

Yong-Liang Jiang

List of Publications by Year in descending order

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47
papers

933
citations

535685

17
h-index

591227

27
g-index

47
all docs

47
docs citations

47
times ranked

1683
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and assembly pattern of a freshwater short-tailed cyanophage Pam1. <i>Structure</i> , 2022, 30, 240-251.e4.	1.6	9
2	Biochemical and structural characterization of the cyanophage- ϕ C encoded phosphate-binding protein: implications for enhanced phosphate uptake of infected cyanobacteria. <i>Environmental Microbiology</i> , 2022, 24, 3037-3050.	1.8	7
3	Complex structure reveals $\langle scp \rangle$ CcmM $\langle /scp \rangle$ and $\langle scp \rangle$ CcmN $\langle /scp \rangle$ form a heterotrimeric adaptor in $\hat{\pm}$ -carboxysome. <i>Protein Science</i> , 2021, 30, 1566-1576.	3.1	5
4	Structures of cyanobacterial bicarbonate transporter SbtA and its complex with PII-like SbtB. <i>Cell Discovery</i> , 2021, 7, 63.	3.1	16
5	Structural basis for juvenile hormone biosynthesis by the juvenile hormone acid methyltransferase. <i>Journal of Biological Chemistry</i> , 2021, 297, 101234.	1.6	15
6	Crystal structure of a novel fold protein Gp72 from the freshwater cyanophage Mic1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1226-1232.	1.5	1
7	The model cyanobacteria <i>Anabaena</i> sp. PCC 7120 possess an intact but partially degenerated gene cluster encoding gas vesicles. <i>BMC Microbiology</i> , 2020, 20, 110.	1.3	8
8	Crystal structure of sulfonic peroxiredoxin Ahp1 in complex with thioredoxin Trx2 mimics a conformational intermediate during the catalytic cycle. <i>International Journal of Biological Macromolecules</i> , 2020, 161, 1055-1060.	3.6	5
9	Cryo-electron Microscopy Structure and Transport Mechanism of a Wall Teichoic Acid ABC Transporter. <i>MBio</i> , 2020, 11, .	1.8	33
10	Cryo-EM structure of human bile salts exporter ABCB11. <i>Cell Research</i> , 2020, 30, 623-625.	5.7	30
11	Structural and functional insights into the Asp1/2/3 complex mediated secretion of pneumococcal serine-rich repeat protein PsrP. <i>Biochemical and Biophysical Research Communications</i> , 2020, 524, 784-790.	1.0	1
12	New structural insights into the recognition of undamaged splayed-arm DNA with a single pair of non-complementary nucleotides by human nucleotide excision repair protein XPA. <i>International Journal of Biological Macromolecules</i> , 2020, 148, 466-474.	3.6	10
13	Genomic Analysis of Mic1 Reveals a Novel Freshwater Long-Tailed Cyanophage. <i>Frontiers in Microbiology</i> , 2020, 11, 484.	1.5	27
14	Molecular basis for the assembly of RuBisCO assisted by the chaperone Raf1. <i>Nature Plants</i> , 2020, 6, 708-717.	4.7	24
15	Capsid Structure of a Freshwater Cyanophage Siphoviridae Mic1. <i>Structure</i> , 2019, 27, 1508-1516.e3.	1.6	21
16	Structural insights into repression of the <i>Pneumococcal</i> fatty acid synthesis pathway by repressor FabT and co-repressor acyl-ACP. <i>FEBS Letters</i> , 2019, 593, 2730-2741.	1.3	20
17	Cryo-EM structure of human lysosomal cobalamin exporter ABCD4. <i>Cell Research</i> , 2019, 29, 1039-1041.	5.7	42
18	Crystal structure of pentameric shell protein CsoS4B of <i>Halothiobacillus neapolitanus</i> $\hat{\pm}$ -carboxysome. <i>Biochemical and Biophysical Research Communications</i> , 2019, 515, 510-515.	1.0	4

