

Min Yao

List of Publications by Year in descending order

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198
papers

7,071
citations

71102

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71685

76
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200
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200
docs citations

200
times ranked

8378
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Redox-Coupled Crystal Structural Changes in Bovine Heart Cytochrome c Oxidase. <i>Science</i> , 1998, 280, 1723-1729. | 12.6 | 1,081 |
| 2 | The low-spin heme of cytochrome c oxidase as the driving element of the proton-pumping process. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15304-15309. | 7.1 | 414 |
| 3 | Roll: a new algorithm for the detection of protein pockets and cavities with a rolling probe sphere. <i>Bioinformatics</i> , 2010, 26, 46-52. | 4.1 | 295 |
| 4 | Insight into a natural Diels-Alder reaction from the structure of macrophomate synthase. <i>Nature</i> , 2003, 422, 185-189. | 27.8 | 187 |
| 5 | Structural reorganization of the bacterial cell-division protein FtsZ from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1175-1188. | 2.5 | 154 |
| 6 | Crystal structure of the octameric pore of staphylococcal β -hemolysin reveals the β -barrel pore formation mechanism by two components. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17314-17319. | 7.1 | 152 |
| 7 | Crystal structure of archaeal toxin-antitoxin RelE-RelB complex with implications for toxin activity and antitoxin effects. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 327-331. | 8.2 | 146 |
| 8 | The Structure of Rat Liver Vault at 3.5 Angstrom Resolution. <i>Science</i> , 2009, 323, 384-388. | 12.6 | 135 |
| 9 | Ammonia Channel Couples Glutaminase with Transamidase Reactions in GatCAB. <i>Science</i> , 2006, 312, 1954-1958. | 12.6 | 123 |
| 10 | Structure of bacterial cellulose synthase subunit D octamer with four inner passageways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17957-17961. | 7.1 | 118 |
| 11 | The crystal structure of human MRP14 (S100A9), a Ca ²⁺ -dependent regulator protein in inflammatory process. <i>Journal of Molecular Biology</i> , 2002, 316, 265-276. | 4.2 | 96 |
| 12 | Structural and Functional Analysis of a Glycoside Hydrolase Family 97 Enzyme from <i>Bacteroides thetaiotaomicron</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 36328-36337. | 3.4 | 87 |
| 13 | Molecular Basis for the Recognition of Long-chain Substrates by Plant β -Glucosidases. <i>Journal of Biological Chemistry</i> , 2013, 288, 19296-19303. | 3.4 | 83 |
| 14 | How Oligomerization Contributes to the Thermostability of an Archaeon Protein. <i>Journal of Biological Chemistry</i> , 2004, 279, 32957-32967. | 3.4 | 78 |
| 15 | Crystal structure of hypothetical protein TTHB192 from <i>Thermus thermophilus</i> HB8 reveals a new protein family with an RNA recognition motif-like domain. <i>Protein Science</i> , 2006, 15, 1494-1499. | 7.6 | 78 |
| 16 | Structural Basis for Multimeric Heme Complexation through a Specific Protein-Heme Interaction. <i>Journal of Biological Chemistry</i> , 2008, 283, 28649-28659. | 3.4 | 75 |
| 17 | Molecular basis of transmembrane beta-barrel formation of staphylococcal pore-forming toxins. <i>Nature Communications</i> , 2014, 5, 4897. | 12.8 | 75 |
| 18 | LAFIRE: software for automating the refinement process of protein-structure analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 189-196. | 2.5 | 71 |

