

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 | 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- ϕ 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 $\hat{\pm}$ -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-ACP. <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> $\hat{\pm}$ -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> , <i>D</i> -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. <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. | 2.5 | 11 |
| 39 | Structural Insights into SraP-Mediated <i>Staphylococcus aureus</i> Adhesion to Host Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004169. | 4.7 | 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. | 3.4 | 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. | 2.3 | 4 |
| 43 | <i>Streptomyces coelicolor</i> SCO4226 Is a Nickel Binding Protein. <i>PLoS ONE</i> , 2014, 9, e109660. | 2.5 | 9 |
| 44 | 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 |
| 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. | 3.4 | 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. | 3.4 | 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. | 3.4 | 4 |