

# Henry van den Bedem

## List of Publications by Year in descending order

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124  
papers

3,585  
citations

201674

27  
h-index

175258

52  
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139  
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139  
docs citations

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times ranked

4405  
citing authors

#	ARTICLE	IF	CITATIONS
1	AtomNet PoseRanker: Enriching Ligand Pose Quality for Dynamic Proteins in Virtual High-Throughput Screens. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 1178-1189.	5.4	13
2	Ligand binding remodels protein side-chain conformational heterogeneity. <i>ELife</i> , 2022, 11, .	6.0	33
3	Modeling of Hidden Structures Using Sparse Chemical Shift Data from NMR Relaxation Dispersion. <i>Biophysical Journal</i> , 2021, 120, 296-305.	0.5	4
4	qFit: 3: Protein and ligand multiconformer modeling for X-ray crystallographic and single-particle cryo-EM density maps. <i>Protein Science</i> , 2021, 30, 270-285.	7.6	34
5	Kinematic Flexibility Analysis of Active and Inactive Kinase Conformations. <i>Proceedings in Applied Mathematics and Mechanics</i> , 2021, 20, e202000166.	0.2	1
6	Reproducibility of protein x-ray diffuse scattering and potential utility for modeling atomic displacement parameters. <i>Structural Dynamics</i> , 2021, 8, 044701.	2.3	5
7	Comparing serial X-ray crystallography and microcrystal electron diffraction (MicroED) as methods for routine structure determination from small macromolecular crystals. <i>IUCr</i> , 2020, 7, 306-323.	2.2	32
8	Sequence-guided protein structure determination using graph convolutional and recurrent networks. , 2020, , .		7
9	Shining light on cysteine modification: connecting protein conformational dynamics to catalysis and regulation. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 958-966.	2.4	18
10	Molecular Recognition of M1-Linked Ubiquitin Chains by Native and Phosphorylated UBAN Domains. <i>Journal of Molecular Biology</i> , 2019, 431, 3146-3156.	4.2	20
11	Transport Properties of Nanoporous, Chemically Forced Biological Lattices. <i>Journal of Physical Chemistry B</i> , 2019, 123, 10331-10342.	2.6	0
12	Cryo-EM structures of <i>Helicobacter pylori</i> vacuolating cytotoxin A oligomeric assemblies at near-atomic resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6800-6805.	7.1	33
13	Kino-Geometric Modeling: Insights into Protein Molecular Mechanisms. <i>Proceedings in Applied Mathematics and Mechanics</i> , 2019, 19, e201900448.	0.2	0
14	Mix-and-inject XFEL crystallography reveals gated conformational dynamics during enzyme catalysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25634-25640.	7.1	56
15	Collision-free poisson motion planning in ultra high-dimensional molecular conformation spaces. <i>Journal of Computational Chemistry</i> , 2018, 39, 711-720.	3.3	5
16	Bridging protein rigidity theory and normal modes using kino-geometric analysis with hierarchical constraint relaxation. <i>Proceedings in Applied Mathematics and Mechanics</i> , 2018, 18, e201800251.	0.2	0
17	qFit-ligand Reveals Widespread Conformational Heterogeneity of Drug-Like Molecules in X-Ray Electron Density Maps. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 11183-11198.	6.4	44
18	Reply to "Misreading chaperone" substrate complexes from random noise™. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 990-991.	8.2	2