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|----|--|------|-----------|
| 19 | Cellulose complementing factor (Ccp) is a new member of the cellulose synthase complex (terminal) Tj ETQq1 1 0.784314 rgBT /Over | 2.2 | 71 |
| 20 | Ribosomal protein S7: a new RNA-binding motif with structural similarities to a DNA architectural factor. <i>Structure</i> , 1997, 5, 1199-1208. | 3.3 | 66 |
| 21 | Structure of the type II-asparaginase from the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> at 2.16 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 294-301. | 2.5 | 63 |
| 22 | Structural analysis of the β -glucosidase HaG provides new insights into substrate specificity and catalytic mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1382-1391. | 2.5 | 63 |
| 23 | Structural and functional characterization of the LldR from <i>Corynebacterium glutamicum</i> : a transcriptional repressor involved in L-lactate and sugar utilization. <i>Nucleic Acids Research</i> , 2008, 36, 7110-7123. | 14.5 | 62 |
| 24 | Structural Change in FtsZ Induced by Intermolecular Interactions between Bound GTP and the T7 Loop. <i>Journal of Biological Chemistry</i> , 2014, 289, 3501-3509. | 3.4 | 62 |
| 25 | RNA helicase module in an acetyltransferase that modifies a specific tRNA anticodon. <i>EMBO Journal</i> , 2009, 28, 1362-1373. | 7.8 | 61 |
| 26 | An automatic diffraction data collection system with an imaging plate. <i>Journal of Applied Crystallography</i> , 1990, 23, 334-339. | 4.5 | 60 |
| 27 | The Three-Dimensional Structure of Septum Site-Determining Protein MinD from <i>Pyrococcus horikoshii</i> OT3 in Complex with Mg-ADP. <i>Structure</i> , 2001, 9, 817-826. | 3.3 | 58 |
| 28 | Crystal Structures of the Multidrug Binding Repressor <i>Corynebacterium glutamicum</i> CgmR in Complex with Inducers and with an Operator. <i>Journal of Molecular Biology</i> , 2010, 403, 174-184. | 4.2 | 58 |
| 29 | Molecular basis of dihydrouridine formation on tRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19593-19598. | 7.1 | 58 |
| 30 | Molecular basis of alanine discrimination in editing site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11669-11674. | 7.1 | 56 |
| 31 | 2-Methyl-2,4-pentanediol induces spontaneous assembly of staphylococcal α -hemolysin into heptameric pore structure. <i>Protein Science</i> , 2011, 20, 448-456. | 7.6 | 54 |
| 32 | Structural and mechanistic insights into guanylation of RNA-splicing ligase RtcB joining RNA between 3'-terminal phosphate and 5'-OH. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15235-15240. | 7.1 | 53 |
| 33 | Crystal Structure of 1-Aminocyclopropane-1-carboxylate Deaminase from <i>Hansenula saturnus</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 34557-34565. | 3.4 | 52 |
| 34 | Crystal Structure of the <i>Pyrococcus horikoshii</i> Isopropylmalate Isomerase Small Subunit Provides Insight into the Dual Substrate Specificity of the Enzyme. <i>Journal of Molecular Biology</i> , 2004, 344, 325-333. | 4.2 | 52 |
| 35 | Structure and Thermodynamics of the Extraordinarily Stable Molten Globule State of Canine Milk Lysozyme. <i>Biochemistry</i> , 2000, 39, 3248-3257. | 2.5 | 51 |
| 36 | Structural Basis for Translation Factor Recruitment to the Eukaryotic/Archaeal Ribosomes. <i>Journal of Biological Chemistry</i> , 2010, 285, 4747-4756. | 3.4 | 51 |

