

# Min Yao

## List of Publications by Year in descending order

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198  
papers

7,071  
citations

71102

41  
h-index

71685

76  
g-index

200  
all docs

200  
docs citations

200  
times ranked

8378  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cellulose-synthesizing machinery in bacteria. <i>Cellulose</i> , 2022, 29, 2755-2777.	4.9	16
2	Structural snapshot of a glycoside hydrolase family 8 endo- $\beta$ -1,4-glucanase capturing the state after cleavage of the scissile bond. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 228-237.	2.3	0
3	Dynamic control of microbial movement by photoswitchable ATP antagonists. <i>Chemistry - A European Journal</i> , 2022, , .	3.3	1
4	Substrate specificity of glycoside hydrolase family 1 $\beta$ -glucosidase AtBGlu42 from <i>Arabidopsis thaliana</i> and its molecular mechanism. <i>Bioscience, Biotechnology and Biochemistry</i> , 2022, 86, 231-245.	1.3	3
5	Molecular Dynamics Simulation of Cellulose Synthase Subunit D Octamer with Cellulose Chains from Acetic Acid Bacteria: Insight into Dynamic Behaviors and Thermodynamics on Substrate Recognition. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 488-496.	5.3	8
6	Structural insights reveal the second base catalyst of isomaltose glucohydrolase. <i>FEBS Journal</i> , 2021, , .	4.7	0
7	Crystal structures clarify cofactor binding of plant tyrosine decarboxylase. <i>Biochemical and Biophysical Research Communications</i> , 2020, 523, 500-505.	2.1	7
8	Biophysical research in Hokkaido University, Japan. <i>Biophysical Reviews</i> , 2020, 12, 233-236.	3.2	3
9	Flexible NAD <sup>+</sup> Binding in Deoxyhypusine Synthase Reflects the Dynamic Hypusine Modification of Translation Factor IF5A. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5509.	4.1	4
10	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
11	Crystallographic analysis of Eisenia hydrolysis-enhancing protein using a long wavelength for native-SAD phasing. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 20-24.	0.8	5
12	A solution-free crystal-mounting platform for native SAD. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 938-945.	2.3	5
13	Cellulose Synthesis in an Acetic Acid Bacterium: Closing in on the Secret Behind an Ultra-Precision Nanomachine Spinning a Cellulose Nanofiber. <i>Kagaku To Seibutsu</i> , 2020, 58, 453-460.	0.0	0
14	The pH-dependent conformational change of eukaryotic translation initiation factor 5: Insights into partner-binding manner. <i>Biochemical and Biophysical Research Communications</i> , 2019, 519, 186-191.	2.1	0
15	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
16	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
17	Neutron crystallographic study of heterotrimeric glutamine amidotransferase CAB. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 193-196.	0.8	2
18	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

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19	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
20	Function and structure of GH13_31 Î±-glucosidase with high (1â€²4)-glucosidic linkage specificity and transglucosylation activity. <i>FEBS Letters</i> , 2018, 592, 2268-2281.	2.8	27
21	Efficient synthesis of Î±-galactosyl oligosaccharides using a mutant <i>Bacteroides thetaiotaomicron</i> retaining Î±-galactosidase (<i>Bt</i> GH97b). <i>FEBS Journal</i> , 2017, 284, 766-783.	4.7	19
22	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
23	Crystal structure of the flexible tandem repeat domain of bacterial cellulose synthesis subunit C. <i>Scientific Reports</i> , 2017, 7, 13018.	3.3	28
24	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
25	Asymmetric Trimeric Ring Structure of the Nucleocapsid Protein of Tospovirus. <i>Journal of Virology</i> , 2017, 91, .	3.4	26
26	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
27	Structural basis for tRNA-dependent cysteine biosynthesis. <i>Nature Communications</i> , 2017, 8, 1521.	12.8	6
28	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
29	Template-dependent nucleotide addition in the reverse (3â€²-5â€²) direction by Thg1-like protein. <i>Science Advances</i> , 2016, 2, e1501397.	10.3	11
30	Structure Determination Software for Macromolecular X-Ray Crystallography. <i>Springer Protocols</i> , 2016, , 293-314.	0.3	0
31	Crystallographic analysis of a subcomplex of the transsulfurase with tRNA for Cys-tRNA <sup>Cys</sup> synthesis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 569-572.	0.8	3
32	Crystallographic study of the 2-thioribothymidine-synthetic complex TtuA-TtuB from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 777-781.	0.8	5
33	Crystal structures of the UDP-diacetylglucosamine pyrophosphohydrolase LpxH from <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2016, 6, 32822.	3.3	18
34	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
35	The loop structure of <i>Actinomyces</i> glycoside hydrolase family 5 mannanases governs substrate recognition. <i>FEBS Journal</i> , 2015, 282, 4001-4014.	4.7	24
36	Structural and functional analysis of the Rpf2-Rrs1 complex in ribosome biogenesis. <i>Nucleic Acids Research</i> , 2015, 43, 4746-4757.	14.5	42

