

Lukasz Jaroszewski

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165
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L-index

#	Paper	IF	Citations
163	The Sorcerer II Global Ocean Sampling expedition: expanding the universe of protein families. <i>PLoS Biology</i> , 2007 , 5, e16	9.7	638
162	FFAS03: a server for profile--profile sequence alignments. <i>Nucleic Acids Research</i> , 2005 , 33, W284-8	20.1	474
161	Comparison of sequence profiles. Strategies for structural predictions using sequence information. <i>Protein Science</i> , 2000 , 9, 232-41	6.3	388
160	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
159	Tolerating some redundancy significantly speeds up clustering of large protein databases. <i>Bioinformatics</i> , 2002 , 18, 77-82	7.2	311
158	XtalPred: a web server for prediction of protein crystallizability. <i>Bioinformatics</i> , 2007 , 23, 3403-5	7.2	219
157	Structural basis of neutralization by a human anti-severe acute respiratory syndrome spike protein antibody, 80R. <i>Journal of Biological Chemistry</i> , 2006 , 281, 34610-6	5.4	174
156	Derivation and testing of pair potentials for protein folding. When is the quasichemical approximation correct?. <i>Protein Science</i> , 1997 , 6, 676-88	6.3	159
155	Three-dimensional structural view of the central metabolic network of <i>Thermotoga maritima</i> . <i>Science</i> , 2009 , 325, 1544-9	33.3	148
154	The importance of alignment accuracy for molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 1229-36		141
153	Caspases. Regulating death since the origin of life. <i>Plant Physiology</i> , 2005 , 137, 841-7	6.6	117
152	FFAS server: novel features and applications. <i>Nucleic Acids Research</i> , 2011 , 39, W38-44	20.1	115
151	Improving the quality of twilight-zone alignments. <i>Protein Science</i> , 2000 , 9, 1487-96	6.3	110
150	PSI-2: structural genomics to cover protein domain family space. <i>Structure</i> , 2009 , 17, 869-81	5.2	108
149	The challenge of protein structure determination--lessons from structural genomics. <i>Protein Science</i> , 2007 , 16, 2472-82	6.3	106
148	Exploration of uncharted regions of the protein universe. <i>PLoS Biology</i> , 2009 , 7, e1000205	9.7	98
147	Numerous proteins with unique characteristics are degraded by the 26S proteasome following monoubiquitination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E4639-47	11.5	91

146	Tyrosine phosphorylation of VHR phosphatase by ZAP-70. <i>Nature Immunology</i> , 2003 , 4, 44-8	19.1	89
145	FFAS-3D: improving fold recognition by including optimized structural features and template re-ranking. <i>Bioinformatics</i> , 2014 , 30, 660-7	7.2	83
144	Structural genomics is the largest contributor of novel structural leverage. <i>Journal of Structural and Functional Genomics</i> , 2009 , 10, 181-91		68
143	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
142	Inhibition of T cell antigen receptor signaling by VHR-related MKPX (VHX), a new dual specificity phosphatase related to VH1 related (VHR). <i>Journal of Biological Chemistry</i> , 2002 , 277, 5524-8	5.4	68
141	In search for more accurate alignments in the twilight zone. <i>Protein Science</i> , 2002 , 11, 1702-13	6.3	63
140	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
139	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
138	The structure of the neurotoxin-associated protein HA33/A from <i>Clostridium botulinum</i> suggests a reoccurring beta-trefoil fold in the progenitor toxin complex. <i>Journal of Molecular Biology</i> , 2005 , 346, 1083-93	6.5	56
137	Crystal structure of the human N-Myc downstream-regulated gene 2 protein provides insight into its role as a tumor suppressor. <i>Journal of Biological Chemistry</i> , 2011 , 286, 12450-60	5.4	54
136	A Distinct Type of Pilus from the Human Microbiome. <i>Cell</i> , 2016 , 165, 690-703	56.2	52
135	PDBFlex: exploring flexibility in protein structures. <i>Nucleic Acids Research</i> , 2016 , 44, D423-8	20.1	51
134	Sequence clustering strategies improve remote homology recognitions while reducing search times. <i>Protein Engineering, Design and Selection</i> , 2002 , 15, 643-9	1.9	51
133	Structural basis of membrane targeting by the Dock180 family of Rho family guanine exchange factors (Rho-GEFs). <i>Journal of Biological Chemistry</i> , 2010 , 285, 13211-22	5.4	49
132	Expansion of the protein repertoire in newly explored environments: human gut microbiome specific protein families. <i>PLoS Computational Biology</i> , 2010 , 6, e1000798	5	48
131	Structure of the D-glutamyl-L-diamino acid endopeptidase YkFC from <i>Bacillus cereus</i> in complex with L-Ala-D-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1354-64		45
130	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
129	Crystal structure of the actin binding domain of the cyclase-associated protein. <i>Biochemistry</i> , 2004 , 43, 10628-41	3.2	44

