

Yong-Liang Jiang

List of Publications by Year in descending order

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47
papers

933
citations

471509

17
h-index

526287

27
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47
all docs

47
docs citations

47
times ranked

1547
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Insights into SraP-Mediated <i>Staphylococcus aureus</i> Adhesion to Host Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004169.	4.7	85
2	Aurora-A mediated phosphorylation of LDHB promotes glycolysis and tumor progression by relieving the substrate-inhibition effect. <i>Nature Communications</i> , 2019, 10, 5566.	12.8	66
3	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.	7.1	65
4	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.	3.4	62
5	Structural basis for receptor recognition and pore formation of a zebrafish aerolysin-like protein. <i>EMBO Reports</i> , 2016, 17, 235-248.	4.5	53
6	Cryo-EM structure of human lysosomal cobalamin exporter ABCD4. <i>Cell Research</i> , 2019, 29, 1039-1041.	12.0	42
7	Structure of a MacAB-like efflux pump from <i>Streptococcus pneumoniae</i> . <i>Nature Communications</i> , 2018, 9, 196.	12.8	34
8	Cryo-electron Microscopy Structure and Transport Mechanism of a Wall Teichoic Acid ABC Transporter. <i>MBio</i> , 2020, 11, .	4.1	33
9	Cryo-EM structure of human bile salts exporter ABCB11. <i>Cell Research</i> , 2020, 30, 623-625.	12.0	30
10	Structural Basis for the Substrate Specificity of a Novel Î ² -N-Acetylhexosaminidase StrH Protein from <i>Streptococcus pneumoniae</i> R6. <i>Journal of Biological Chemistry</i> , 2011, 286, 43004-43012.	3.4	29
11	Structural insights into HetR~PatS interaction involved in cyanobacterial pattern formation. <i>Scientific Reports</i> , 2015, 5, 16470.	3.3	29
12	Genomic Analysis of Mic1 Reveals a Novel Freshwater Long-Tailed Cyanophage. <i>Frontiers in Microbiology</i> , 2020, 11, 484.	3.5	27
13	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.	3.4	26
14	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.	3.4	25
15	Structural Analysis of the Catalytic Mechanism and Substrate Specificity of Anabaena Alkaline Invertase InvA Reveals a Novel Glucosidase. <i>Journal of Biological Chemistry</i> , 2016, 291, 25667-25677.	3.4	24
16	Molecular basis for the assembly of RuBisCO assisted by the chaperone Raf1. <i>Nature Plants</i> , 2020, 6, 708-717.	9.3	24
17	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
18	Capsid Structure of a Freshwater Cyanophage Siphoviridae Mic1. <i>Structure</i> , 2019, 27, 1508-1516.e3.	3.3	21

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19	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.	2.8	20
20	Structure of the adenylation-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
21	Structures of cyanobacterial bicarbonate transporter SbtA and its complex with PII-like SbtB. <i>Cell Discovery</i> , 2021, 7, 63.	6.7	16
22	Structural basis for juvenile hormone biosynthesis by the juvenile hormone acid methyltransferase. <i>Journal of Biological Chemistry</i> , 2021, 297, 101234.	3.4	15
23	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.	3.7	13
24	Structural Insights into the Neutralization Mechanism of Monoclonal Antibody 6C2 against Ricin. <i>Journal of Biological Chemistry</i> , 2013, 288, 25165-25172.	3.4	12
25	Structure of a variable lymphocyte receptor-like protein from the amphioxus <i>Branchiostoma floridae</i> . <i>Scientific Reports</i> , 2016, 6, 19951.	3.3	12
26	Structural and enzymatic analyses of <i>Anabaena</i> heterocyst-specific alkaline invertase InvB. <i>FEBS Letters</i> , 2018, 592, 1589-1601.	2.8	12
27	Structural characterization of the redefined DNA-binding domain of human XPA. <i>Biochemical and Biophysical Research Communications</i> , 2019, 514, 985-990.	2.1	11
28	Structural and Enzymatic Characterization of the Choline Kinase LicA from <i>Streptococcus pneumoniae</i> . <i>PLoS ONE</i> , 2015, 10, e0120467.	2.5	11
29	Crystal structure of the choline-binding protein CbpJ from <i>Streptococcus pneumoniae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 514, 1192-1197.	2.1	10
30	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.	7.5	10
31	<i>Streptomyces coelicolor</i> SCO4226 Is a Nickel Binding Protein. <i>PLoS ONE</i> , 2014, 9, e109660.	2.5	9
32	Structure and assembly pattern of a freshwater short-tailed cyanophage Pam1. <i>Structure</i> , 2022, 30, 240-251.e4.	3.3	9
33	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.	3.3	8
34	Biochemical and structural characterization of the cyanophage-encoded phosphate-binding protein: implications for enhanced phosphate uptake of infected cyanobacteria. <i>Environmental Microbiology</i> , 2022, 24, 3037-3050.	3.8	7
35	Structural insights into the catalysis and substrate specificity of cyanobacterial aspartate racemase McyF. <i>Biochemical and Biophysical Research Communications</i> , 2019, 514, 1108-1114.	2.1	6
36	Multi-functional regulator MapZ controls both positioning and timing of FtsZ polymerization. <i>Biochemical Journal</i> , 2019, 476, 1433-1444.	3.7	6

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37	Crystal structure of sulfonic peroxidoredoxin 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.	7.5	5
38	Complex structure reveals <i>CcmM</i> and <i>CcmN</i> form a heterotrimeric adaptor in γ -carboxysome. <i>Protein Science</i> , 2021, 30, 1566-1576.	7.6	5
39	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.	3.4	4
40	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.	2.3	4
41	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.	2.5	4
42	Crystal structure of pentameric shell protein CsoS4B of <i>Halothiobacillus neapolitanus</i> γ -carboxysome. <i>Biochemical and Biophysical Research Communications</i> , 2019, 515, 510-515.	2.1	4
43	Structural and biochemical analyses of the <i>Streptococcus pneumoniae</i> <i>L</i> , <i>D</i> -carboxypeptidase DacB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 283-292.	2.5	2
44	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.	0.8	1
45	Crystal structure of a novel fold protein Gp72 from the freshwater cyanophage Mic1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1226-1232.	2.6	1
46	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.	2.1	1
47	Structural Comparison and Simulation of Pneumococcal Peptidoglycan Hydrolase LytB. <i>Methods in Molecular Biology</i> , 2016, 1440, 271-283.	0.9	0