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37	Crystallization and preliminary X-ray crystallographic study of a 3.8-MDa respiratory supermolecule hemocyanin. <i>Journal of Structural Biology</i> , 2015, 190, 379-382.	2.8	9
38	Structural analysis of the Î±-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
39	Structural insights into the catalytic reaction that is involved in the reorientation of Trp238 at the substrate-binding site in GH13 dextran glucosidase. <i>FEBS Letters</i> , 2015, 589, 484-489.	2.8	17
40	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
41	Structural Advantage of Sugar Beet Î±-Glucosidase to Stabilize the Michaelis Complex with Long-chain Substrate. <i>Journal of Biological Chemistry</i> , 2015, 290, 1796-1803.	3.4	11
42	Crystal Structure of the 3.8-MDa Respiratory Supermolecule Hemocyanin at 3.0Å... Resolution. <i>Structure</i> , 2015, 23, 2204-2212.	3.3	29
43	Structural basis for pore-forming mechanism of staphylococcal Î±-hemolysin. <i>Toxicon</i> , 2015, 108, 226-231.	1.6	48
44	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
45	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
46	X-ray structures of eIF5B and the eIF5B-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
47	Molecular insights into the interaction of the ribosomal stalk protein with elongation factor 1Î±. <i>Nucleic Acids Research</i> , 2014, 42, 14042-14052.	14.5	35
48	Crystallization and preliminary X-ray crystallographic analysis of Î±-glucosidase HaG from <i>Halomonas</i> sp. strain H11. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 464-466.	0.8	4
49	Structural Insights into the Epimerization of Î²-1,4-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
50	Anchoring protein crystals to mounting loops with hydrogel using inkjet technology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2794-2799.	2.5	2
51	Crystallization and preliminary X-ray crystallographic analysis of a bacterial Asn-transamidosome. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 790-793.	0.8	3
52	Crystallization and preliminary X-ray crystallographic analysis of ribosome assembly factors: the Rpf2-Rrs1 complex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1649-1652.	0.8	4
53	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
54	Molecular basis of transmembrane beta-barrel formation of staphylococcal pore-forming toxins. <i>Nature Communications</i> , 2014, 5, 4897.	12.8	75

