

Cong-Zhao Zhou

List of Publications by Year in descending order

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138
papers

7,529
citations

147801

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56724

83
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141
all docs

141
docs citations

141
times ranked

15370
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Guidelines for the use and interpretation of assays for monitoring autophagy. <i>Autophagy</i> , 2012, 8, 445-544. | 9.1 | 3,122 |
| 2 | Silk fibroin: Structural implications of a remarkable amino acid sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 44, 119-122. | 2.6 | 606 |
| 3 | Fine organization of <i>Bombyx mori</i> fibroin heavy chain gene. <i>Nucleic Acids Research</i> , 2000, 28, 2413-2419. | 14.5 | 603 |
| 4 | Carbon/Nitrogen Metabolic Balance: Lessons from Cyanobacteria. <i>Trends in Plant Science</i> , 2018, 23, 1116-1130. | 8.8 | 117 |
| 5 | N-Terminal Domain of <i>Bombyx mori</i> Fibroin Mediates the Assembly of Silk in Response to pH Decrease. <i>Journal of Molecular Biology</i> , 2012, 418, 197-207. | 4.2 | 107 |
| 6 | Structural basis for the allosteric control of the global transcription factor NtcA by the nitrogen starvation signal 2-oxoglutarate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12487-12492. | 7.1 | 102 |
| 7 | Structural Insights into SraP-Mediated <i>Staphylococcus aureus</i> Adhesion to Host Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004169. | 4.7 | 85 |
| 8 | Cloning of novel laccase isozyme genes from <i>Trametes</i> sp. AH28-2 and analyses of their differential expression. <i>Applied Microbiology and Biotechnology</i> , 2006, 71, 493-501. | 3.6 | 81 |
| 9 | Crystal Structure and Functional Characterization of Yeast YLR011wp, an Enzyme with NAD(P)H-FMN and Ferric Iron Reductase Activities. <i>Journal of Biological Chemistry</i> , 2004, 279, 34890-34897. | 3.4 | 71 |
| 10 | 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 |
| 11 | 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 |
| 12 | Crystal Structure of the Yeast Phox Homology (PX) Domain Protein Grd19p Complexed to Phosphatidylinositol-3-phosphate. <i>Journal of Biological Chemistry</i> , 2003, 278, 50371-50376. | 3.4 | 64 |
| 13 | Activation of the LicT Transcriptional Antiterminator Involves a Domain Swing/Lock Mechanism Provoking Massive Structural Changes. <i>Journal of Biological Chemistry</i> , 2005, 280, 14780-14789. | 3.4 | 64 |
| 14 | 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 |
| 15 | Catalytic Mechanism and Structure of Viral Flavin-dependent Thymidylate Synthase ThyX. <i>Journal of Biological Chemistry</i> , 2006, 281, 24048-24057. | 3.4 | 53 |
| 16 | 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 |
| 17 | Systematic cloning and analysis of autophagy-related genes from the silkworm <i>Bombyx mori</i> . <i>BMC Molecular Biology</i> , 2009, 10, 50. | 3.0 | 51 |
| 18 | Crystal structure of LZα8 from the medicinal fungus <i>Ganoderma lucidum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 524-527. | 2.6 | 50 |