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|----|---|------|-----------|
| 37 | Structural Insights into the Epimerization of β -1,4-Linked Oligosaccharides Catalyzed by Cellobiose 2-Epimerase, the Sole Enzyme Epimerizing Non-anomeric Hydroxyl Groups of Unmodified Sugars. <i>Journal of Biological Chemistry</i> , 2014, 289, 3405-3415. | 3.4 | 49 |
| 38 | Structure of the Monomeric Isocitrate Dehydrogenase. <i>Structure</i> , 2002, 10, 1637-1648. | 3.3 | 48 |
| 39 | Archaeal ribosomal stalk protein interacts with translation factors in a nucleotide-independent manner via its conserved C terminus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3748-3753. | 7.1 | 48 |
| 40 | Structural basis for pore-forming mechanism of staphylococcal α -hemolysin. <i>Toxicon</i> , 2015, 108, 226-231. | 1.6 | 48 |
| 41 | Structural characterization of the <i>Acetobacter xylinum</i> endo- β -1,4-glucanase CMCax required for cellulose biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 1069-1077. | 2.6 | 47 |
| 42 | Structure of archaeal translational initiation factor 2 β -GDP reveals significant conformational change of the β -subunit and switch 1 region. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13016-13021. | 7.1 | 45 |
| 43 | Structural implications for heavy metal-induced reversible assembly and aggregation of a protein: the case of <i>Pyrococcus horikoshii</i> CutA1. <i>FEBS Letters</i> , 2004, 556, 167-174. | 2.8 | 43 |
| 44 | Snapshots of Dynamics in Synthesizing 6 -Isopentenyladenosine at the tRNA Anticodon. <i>Biochemistry</i> , 2009, 48, 5057-5065. | 2.5 | 43 |
| 45 | Directed Evolution and Structural Analysis of NADPH-Dependent Acetoacetyl Coenzyme A (Acetoacetyl-CoA) Reductase from <i>Ralstonia eutropha</i> Reveals Two Mutations Responsible for Enhanced Kinetics. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6134-6139. | 3.1 | 43 |
| 46 | The c-di-GMP recognition mechanism of the PilZ domain of bacterial cellulose synthase subunit A. <i>Biochemical and Biophysical Research Communications</i> , 2013, 431, 802-807. | 2.1 | 42 |
| 47 | Structural and functional analysis of the Rpf2-Rrs1 complex in ribosome biogenesis. <i>Nucleic Acids Research</i> , 2015, 43, 4746-4757. | 14.5 | 42 |
| 48 | Crystal Structure of the Monomeric Isocitrate Dehydrogenase in the Presence of NADP ⁺ . <i>Journal of Biological Chemistry</i> , 2003, 278, 36897-36904. | 3.4 | 41 |
| 49 | Crystal structure of BinB: A receptor binding component of the binary toxin from <i>Lysinibacillus sphaericus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2703-2712. | 2.6 | 41 |
| 50 | Crystal Structure of a Ribonuclease P Protein Ph1601p from <i>Pyrococcus horikoshii</i> OT3: An Archaeal Homologue of Human Nuclear Ribonuclease P Protein Rpp21. <i>Biochemistry</i> , 2005, 44, 12086-12093. | 2.5 | 40 |
| 51 | The structure of alanyl-tRNA synthetase with editing domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11028-11033. | 7.1 | 40 |
| 52 | Structural and Mutational Analyses of Drp35 from <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 5770-5780. | 3.4 | 39 |
| 53 | Crystal structure of <i>Ruminococcus albus</i> cellobiose 2-epimerase: Structural insights into epimerization of unmodified sugar. <i>FEBS Letters</i> , 2013, 587, 840-846. | 2.8 | 39 |
| 54 | Crystal Structure of Hyperthermophilic Archaeal Initiation Factor 5A: A Homologue of Eukaryotic Initiation Factor 5A (eIF-5A). <i>Journal of Biochemistry</i> , 2003, 133, 75-81. | 1.7 | 38 |

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|----|---|------|-----------|
| 55 | Crystal structure of hypothetical protein PH0642 from <i>Pyrococcus horikoshii</i> at 1.6Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 869-873. | 2.6 | 38 |
| 56 | Structural and Enzymatic Properties of 1-Aminocyclopropane-1-carboxylate Deaminase Homologue from <i>Pyrococcus horikoshii</i> . <i>Journal of Molecular Biology</i> , 2004, 341, 999-1013. | 4.2 | 37 |
| 57 | Biochemical and structural characterization of oxygen-sensitive 2-thiouridine synthesis catalyzed by an iron-sulfur protein TtuA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4954-4959. | 7.1 | 37 |
| 58 | X-ray structure of azide-bound fully oxidized cytochromecoxidase from bovine heart at 2.9Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 529-535. | 2.5 | 36 |
| 59 | DNA Recognition Mechanism of the ONECUT Homeodomain of Transcription Factor HNF-6. <i>Structure</i> , 2007, 15, 75-83. | 3.3 | 35 |
| 60 | Cellulose production by <i>Enterobacter</i> sp. CJF-002 and identification of genes for cellulose biosynthesis. <i>Cellulose</i> , 2012, 19, 1989-2001. | 4.9 | 35 |
| 61 | Molecular insights into the interaction of the ribosomal stalk protein with elongation factor 1 β . <i>Nucleic Acids Research</i> , 2014, 42, 14042-14052. | 14.5 | 35 |
| 62 | The CGL2612 Protein from <i>Corynebacterium glutamicum</i> Is a Drug Resistance-related Transcriptional Repressor. <i>Journal of Biological Chemistry</i> , 2005, 280, 38711-38719. | 3.4 | 33 |
| 63 | Crystal structure of an RtcB homolog protein (PH1602-extein protein) from <i>Pyrococcus horikoshii</i> reveals a novel fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 1119-1122. | 2.6 | 33 |
| 64 | Structure of the <i>Pseudomonas aeruginosa</i> transamidosome reveals unique aspects of bacterial tRNA-dependent asparagine biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 382-387. | 7.1 | 33 |
| 65 | Reaction Intermediate Structures of 1-Aminocyclopropane-1-carboxylate Deaminase. <i>Journal of Biological Chemistry</i> , 2003, 278, 41069-41076. | 3.4 | 31 |
| 66 | Structure of the catalytic nucleotide-binding subunit A of A-type ATP synthase from <i>Pyrococcus horikoshii</i> reveals a novel domain related to the peripheral stalk. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 483-488. | 2.5 | 31 |
| 67 | Crystal Structure of the Ectodomain of Human Fc γ RI. <i>Journal of Biological Chemistry</i> , 2003, 278, 27966-27970. | 3.4 | 30 |
| 68 | Crystal Structure of the 3.8-MDa Respiratory Supermolecule Hemocyanin at 3.0Å... Resolution. <i>Structure</i> , 2015, 23, 2204-2212. | 3.3 | 29 |
| 69 | Structural Analysis of an Insect Lysozyme Exhibiting Catalytic Efficiency at Low Temperatures. <i>Biochemistry</i> , 2002, 41, 12086-12092. | 2.5 | 28 |
| 70 | Crystal structure of the flexible tandem repeat domain of bacterial cellulose synthesis subunit C. <i>Scientific Reports</i> , 2017, 7, 13018. | 3.3 | 28 |
| 71 | pH regulates pore formation of a protease activated Vip3Aa from <i>Bacillus thuringiensis</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017, 1859, 2234-2241. | 2.6 | 28 |
| 72 | ID14 'Quadriga', a Beamline for Protein Crystallography at the ESRF. <i>Journal of Synchrotron Radiation</i> , 1998, 5, 215-221. | 2.4 | 27 |

