

# Yong-Liang Jiang

## List of Publications by Year in descending order

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47  
papers

933  
citations

471477

17  
h-index

526264

27  
g-index

47  
all docs

47  
docs citations

47  
times ranked

1547  
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.	3.3	9
2	Biochemical and structural characterization of the cyanophage- $\phi$ C encoded phosphate-binding protein: implications for enhanced phosphate uptake of infected cyanobacteria. <i>Environmental Microbiology</i> , 2022, 24, 3037-3050.	3.8	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 $\beta$ -carboxysome. <i>Protein Science</i> , 2021, 30, 1566-1576.	7.6	5
4	Structures of cyanobacterial bicarbonate transporter SbtA and its complex with PII-like SbtB. <i>Cell Discovery</i> , 2021, 7, 63.	6.7	16
5	Structural basis for juvenile hormone biosynthesis by the juvenile hormone acid methyltransferase. <i>Journal of Biological Chemistry</i> , 2021, 297, 101234.	3.4	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.	2.6	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.	3.3	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.	7.5	5
9	Cryo-electron Microscopy Structure and Transport Mechanism of a Wall Teichoic Acid ABC Transporter. <i>MBio</i> , 2020, 11, .	4.1	33
10	Cryo-EM structure of human bile salts exporter ABCB11. <i>Cell Research</i> , 2020, 30, 623-625.	12.0	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.	2.1	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.	7.5	10
13	Genomic Analysis of Mic1 Reveals a Novel Freshwater Long-Tailed Cyanophage. <i>Frontiers in Microbiology</i> , 2020, 11, 484.	3.5	27
14	Molecular basis for the assembly of RuBisCO assisted by the chaperone Raf1. <i>Nature Plants</i> , 2020, 6, 708-717.	9.3	24
15	Capsid Structure of a Freshwater Cyanophage Siphoviridae Mic1. <i>Structure</i> , 2019, 27, 1508-1516.e3.	3.3	21
16	Structural insights into repression of the <i>Pneumococcal</i> fatty acid synthesis pathway by repressor FabT and co-repressor acyl-CoA. <i>FEBS Letters</i> , 2019, 593, 2730-2741.	2.8	20
17	Cryo-EM structure of human lysosomal cobalamin exporter ABCD4. <i>Cell Research</i> , 2019, 29, 1039-1041.	12.0	42
18	Crystal structure of pentameric shell protein CsoS4B of <i>Halothiobacillus neapolitanus</i> $\beta$ -carboxysome. <i>Biochemical and Biophysical Research Communications</i> , 2019, 515, 510-515.	2.1	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.	2.1	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.	2.1	6
21	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
22	Multi-functional regulator MapZ controls both positioning and timing of FtsZ polymerization. <i>Biochemical Journal</i> , 2019, 476, 1433-1444.	3.7	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.	12.8	66
24	Structural and enzymatic analyses of <i>Anabaena</i> heterocyst-specific alkaline invertase InvB. <i>FEBS Letters</i> , 2018, 592, 1589-1601.	2.8	12
25	Structure of a MacAB-like efflux pump from <i>Streptococcus pneumoniae</i> . <i>Nature Communications</i> , 2018, 9, 196.	12.8	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.	7.1	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.	3.7	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.	3.4	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.	3.4	24
30	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
31	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
32	Structural Comparison and Simulation of Pneumococcal Peptidoglycan Hydrolase LytB. <i>Methods in Molecular Biology</i> , 2016, 1440, 271-283.	0.9	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.	2.5	4
34	Structural insights into HetR~PatS interaction involved in cyanobacterial pattern formation. <i>Scientific Reports</i> , 2015, 5, 16470.	3.3	29
35	Structural and biochemical analyses of the <i>Streptococcus pneumoniae</i> <i>L</i> -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.	0.8	1

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37	Structure of the adenylationâ€“peptidyl carrier protein didomain of the<i>Microcystis aeruginosa</i> microcystin synthetase McyG. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 873-881.	2.5	18
38	Structural and Enzymatic Characterization of the Choline Kinase LicA from Streptococcus pneumoniae. PLoS ONE, 2015, 10, e0120467.	2.5	11
39	Structural Insights into SraP-Mediated Staphylococcus aureus Adhesion to Host Cells. PLoS Pathogens, 2014, 10, e1004169.	4.7	85
40	Structure of Pneumococcal Peptidoglycan Hydrolase LytB Reveals Insights into the Bacterial Cell Wall Remodeling and Pathogenesis. Journal of Biological Chemistry, 2014, 289, 23403-23416.	3.4	62
41	Crystal structures and catalytic mechanism of the<i>C</i>-methyltransferase Coq5 provide insights into a key step of the yeast coenzyme Q synthesis pathway. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2085-2092.	2.5	22
42	Structural and biochemical analyses of Microcystis aeruginosa O-acetylserine sulfhydrylases reveal a negative feedback regulation of cysteine biosynthesis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 308-315.	2.3	4
43	Streptomyces coelicolor SCO4226 Is a Nickel Binding Protein. PLoS ONE, 2014, 9, e109660.	2.5	9
44	Structural Insights into the Neutralization Mechanism of Monoclonal Antibody 6C2 against Ricin. Journal of Biological Chemistry, 2013, 288, 25165-25172.	3.4	12
45	Structure of Yeast Sulfhydryl Oxidase Erv1 Reveals Electron Transfer of the Disulfide Relay System in the Mitochondrial Intermembrane Space. Journal of Biological Chemistry, 2012, 287, 34961-34969.	3.4	25
46	Structural Basis for the Substrate Specificity of a Novel Î²-N-Acetylhexosaminidase StrH Protein from Streptococcus pneumoniae R6. Journal of Biological Chemistry, 2011, 286, 43004-43012.	3.4	29
47	Structural and Enzymatic Characterization of the Streptococcal ATP/Diadenosine Polyphosphate and Phosphodiester Hydrolase Spr1479/SapH*. Journal of Biological Chemistry, 2011, 286, 35906-35914.	3.4	4