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|----|--|------|-----------|
| 19 | Refolding strategies from inclusion bodies in a structural genomics project. <i>Journal of Structural and Functional Genomics</i> , 2004, 5, 195-204. | 1.2 | 49 |
| 20 | Structure of a Novel O-Linked N-Acetyl-d-glucosamine (O-GlcNAc) Transferase, GtfA, Reveals Insights into the Glycosylation of Pneumococcal Serine-rich Repeat Adhesins. <i>Journal of Biological Chemistry</i> , 2014, 289, 20898-20907. | 3.4 | 49 |
| 21 | Crystal structure of glutathione reductase Glr1 from the yeast <i>Saccharomyces cerevisiae</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 972-979. | 2.6 | 47 |
| 22 | The Ternary Structure of the Double-headed Arrowhead Protease Inhibitor API-A Complexed with Two Trypsins Reveals a Novel Reactive Site Conformation. <i>Journal of Biological Chemistry</i> , 2009, 284, 26676-26684. | 3.4 | 46 |
| 23 | Structural and Biochemical Characterization of Yeast Monothiol Glutaredoxin Grx6. <i>Journal of Molecular Biology</i> , 2010, 398, 614-622. | 4.2 | 45 |
| 24 | Structures of the substrate-binding protein provide insights into the multiple compatible solute binding specificities of the <i>Bacillus subtilis</i> ABC transporter OpuC. <i>Biochemical Journal</i> , 2011, 436, 283-289. | 3.7 | 45 |
| 25 | Cryo-EM structure of human lysosomal cobalamin exporter ABCD4. <i>Cell Research</i> , 2019, 29, 1039-1041. | 12.0 | 42 |
| 26 | Glutathionylation-triggered conformational changes of glutaredoxin Grx1 from the yeast <i>Saccharomyces cerevisiae</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 1077-1083. | 2.6 | 41 |
| 27 | Structural Snapshots of Yeast Alkyl Hydroperoxide Reductase Ahp1 Peroxiredoxin Reveal a Novel Two-cysteine Mechanism of Electron Transfer to Eliminate Reactive Oxygen Species. <i>Journal of Biological Chemistry</i> , 2012, 287, 17077-17087. | 3.4 | 39 |
| 28 | Crystal Structure of the Cyanobacterial Signal Transduction Protein PII in Complex with PipX. <i>Journal of Molecular Biology</i> , 2010, 402, 552-559. | 4.2 | 36 |
| 29 | Crystal structure of <i>Saccharomyces cerevisiae</i> 6-phosphogluconate dehydrogenase Gnd1. <i>BMC Structural Biology</i> , 2007, 7, 38. | 2.3 | 34 |
| 30 | Gloverins of the silkworm <i>Bombyx mori</i> : Structural and binding properties and activities. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 612-625. | 2.7 | 34 |
| 31 | Characterization of the First Fungal Glycosyl Hydrolase Family 19 Chitinase (NbchiA) from <i>Nosema bombycis</i> (Nb). <i>Journal of Eukaryotic Microbiology</i> , 2016, 63, 37-45. | 1.7 | 34 |
| 32 | Structure of a MacAB-like efflux pump from <i>Streptococcus pneumoniae</i> . <i>Nature Communications</i> , 2018, 9, 196. | 12.8 | 34 |
| 33 | Neofunctionalization of zona pellucida proteins enhances freeze-prevention in the eggs of Antarctic notothenioids. <i>Nature Communications</i> , 2016, 7, 12987. | 12.8 | 33 |
| 34 | Cryo-electron Microscopy Structure and Transport Mechanism of a Wall Teichoic Acid ABC Transporter. <i>MBio</i> , 2020, 11, . | 4.1 | 33 |
| 35 | Structural Insights into the Substrate Specificity of <i>Streptococcus pneumoniae</i> $\hat{1}$ (1,3)-Galactosidase BgaC. <i>Journal of Biological Chemistry</i> , 2012, 287, 22910-22918. | 3.4 | 32 |
| 36 | Crystal Structure of the YDR533c <i>S. cerevisiae</i> Protein, a Class II Member of the Hsp31 Family. <i>Structure</i> , 2004, 12, 839-847. | 3.3 | 31 |

