

Adam Godzik

List of Publications by Year in descending order

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Version: 2024-02-01

377
papers

42,279
citations

5558

82
h-index

3021

188
g-index

404
all docs

404
docs citations

404
times ranked

57850
citing authors

#	ARTICLE	IF	CITATIONS
1	Novel putative polyethylene terephthalate (PET) plastic degrading enzymes from the environmental metagenome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 504-511.	1.5	17
2	Multiple expansions of globally uncommon SARS-CoV-2 lineages in Nigeria. <i>Nature Communications</i> , 2022, 13, 688.	5.8	23
3	Defining the risk of SARS-CoV-2 variants on immune protection. <i>Nature</i> , 2022, 605, 640-652.	13.7	117
4	Actin Cross-Linking Effector Domain of the <i>Vibrio vulnificus</i> F-Type MARTX Toxin Dominates Disease Progression During Intestinal Infection. <i>Infection and Immunity</i> , 2022, , e0062721.	1.0	1
5	A Genomic Island of <i>Vibrio cholerae</i> Encodes a Three-Component Cytotoxin with Monomer and Protomer Forms Structurally Similar to Alpha-Pore-Forming Toxins. <i>Journal of Bacteriology</i> , 2022, 204, e0055521.	1.0	3
6	What the protein data bank tells us about the evolutionary conservation of protein conformational diversity. <i>Protein Science</i> , 2022, 31, .	3.1	2
7	Identification and phylogenetic analysis of RNA binding domain abundant in apicomplexans or RAP proteins. <i>Microbial Genomics</i> , 2021, 7, .	1.0	5
8	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021, 592, 438-443.	13.7	1,381
9	ModFlex: Towards Function Focused Protein Modeling. <i>Journal of Molecular Biology</i> , 2021, 433, 166828.	2.0	2
10	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. <i>Cell Host and Microbe</i> , 2021, 29, 1093-1110.	5.1	73
11	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.	1.5	35
12	NMR in structural genomics to increase structural coverage of the protein universe. , 2021, , 143-154.		0
13	Dynamic changes in human single-cell transcriptional signatures during fatal sepsis. <i>Journal of Leukocyte Biology</i> , 2021, 110, 1253-1268.	1.5	26
14	Structure of galactarate dehydratase, a new fold in an enolase involved in bacterial fitness after antibiotic treatment. <i>Protein Science</i> , 2020, 29, 711-722.	3.1	4
15	Protein structure, amino acid composition and sequence determine proteome vulnerability to oxidation-induced damage. <i>EMBO Journal</i> , 2020, 39, e104523.	3.5	34
16	Microbial function and genital inflammation in young South African women at high risk of HIV infection. <i>Microbiome</i> , 2020, 8, 165.	4.9	23
17	FATCAT 2.0: towards a better understanding of the structural diversity of proteins. <i>Nucleic Acids Research</i> , 2020, 48, W60-W64.	6.5	134
18	Coronavirus3D: 3D structural visualization of COVID-19 genomic divergence. <i>Bioinformatics</i> , 2020, 36, 4360-4362.	1.8	39