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|----|---|------|-----------|
| 73 | A Helical String of Alternately Connected Three-Helix Bundles for the Cell Wall-Associated Adhesion Protein Ehb from <i>Staphylococcus aureus</i> . <i>Structure</i> , 2008, 16, 488-496. | 3.3 | 27 |
| 74 | <i>Staphylococcus aureus</i> surface protein SasG contributes to intercellular autoaggregation of <i>Staphylococcus aureus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2008, 377, 1102-1106. | 2.1 | 27 |
| 75 | Catalytic Mechanism of Retaining α -Galactosidase Belonging to Glycoside Hydrolase Family 97. <i>Journal of Molecular Biology</i> , 2009, 392, 1232-1241. | 4.2 | 27 |
| 76 | The C-terminal helix of ribosomal P stalk recognizes a hydrophobic groove of elongation factor 2 in a novel fashion. <i>Nucleic Acids Research</i> , 2018, 46, 3232-3244. | 14.5 | 27 |
| 77 | Function and structure of GH13_31 α -glucosidase with high α -glucosidic linkage specificity and transglucosylation activity. <i>FEBS Letters</i> , 2018, 592, 2268-2281. | 2.8 | 27 |
| 78 | Crystal Structures of the Ribonuclease MC1 from Bitter Gourd Seeds, Complexed with 2α -UMP or 3α -UMP, Reveal Structural Basis for Uridine Specificity. <i>Biochemical and Biophysical Research Communications</i> , 2000, 275, 572-576. | 2.1 | 26 |
| 79 | Two distinct regions in <i>Staphylococcus aureus</i> GatCAB guarantee accurate tRNA recognition. <i>Nucleic Acids Research</i> , 2010, 38, 672-682. | 14.5 | 26 |
| 80 | Asymmetric Trimeric Ring Structure of the Nucleocapsid Protein of Tosopovirus. <i>Journal of Virology</i> , 2017, 91, . | 3.4 | 26 |
| 81 | Structural basis of reverse nucleotide polymerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20970-20975. | 7.1 | 25 |
| 82 | Crystal structure of the regulatory subunit of archaeal initiation factor 2B (aIF2B) from hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT3: a proposed structure of the regulatory subcomplex of eukaryotic IF2B. <i>Biochemical and Biophysical Research Communications</i> , 2004, 319, 725-732. | 2.1 | 24 |
| 83 | The loop structure of <i>Actinomycete</i> glycoside hydrolase family 5 mannanases governs substrate recognition. <i>FEBS Journal</i> , 2015, 282, 4001-4014. | 4.7 | 24 |
| 84 | Detailed analysis of RNA-protein interactions within the bacterial ribosomal protein L5/5S rRNA complex. <i>Rna</i> , 2002, 8, 1548-57. | 3.5 | 22 |
| 85 | In-crystal affinity ranking of fragment hit compounds reveals a relationship with their inhibitory activities. <i>Journal of Applied Crystallography</i> , 2011, 44, 798-804. | 4.5 | 21 |
| 86 | Structures of AzrA and of AzrC complexed with substrate or inhibitor: insight into substrate specificity and catalytic mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 553-564. | 2.5 | 21 |
| 87 | Biochemical and structural characterization of <i>Marinomonas mediterranea</i> d-mannose isomerase Marme_2490 phylogenetically distant from known enzymes. <i>Biochimie</i> , 2018, 144, 63-73. | 2.6 | 21 |
| 88 | Ribosomal protein L5 has a highly twisted concave surface and flexible arms responsible for rRNA binding. <i>Rna</i> , 2001, 7, 692-701. | 3.5 | 19 |
| 89 | Crystal structure analysis reveals a novel forkhead-associated domain of ESAT-6 secretion system C protein in <i>Staphylococcus aureus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 659-664. | 2.6 | 19 |
| 90 | Structural and mutational analyses of the receptor binding domain of botulinum D/C mosaic neurotoxin: Insight into the ganglioside binding mechanism. <i>Biochemical and Biophysical Research Communications</i> , 2011, 411, 433-439. | 2.1 | 19 |