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19	Kinematic Flexibility Analysis: Hydrogen Bonding Patterns Impart a Spatial Hierarchy of Protein Motion. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 2108-2122.	5.4	11
20	Cryo Electron Tomography and Reaction-Diffusion Simulations Reveal a Molecular and Evolutionary Basis for Charged Archaeal Surface Layer Proteins. <i>Biophysical Journal</i> , 2018, 114, 495a.	0.5	1
21	Nutrient transport suggests an evolutionary basis for charged archaeal surface layer proteins. <i>ISME Journal</i> , 2018, 12, 2389-2402.	9.8	51
22	Conformational variation of proteins at room temperature is not dominated by radiation damage. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 73-82.	2.4	50
23	Frustration-guided motion planning reveals conformational transitions in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1795-1807.	2.6	7
24	Fast, clash-free RNA conformational morphing using molecular junctions. <i>Bioinformatics</i> , 2017, 33, 2114-2122.	4.1	4
25	Molecular mechanisms of chronic traumatic encephalopathy. <i>Current Opinion in Biomedical Engineering</i> , 2017, 1, 23-30.	3.4	15
26	Integrated structural biology and molecular ecology of N <sub>2</sub> -fixing enzymes from ammonia-oxidizing archaea. <i>Environmental Microbiology Reports</i> , 2017, 9, 484-491.	2.4	26
27	Probing RNA Native Conformational Ensembles with Structural Constraints. <i>Journal of Computational Biology</i> , 2016, 23, 362-371.	1.6	4
28	Atomic resolution experimental phase information reveals extensive disorder and bound 2-methyl-2,4-pentanediol in Ca <sup>2+</sup> -calmodulin. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 83-92.	2.3	6
29	Visualizing chaperone-assisted protein folding. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 691-697.	8.2	52
30	Coupled Motions in $\hat{I}^2$ AR-G $\hat{I}$ 's Conformational Ensembles. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 946-956.	5.3	12
31	A geometric approach to characterize rigidity in proteins. <i>Proceedings in Applied Mathematics and Mechanics</i> , 2015, 15, 89-90.	0.2	0
32	Exposing Hidden Alternative Backbone Conformations in X-ray Crystallography Using qFit. <i>PLoS Computational Biology</i> , 2015, 11, e1004507.	3.2	81
33	KGSrna: Efficient 3D Kinematics-Based Sampling for Nucleic Acids. <i>Lecture Notes in Computer Science</i> , 2015, , 80-95.	1.3	4
34	Tau-ism: The Yin and Yang of Microtubule Sliding, Detachment, and Rupture. <i>Biophysical Journal</i> , 2015, 109, 2215-2217.	0.5	25
35	Geometric analysis characterizes molecular rigidity in generic and non-generic protein configurations. <i>Journal of the Mechanics and Physics of Solids</i> , 2015, 83, 36-47.	4.8	14
36	Integrative, dynamic structural biology at atomic resolution – it's about time. <i>Nature Methods</i> , 2015, 12, 307-318.	19.0	220

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37	Nullspace Sampling with Holonomic Constraints Reveals Molecular Mechanisms of Protein G $\hat{I}$ s. PLoS Computational Biology, 2015, 11, e1004361.	3.2	10
38	Mapping the conformational landscape of a dynamic enzyme by multitemperature and XFEL crystallography. ELife, 2015, 4, .	6.0	143
39	Integrated description of protein dynamics from room-temperature X-ray crystallography and NMR. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E445-54.	7.1	142
40	Characterizing RNA ensembles from NMR data with kinematic models. Nucleic Acids Research, 2014, 42, 9562-9572.	14.5	25
41	Crystal Cryocooling Distorts Conformational Heterogeneity in a Model Michaelis Complex of DHFR. Structure, 2014, 22, 899-910.	3.3	131
42	Discovering and Manipulating Protein Conformational Heterogeneity and Function. Biophysical Journal, 2014, 106, 635a-636a.	0.5	0
43	Radiation damage effects on protein conformation at room temperature and 100K. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C344-C344.	0.1	0
44	Automated identification of functional dynamic contact networks from X-ray crystallography. Nature Methods, 2013, 10, 896-902.	19.0	130
45	Distributed structure determination at the JCSG. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 368-375.	2.5	24
46	Accessing protein conformational ensembles using room-temperature X-ray crystallography. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16247-16252.	7.1	511
47	Structure of an essential bacterial protein YeaZ (TM0874) from <i>Thermotoga maritima</i> at 2.5 Å resolution. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1230-1236.	0.7	17
48	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. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1198-1204.	0.7	9
49	Structure of the $\beta$ -glutamyl-L-diamino acid endopeptidase YkfC from <i>Bacillus cereus</i> in complex with L-Ala- $\beta$ -D-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1354-1364.	0.7	64
50	The structure of Haemophilus influenzae prephenate dehydrogenase suggests unique features of bifunctional TyrA enzymes. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1317-1325.	0.7	11
51	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. Protein Science, 2010, 19, 2131-2140.	7.6	12
52	Bacterial Pleckstrin Homology Domains: A Prokaryotic Origin for the PH Domain. Journal of Molecular Biology, 2010, 396, 31-46.	4.2	32
53	Crystal Structure of the First Eubacterial Mre11 Nuclease Reveals Novel Features that May Discriminate Substrates During DNA Repair. Journal of Molecular Biology, 2010, 397, 647-663.	4.2	41
54	Structural and Functional Characterizations of SsgB, a Conserved Activator of Developmental Cell Division in Morphologically Complex Actinomycetes. Journal of Biological Chemistry, 2009, 284, 25268-25279.	3.4	23

