

Mitchell D Miller

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156
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L-index

#	Paper	IF	Citations
146	Structural genomics of the <i>Thermotoga maritima</i> proteome implemented in a high-throughput structure determination pipeline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 11664-9	11.5	381
145	An automated system to mount cryo-cooled protein crystals on a synchrotron beam line, using compact sample cassettes and a small-scale robot. <i>Journal of Applied Crystallography</i> , 2002 , 35, 720-726	3.8	216
144	Drop-on-demand sample delivery for studying biocatalysts in action at X-ray free-electron lasers. <i>Nature Methods</i> , 2017 , 14, 443-449	21.6	107
143	Chemical Generation of C602- and Electron Transfer Mechanism for the Reactions with Alkyl Bromides. <i>The Journal of Physical Chemistry</i> , 1996 , 100, 16327-16335		93
142	The active site of Serratia endonuclease contains a conserved magnesium-water cluster. <i>Journal of Molecular Biology</i> , 1999 , 288, 975-87	6.5	82
141	2.1 A structure of Serratia endonuclease suggests a mechanism for binding to double-stranded DNA. <i>Nature Structural and Molecular Biology</i> , 1994 , 1, 461-8	17.6	77
140	Enzyme intermediates captured "on the fly" by mix-and-inject serial crystallography. <i>BMC Biology</i> , 2018 , 16, 59	7.3	73
139	Crystal structures of two novel dye-decolorizing peroxidases reveal a beta-barrel fold with a conserved heme-binding motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 223-33	4.2	68
138	Identification and structural characterization of heme binding in a novel dye-decolorizing peroxidase, TyrA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 234-43	4.2	61
137	Structural basis of murein peptide specificity of a gamma-D-glutamyl-L-diamino acid endopeptidase. <i>Structure</i> , 2009 , 17, 303-13	5.2	57
136	Identification of the Serratia endonuclease dimer: structural basis and implications for catalysis. <i>Protein Science</i> , 1996 , 5, 24-33	6.3	50
135	Structure of the ED-glutamyl-L-diamino acid endopeptidase YkFC from <i>Bacillus cereus</i> in complex with L-Ala-ED-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1354-64		45
134	Crystal structure of the global regulatory protein CsrA from <i>Pseudomonas putida</i> at 2.05 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 449-53	4.2	45
133	Crystal structure of the first eubacterial Mre11 nuclease reveals novel features that may discriminate substrates during DNA repair. <i>Journal of Molecular Biology</i> , 2010 , 397, 647-63	6.5	37
132	Functional and structural characterization of a thermostable acetyl esterase from <i>Thermotoga maritima</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 1545-59	4.2	36
131	Structure-based discovery of NANOG variant with enhanced properties to promote self-renewal and reprogramming of pluripotent stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 4666-71	11.5	32
130	Reader domain specificity and lysine demethylase-4 family function. <i>Nature Communications</i> , 2016 , 7, 13387	17.4	30