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|-----|--|------|-----------|
| 91 | Efficient synthesis of Î±-galactosyl oligosaccharides using a mutant <i>Bacteroides thetaiotaomicron</i> retaining Î±-galactosidase (GH₉₇). <i>FEBS Journal</i> , 2017, 284, 766-783. | 4.7 | 19 |
| 92 | The X-ray crystal structure of pyrrolidone-carboxylate peptidase from hyperthermophilic archaea <i>Pyrococcus horikoshii</i> . <i>Journal of Structural and Functional Genomics</i> , 2002, 2, 145-154. | 1.2 | 18 |
| 93 | Structural evidence for guanidineâ€“protein side chain interactions: crystal structure of CutA from <i>Pyrococcus horikoshii</i> in 3M guanidine hydrochloride. <i>Biochemical and Biophysical Research Communications</i> , 2004, 323, 185-191. | 2.1 | 18 |
| 94 | Crystal structures of the UDP-diacylglucosamine pyrophosphohydrolase LpxH from <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2016, 6, 32822. | 3.3 | 18 |
| 95 | Inulin with a low degree of polymerization protects human umbilical vein endothelial cells from hypoxia/reoxygenation-induced injury. <i>Carbohydrate Polymers</i> , 2019, 216, 97-106. | 10.2 | 18 |
| 96 | Amino Acid Residues in Ribonuclease MC1 from Bitter Gourd Seeds Which Are Essential for Uridine Specificity. <i>Biochemistry</i> , 2001, 40, 524-530. | 2.5 | 17 |
| 97 | Crystal structure of the functional region of Uroâ€“adherence factor A from <i>Staphylococcus saprophyticus</i> reveals participation of the B domain in ligand binding. <i>Protein Science</i> , 2011, 20, 406-416. | 7.6 | 17 |
| 98 | X-ray structures of eIF5B and the eIF5Bâ€“eIF1A complex: the conformational flexibility of eIF5B is restricted on the ribosome by interaction with eIF1A. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3090-3098. | 2.5 | 17 |
| 99 | Ancient translation factor is essential for tRNA-dependent cysteine biosynthesis in methanogenic archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10520-10525. | 7.1 | 17 |
| 100 | Structural insights into the catalytic reaction that is involved in the reorientation of Trp238 at the substrateâ€“binding site in GH13 dextran glucosidase. <i>FEBS Letters</i> , 2015, 589, 484-489. | 2.8 | 17 |
| 101 | The [4Fe-4S] cluster of sulfurtransferase TtuA desulfurizes TtuB during tRNA modification in <i>Thermus thermophilus</i> . <i>Communications Biology</i> , 2020, 3, 168. | 4.4 | 17 |
| 102 | Crystal Structures of the Ribonuclease MC1 Mutants N71T and N71S in Complex with 5â€“GMP:Â Structural Basis for Alterations in Substrate Specificityâ€. <i>Biochemistry</i> , 2003, 42, 5270-5278. | 2.5 | 16 |
| 103 | Structure analysis of geranyl pyrophosphate methyltransferase and the proposed reaction mechanism of SAM-dependent C-methylation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1558-1569. | 2.5 | 16 |
| 104 | Cellulose-synthesizing machinery in bacteria. <i>Cellulose</i> , 2022, 29, 2755-2777. | 4.9 | 16 |
| 105 | Crystal structure of the ATP-binding cassette of multisugar transporter from <i>Pyrococcus horikoshii</i> OT3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 635-638. | 2.6 | 15 |
| 106 | New algorithm for protein model building: extending a partial model in a map segment. <i>Journal of Applied Crystallography</i> , 2006, 39, 57-63. | 4.5 | 15 |
| 107 | A novel glycoside hydrolase family 97 enzyme: Bifunctional Î²-L-arabinopyranosidase/Î±-galactosidase from <i>Bacteroides thetaiotaomicron</i> . <i>Biochimie</i> , 2017, 142, 41-50. | 2.6 | 15 |
| 108 | Structure of macrophomate synthase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1187-1197. | 2.5 | 14 |