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|----|---|------|-----------|
| 37 | Crystal structure of <i>Saccharomyces cerevisiae</i> glutamine synthetase Gln1 suggests a nanotube-like supramolecular assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 249-254. | 2.6 | 31 |
| 38 | Crystal structure of the mucin-binding domain of Spr1345 from <i>Streptococcus pneumoniae</i> . <i>Journal of Structural Biology</i> , 2011, 174, 252-257. | 2.8 | 31 |
| 39 | Indian hedgehog mutations causing brachydactyly type A1 impair Hedgehog signal transduction at multiple levels. <i>Cell Research</i> , 2011, 21, 1343-1357. | 12.0 | 31 |
| 40 | ATHB17 enhances stress tolerance by coordinating photosynthesis associated nuclear gene and ATSIG5 expression in response to abiotic stress. <i>Scientific Reports</i> , 2017, 7, 45492. | 3.3 | 31 |
| 41 | Solution Structure of Kti11p from <i>Saccharomyces cerevisiae</i> Reveals a Novel Zinc-Binding Module. <i>Biochemistry</i> , 2005, 44, 8801-8809. | 2.5 | 30 |
| 42 | Cryo-EM structure of human bile salts exporter ABCB11. <i>Cell Research</i> , 2020, 30, 623-625. | 12.0 | 30 |
| 43 | Structures of <i>Streptococcus pneumoniae</i> PiaA and Its Complex with Ferrichrome Reveal Insights into the Substrate Binding and Release of High Affinity Iron Transporters. <i>PLoS ONE</i> , 2013, 8, e71451. | 2.5 | 30 |
| 44 | Structural Basis for the Substrate Specificity of a Novel β -N-Acetylhexosaminidase StrH Protein from <i>Streptococcus pneumoniae</i> R6. <i>Journal of Biological Chemistry</i> , 2011, 286, 43004-43012. | 3.4 | 29 |
| 45 | Crystal structure of the 30 K protein from the silkworm <i>Bombyx mori</i> reveals a new member of the β -trefoil superfamily. <i>Journal of Structural Biology</i> , 2011, 175, 97-103. | 2.8 | 29 |
| 46 | Structural insights into HetR \sim PatS interaction involved in cyanobacterial pattern formation. <i>Scientific Reports</i> , 2015, 5, 16470. | 3.3 | 29 |
| 47 | Structural insights into the substrate tunnel of <i>Saccharomyces cerevisiae</i> carbonic anhydrase Nce103. <i>BMC Structural Biology</i> , 2009, 9, 67. | 2.3 | 27 |
| 48 | Structures of yeast glutathione S-transferase Gtt2 reveal a new catalytic type of GST family. <i>EMBO Reports</i> , 2009, 10, 1320-1326. | 4.5 | 27 |
| 49 | Genomic Analysis of Mic1 Reveals a Novel Freshwater Long-Tailed Cyanophage. <i>Frontiers in Microbiology</i> , 2020, 11, 484. | 3.5 | 27 |
| 50 | Structural Plasticity of the Thioredoxin Recognition Site of Yeast Methionine S-Sulfoxide Reductase Mxr1. <i>Journal of Biological Chemistry</i> , 2011, 286, 13430-13437. | 3.4 | 26 |
| 51 | 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 |
| 52 | 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 |
| 53 | Crystal structure of <i>Saccharomyces cerevisiae</i> cytoplasmic thioredoxin reductase Trr1 reveals the structural basis for species-specific recognition of thioredoxin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 124-128. | 2.3 | 24 |
| 54 | 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 |

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| 55 | Molecular basis for the assembly of RuBisCO assisted by the chaperone Raf1. <i>Nature Plants</i> , 2020, 6, 708-717. | 9.3 | 24 |
| 56 | Structural and Biochemical Insights into the Multiple Functions of Yeast Grx3. <i>Journal of Molecular Biology</i> , 2018, 430, 1235-1248. | 4.2 | 23 |
| 57 | Structural and kinetic analysis of <i>Saccharomyces cerevisiae</i> thioredoxin Trx1: Implications for the catalytic mechanism of GSSG reduced by the thioredoxin system. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 1218-1223. | 2.3 | 22 |
| 58 | 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 |
| 59 | Structure of the gas vesicle protein GvpF from the cyanobacterium <i>Microcystis aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3013-3022. | 2.5 | 22 |
| 60 | Full-length structure of the major autolysin LytA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1373-1381. | 2.5 | 22 |
| 61 | Crystal Structure and Computational Analyses Provide Insights into the Catalytic Mechanism of 2,4-Diacetylphloroglucinol Hydrolase PhlG from <i>Pseudomonas fluorescens</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 4603-4611. | 3.4 | 21 |
| 62 | Capsid Structure of a Freshwater Cyanophage Siphoviridae Mic1. <i>Structure</i> , 2019, 27, 1508-1516.e3. | 3.3 | 21 |
| 63 | A structural genomics initiative on yeast proteins. <i>Journal of Synchrotron Radiation</i> , 2003, 10, 4-8. | 2.4 | 20 |
| 64 | Crystal structure of the yeast cytoplasmic thioredoxin Trx2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 246-249. | 2.6 | 20 |
| 65 | Comparative analyses of secreted proteins from the phytopathogenic fungus <i>Verticillium dahliae</i> in response to nitrogen starvation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 437-448. | 2.3 | 20 |
| 66 | Structural insights into repression of the <i>Pneumococcal</i> fatty acid synthesis pathway by repressor FabT and corepressor acyl-CoA:ACP. <i>FEBS Letters</i> , 2019, 593, 2730-2741. | 2.8 | 20 |
| 67 | Crystal structure of glutathione-dependent phospholipid peroxidase Hyr1 from the yeast <i>Saccharomyces cerevisiae</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 1058-1062. | 2.6 | 19 |
| 68 | The Paris-Sud yeast structural genomics pilot-project: from structure to function. <i>Biochimie</i> , 2004, 86, 617-623. | 2.6 | 18 |
| 69 | Structural Insights into the Substrate Specificity of a 6-Phospho- β -glucosidase BglA-2 from <i>Streptococcus pneumoniae</i> TIGR4. <i>Journal of Biological Chemistry</i> , 2013, 288, 14949-14958. | 3.4 | 18 |
| 70 | Crystal structure of juvenile hormone epoxide hydrolase from the silkworm <i>Bombyx mori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3224-3229. | 2.6 | 18 |
| 71 | 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 |
| 72 | Structure and transport mechanism of the human cholesterol transporter ABCG1. <i>Cell Reports</i> , 2022, 38, 110298. | 6.4 | 18 |