129	Crystal structure of a tandem cystathionine-beta-synthase (CBS) domain protein (TM0935) from <i>Thermotoga maritima</i> at 1.87 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 57, 213-7	4.2	30
128	Automated identification of elemental ions in macromolecular crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 1104-14		27
127	Crystal structure of an iron-containing 1,3-propanediol dehydrogenase (TM0920) from <i>Thermotoga maritima</i> at 1.3 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 174-7	4.2	27
126	Structure of a membrane-attack complex/perforin (MACPF) family protein from the human gut symbiont <i>Bacteroides thetaiotaomicron</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1297-305		26
125	Crystal structure of a PIN (PilT N-terminus) domain (AF0591) from <i>Archaeoglobus fulgidus</i> at 1.90 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 404-8	4.2	26
124	Pro-metastatic collagen lysyl hydroxylase dimer assemblies stabilized by Fe-binding. <i>Nature Communications</i> , 2018 , 9, 512	17.4	25
123	Bacterial pleckstrin homology domains: a prokaryotic origin for the PH domain. <i>Journal of Molecular Biology</i> , 2010 , 396, 31-46	6.5	25
122	Crystal structure of acireductone dioxygenase (ARD) from <i>Mus musculus</i> at 2.06 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 808-13	4.2	25
121	Structure and functional characterization of a bile acid 7 α -dehydratase BaiE in secondary bile acid synthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84, 316-31	4.2	24
120	Insights into substrate specificity of geranylgeranyl reductases revealed by the structure of digeranylgeranyl glycerophospholipid reductase, an essential enzyme in the biosynthesis of archaeal membrane lipids. <i>Journal of Molecular Biology</i> , 2010 , 404, 403-17	6.5	23
119	Crystal structure of a glycerophosphodiester phosphodiesterase (GDPD) from <i>Thermotoga maritima</i> (TM1621) at 1.60 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 167-70	4.2	23
118	Structures of a bifunctional cell wall hydrolase CwlT containing a novel bacterial lysozyme and an NlpC/P60 DL-endopeptidase. <i>Journal of Molecular Biology</i> , 2014 , 426, 169-84	6.5	22
117	Crystal structure of a novel manganese-containing cupin (TM1459) from <i>Thermotoga maritima</i> at 1.65 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 611-4	4.2	22
116	Structure-guided functional characterization of enediyne self-sacrifice resistance proteins, CalU16 and CalU19. <i>ACS Chemical Biology</i> , 2014 , 9, 2347-58	4.9	20
115	Crystallization and preliminary crystallographic analysis of a novel nuclease from <i>Serratia marcescens</i> . <i>Journal of Molecular Biology</i> , 1991 , 222, 27-30	6.5	20
114	Crystal structure of the Fic (Filamentation induced by cAMP) family protein SO4266 (gi 24375750) from <i>Shewanella oneidensis</i> MR-1 at 1.6 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 75, 264-71	4.2	19
113	Crystal structure of an Udp-n-acetylmuramate-alanine ligase MurC (TM0231) from <i>Thermotoga maritima</i> at 2.3 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 1078-81	4.2	19
112	Structural analysis of papain-like NlpC/P60 superfamily enzymes with a circularly permuted topology reveals potential lipid binding sites. <i>PLoS ONE</i> , 2011 , 6, e22013	3.7	19

111	Crystal structure of a type II quinolic acid phosphoribosyltransferase (TM1645) from <i>Thermotoga maritima</i> at 2.50 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 768-71	4.2	18
110	Structural and functional characterizations of SsgB, a conserved activator of developmental cell division in morphologically complex actinomycetes. <i>Journal of Biological Chemistry</i> , 2009 , 284, 25268-79	5.4	17
109	Crystal structure of O-acetylserine sulfhydrylase (TM0665) from <i>Thermotoga maritima</i> at 1.8 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 387-91	4.2	17
108	Crystal structure of a putative PII-like signaling protein (TM0021) from <i>Thermotoga maritima</i> at 2.5 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 810-3	4.2	17
107	Structure of a tryptophanyl-tRNA synthetase containing an iron-sulfur cluster. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1326-34		16
106	Crystal structure of a putative oxalate decarboxylase (TM1287) from <i>Thermotoga maritima</i> at 1.95 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 392-5	4.2	16
105	Structure of the pilus assembly protein TadZ from <i>Eubacterium rectale</i> : implications for polar localization. <i>Molecular Microbiology</i> , 2012 , 83, 712-27	4.1	15
104	Structural and sequence analysis of imelysin-like proteins implicated in bacterial iron uptake. <i>PLoS ONE</i> , 2011 , 6, e21875	3.7	15
103	Structure of the first representative of Pfam Family PF09410 (DUF2006) reveals a structural signature of the calycin superfamily that suggests a role in lipid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1153-9		15
102	The structure of SSO2064, the first representative of Pfam family PF01796, reveals a novel two-domain zinc-ribbon OB-fold architecture with a potential acyl-CoA-binding role. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1160-6		15
101	Genomics, evolution, and crystal structure of a new family of bacterial spore kinases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 1470-82	4.2	15
100	Structure and function of the first full-length murein peptide ligase (Mpl) cell wall recycling protein. <i>PLoS ONE</i> , 2011 , 6, e17624	3.7	15
99	Structure and function of a novel LD-carboxypeptidase involved in peptidoglycan recycling. <i>Journal of Bacteriology</i> , 2013 , 195, 5555-66	3.5	14
98	Crystal structure of a novel Sm-like protein of putative cyanophage origin at 2.60 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 75, 296-307	4.2	14
97	Structure of a virulence regulatory factor CvfB reveals a novel winged helix RNA binding module. <i>Structure</i> , 2010 , 18, 537-47	5.2	14
96	Structure of an essential bacterial protein YeaZ (TM0874) from <i>Thermotoga maritima</i> at 2.5 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1230-6		14
95	Crystal structure of a ribose-5-phosphate isomerase RpiB (TM1080) from <i>Thermotoga maritima</i> at 1.90 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 171-5	4.2	14
94	Crystal structure of gamma-glutamyl phosphate reductase (TM0293) from <i>Thermotoga maritima</i> at 2.0 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 157-61	4.2	14