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55	Structural and genomic DNA analysis of the putative TetR transcriptional repressor SCO7518 from <i>Streptomyces coelicolor</i> A3(2). FEBS Letters, 2014, 588, 4311-4318.	2.8	7
56	Catalytic role of the calcium ion in GH97 inverting glycoside hydrolase. FEBS Letters, 2014, 588, 3213-3217.	2.8	12
57	Ancient translation factor is essential for tRNA-dependent cysteine biosynthesis in methanogenic archaea. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10520-10525.	7.1	17
58	Direct interaction between EFL1 and SBDS is mediated by an intrinsically disordered insertion domain. Biochemical and Biophysical Research Communications, 2014, 443, 1251-1256.	2.1	14
59	Crystal structure of <i>Ruminococcus albus</i> cellobiose 2-epimerase: Structural insights into epimerization of unmodified sugar. FEBS Letters, 2013, 587, 840-846.	2.8	39
60	The c-di-GMP recognition mechanism of the PilZ domain of bacterial cellulose synthase subunit A. Biochemical and Biophysical Research Communications, 2013, 431, 802-807.	2.1	42
61	Cellulose complementing factor (Ccp) is a new member of the cellulose synthase complex (terminal) Tj ETQq1 1 0.784314 rgBT /Over	2.2	71
62	Structural and genomic DNA analysis of a putative transcription factor SCO5550 from <i>Streptomyces coelicolor</i> A3(2): Regulating the expression of gene sco5551 as a transcriptional activator with a novel dimer shape. Biochemical and Biophysical Research Communications, 2013, 435, 28-33.	2.1	3
63	SCO4008, a Putative TetR Transcriptional Repressor from <i>Streptomyces coelicolor</i> A3(2), Regulates Transcription of sco4007 by Multidrug Recognition. Journal of Molecular Biology, 2013, 425, 3289-3300.	4.2	14
64	Crystallization and preliminary X-ray crystallographic analysis of the functional form of BinB binary toxin from <i>Bacillus sphaericus</i> . Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 170-173.	0.7	3
65	Preliminary X-ray crystallographic study of staphylococcal $\beta$ -haemolysin monomer. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 868-870.	0.7	2
66	Molecular dissection of the silkworm ribosomal stalk complex: the role of multiple copies of the stalk proteins. Nucleic Acids Research, 2013, 41, 3635-3643.	14.5	11
67	New model-fitting and model-completion programs for automated iterative nucleic acid refinement. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1171-1179.	2.5	7
68	Crystal structure analysis, overexpression and refolding behaviour of a DING protein with single mutation. Journal of Synchrotron Radiation, 2013, 20, 854-858.	2.4	4
69	Expression, purification, crystallization and preliminary X-ray crystallographic study of the nucleocapsid protein of Tomato spotted wilt virus. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 700-703.	0.7	3
70	Structure of dihydrouridine synthase C (DusC) from <i>Escherichia coli</i> . Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 834-838.	0.7	12
71	Molecular Basis for the Recognition of Long-chain Substrates by Plant $\beta$ -Glucosidases. Journal of Biological Chemistry, 2013, 288, 19296-19303.	3.4	83
72	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. Applied and Environmental Microbiology, 2013, 79, 6134-6139.	3.1	43

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73	Structural basis of reverse nucleotide polymerization. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20970-20975.	7.1	25
74	Crystal Structure of a Putative Methyltransferase SAV1081 from <i>Staphylococcus aureus</i> . Protein and Peptide Letters, 2013, 20, 530-537.	0.9	3
75	Structural and mechanistic insights into guanylation of RNA-splicing ligase RtcB joining RNA between 3' terminal phosphate and 5' OH. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15235-15240.	7.1	53
76	Archaeal ribosomal stalk protein interacts with translation factors in a nucleotide-independent manner via its conserved C terminus. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3748-3753.	7.1	48
77	Structural reorganization of the bacterial cell-division protein FtsZ from <i>Staphylococcus aureus</i> . Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1175-1188.	2.5	154
78	The binding mechanism of eIF2 <sup>2</sup> with its partner proteins, eIF5 and eIF2B $\mu$ . Biochemical and Biophysical Research Communications, 2012, 423, 515-519.	2.1	3
79	Structure analysis of geranyl pyrophosphate methyltransferase and the proposed reaction mechanism of SAM-dependent C-methylation. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1558-1569.	2.5	16
80	Cellulose production by <i>Enterobacter</i> sp. CJF-002 and identification of genes for cellulose biosynthesis. Cellulose, 2012, 19, 1989-2001.	4.9	35
81	Flavin-binding of azoreductase: Direct evidences for dual-binding property of apo-azoreductase with FMN and FAD. Journal of Molecular Catalysis B: Enzymatic, 2012, 74, 204-208.	1.8	7
82	Structural and mutational analyses of the receptor binding domain of botulinum D/C mosaic neurotoxin: Insight into the ganglioside binding mechanism. Biochemical and Biophysical Research Communications, 2011, 411, 433-439.	2.1	19
83	In-crystal affinity ranking of fragment hit compounds reveals a relationship with their inhibitory activities. Journal of Applied Crystallography, 2011, 44, 798-804.	4.5	21
84	Crystallization and preliminary X-ray crystallographic study of a methyltransferase involved in 2-methylisoborneol biosynthesis in <i>Streptomyces lasaliensis</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 417-420.	0.7	5
85	Crystallization and preliminary X-ray crystallographic analysis of dihydrouridine synthase from <i>Thermus thermophilus</i> and its complex with tRNA. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 685-688.	0.7	2
86	Crystallization and preliminary X-ray crystallographic analysis of eIF5B <sup>N</sup> and the eIF5B <sup>N</sup> -eIF1A <sup>N</sup> complex. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 730-733.	0.7	3
87	Crystallization and preliminary X-ray structure analysis of human ribosomal protein L30e. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1516-1518.	0.7	1
88	Crystal structure of the functional region of Urokinase adherence factor A from <i>Staphylococcus saprophyticus</i> reveals participation of the B domain in ligand binding. Protein Science, 2011, 20, 406-416.	7.6	17
89	2-Methyl-2,4-pentanediol induces spontaneous assembly of staphylococcal $\beta$ -hemolysin into heptameric pore structure. Protein Science, 2011, 20, 448-456.	7.6	54
90	Molecular basis of dihydrouridine formation on tRNA. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19593-19598.	7.1	58

