

Cong-Zhao Zhou

List of Publications by Year in descending order

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Version: 2024-02-01

138
papers

7,529
citations

147801

31
h-index

56724

83
g-index

141
all docs

141
docs citations

141
times ranked

15370
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	Structure and transport mechanism of the human cholesterol transporter ABCG1. <i>Cell Reports</i> , 2022, 38, 110298.	6.4	18
3	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
4	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
5	Inhibition of <i>Streptococcus pneumoniae</i> growth by masarimycin. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	1.8	0
6	Biochemical and structural characterization of the cyanophage-encoded phosphate-binding protein: implications for enhanced phosphate uptake of infected cyanobacteria. <i>Environmental Microbiology</i> , 2022, 24, 3037-3050.	3.8	7
7	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
8	Complex structure reveals <i>CcmM</i> and <i>CcmN</i> form a heterotrimeric adaptor in <i>Paracoccus carboxysome</i> . <i>Protein Science</i> , 2021, 30, 1566-1576.	7.6	5
9	Structures of cyanobacterial bicarbonate transporter SbtA and its complex with PII-like SbtB. <i>Cell Discovery</i> , 2021, 7, 63.	6.7	16
10	Capsid Structure of <i>Anabaena</i> Cyanophage A-1(L). <i>Journal of Virology</i> , 2021, 95, e0135621.	3.4	4
11	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
12	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
13	Cryo-electron Microscopy Structure and Transport Mechanism of a Wall Teichoic Acid ABC Transporter. <i>MBio</i> , 2020, 11, .	4.1	33
14	Cryo-EM structure of human bile salts exporter ABCB11. <i>Cell Research</i> , 2020, 30, 623-625.	12.0	30
15	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
16	Genomic Analysis of Mic1 Reveals a Novel Freshwater Long-Tailed Cyanophage. <i>Frontiers in Microbiology</i> , 2020, 11, 484.	3.5	27
17	Molecular basis for the assembly of RuBisCO assisted by the chaperone Raf1. <i>Nature Plants</i> , 2020, 6, 708-717.	9.3	24
18	Capsid Structure of a Freshwater Cyanophage Siphoviridae Mic1. <i>Structure</i> , 2019, 27, 1508-1516.e3.	3.3	21

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19	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
20	Cryo-EM structure of human lysosomal cobalamin exporter ABCD4. <i>Cell Research</i> , 2019, 29, 1039-1041.	12.0	42
21	Crystal structure of pentameric shell protein CsoS4B of <i>Halothiobacillus neapolitanus</i> $\hat{\iota}$ -carboxysome. <i>Biochemical and Biophysical Research Communications</i> , 2019, 515, 510-515.	2.1	4
22	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
23	Multi-functional regulator MapZ controls both positioning and timing of FtsZ polymerization. <i>Biochemical Journal</i> , 2019, 476, 1433-1444.	3.7	6
24	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
25	Structural and enzymatic analyses of <i>Anabaena</i> heterocyst-specific alkaline invertase InvB. <i>FEBS Letters</i> , 2018, 592, 1589-1601.	2.8	12
26	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
27	Structure of a MacAB-like efflux pump from <i>Streptococcus pneumoniae</i> . <i>Nature Communications</i> , 2018, 9, 196.	12.8	34
28	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
29	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
30	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
31	Structural and Biochemical Insights into the Multiple Functions of Yeast Grx3. <i>Journal of Molecular Biology</i> , 2018, 430, 1235-1248.	4.2	23
32	Carbon/Nitrogen Metabolic Balance: Lessons from Cyanobacteria. <i>Trends in Plant Science</i> , 2018, 23, 1116-1130.	8.8	117
33	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
34	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
35	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
36	Structural features of the aromatic/arginine constriction in the aquaglyceroporin GintAQPF2 are responsible for glycerol impermeability in arbuscular mycorrhizal symbiosis. <i>Fungal Biology</i> , 2017, 121, 95-102.	2.5	4