128	Crystal structure of thy1, a thymidylate synthase complementing protein from <i>Thermotoga maritima</i> at 2.25 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 49, 142-5	4.2	43
127	The interplay of fold recognition and experimental structure determination in structural genomics. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 307-12	8.1	38
126	Improving the chances of successful protein structure determination with a random forest classifier. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 627-35		37
125	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
124	AIDA: ab initio domain assembly server. <i>Nucleic Acids Research</i> , 2014 , 42, W308-13	20.1	35
123	Domain analysis of the tubulin cofactor system: a model for tubulin folding and dimerization. <i>BMC Bioinformatics</i> , 2003 , 4, 46	3.6	35
122	AIDA: ab initio domain assembly for automated multi-domain protein structure prediction and domain-domain interaction prediction. <i>Bioinformatics</i> , 2015 , 31, 2098-105	7.2	34
121	An Efficient Monte Carlo Model of Protein Chains. Modeling the Short-Range Correlations between Side Group Centers of Mass. <i>Journal of Physical Chemistry B</i> , 1998 , 102, 4628-4637	3.4	34
120	The JCSG MR pipeline: optimized alignments, multiple models and parallel searches. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008 , 64, 133-40		30
119	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
118	A segment alignment approach to protein comparison. <i>Bioinformatics</i> , 2003 , 19, 742-9	7.2	28
117	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
116	ATP-activated oligomerization as a mechanism for apoptosis regulation: fold and mechanism prediction for CED-4. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 39, 197-203	4.2	27
115	FATCAT 2.0: towards a better understanding of the structural diversity of proteins. <i>Nucleic Acids Research</i> , 2020 , 48, W60-W64	20.1	26
114	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
113	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
112	Insights into Substrate Specificity of NlpC/P60 Cell Wall Hydrolases Containing Bacterial SH3 Domains. <i>MBio</i> , 2015 , 6, e02327-14	7.8	25
111	Bacterial pleckstrin homology domains: a prokaryotic origin for the PH domain. <i>Journal of Molecular Biology</i> , 2010 , 396, 31-46	6.5	25

110	Crystal structure of acireductone dioxygenase (ARD) from <i>Mus musculus</i> at 2.06 angstrom resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 808-13	4.2	25
109	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
108	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
107	Coronavirus3D: 3D structural visualization of COVID-19 genomic divergence. <i>Bioinformatics</i> , 2020 , 36, 4360-4362	7.2	22
106	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
105	Multiple Model Approach: Exploring the Limits of Comparative Modeling. <i>Journal of Molecular Modeling</i> , 1998 , 4, 294-309	2	22
104	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
103	UHM-ULM interactions in the RBM39-U2AF65 splicing-factor complex. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 497-511	5.5	21
102	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
101	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
100	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
99	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
98	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
97	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
96	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
95	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
94	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
93	Structural and sequence analysis of imelysin-like proteins implicated in bacterial iron uptake. <i>PLoS ONE</i> , 2011 , 6, e21875	3.7	15