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91	Crystal structure of the octameric pore of staphylococcal $\beta$ -hemolysin reveals the $\beta$ -barrel pore formation mechanism by two components. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17314-17319.	7.1	152
92	In-crystal chemical ligation for lead compound generation. Journal of Applied Crystallography, 2010, 43, 1329-1337.	4.5	8
93	Crystallization and preliminary X-ray studies of azoreductases from <i>Bacillus</i> sp. B29. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 503-505.	0.7	5
94	Preliminary X-ray crystallographic study of the receptor-binding domain of the D/C mosaic neurotoxin from <i>Clostridium botulinum</i> . Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 608-610.	0.7	4
95	Structure of bacterial cellulose synthase subunit D octamer with four inner passageways. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17957-17961.	7.1	118
96	Two distinct regions in <i>Staphylococcus aureus</i> GatCAB guarantee accurate tRNA recognition. Nucleic Acids Research, 2010, 38, 672-682.	14.5	26
97	Structural Basis for Translation Factor Recruitment to the Eukaryotic/Archaeal Ribosomes. Journal of Biological Chemistry, 2010, 285, 4747-4756.	3.4	51
98	Roll: a new algorithm for the detection of protein pockets and cavities with a rolling probe sphere. Bioinformatics, 2010, 26, 46-52.	4.1	295
99	Crystal Structures of the Multidrug Binding Repressor <i>Corynebacterium glutamicum</i> CgmR in Complex with Inducers and with an Operator. Journal of Molecular Biology, 2010, 403, 174-184.	4.2	58
100	Deduced RNA binding mechanism of Thil based on structural and binding analyses of a minimal RNA ligand. Rna, 2009, 15, 1498-1506.	3.5	11
101	The structure of alanyl-tRNA synthetase with editing domain. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11028-11033.	7.1	40
102	Cloning, expression, purification and preliminary crystallographic studies of the adenylate/uridylate-rich element-binding protein HuR complexed with its target RNA. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 285-287.	0.7	3
103	RNA helicase module in an acetyltransferase that modifies a specific tRNA anticodon. EMBO Journal, 2009, 28, 1362-1373.	7.8	61
104	Catalytic Mechanism of Retaining $\beta$ -Galactosidase Belonging to Glycoside Hydrolase Family 97. Journal of Molecular Biology, 2009, 392, 1232-1241.	4.2	27
105	The Structure of Rat Liver Vault at 3.5 Angstrom Resolution. Science, 2009, 323, 384-388.	12.6	135
106	Snapshots of Dynamics in Synthesizing $\epsilon$ -Isopentenyladenosine at the tRNA Anticodon. Biochemistry, 2009, 48, 5057-5065.	2.5	43
107	Crystal structure of the PH1932 protein, a unique archaeal ArsR type winged $\alpha$ HTH transcription factor from <i>Pyrococcus horikoshii</i> OT3. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1631-1634.	2.6	4
108	Structural and functional analysis of the TetR-family transcriptional regulator SCO0332 from <i>Streptomyces coelicolor</i> . Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 198-205.	2.5	12