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37	The N-terminal polypeptide derived from viral macrophage inflammatory protein II reverses breast cancer epithelial-to-mesenchymal transition via a PDGFR α -dependent mechanism. <i>Oncotarget</i> , 2017, 8, 37448-37463.	1.8	7
38	Crystal structure of yeast monothiol glutaredoxin Grx6 in complex with a glutathione-coordinated [2Fe μ -2S] cluster. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 732-737.	0.8	12
39	Structural Analysis of the Catalytic Mechanism and Substrate Specificity of Anabaena Alkaline Invertase InvA Reveals a Novel Glucosidase. <i>Journal of Biological Chemistry</i> , 2016, 291, 25667-25677.	3.4	24
40	Neofunctionalization of zona pellucida proteins enhances freeze-prevention in the eggs of Antarctic notothenioids. <i>Nature Communications</i> , 2016, 7, 12987.	12.8	33
41	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
42	Structural basis for receptor recognition and pore formation of a zebrafish aerolysin α -like protein. <i>EMBO Reports</i> , 2016, 17, 235-248.	4.5	53
43	Structural Comparison and Simulation of Pneumococcal Peptidoglycan Hydrolase LytB. <i>Methods in Molecular Biology</i> , 2016, 1440, 271-283.	0.9	0
44	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
45	Structures of an all- β protein running along the DNA major groove. <i>Nucleic Acids Research</i> , 2016, 44, 3936-3945.	14.5	5
46	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
47	Structural insights into HetR \sim PatS interaction involved in cyanobacterial pattern formation. <i>Scientific Reports</i> , 2015, 5, 16470.	3.3	29
48	Activity Augmentation of Amphioxus Peptidoglycan Recognition Protein BbtPGRP3 via Fusion with a Chitin Binding Domain. <i>PLoS ONE</i> , 2015, 10, e0140953.	2.5	3
49	Full-length structure of the major autolysin LytA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1373-1381.	2.5	22
50	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
51	Structural and biochemical analyses of the <i>Streptococcus pneumoniae</i> L α -D-carboxypeptidase DacB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 283-292.	2.5	2
52	Structure of the adenylation α -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
53	Structural and Enzymatic Characterization of the Choline Kinase LicA from <i>Streptococcus pneumoniae</i> . <i>PLoS ONE</i> , 2015, 10, e0120467.	2.5	11
54	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

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55	Structural Insights into SraP-Mediated <i>Staphylococcus aureus</i> Adhesion to Host Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004169.	4.7	85
56	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
57	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
58	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
59	Structure-Guided Activity Enhancement and Catalytic Mechanism of Yeast Grx8. <i>Biochemistry</i> , 2014, 53, 2185-2196.	2.5	12
60	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
61	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
62	<i>Streptomyces coelicolor</i> SCO4226 Is a Nickel Binding Protein. <i>PLoS ONE</i> , 2014, 9, e109660.	2.5	9
63	Structures of Yeast Apa2 Reveal Catalytic Insights into a Canonical Ap4A Phosphorylase of the Histidine Triad Superfamily. <i>Journal of Molecular Biology</i> , 2013, 425, 2687-2698.	4.2	6
64	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
65	Structure and Catalytic Mechanism of Yeast 4-Amino-4-deoxychorismate Lyase. <i>Journal of Biological Chemistry</i> , 2013, 288, 22985-22992.	3.4	5
66	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
67	ATPase as a switch in P _{II} signal transduction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12863-12864.	7.1	3
68	The N-Terminal β -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
69	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
70	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
71	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
72	Structural Insights into the Substrate Specificity of <i>Streptococcus pneumoniae</i> β (1,3)-Galactosidase BgaC. <i>Journal of Biological Chemistry</i> , 2012, 287, 22910-22918.	3.4	32