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19	Difference contact maps: From what to why in the analysis of the conformational flexibility of proteins. PLoS ONE, 2020, 15, e0226702.	1.1	11
20	Understanding oncogenicity of cancer driver genes and mutations in the cancer genomics era. FEBS Letters, 2020, 594, 4233-4246.	1.3	20
21	Crystal structure of Nsp15 endoribonuclease <sc>NendoU</sc> from <sc>SARSâ€CoV</sc>â€2. Protein Science, 2020, 29, 1596-1605.	3.1	294
22	Comparison of metalâ€bound and unbound structures of aminopeptidase B proteins from <sc><i>Escherichia coli</i></sc> and <sc><i>Yersinia pestis</i></sc>. Protein Science, 2020, 29, 1618-1628.	3.1	3
23	Structures of singleâ€layer Î²â€sheet proteins evolved from Î²â€hairpin repeats. Protein Science, 2019, 28, 1676-1689.	3.1	4
24	Stratification of amyotrophic lateral sclerosis patients: a crowdsourcing approach. Scientific Reports, 2019, 9, 690.	1.6	46
25	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	5.8	240
26	Cancer3D 2.0: interactive analysis of 3D patterns of cancer mutations in cancer subsets. Nucleic Acids Research, 2019, 47, D895-D899.	6.5	12
27	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
28	Draft Genome Sequences of Two Vibrio parahaemolyticus Strains Associated with Gastroenteritis after Raw Seafood Ingestion in Colorado. Genome Announcements, 2018, 6, .	0.8	3
29	The â€Sticky Patchâ€ Model of Crystallization and Modification of Proteins for Enhanced Crystallizability. Methods in Molecular Biology, 2017, 1607, 77-115.	0.4	17
30	The Functional Impact of Alternative Splicing in Cancer. Cell Reports, 2017, 20, 2215-2226.	2.9	517
31	Comparison of algorithms for the detection of cancer drivers at subgene resolution. Nature Methods, 2017, 14, 782-788.	9.0	72
32	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. Genome Medicine, 2017, 9, 113.	3.6	47
33	Neutralizing antibody affords comparable protection against vaginal and rectal simian/human immunodeficiency virus challenge in macaques. Aids, 2016, 30, 1543-1551.	1.0	47
34	<sc>NMR</sc> in structural genomics to increase structural coverage of the protein universe. FEBS Journal, 2016, 283, 3870-3881.	2.2	5
35	Numerous proteins with unique characteristics are degraded by the 26S proteasome following monoubiquitination. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4639-47.	3.3	127
36	UHMâ€ULM interactions in the RBM39â€U2AF65 splicing-factor complex. Acta Crystallographica Section D: Structural Biology, 2016, 72, 497-511.	1.1	36

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37	A Distinct Type of Pilus from the Human Microbiome. <i>Cell</i> , 2016, 165, 690-703.	13.5	78
38	Mutation Drivers of Immunological Responses to Cancer. <i>Cancer Immunology Research</i> , 2016, 4, 789-798.	1.6	32
39	Revealing aperiodic aspects of solenoid proteins from sequence information. <i>Bioinformatics</i> , 2016, 32, 2776-2782.	1.8	3
40	PDBFlex: exploring flexibility in protein structures. <i>Nucleic Acids Research</i> , 2016, 44, D423-D428.	6.5	70
41	Protael: protein data visualization library for the web. <i>Bioinformatics</i> , 2016, 32, 602-604.	1.8	9
42	Crystal Structure and Activity Studies of the C11 Cysteine Peptidase from <i>Parabacteroides merdae</i> in the Human Gut Microbiome. <i>Journal of Biological Chemistry</i> , 2016, 291, 9482-9491.	1.6	15
43	Broadly Neutralizing Antibody Responses in a Large Longitudinal Sub-Saharan HIV Primary Infection Cohort. <i>PLoS Pathogens</i> , 2016, 12, e1005369.	2.1	241
44	PROPER: Performance visualization for optimizing and comparing ranking classifiers in MATLAB. <i>Source Code for Biology and Medicine</i> , 2015, 10, 15.	1.7	3
45	Cofactor-induced reversible folding of <i>Flavodoxin</i> from <i>Actinobacillus acidophilus</i> . <i>Protein Science</i> , 2015, 24, 1600-1608.	3.1	2
46	A Pan-Cancer Catalogue of Cancer Driver Protein Interaction Interfaces. <i>PLoS Computational Biology</i> , 2015, 11, e1004518.	1.5	122
47	Structure and sequence analyses of <i>Bacteroides</i> proteins BVU_4064 and BF1687 reveal presence of two novel predominantly-beta domains, predicted to be involved in lipid and cell surface interactions. <i>BMC Bioinformatics</i> , 2015, 16, 7.	1.2	8
48	AIDA: <i>ab initio</i> domain assembly for automated multi-domain protein structure prediction and domain-domain interaction prediction. <i>Bioinformatics</i> , 2015, 31, 2098-2105.	1.8	59
49	Analysis of Individual Protein Regions Provides Novel Insights on Cancer Pharmacogenomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004024.	1.5	10
50	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, 4666-4671.	3.3	43
51	Cancer3D: understanding cancer mutations through protein structures. <i>Nucleic Acids Research</i> , 2015, 43, D968-D973.	6.5	46
52	Insights into Substrate Specificity of NlpC/P60 Cell Wall Hydrolases Containing Bacterial SH3 Domains. <i>MBio</i> , 2015, 6, e02327-14.	1.8	46
53	POSA: a user-driven, interactive multiple protein structure alignment server. <i>Nucleic Acids Research</i> , 2014, 42, W240-W245.	6.5	50
54	Improving the chances of successful protein structure determination with a random forest classifier. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 627-635.	2.5	46

