxococcus xanthus</i> DK1622. <i>Frontiers in Microbiology</i> , 2017, 8, 122.	3.5	10
27	<i>Myxococcus xanthus</i> DK1622 Coordinates Expressions of the Duplicate groEL and Single groES Genes for Synergistic Functions of GroELs and GroES. <i>Frontiers in Microbiology</i> , 2017, 8, 733.	3.5	10
28	Analysis of the Sequences, Structures, and Functions of Product-Releasing Enzyme Domains in Fungal Polyketide Synthases. <i>Frontiers in Microbiology</i> , 2017, 8, 1685.	3.5	12
29	Bioinformatics analysis of the structural and evolutionary characteristics for toll-like receptor 15. <i>PeerJ</i> , 2016, 4, e2079.	2.0	13
30	Interleukin-22 ameliorates acute severe pancreatitis-associated lung injury in mice. <i>World Journal of Gastroenterology</i> , 2016, 22, 5023.	3.3	18
31	Ectodomain Architecture Affects Sequence and Functional Evolution of Vertebrate Toll-like Receptors. <i>Scientific Reports</i> , 2016, 6, 26705.	3.3	37
32	Bioinformatical Analysis of the Sequences, Structures and Functions of Fungal Polyketide Synthase Product Template Domains. <i>Scientific Reports</i> , 2015, 5, 10463.	3.3	38
33	Structural characterization and evolutionary analysis of fish-specific TLR27. <i>Fish and Shellfish Immunology</i> , 2015, 45, 940-945.	3.6	39
34	Structural and evolutionary characteristics of fish-specific TLR19. <i>Fish and Shellfish Immunology</i> , 2015, 47, 271-279.	3.6	16
35	TRPM7 promotes the metastatic process in human nasopharyngeal carcinoma. <i>Cancer Letters</i> , 2015, 356, 483-490.	7.2	31
36	Mechanisms Involved in the Functional Divergence of Duplicated GroEL Chaperonins in <i>Myxococcus xanthus</i> DK1622. <i>PLoS Genetics</i> , 2013, 9, e1003306.	3.5	27

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37	IndelFR: a database of indels in protein structures and their flanking regions. <i>Nucleic Acids Research</i> , 2012, 40, D512-D518.	14.5	14
38	Impact of Indels on the Flanking Regions in Structural Domains. <i>Molecular Biology and Evolution</i> , 2011, 28, 291-301.	8.9	35
39	The Combined Effects of Amino Acid Substitutions and Indels on the Evolution of Structure within Protein Families. <i>PLoS ONE</i> , 2010, 5, e14316.	2.5	25