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| 73 | Crystal structure of the YGR205w protein from <i>Saccharomyces cerevisiae</i> : Close structural resemblance to <i>E. coli</i> pantothenate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 54, 776-783. | 2.6 | 17 |
| 74 | Structural insights into the catalytic mechanism of the yeast pyridoxal 5-phosphate synthase Snz1. <i>Biochemical Journal</i> , 2010, 432, 445-454. | 3.7 | 17 |
| 75 | Structures of human bile acid exporter ABCB11 reveal a transport mechanism facilitated by two tandem substrate-binding pockets. <i>Cell Research</i> , 2022, 32, 501-504. | 12.0 | 17 |
| 76 | Structural and mechanistic analyses of yeast mitochondrial thioredoxin Trx3 reveal putative function of its additional cysteine residues. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 716-721. | 2.3 | 16 |
| 77 | The pore-forming protein Aep1 is an innate immune molecule that prevents zebrafish from bacterial infection. <i>Developmental and Comparative Immunology</i> , 2018, 82, 49-54. | 2.3 | 16 |
| 78 | Structures of cyanobacterial bicarbonate transporter SbtA and its complex with PII-like SbtB. <i>Cell Discovery</i> , 2021, 7, 63. | 6.7 | 16 |
| 79 | Crystal structures and putative interface of <i>Saccharomyces cerevisiae</i> mitochondrial matrix proteins Mmf1 and Mam33. <i>Journal of Structural Biology</i> , 2011, 175, 469-474. | 2.8 | 15 |
| 80 | Structural insights into the activation of autoinhibited human lipid flippase ATP8B1 upon substrate binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118656119. | 7.1 | 15 |
| 81 | Identification and characterization of a silk gland-related matrix association region in <i>Bombyx mori</i> . <i>Gene</i> , 2001, 277, 139-144. | 2.2 | 14 |
| 82 | Structural basis for the different activities of yeast Grx1 and Grx2. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 1542-1547. | 2.3 | 14 |
| 83 | Structural insights into the cofactor-assisted substrate recognition of yeast quinone oxidoreductase Zta1. <i>Journal of Structural Biology</i> , 2011, 176, 112-118. | 2.8 | 14 |
| 84 | Crystal structures of Aflatoxin-oxidase from <i>Armillariella tabescens</i> reveal a dual activity enzyme. <i>Biochemical and Biophysical Research Communications</i> , 2017, 494, 621-625. | 2.1 | 14 |
| 85 | Cloning, Production, and Purification of Proteins for a Medium-Scale Structural Genomics Project. <i>Methods in Molecular Biology</i> , 2007, 363, 21-37. | 0.9 | 14 |
| 86 | Crystal structure of the YML079w protein from <i>Saccharomyces cerevisiae</i> reveals a new sequence family of the jelly-roll fold. <i>Protein Science</i> , 2009, 14, 209-215. | 7.6 | 13 |
| 87 | 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 |
| 88 | Structural basis of substrate recognition and translocation by human very long-chain fatty acid transporter ABCD1. <i>Nature Communications</i> , 2022, 13, . | 12.8 | 13 |
| 89 | Crystal structure and confirmation of the alanine:glyoxylate aminotransferase activity of the YFL030w yeast protein. <i>Biochimie</i> , 2005, 87, 1041-1047. | 2.6 | 12 |
| 90 | Structure-Guided Activity Enhancement and Catalytic Mechanism of Yeast Grx8. <i>Biochemistry</i> , 2014, 53, 2185-2196. | 2.5 | 12 |