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55	AIDA: ab initio domain assembly server. <i>Nucleic Acids Research</i> , 2014, 42, W308-W313.	6.5	47
56	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, 1086-1092.	1.5	7
57	Structure-Guided Functional Characterization of DUF1460 Reveals a Highly Specific NlpC/P60 Amidase Family. <i>Structure</i> , 2014, 22, 1799-1809.	1.6	10
58	Molecular characterization of novel pyridoxal-5-phosphate-dependent enzymes from the human microbiome. <i>Protein Science</i> , 2014, 23, 1060-1076.	3.1	8
59	Structural genomics analysis of uncharacterized protein families overrepresented in human gut bacteria identifies a novel glycoside hydrolase. <i>BMC Bioinformatics</i> , 2014, 15, 112.	1.2	13
60	Phylogenomic analysis of glycogen branching and debranching enzymatic duo. <i>BMC Evolutionary Biology</i> , 2014, 14, 183.	3.2	27
61	PubServer: literature searches by homology. <i>Nucleic Acids Research</i> , 2014, 42, W430-W435.	6.5	13
62	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, 2640-2651.	2.5	0
63	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, 169-184.	2.0	25
64	bNAber: database of broadly neutralizing HIV antibodies. <i>Nucleic Acids Research</i> , 2014, 42, D1133-D1139.	6.5	69
65	FFAS-3D: improving fold recognition by including optimized structural features and template re-ranking. <i>Bioinformatics</i> , 2014, 30, 660-667.	1.8	97
66	Crystal structures of three representatives of a new <i>scp</i> family PF14869 (DUF4488) suggest they function in sugar binding/uptake. <i>Protein Science</i> , 2014, 23, 1380-1391.	3.1	3
67	Structure- and context-based analysis of the GxGYxYP family reveals a new putative class of Glycoside Hydrolase. <i>BMC Bioinformatics</i> , 2014, 15, 196.	1.2	8
68	Basis for substrate recognition and distinction by matrix metalloproteinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4148-55.	3.3	75
69	S-Nitrosylation-Mediated Redox Transcriptional Switch Modulates Neurogenesis and Neuronal Cell Death. <i>Cell Reports</i> , 2014, 8, 217-228.	2.9	58
70	ConSole: using modularity of Contact maps to locate Solenoid domains in protein structures. <i>BMC Bioinformatics</i> , 2014, 15, 119.	1.2	23
71	Structure and computational analysis of a novel protein with metallopeptidase-like and circularly permuted winged-helix-turn-helix domains reveals a possible role in modified polysaccharide biosynthesis. <i>BMC Bioinformatics</i> , 2014, 15, 75.	1.2	1
72	Structural systems biology: from bacterial to cancer networks. <i>BMC Genomics</i> , 2014, 15, O14.	1.2	0