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109	Structure of protein PH0536 from <i>Pyrococcus horikoshii</i> at 1.7 Å... resolution reveals a novel assembly of an oligonucleotide/oligosaccharide-binding fold and an $\alpha$ -helical bundle. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 503-508.	2.6	1
110	A Helical String of Alternately Connected Three-Helix Bundles for the Cell Wall-Associated Adhesion Protein Ebh from <i>Staphylococcus aureus</i> . <i>Structure</i> , 2008, 16, 488-496.	3.3	27
111	Electron microscopy and computational studies of Ebh, a giant cell-wall-associated protein from <i>Staphylococcus aureus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2008, 376, 261-266.	2.1	7
112	<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
113	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
114	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
115	Purification, Crystallization and Preliminary X-Ray Studies of AxcesD Required for Efficient Cellulose Biosynthesis in <i>Acetobacter xylinum</i> . <i>Protein and Peptide Letters</i> , 2008, 15, 115-117.	0.9	4
116	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
117	2P-029 Structural analysis of eukaryotic translation initiation factor eIF5B(The 46th Annual Meeting) Tj ETQq1 1 0.784314 rgBT /Over	0.1	0
118	Crystal Structure of SCO6571 from <i>Streptomyces coelicolor</i> A3(2). <i>Protein and Peptide Letters</i> , 2008, 15, 709-712.	0.9	1
119	Structural and Mutational Analyses of Drp35 from <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 5770-5780.	3.4	39
120	Crystallization and Preliminary X-Ray Studies of the Unliganded Wild-Type Bovine Thrombin. <i>Protein and Peptide Letters</i> , 2007, 14, 923-924.	0.9	1
121	S06A1 Mechanistic insight into RNA acetylation to maintain the decoding fidelity in bacteria(Structural Biology of ncRNA Processing and Function). <i>Seibutsu Butsuru</i> , 2007, 47, S8.	0.1	0
122	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
123	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
124	DNA Recognition Mechanism of the ONECUT Homeodomain of Transcription Factor HNF-6. <i>Structure</i> , 2007, 15, 75-83.	3.3	35
125	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
126	Crystal structure of an archaeal Ski2p-like protein from <i>Pyrococcus horikoshii</i> OT3. <i>Protein Science</i> , 2007, 17, 136-145.	7.6	8



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127	Structural basis of CoA recognition by the Pyrococcus single-domain CoA-binding proteins. Journal of Structural and Functional Genomics, 2007, 7, 119-129.	1.2	3
128	S2c1-2 Mechanistic insights into RNA dependent transamidation by GatCAB(S2-c1: "Crystallographic) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.1	0
129	2P034 Crystal structure of Atlantic cod trypsin(29. Protein structure and dynamics (II),Poster) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.1	0
130	LAFIRE: software for automating the refinement process of protein-structure analysis. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 189-196.	2.5	71
131	Structure of the catalytic nucleotide-binding subunit A of A-type ATP synthase from Pyrococcus horikoshii reveals a novel domain related to the peripheral stalk. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 483-488.	2.5	31
132	The structure of Pyrococcus horikoshii 2â€²-5â€² RNA ligase at 1.94â€š resolution reveals a possible open form with a wider active-site cleft. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 1196-1200.	0.7	8
133	New algorithm for protein model building: extending a partial model in a map segment. Journal of Applied Crystallography, 2006, 39, 57-63.	4.5	15
134	Crystal structure of an RtcB homolog protein (PH1602-extein protein) from Pyrococcus horikoshii reveals a novel fold. Proteins: Structure, Function and Bioinformatics, 2006, 63, 1119-1122.	2.6	33
135	Structural analysis of the transcriptional regulator homolog protein from Pyrococcus horikoshii OT3. Proteins: Structure, Function and Bioinformatics, 2006, 63, 1084-1086.	2.6	7
136	Structural characterization of the Acetobacter xylinum endo-1,4-glucanase CMCax required for cellulose biosynthesis. Proteins: Structure, Function and Bioinformatics, 2006, 64, 1069-1077.	2.6	47
137	Crystal structure of hypothetical protein TTHB192 from Thermus thermophilus HB8 reveals a new protein family with an RNA recognition motif-like domain. Protein Science, 2006, 15, 1494-1499.	7.6	78
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