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|-----|--|-----|-----------|
| 91 | Crystal structure of yeast monothiol glutaredoxin Grx6 in complex with a glutathione-coordinated [2Feâ€“2S] cluster. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 732-737. | 0.8 | 12 |
| 92 | 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 |
| 93 | Structural and enzymatic analyses of <i>Anabaena</i> heterocystâ€“specific alkaline invertase InvB. <i>FEBS Letters</i> , 2018, 592, 1589-1601. | 2.8 | 12 |
| 94 | The 62-kb upstream region of <i>Bombyx mori</i> fibroin heavy chain gene is clustered of repetitive elements and candidate matrix association regions. <i>Gene</i> , 2003, 312, 189-195. | 2.2 | 11 |
| 95 | Structure of the thioredoxin-fold domain of human phosphatidylethanolamine transferase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 67-70. | 0.7 | 11 |
| 96 | Crystal structures of holo and Cuâ€“deficient Cu/Znâ€“SOD from the silkworm <i>Bombyx mori</i> and the implications in amyotrophic lateral sclerosis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1999-2004. | 2.6 | 11 |
| 97 | Structural and Enzymatic Characterization of the Choline Kinase LicA from <i>Streptococcus pneumoniae</i> . <i>PLoS ONE</i> , 2015, 10, e0120467. | 2.5 | 11 |
| 98 | Crystal structure of <i>Arabidopsis</i> translation initiation factor eIFâ€“5A2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 736-740. | 2.6 | 10 |
| 99 | The N-Terminal Î²-Sheet of Peroxiredoxin 4 in the Large Yellow Croaker <i>Pseudosciaena crocea</i> Is Involved in Its Biological Functions. <i>PLoS ONE</i> , 2013, 8, e57061. | 2.5 | 10 |
| 100 | Structure-Guided Activity Restoration of the Silkworm Glutathione Transferase Omega GSTO3-3. <i>Journal of Molecular Biology</i> , 2011, 412, 204-211. | 4.2 | 9 |
| 101 | <i>Streptomyces coelicolor</i> SCO4226 Is a Nickel Binding Protein. <i>PLoS ONE</i> , 2014, 9, e109660. | 2.5 | 9 |
| 102 | Structure and assembly pattern of a freshwater short-tailed cyanophage Pam1. <i>Structure</i> , 2022, 30, 240-251.e4. | 3.3 | 9 |
| 103 | The gene expression profile of <i>Bombyx mori</i> silk gland. <i>Gene</i> , 2007, 396, 369-372. | 2.2 | 8 |
| 104 | Crystal structure of the dimeric Urm1 from the yeast <i>Saccharomyces cerevisiae</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1050-1055. | 2.6 | 8 |
| 105 | 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 |
| 106 | Unique Conformation in a Natural Interruption Sequence of Type XIX Collagen Revealed by Its High-Resolution Crystal Structure. <i>Biochemistry</i> , 2018, 57, 1087-1095. | 2.5 | 7 |
| 107 | The N-terminal polypeptide derived from viral macrophage inflammatory protein II reverses breast cancer epithelial-to-mesenchymal transition via a PDGFRÎ±-dependent mechanism. <i>Oncotarget</i> , 2017, 8, 37448-37463. | 1.8 | 7 |
| 108 | Biochemical and structural characterization of the cyanophageâ€“encoded phosphateâ€“binding protein: implications for enhanced phosphate uptake of infected cyanobacteria. <i>Environmental Microbiology</i> , 2022, 24, 3037-3050. | 3.8 | 7 |