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|-----|--|------|-----------|
| 109 | SCO4008, a Putative TetR Transcriptional Repressor from <i>Streptomyces coelicolor</i> A3(2), Regulates Transcription of sco4007 by Multidrug Recognition. <i>Journal of Molecular Biology</i> , 2013, 425, 3289-3300. | 4.2 | 14 |
| 110 | Direct interaction between EFL1 and SBDS is mediated by an intrinsically disordered insertion domain. <i>Biochemical and Biophysical Research Communications</i> , 2014, 443, 1251-1256. | 2.1 | 14 |
| 111 | Production and crystallization of lobster muscle tropomyosin expressed in Sf9 cells. <i>FEBS Letters</i> , 1996, 394, 201-205. | 2.8 | 13 |
| 112 | Structural insights into the difference in substrate recognition of two mannoside phosphorylases from two GH130 subfamilies. <i>FEBS Letters</i> , 2016, 590, 828-837. | 2.8 | 13 |
| 113 | Structural basis for recognition of a kink-turn motif by an archaeal homologue of human RNase P protein Rpp38. <i>Biochemical and Biophysical Research Communications</i> , 2016, 474, 541-546. | 2.1 | 13 |
| 114 | Encapsulation of biomacromolecules by soaking and co-crystallization into porous protein crystals of hemocyanin. <i>Biochemical and Biophysical Research Communications</i> , 2019, 509, 577-584. | 2.1 | 13 |
| 115 | Structure analysis of PH1161 protein, a transcriptional activator TenA homologue from the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1094-1100. | 2.5 | 12 |
| 116 | Structural and functional analysis of the TetR-family transcriptional regulator SCO0332 from <i>Streptomyces coelicolor</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 198-205. | 2.5 | 12 |
| 117 | Structure of dihydrouridine synthase C (DusC) from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 834-838. | 0.7 | 12 |
| 118 | Catalytic role of the calcium ion in GH97 inverting glycoside hydrolase. <i>FEBS Letters</i> , 2014, 588, 3213-3217. | 2.8 | 12 |
| 119 | Production, crystallization, and preliminary X-ray analysis of rabbit skeletal muscle troponin complex consisting of troponin C and fragment (1-47) of troponin I. <i>Protein Science</i> , 1997, 6, 916-918. | 7.6 | 11 |
| 120 | Deduced RNA binding mechanism of Thil based on structural and binding analyses of a minimal RNA ligand. <i>Rna</i> , 2009, 15, 1498-1506. | 3.5 | 11 |
| 121 | Molecular dissection of the silkworm ribosomal stalk complex: the role of multiple copies of the stalk proteins. <i>Nucleic Acids Research</i> , 2013, 41, 3635-3643. | 14.5 | 11 |
| 122 | Structural Advantage of Sugar Beet β -Glucosidase to Stabilize the Michaelis Complex with Long-chain Substrate. <i>Journal of Biological Chemistry</i> , 2015, 290, 1796-1803. | 3.4 | 11 |
| 123 | Template-dependent nucleotide addition in the reverse (3' to 5') direction by Thg1-like protein. <i>Science Advances</i> , 2016, 2, e1501397. | 10.3 | 11 |
| 124 | Crystal structure of human p120 homologue protein PH1374 from <i>Pyrococcus horikoshii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 54, 814-816. | 2.6 | 10 |
| 125 | Molecular properties of two proteins homologous to PduO-type ATP:cob(I)alamin adenosyltransferase from <i>Sulfolobus tokodaii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 446-457. | 2.6 | 10 |
| 126 | The structures of transcription factor CGL2947 from <i>Corynebacterium glutamicum</i> in two crystal forms: A novel homodimer assembling and the implication for effector binding mode. <i>Protein Science</i> , 2007, 16, 1878-1886. | 7.6 | 9 |

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