

Mitchell D Miller

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

146
papers

2,805
citations

25
h-index

45
g-index

156
ext. papers

3,121
ext. citations

4.8
avg. IF

3.85
L-index

#	Paper	IF	Citations
146	The crystal structure of DynF from the dynemicin-biosynthesis pathway of <i>Micromonospora chersina</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022 , 78, 1-7	1.1	0
145	The Structure of the PEX4-PEX22 Peroxin Complex-Insights Into Ubiquitination at the Peroxisomal Membrane.. <i>Frontiers in Cell and Developmental Biology</i> , 2022 , 10, 838923	5.7	0
144	Structure and Function of a Dual Reductase-Dehydratase Enzyme System Involved in -Terphenyl Biosynthesis. <i>ACS Chemical Biology</i> , 2021 ,	4.9	1
143	A collagen glucosyltransferase drives lung adenocarcinoma progression in mice. <i>Communications Biology</i> , 2021 , 4, 482	6.7	3
142	Moving beyond static snapshots: Protein dynamics and the Protein Data Bank. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100749	5.4	7
141	Structural characterization of DynU16, a START/Bet v1-like protein involved in dynemicin biosynthesis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021 , 77, 328-333	1.1	0
140	phage ferredoxin: structural characterization and electron transfer to cyanobacterial sulfite reductases. <i>Journal of Biological Chemistry</i> , 2020 , 295, 10610-10623	5.4	3
139	Methionine Adenosyltransferase Engineering to Enable Bioorthogonal Platforms for AdoMet-Utilizing Enzymes. <i>ACS Chemical Biology</i> , 2020 , 15, 695-705	4.9	10
138	Molecular-replacement phasing using predicted protein structures from. <i>IUCrJ</i> , 2020 , 7, 1168-1178	4.7	4
137	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
136	Covalent Capture of Collagen Triple Helices Using Lysine-Aspartate and Lysine-Glutamate Pairs. <i>Biomacromolecules</i> , 2020 , 21, 3772-3781	6.9	6
135	Pro-metastatic collagen lysyl hydroxylase dimer assemblies stabilized by Fe-binding. <i>Nature Communications</i> , 2018 , 9, 512	17.4	25
134	Enzyme intermediates captured "on the fly" by mix-and-inject serial crystallography. <i>BMC Biology</i> , 2018 , 16, 59	7.3	73
133	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
132	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
131	Reader domain specificity and lysine demethylase-4 family function. <i>Nature Communications</i> , 2016 , 7, 13387	17.4	30
130	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

129	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
128	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
127	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
126	Crystal structure of a two-subunit TrkA octameric gating ring assembly. <i>PLoS ONE</i> , 2015 , 10, e0122512	3.7	1
125	Crystal structures of three representatives of a new Pfam family PF14869 (DUF4488) suggest they function in sugar binding/uptake. <i>Protein Science</i> , 2014 , 23, 1380-91	6.3	1
124	Automated identification of elemental ions in macromolecular crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 1104-14		27
123	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
122	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
121	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
120	Molecular characterization of novel pyridoxal-5P-phosphate-dependent enzymes from the human microbiome. <i>Protein Science</i> , 2014 , 23, 1060-76	6.3	8
119	Structural analysis of arabinose-5-phosphate isomerase from <i>Bacteroides fragilis</i> and functional implications. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 2640-51		
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 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
116	Structure and function of a novel LD-carboxypeptidase a involved in peptidoglycan recycling. <i>Journal of Bacteriology</i> , 2013 , 195, 5555-66	3.5	14
115	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
114	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
113	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
112	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

111	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
110	Structural and sequence analysis of imelysin-like proteins implicated in bacterial iron uptake. <i>PLoS ONE</i> , 2011 , 6, e21875	3.7	15
109	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
108	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
107	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
106	Bacterial pleckstrin homology domains: a prokaryotic origin for the PH domain. <i>Journal of Molecular Biology</i> , 2010 , 396, 31-46	6.5	25
105	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
104	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
103	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
102	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
101	The structure of KPN03535 (gi 152972051), a novel putative lipoprotein from <i>Klebsiella pneumoniae</i> , reveals an OB-fold. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1254-60		3
100	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
99	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
98	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
97	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
96	Structure of LP2179, the first representative of Pfam family PF08866, suggests a new fold with a role in amino-acid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1205-10		2
95	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
94	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

93	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
92	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
91	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
90	Structures of the first representatives of Pfam family PF06684 (DUF1185) reveal a novel variant of the <i>Bacillus</i> chorismate mutase fold and suggest a role in amino-acid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1182-9		2
89	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
88	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
87	Structure of the first representative of Pfam family PF04016 (DUF364) reveals enolase and Rossmann-like folds that combine to form a unique active site with a possible role in heavy-metal chelation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1167-73		3
86	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
85	Structure of the β -glutamyl-L-diamino acid endopeptidase YkFC from <i>Bacillus cereus</i> in complex with L-Ala- β -Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1354-64		45
84	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
83	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
82	Structure of a putative NTP pyrophosphohydrolase: YP_001813558.1 from <i>Exiguobacterium sibiricum</i> 255-15. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1237-44		2
81	Structure of <i>Bacteroides thetaiotaomicron</i> BT2081 at 2.05 Å resolution: the first structural representative of a new protein family that may play a role in carbohydrate metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1287-96		1
80	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
79	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
78	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
77	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
76	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

75	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
74	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
73	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
72	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
71	A structural basis for the regulatory inactivation of DnaA. <i>Journal of Molecular Biology</i> , 2009 , 385, 368-80	6.5	13
70	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
69	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
68	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
67	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
66	Crystal structures of MW1337R and lin2004: representatives of a novel protein family that adopt a four-helical bundle fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 1589-96	4.2	3
65	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
64	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
63	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
62	Crystal structure of NMA1982 from <i>Neisseria meningitidis</i> at 1.5 angstroms resolution provides a structural scaffold for nonclassical, eukaryotic-like phosphatases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 415-21	4.2	7
61	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
60	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
59	Crystal structure of MtnX phosphatase from <i>Bacillus subtilis</i> at 2.0 angstroms 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, 433-9	4.2	6
58	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

57	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
56	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
55	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
54	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
53	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
52	Crystal structure of 2-phosphosulfolactate phosphatase (ComB) from <i>Clostridium acetobutylicum</i> at 2.6 Å resolution reveals a new fold with a novel active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 771-6	4.2	3
51	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
50	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
49	Comparative structural analysis of a novel glutathioneS-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
48	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
47	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
46	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
45	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
44	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
43	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
42	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
41	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
40	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

39	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
38	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
37	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
36	Technical Reports: Automation of High-Throughput Protein Crystal Screening at SSRL. <i>Synchrotron Radiation News</i> , 2005 , 18, 28-35	0.6	6
35	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
34	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
33	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
32	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
31	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
30	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
29	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
28	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
27	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
26	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
25	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
24	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
23	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
22	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

21	Crystal structure of an allantoicase (YIR029W) from <i>Saccharomyces cerevisiae</i> at 2.4 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 619-24	4.2	1
20	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
19	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
18	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
17	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
16	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
15	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
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