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73	e-Driver: a novel method to identify protein regions driving cancer. <i>Bioinformatics</i> , 2014, 30, 3109-3114.	1.8	116
74	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, 164-170.	1.5	15
75	OUR EXPANDING PROTEIN UNIVERSE. , 2014, , .		0
76	THE MICROBIOME(S): MICROBIOTA, FAMILIES, FUNCTIONS. , 2014, , .		0
77	JCSG â€œ Adapting Structural Genomics to Eukaryotic Complexes. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C1148-C1148.	0.0	0
78	MORPH-PRO: a novel algorithm and web server for protein morphing. <i>Algorithms for Molecular Biology</i> , 2013, 8, 19.	0.3	9
79	Evolution of the Animal Apoptosis Network. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a008649-a008649.	2.3	63
80	Two Pfam protein families characterized by a crystal structure of protein lpg2210 from <i>Legionella pneumophila</i> . <i>BMC Bioinformatics</i> , 2013, 14, 265.	1.2	3
81	Polysaccharides utilization in human gut bacterium <i>Bacteroides thetaiotaomicron</i> : comparative genomics reconstruction of metabolic and regulatory networks. <i>BMC Genomics</i> , 2013, 14, 873.	1.2	122
82	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1243-1249.	3.6	153
83	Structural Systems Biology Evaluation of Metabolic Thermotolerance in <i>Escherichia coli</i> . <i>Science</i> , 2013, 340, 1220-1223.	6.0	111
84	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013, 14, 341.	1.2	8
85	Structure and Function of a Novel <i>Id</i> -Carboxypeptidase A Involved in Peptidoglycan Recycling. <i>Journal of Bacteriology</i> , 2013, 195, 5555-5566.	1.0	16
86	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.	1.6	7
87	This DÃ©jÃ Vu Feelingâ€”Analysis of Multidomain Protein Evolution in Eukaryotic Genomes. <i>PLoS Computational Biology</i> , 2012, 8, e1002701.	1.5	37
88	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, 2987-2999.	1.0	14
89	A Blueprint for HIV Vaccine Discovery. <i>Cell Host and Microbe</i> , 2012, 12, 396-407.	5.1	348
90	MORPH-PRO: A Novel Algorithm and Web Server for Protein Morphing. <i>Lecture Notes in Computer Science</i> , 2012, , 262-273.	1.0	0

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91	Structure of a Novel Winged-Helix Like Domain from Human NFRKB Protein. PLoS ONE, 2012, 7, e43761.	1.1	5
92	Structure of the pilus assembly protein TadZ from <i>Eubacterium rectale</i> : implications for polar localization. Molecular Microbiology, 2012, 83, 712-727.	1.2	22
93	Structure of an MmyB-Like Regulator from <i>C. aurantiacus</i> , Member of a New Transcription Factor Family Linked to Antibiotic Metabolism in Actinomycetes. PLoS ONE, 2012, 7, e41359.	1.1	14
94	Structural Determinants of Limited Proteolysis. Journal of Proteome Research, 2011, 10, 3642-3651.	1.8	68
95	Strong functional patterns in the evolution of eukaryotic genomes revealed by the reconstruction of ancestral protein domain repertoires. Genome Biology, 2011, 12, R4.	13.9	84
96	TIR domain-containing adaptor SARM is a late addition to the ongoing microbe-host dialog. Developmental and Comparative Immunology, 2011, 35, 461-468.	1.0	66
97	Dynamics of coregulator-induced conformational perturbations in androgen receptor ligand binding domain. Molecular and Cellular Endocrinology, 2011, 341, 1-8.	1.6	8
98	Structural and Sequence Analysis of Imelysin-Like Proteins Implicated in Bacterial Iron Uptake. PLoS ONE, 2011, 6, e21875.	1.1	17
99	Metagenomics and the protein universe. Current Opinion in Structural Biology, 2011, 21, 398-403.	2.6	62
100	Crystal structure of a metal-dependent phosphoesterase (YP_910028.1) from <i>Bifidobacterium adolescentis</i> : Computational prediction and experimental validation of phosphoesterase activity. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2146-2160.	1.5	11
101	Internal organization of large protein families: Relationship between the sequence, structure, and function-based clustering. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2389-2402.	1.5	4
102	TOPSAN: a dynamic web database for structural genomics. Nucleic Acids Research, 2011, 39, D494-D496.	6.5	17
103	Structural Insights into Inhibition of <i>Bacillus anthracis</i> Sporulation by a Novel Class of Non-heme Globin Sensor Domains. Journal of Biological Chemistry, 2011, 286, 8448-8458.	1.6	22
104	The FGGY Carbohydrate Kinase Family: Insights into the Evolution of Functional Specificities. PLoS Computational Biology, 2011, 7, e1002318.	1.5	48
105	FFAS server: novel features and applications. Nucleic Acids Research, 2011, 39, W38-W44.	6.5	130
106	Structure and Function of the First Full-Length Murein Peptide Ligase (Mpl) Cell Wall Recycling Protein. PLoS ONE, 2011, 6, e17624.	1.1	30
107	Structural Analysis of Papain-Like NlpC/P60 Superfamily Enzymes with a Circularly Permuted Topology Reveals Potential Lipid Binding Sites. PLoS ONE, 2011, 6, e22013.	1.1	22
108	CARD8 and NLRP1 Undergo Autoproteolytic Processing through a ZU5-Like Domain. PLoS ONE, 2011, 6, e27396.	1.1	168