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73	N-Terminal Domain of Bombyx mori Fibroin Mediates the Assembly of Silk in Response to pH Decrease. <i>Journal of Molecular Biology</i> , 2012, 418, 197-207.	4.2	107
74	Guidelines for the use and interpretation of assays for monitoring autophagy. <i>Autophagy</i> , 2012, 8, 445-544.	9.1	3,122
75	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
76	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
77	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
78	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
79	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
80	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
81	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
82	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
83	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
84	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
85	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
86	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
87	Crystal structures of holo and Cu-deficient Cu/Zn-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
88	Crystal structures of the apo and GDP-bound forms of a cupin-like protein BbDUF985 from <i>Branchiostoma belcheri tsingtauense</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2714-2719.	2.6	3
89	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
90	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

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91	Structural and Biochemical Characterization of Yeast Monothiol Glutaredoxin Grx6. <i>Journal of Molecular Biology</i> , 2010, 398, 614-622.	4.2	45
92	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
93	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
94	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
95	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
96	Crystal structure of <i>Arabidopsis</i> translation initiation factor eIF5A2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 736-740.	2.6	10
97	Structure of the thioredoxin-fold domain of human phosphocyanin-like protein 2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 67-70.	0.7	11
98	Purification, crystallization and preliminary X-ray diffraction analysis of glutathionylated Trx1 C33S mutant from yeast. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 39-41.	0.7	1
99	Cloning, overproduction, purification, crystallization and preliminary X-ray diffraction analysis of yeast glutaredoxin Grx5. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 651-653.	0.7	1
100	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
101	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
102	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
103	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
104	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
105	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
106	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
107	Expression, purification, crystallization and preliminary X-ray diffraction analysis of thioredoxin Trx1 from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 323-325.	0.7	5
108	Structure of Ynk1 from the yeast <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 572-576.	0.7	6

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109	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
110	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
111	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
112	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
113	The gene expression profile of <i>Bombyx mori</i> silk gland. <i>Gene</i> , 2007, 396, 369-372.	2.2	8
114	Purification, crystallization and preliminary X-ray analysis of Hsp33 from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 114-116.	0.7	1
115	Crystal structure of <i>Saccharomyces cerevisiae</i> 6-phosphogluconate dehydrogenase Gnd1. <i>BMC Structural Biology</i> , 2007, 7, 38.	2.3	34
116	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
117	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
118	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
119	Expression, purification, crystallization and preliminary X-ray diffraction analysis of mitochondrial thioredoxin Trx3 from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1161-1163.	0.7	4
120	Crystal structure of the yeast cytoplasmic thioredoxin Trx2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 246-249.	2.6	20
121	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
122	Catalytic Mechanism and Structure of Viral Flavin-dependent Thymidylate Synthase ThyX. <i>Journal of Biological Chemistry</i> , 2006, 281, 24048-24057.	3.4	53
123	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
124	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
125	Crystal structure and confirmation of the alanine:glyoxylate aminotransferase activity of the YFLO30w yeast protein. <i>Biochimie</i> , 2005, 87, 1041-1047.	2.6	12
126	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

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127	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
128	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
129	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
130	The Paris-Sud yeast structural genomics pilot-project: from structure to function. <i>Biochimie</i> , 2004, 86, 617-623.	2.6	18
131	Developments in Structural Genomics: Protein Purification and Function Interpretation. <i>Current Genomics</i> , 2004, 5, 37-48.	1.6	3
132	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
133	A structural genomics initiative on yeast proteins. <i>Journal of Synchrotron Radiation</i> , 2003, 10, 4-8.	2.4	20
134	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
135	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
136	Identification and characterization of a silkgland-related matrix association region in <i>Bombyx mori</i> . <i>Gene</i> , 2001, 277, 139-144.	2.2	14
137	Silk fibroin: Structural implications of a remarkable amino acid sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 44, 119-122.	2.6	606
138	Fine organization of <i>Bombyx mori</i> fibroin heavy chain gene. <i>Nucleic Acids Research</i> , 2000, 28, 2413-2419.	14.5	603