92	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
91	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
90	Protein structure prediction based on sequence similarity. <i>Methods in Molecular Biology</i> , 2009 , 569, 129-56		15
89	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
88	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
87	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
86	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
85	A structural basis for the regulatory inactivation of DnaA. <i>Journal of Molecular Biology</i> , 2009 , 385, 368-80.5		13
84	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
83	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
82	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
81	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
80	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
79	Genome pool strategy for structural coverage of protein families. <i>Structure</i> , 2008 , 16, 1659-67	5.2	12
78	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
77	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
76	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
75	The interplay of SARS-CoV-2 evolution and constraints imposed by the structure and functionality of its proteins. <i>PLoS Computational Biology</i> , 2021 , 17, e1009147	5	12

74	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
73	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
72	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
71	Crystal structure of a glycerate kinase (TM1585) from <i>Thermotoga maritima</i> at 2.70 Å resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 243-8	4.2	10
70	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
69	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
68	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
67	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
66	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
65	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
64	Protacel: protein data visualization library for the web. <i>Bioinformatics</i> , 2016 , 32, 602-4	7.2	8
63	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
62	Molecular characterization of novel pyridoxal-5-phosphate-dependent enzymes from the human microbiome. <i>Protein Science</i> , 2014 , 23, 1060-76	6.3	8
61	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
60	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
59	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
58	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
57	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

56	Comparative structural analysis of a novel glutathioneS-transferase (ATU5508) from <i>Agrobacterium tumefaciens</i> at 2.0 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 527-37	4.2	8
55	Integrated web service for improving alignment quality based on segments comparison. <i>BMC Bioinformatics</i> , 2004 , 5, 98	3.6	8
54	Crystal structure of a phosphoribosylaminoimidazole mutase PurE (TM0446) from <i>Thermotoga maritima</i> at 1.77-A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 474-8	4.2	8
53	Crystal structure of a methionine aminopeptidase (TM1478) from <i>Thermotoga maritima</i> at 1.9 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 396-400	4.2	8
52	Crystal structure of a putative NADPH-dependent oxidoreductase (GI: 18204011) from mouse at 2.10 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 629-33	4.2	8
51	Molecular modeling of phosphorylation sites in proteins using a database of local structure segments. <i>Journal of Molecular Modeling</i> , 2005 , 11, 431-8	2	8
50	Crystal structure of a putative modulator of DNA gyrase (pmbA) from <i>Thermotoga maritima</i> at 1.95 A resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 444-8	4.2	8
49	Structure-guided functional characterization of DUF1460 reveals a highly specific NlpC/P60 amidase family. <i>Structure</i> , 2014 , 22, 1799-1809	5.2	7
48	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
47	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
46	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
45	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
44	Crystal structure of phosphoribosylformylglycinamide synthase II (smPurL) from <i>Thermotoga maritima</i> at 2.15 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 1106-11	4.2	7
43	Crystal structure of an ORFan protein (TM1622) from <i>Thermotoga maritima</i> at 1.75 A 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
42	Crystal structure of an HEPN domain protein (TM0613) from <i>Thermotoga maritima</i> at 1.75 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 806-9	4.2	7
41	Crystal structure of a zinc-containing glycerol dehydrogenase (TM0423) from <i>Thermotoga maritima</i> at 1.5 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 50, 371-4	4.2	7
40	Crystal structure of uronate isomerase (TM0064) from <i>Thermotoga maritima</i> at 2.85 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53, 142-5	4.2	7
39	Synthesis, cloning and expression in <i>Escherichia coli</i> of a gene coding for the Met8-->Leu CMTI I--a representative of the squash inhibitors of serine proteinases. <i>FEBS Letters</i> , 1995 , 377, 172-4	3.8	7

38	Cancer3D 2.0: interactive analysis of 3D patterns of cancer mutations in cancer subsets. <i>Nucleic Acids Research</i> , 2019 , 47, D895-D899	20.1	7
37	PubServer: literature searches by homology. <i>Nucleic Acids Research</i> , 2014 , 42, W430-5	20.1	6
36	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
35	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
34	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
33	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
32	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
31	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
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