93	Biochemical and Structural Characterization of TtnD, a Prenylated FMN-Dependent Decarboxylase from the Tautomycetin Biosynthetic Pathway. <i>ACS Chemical Biology</i> , 2018 , 13, 2728-2738	4.9	14
92	A structural basis for the regulatory inactivation of DnaA. <i>Journal of Molecular Biology</i> , 2009 , 385, 368-806.5	6.5	13
91	Crystal structure of a single-stranded DNA-binding protein (TM0604) from <i>Thermotoga maritima</i> at 2.60 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 256-60	4.2	13
90	Crystal structure of S-adenosylmethionine:tRNA ribosyltransferase-isomerase (QueA) from <i>Thermotoga maritima</i> at 2.0 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 59, 869-74	4.2	13
89	Crystal structure of Hsp33 chaperone (TM1394) from <i>Thermotoga maritima</i> at 2.20 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 669-73	4.2	13
88	Crystal structure of histidine phosphotransfer protein ShpA, an essential regulator of stalk biogenesis in <i>Caulobacter crescentus</i> . <i>Journal of Molecular Biology</i> , 2009 , 390, 686-98	6.5	12
87	The crystal structure of a bacterial Sufu-like protein defines a novel group of bacterial proteins that are similar to the N-terminal domain of human Sufu. <i>Protein Science</i> , 2010 , 19, 2131-40	6.3	12
86	Crystal structure of an aspartate aminotransferase (TM1255) from <i>Thermotoga maritima</i> at 1.90 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 759-63	4.2	12
85	Crystal structure of an indigoidine synthase A (IndA)-like protein (TM1464) from <i>Thermotoga maritima</i> at 1.90 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 59, 864-8	4.2	12
84	Structure of an MmyB-like regulator from <i>C. aurantiacus</i> , member of a new transcription factor family linked to antibiotic metabolism in actinomycetes. <i>PLoS ONE</i> , 2012 , 7, e41359	3.7	12
83	Photoreversible interconversion of a phytochrome photosensory module in the crystalline state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 300-307	11.5	12
82	Crystal structure of a metal-dependent phosphoesterase (YP_910028.1) from <i>Bifidobacterium adolescentis</i> : Computational prediction and experimental validation of phosphoesterase activity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 2146-60	4.2	11
81	TM0486 from the hyperthermophilic anaerobe <i>Thermotoga maritima</i> is a thiamin-binding protein involved in response of the cell to oxidative conditions. <i>Journal of Molecular Biology</i> , 2010 , 400, 463-76	6.5	11
80	Crystal structure of homoserine O-succinyltransferase from <i>Bacillus cereus</i> at 2.4 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 68, 999-1005	4.2	11
79	Crystal structure of an alanine-glyoxylate aminotransferase from <i>Anabaena</i> sp. at 1.70 Å resolution reveals a noncovalently linked PLP cofactor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 971-5	4.2	11
78	Nucleotide sequence of the glyceraldehyde-3-phosphate dehydrogenase gene from <i>Thermus aquaticus</i> YT1. <i>Nucleic Acids Research</i> , 1989 , 17, 10123	20.1	11
77	Methionine Adenosyltransferase Engineering to Enable Bioorthogonal Platforms for AdoMet-Utilizing Enzymes. <i>ACS Chemical Biology</i> , 2020 , 15, 695-705	4.9	10
76	Crystal structure of the ApbE protein (TM1553) from <i>Thermotoga maritima</i> at 1.58 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 1083-90	4.2	10