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|-----|---|------|-----------|
| 109 | Structure of Ynk1 from the yeast <i>Saccharomyces cerevisiae</i> . Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 572-576. | 0.7 | 6 |
| 110 | Structures of Yeast Apa2 Reveal Catalytic Insights into a Canonical Ap4A Phosphorylase of the Histidine Triad Superfamily. Journal of Molecular Biology, 2013, 425, 2687-2698. | 4.2 | 6 |
| 111 | Structural insights into the catalysis and substrate specificity of cyanobacterial aspartate racemase McyF. Biochemical and Biophysical Research Communications, 2019, 514, 1108-1114. | 2.1 | 6 |
| 112 | Multi-functional regulator MapZ controls both positioning and timing of FtsZ polymerization. Biochemical Journal, 2019, 476, 1433-1444. | 3.7 | 6 |
| 113 | Expression, purification, crystallization and preliminary X-ray diffraction analysis of thioredoxin Trx1 from <i>Saccharomyces cerevisiae</i> . Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 323-325. | 0.7 | 5 |
| 114 | Structure and Catalytic Mechanism of Yeast 4-Amino-4-deoxychorismate Lyase. Journal of Biological Chemistry, 2013, 288, 22985-22992. | 3.4 | 5 |
| 115 | Structures of an all- α protein running along the DNA major groove. Nucleic Acids Research, 2016, 44, 3936-3945. | 14.5 | 5 |
| 116 | Complex structure reveals <i>CcmM</i> and <i>CcmN</i> form a heterotrimeric adaptor in α -carboxysome. Protein Science, 2021, 30, 1566-1576. | 7.6 | 5 |
| 117 | Expression, purification, crystallization and preliminary X-ray diffraction analysis of mitochondrial thioredoxin Trx3 from <i>Saccharomyces cerevisiae</i> . Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 1161-1163. | 0.7 | 4 |
| 118 | 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 |
| 119 | Structural and biochemical analyses of <i>Microcystis aeruginosa</i> 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 |
| 120 | Structural and enzymatic analyses of a glucosyltransferase Alr3699/HepE involved in <i>Anabaena</i> heterocyst envelop polysaccharide biosynthesis. Glycobiology, 2016, 26, 520-531. | 2.5 | 4 |
| 121 | Structural features of the aromatic/arginine constriction in the aquaglyceroporin GintAQP2 are responsible for glycerol impermeability in arbuscular mycorrhizal symbiosis. Fungal Biology, 2017, 121, 95-102. | 2.5 | 4 |
| 122 | Crystal structure of pentameric shell protein CsoS4B of <i>Halothiobacillus neapolitanus</i> α -carboxysome. Biochemical and Biophysical Research Communications, 2019, 515, 510-515. | 2.1 | 4 |
| 123 | Capsid Structure of <i>Anabaena</i> Cyanophage A-1(L). Journal of Virology, 2021, 95, e0135621. | 3.4 | 4 |
| 124 | Crystal structures of the apo and GDP-bound forms of a cupin-like protein BbDUF985 from <i>Branchiostoma belcheri tsingtauense</i> . Proteins: Structure, Function and Bioinformatics, 2010, 78, 2714-2719. | 2.6 | 3 |
| 125 | ATPase as a switch in P _{II} signal transduction. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12863-12864. | 7.1 | 3 |
| 126 | Activity Augmentation of Amphioxus Peptidoglycan Recognition Protein BbtPGRP3 via Fusion with a Chitin Binding Domain. PLoS ONE, 2015, 10, e0140953. | 2.5 | 3 |

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|-----|--|-----|-----------|
| 127 | Developments in Structural Genomics: Protein Purification and Function Interpretation. <i>Current Genomics</i> , 2004, 5, 37-48. | 1.6 | 3 |
| 128 | Purification, crystallization and preliminary X-ray analysis of glutathione peroxidase Gpx3 from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 593-596. | 0.7 | 2 |
| 129 | Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of hypothetical protein SCO4226 from <i>Streptomyces coelicolor</i> A3(2). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 847-850. | 0.7 | 2 |
| 130 | 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 |
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| 136 | Structural Comparison and Simulation of Pneumococcal Peptidoglycan Hydrolase LytB. <i>Methods in Molecular Biology</i> , 2016, 1440, 271-283. | 0.9 | 0 |
| 137 | Inhibition of <i>Streptococcus pneumoniae</i> growth by masarimycin. <i>Microbiology (United Kingdom)</i> , 2022, 168, . | 1.8 | 0 |
| 138 | Crystal Structure of the YDR533c <i>S. cerevisiae</i> Protein, a Class II Member of the Hsp31 Family. <i>Structure</i> , 2004, 12, 839-847. | 3.3 | 0 |