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109	Domain architecture evolution of pattern-recognition receptors. <i>Immunogenetics</i> , 2010, 62, 263-272.	1.2	68
110	Structure of a Virulence Regulatory Factor CvfB Reveals a Novel Winged Helix RNA Binding Module. <i>Structure</i> , 2010, 18, 537-547.	1.6	23
111	TOPSAN: a collaborative annotation environment for structural genomics. <i>BMC Bioinformatics</i> , 2010, 11, 426.	1.2	19
112	A widespread peroxiredoxin-like domain present in tumor suppression- and progression-implicated proteins. <i>BMC Genomics</i> , 2010, 11, 590.	1.2	26
113	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, 1254-1260.	0.7	3
114	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, 1347-1353.	0.7	5
115	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, 1230-1236.	0.7	17
116	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, 1174-1181.	0.7	8
117	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, 1211-1217.	0.7	10
118	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, 1205-1210.	0.7	3
119	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, 1198-1204.	0.7	9
120	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, 1153-1159.	0.7	18
121	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, 1245-1253.	0.7	8
122	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, 1265-1273.	0.7	8
123	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, 1218-1225.	0.7	8
124	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, 1182-1189.	0.7	3
125	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, 1160-1166.	0.7	20
126	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, 1281-1286.	0.7	9

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127	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, 1167-1173.	0.7	3
128	Structures of three members of Pfam PF02663 (FmdE) implicated in microbial methanogenesis reveal a conserved $\hat{1}\pm+\hat{1}^2$ core domain and an auxiliary C-terminal treble-clef zinc finger. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1335-1346.	0.7	8
129	Structure of the $\hat{1}^3$ -D<sc>L</sc>-glutamyl-<sc>L</sc>-diamino acid endopeptidase YkfC from <i>Bacillus cereus</i> in complex with L<sc>L</sc>-Ala- $\hat{1}^3$ -D<sc>L</sc>-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1354-1364.	0.7	64
130	The structure of Haemophilus influenzae prephenate dehydrogenase suggests unique features of bifunctional TyrA enzymes. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1317-1325.	0.7	11
131	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, 1297-1305.	0.7	30
132	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, 1237-1244.	0.7	2
133	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, 1287-1296.	0.7	2
134	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, 1274-1280.	0.7	11
135	TOPSAN: use of a collaborative environment for annotating, analyzing and disseminating data on JCSG and PSI structures. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1143-1147.	0.7	33
136	Structure of a tryptophanyl-tRNA synthetase containing an iron-sulfur cluster. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1326-1334.	0.7	19
137	The JCSG high-throughput structural biology pipeline. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1137-1142.	0.7	99
138	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, 2131-2140.	3.1	12
139	Expansion of the Protein Repertoire in Newly Explored Environments: Human Gut Microbiome Specific Protein Families. <i>PLoS Computational Biology</i> , 2010, 6, e1000798.	1.5	52
140	Pre-calculated protein structure alignments at the RCSB PDB website. <i>Bioinformatics</i> , 2010, 26, 2983-2985.	1.8	183
141	A Primer on Metagenomics. <i>PLoS Computational Biology</i> , 2010, 6, e1000667.	1.5	523
142	S-Nitrosylation of Drp1 links excessive mitochondrial fission to neuronal injury in neurodegeneration. <i>Mitochondrion</i> , 2010, 10, 573-578.	1.6	120
143	Bacterial Pleckstrin Homology Domains: A Prokaryotic Origin for the PH Domain. <i>Journal of Molecular Biology</i> , 2010, 396, 31-46.	2.0	32
144	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, 647-663.	2.0	41

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145	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, 403-417.	2.0	36
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