75	Crystal structure of an alpha/beta serine hydrolase (YDR428C) from <i>Saccharomyces cerevisiae</i> at 1.85 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 755-8	4.2	10
74	Crystal structure of an Apo mRNA decapping enzyme (DcpS) from Mouse at 1.83 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 797-802	4.2	10
73	The structure of Mlc titration factor A (MtfA/Yeel) reveals a prototypical zinc metallopeptidase related to anthrax lethal factor. <i>Journal of Bacteriology</i> , 2012 , 194, 2987-99	3.5	9
72	The structure of Jann_2411 (DUF1470) from <i>Jannaschia</i> sp. at 1.45 Å resolution reveals a new fold (the ABATE domain) and suggests its possible role as a transcription regulator. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1198-204		9
71	The structure of <i>Haemophilus influenzae</i> prephenate dehydrogenase suggests unique features of bifunctional TyrA enzymes. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1317-25		9
70	Structure of BT_3984, a member of the SusD/RagB family of nutrient-binding molecules. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1274-80		9
69	Simulation of electrostatic and hydrodynamic properties of <i>Serratia</i> endonuclease. <i>Biopolymers</i> , 1997 , 41, 443-50	2.2	9
68	Crystal structure of a conserved hypothetical protein (gi: 13879369) from Mouse at 1.90 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 1132-6	4.2	9
67	Crystal structure of a member of a novel family of dioxygenases (PF10014) reveals a conserved cupin fold and active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 164-70	4.2	8
66	Structural Basis for the Stereochemical Control of Amine Installation in Nucleotide Sugar Aminotransferases. <i>ACS Chemical Biology</i> , 2015 , 10, 2048-56	4.9	8
65	Molecular characterization of novel pyridoxal-5P-phosphate-dependent enzymes from the human microbiome. <i>Protein Science</i> , 2014 , 23, 1060-76	6.3	8
64	Crystal structure of a novel archaeal AAA+ ATPase SSO1545 from <i>Sulfolobus solfataricus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 74, 1041-9	4.2	8
63	The structure of the first representative of Pfam family PF06475 reveals a new fold with possible involvement in glycolipid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1211-7		8
62	Open and closed conformations of two SpoIIAA-like proteins (YP_749275.1 and YP_001095227.1) provide insights into membrane association and ligand binding. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1245-53		8
61	A conserved fold for fimbrial components revealed by the crystal structure of a putative fimbrial assembly protein (BT1062) from <i>Bacteroides thetaiotaomicron</i> at 2.2 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1281-6		8
60	Crystal structure of 2-keto-3-deoxygluconate kinase (TM0067) from <i>Thermotoga maritima</i> at 2.05 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 603-8	4.2	8
59	Comparative structural analysis of a novel glutathione S-transferase (ATU5508) from <i>Agrobacterium tumefaciens</i> at 2.0 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 527-37	4.2	8
58	Crystal structure of a phosphoribosylaminoimidazole mutase PurE (TM0446) from <i>Thermotoga maritima</i> at 1.77-Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 474-8	4.2	8

57	Crystal structure of a methionine aminopeptidase (TM1478) from <i>Thermotoga maritima</i> at 1.9 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 396-400	4.2	8
56	Crystal structure of a putative NADPH-dependent oxidoreductase (GI: 18204011) from mouse at 2.10 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 629-33	4.2	8
55	Crystal structure of a putative modulator of DNA gyrase (pmbA) from <i>Thermotoga maritima</i> at 1.95 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 444-8	4.2	8
54	Improving the efficiency of molecular replacement by utilizing a new iterative transform phasing algorithm. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016 , 72, 539-47	1.7	7
53	Structure and function of the DUF2233 domain in bacteria and in the human mannose 6-phosphate uncovering enzyme. <i>Journal of Biological Chemistry</i> , 2013 , 288, 16789-16799	5.4	7
52	The structure of the first representative of Pfam family PF09836 reveals a two-domain organization and suggests involvement in transcriptional regulation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1174-81		7
51	Structures of the first representatives of Pfam family PF06938 (DUF1285) reveal a new fold with repeated structural motifs and possible involvement in signal transduction. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1218-25		7
50	Structures of three members of Pfam PF02663 (FmdE) implicated in microbial methanogenesis reveal a conserved core domain and an auxiliary C-terminal treble-clef zinc finger. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1335-46		7
49	An X-ray microsource based system for crystal screening and beamline development during synchrotron shutdown periods. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2007 , 582, 233-235	1.2	7
48	Crystal structure of NMA1982 from <i>Neisseria meningitidis</i> at 1.5 Å resolution provides a structural scaffold for nonclassical, eukaryotic-like phosphatases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 415-21	4.2	7
47	Crystal structure of phosphoribosylformylglycinamide synthase II (smPurL) from <i>Thermotoga maritima</i> at 2.15 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 1106-11	4.2	7
46	Crystal structure of an ORFan protein (TM1622) from <i>Thermotoga maritima</i> at 1.75 Å resolution reveals a fold similar to the Ran-binding protein Mog1p. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 777-82	4.2	7
45	Crystal structure of an HEPN domain protein (TM0613) from <i>Thermotoga maritima</i> at 1.75 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 806-9	4.2	7
44	Crystal structure of a zinc-containing glycerol dehydrogenase (TM0423) from <i>Thermotoga maritima</i> at 1.5 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 50, 371-4	4.2	7
43	Crystal structure of human protein N-terminal glutamine amidohydrolase, an initial component of the N-end rule pathway. <i>PLoS ONE</i> , 2014 , 9, e111142	3.7	7
42	Moving beyond static snapshots: Protein dynamics and the Protein Data Bank. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100749	5.4	7
41	The structure of BVU2987 from <i>Bacteroides vulgatus</i> reveals a superfamily of bacterial periplasmic proteins with possible inhibitory function. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1265-73		6
40	Crystal structure of MtnX phosphatase from <i>Bacillus subtilis</i> at 2.0 Å resolution provides a structural basis for bipartite phosphomonoester hydrolysis of 2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 422-9	4.2	6