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19	Crystal structure of the choline-binding protein CbpJ from <i>Streptococcus pneumoniae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 514, 1192-1197.	1.0	10
20	Structural insights into the catalysis and substrate specificity of cyanobacterial aspartate racemase McyF. <i>Biochemical and Biophysical Research Communications</i> , 2019, 514, 1108-1114.	1.0	6
21	Structural characterization of the redefined DNA-binding domain of human XPA. <i>Biochemical and Biophysical Research Communications</i> , 2019, 514, 985-990.	1.0	11
22	Multi-functional regulator MapZ controls both positioning and timing of FtsZ polymerization. <i>Biochemical Journal</i> , 2019, 476, 1433-1444.	1.7	6
23	Aurora-A mediated phosphorylation of LDHB promotes glycolysis and tumor progression by relieving the substrate-inhibition effect. <i>Nature Communications</i> , 2019, 10, 5566.	5.8	66
24	Structural and enzymatic analyses of <i>Anabaena</i> heterocyst-specific alkaline invertase InvB. <i>FEBS Letters</i> , 2018, 592, 1589-1601.	1.3	12
25	Structure of a MacAB-like efflux pump from <i>Streptococcus pneumoniae</i> . <i>Nature Communications</i> , 2018, 9, 196.	5.8	34
26	Coordinating carbon and nitrogen metabolic signaling through the cyanobacterial global repressor NdhR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 403-408.	3.3	65
27	The GDP-switched GAF domain of DcpA modulates the concerted synthesis/hydrolysis of c-di-GMP in <i>Mycobacterium smegmatis</i> . <i>Biochemical Journal</i> , 2018, 475, 1295-1308.	1.7	13
28	Defining the enzymatic pathway for polymorphic O-glycosylation of the pneumococcal serine-rich repeat protein PsrP. <i>Journal of Biological Chemistry</i> , 2017, 292, 6213-6224.	1.6	26
29	Structural Analysis of the Catalytic Mechanism and Substrate Specificity of <i>Anabaena</i> Alkaline Invertase InvA Reveals a Novel Glucosidase. <i>Journal of Biological Chemistry</i> , 2016, 291, 25667-25677.	1.6	24
30	Structure of a variable lymphocyte receptor-like protein from the amphioxus <i>Branchiostoma floridae</i> . <i>Scientific Reports</i> , 2016, 6, 19951.	1.6	12
31	Structural basis for receptor recognition and pore formation of a zebrafish aerolysin-like protein. <i>EMBO Reports</i> , 2016, 17, 235-248.	2.0	53
32	Structural Comparison and Simulation of Pneumococcal Peptidoglycan Hydrolase LytB. <i>Methods in Molecular Biology</i> , 2016, 1440, 271-283.	0.4	0
33	Structural and enzymatic analyses of a glucosyltransferase Alr3699/HepE involved in <i>Anabaena</i> heterocyst envelop polysaccharide biosynthesis. <i>Glycobiology</i> , 2016, 26, 520-531.	1.3	4
34	Structural insights into HetR~PatS interaction involved in cyanobacterial pattern formation. <i>Scientific Reports</i> , 2015, 5, 16470.	1.6	29
35	Structural and biochemical analyses of the <i>Streptococcus pneumoniae</i> L, D-carboxypeptidase DacB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 283-292.	2.5	2
36	Crystallization and preliminary X-ray diffraction analysis of a putative carbon-carbon bond hydrolase from <i>Mycobacterium abscessus</i> 103. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 239-242.	0.4	1

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37	Structure of the adenylationâ€“peptidyl carrier protein didomain of the <i>Microcystis aeruginosa</i> microcystin synthetase McyG. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 873-881.	2.5	18
38	Structural and Enzymatic Characterization of the Choline Kinase LicA from <i>Streptococcus pneumoniae</i> . <i>PLoS ONE</i> , 2015, 10, e0120467.	1.1	11
39	Structural Insights into SraP-Mediated <i>Staphylococcus aureus</i> Adhesion to Host Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004169.	2.1	85
40	Structure of Pneumococcal Peptidoglycan Hydrolase LytB Reveals Insights into the Bacterial Cell Wall Remodeling and Pathogenesis. <i>Journal of Biological Chemistry</i> , 2014, 289, 23403-23416.	1.6	62
41	Crystal structures and catalytic mechanism of the C-methyltransferase Coq5 provide insights into a key step of the yeast coenzyme Q synthesis pathway. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2085-2092.	2.5	22
42	Structural and biochemical analyses of <i>Microcystis aeruginosa</i> O-acetylserine sulfhydrylases reveal a negative feedback regulation of cysteine biosynthesis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 308-315.	1.1	4
43	<i>Streptomyces coelicolor</i> SCO4226 Is a Nickel Binding Protein. <i>PLoS ONE</i> , 2014, 9, e109660.	1.1	9
44	Structural Insights into the Neutralization Mechanism of Monoclonal Antibody 6C2 against Ricin. <i>Journal of Biological Chemistry</i> , 2013, 288, 25165-25172.	1.6	12
45	Structure of Yeast Sulfhydryl Oxidase Erv1 Reveals Electron Transfer of the Disulfide Relay System in the Mitochondrial Intermembrane Space. <i>Journal of Biological Chemistry</i> , 2012, 287, 34961-34969.	1.6	25
46	Structural Basis for the Substrate Specificity of a Novel Î²-N-Acetylhexosaminidase StrH Protein from <i>Streptococcus pneumoniae</i> R6. <i>Journal of Biological Chemistry</i> , 2011, 286, 43004-43012.	1.6	29
47	Structural and Enzymatic Characterization of the Streptococcal ATP/Diadenosine Polyphosphate and Phosphodiester Hydrolase Spr1479/SapH*. <i>Journal of Biological Chemistry</i> , 2011, 286, 35906-35914.	1.6	4