39	Crystal structure of AICAR transformylase IMP cyclohydrolase (TM1249) from <i>Thermotoga maritima</i> at 1.88 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 1042-9	4.2	6
38	Crystal structure of an ADP-ribosylated protein with a cytidine deaminase-like fold, but unknown function (TM1506), from <i>Thermotoga maritima</i> at 2.70 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 1546-52	4.2	6
37	Crystal structure of TM1367 from <i>Thermotoga maritima</i> at 1.90 Å resolution reveals an atypical member of the cyclophilin (peptidylprolyl isomerase) fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 1112-8	4.2	6
36	Crystal structure of phosphoribosylformyl-glycinamide synthase II, PurS subunit (TM1244) from <i>Thermotoga maritima</i> at 1.90 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 249-54	4.2	6
35	Crystal structure of an orphan protein (TM0875) from <i>Thermotoga maritima</i> at 2.00-Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 607-10	4.2	6
34	Crystal structure of virulence factor CJ0248 from <i>Campylobacter jejuni</i> at 2.25 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 62, 292-6	4.2	6
33	Technical Reports: Automation of High-Throughput Protein Crystal Screening at SSRL. <i>Synchrotron Radiation News</i> , 2005 , 18, 28-35	0.6	6
32	Covalent Capture of Collagen Triple Helices Using Lysine-Aspartate and Lysine-Glutamate Pairs. <i>Biomacromolecules</i> , 2020 , 21, 3772-3781	6.9	6
31	Crystal structure of a transcription regulator (TM1602) from <i>Thermotoga maritima</i> at 2.3 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 67, 247-52	4.2	5
30	Crystal structure of TM1030 from <i>Thermotoga maritima</i> at 2.3 Å resolution reveals molecular details of its transcription repressor function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 68, 418-24	4.2	5
29	Crystal structure of a novel <i>Thermotoga maritima</i> enzyme (TM1112) from the cupin family at 1.83 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 615-8	4.2	5
28	Crystal structure of a putative glutamine amido transferase (TM1158) from <i>Thermotoga maritima</i> at 1.7 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 801-5	4.2	5
27	Finding a cold needle in a warm haystack: infrared imaging applied to locating cryocooled crystals in loops. <i>Journal of Applied Crystallography</i> , 2005 , 38, 69-77	3.8	5
26	Crystal structure of a putative quorum sensing-regulated protein (PA3611) from the <i>Pseudomonas</i> -specific DUF4146 family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 1086-92	4.2	4
25	Conformational changes associated with the binding of zinc acetate at the putative active site of XcTcmJ, a cupin from <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1347-53		4
24	Crystal structure of a formiminotetrahydrofolate cyclodeaminase (TM1560) from <i>Thermotoga maritima</i> at 2.80 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 976-81	4.2	4
23	Molecular-replacement phasing using predicted protein structures from. <i>IUCrJ</i> , 2020 , 7, 1168-1178	4.7	4
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