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55	Structural Basis of Murein Peptide Specificity of a $\hat{I}^3$ -D-Glutamyl-L-Diamino Acid Endopeptidase. Structure, 2009, 17, 303-313.	3.3	73
56	Crystal structure of a novel archaeal AAA+ ATPase SSO1545 from <i>Sulfolobus solfataricus</i> . Proteins: Structure, Function and Bioinformatics, 2009, 74, 1041-1049.	2.6	8
57	Crystal structure of the Fic (Filamentation induced by cAMP) family protein SO4266 (gi   24375750) from <i>Shewanella oneidensis</i> MR $\hat{C}1$ at 1.6 Å... resolution. Proteins: Structure, Function and Bioinformatics, 2009, 75, 264-271.	2.6	23
58	Crystal structure of a novel Sm $\hat{C}$ -like protein of putative cyanophage origin at 2.60 Å... resolution. Proteins: Structure, Function and Bioinformatics, 2009, 75, 296-307.	2.6	18
59	Modeling discrete heterogeneity in X-ray diffraction data by fitting multi-conformers. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1107-1117.	2.5	104
60	A Structural Basis for the Regulatory Inactivation of DnaA. Journal of Molecular Biology, 2009, 385, 368-380.	4.2	15
61	Crystal Structure of Histidine Phosphotransfer Protein ShpA, an Essential Regulator of Stalk Biogenesis in <i>Caulobacter crescentus</i> . Journal of Molecular Biology, 2009, 390, 686-698.	4.2	13
62	Modeling Structural Heterogeneity in Proteins from X-Ray Data. Springer Tracts in Advanced Robotics, 2009, , 551-566.	0.4	2
63	Crystal structure of 2 $\hat{C}$ -keto $\hat{C}3$ -deoxygluconate kinase (TM0067) from <i>Thermotoga maritima</i> at 2.05 Å... resolution. Proteins: Structure, Function and Bioinformatics, 2008, 70, 603-608.	2.6	9
64	Crystal structure of AICAR transformylase IMP cyclohydrolase (TM1249) from <i>Thermotoga maritima</i> at 1.88 Å... resolution. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1042-1049.	2.6	7
65	Crystal structure of an ADP $\hat{C}$ -ribosylated protein with a cytidine deaminase $\hat{C}$ -like fold, but unknown function (TM1506), from <i>Thermotoga maritima</i> at 2.70 Å... resolution. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1546-1552.	2.6	6
66	Crystal structures of MW1337R and lin2004: Representatives of a novel protein family that adopt a four $\hat{C}$ -helical bundle fold. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1589-1596.	2.6	3
67	Efficient Algorithms to Explore Conformation Spaces of Flexible Protein Loops. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 534-545.	3.0	37
68	Crystal structure of homoserine O-succinyltransferase from <i>Bacillus cereus</i> at 2.4 Å... resolution. Proteins: Structure, Function and Bioinformatics, 2007, 68, 999-1005.	2.6	13
69	Crystal structure of a transcription regulator (TM1602) from <i>Thermotoga maritima</i> at 2.3 Å... resolution. Proteins: Structure, Function and Bioinformatics, 2007, 67, 247-252.	2.6	5
70	Crystal structure of NMA1982 from <i>Neisseria meningitidis</i> at 1.5 Å... resolution provides a structural scaffold for nonclassical, eukaryotic $\hat{C}$ -like phosphatases. Proteins: Structure, Function and Bioinformatics, 2007, 69, 415-421.	2.6	11
71	Crystal structure of TM1030 from <i>Thermotoga maritima</i> at 2.3 Å... resolution reveals molecular details of its transcription repressor function. Proteins: Structure, Function and Bioinformatics, 2007, 68, 418-424.	2.6	5
72	Crystal structures of two novel dye $\hat{C}$ -decolorizing peroxidases reveal a $\hat{I}^2$ $\hat{C}$ -barrel fold with a conserved heme $\hat{C}$ -binding motif. Proteins: Structure, Function and Bioinformatics, 2007, 69, 223-233.	2.6	81

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73	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, 433-439.	2.6	6
74	Identification and structural characterization of heme binding in a novel dye-decolorizing peroxidase, TyrA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 234-243.	2.6	67
75	Efficient Algorithms to Explore Conformation Spaces of Flexible Protein Loops. <i>Lecture Notes in Computer Science</i> , 2007, , 265-276.	1.3	3
76	Automated diffraction image analysis and spot searching for high-throughput crystal screening. <i>Journal of Applied Crystallography</i> , 2006, 39, 112-119.	4.5	106
77	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, 1106-1111.	2.6	7
78	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, 256-260.	2.6	15
79	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, 1112-1118.	2.6	6
80	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, 808-813.	2.6	28
81	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, 1083-1090.	2.6	10
82	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, 771-776.	2.6	3
83	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, 777-782.	2.6	7
84	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, 249-254.	2.6	6
85	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, 243-248.	2.6	10
86	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, 527-537.	2.6	8
87	Real-space protein-model completion: an inverse-kinematics approach. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 2-13.	2.5	47
88	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, 971-975.	2.6	14
89	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, 976-981.	2.6	4
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, 869-874.	2.6	16

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91	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, 864-868.	2.6	13
92	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.	2.6	12
93	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, 444-448.	2.6	10
94	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, 449-453.	2.6	69
95	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, 669-673.	2.6	13
96	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, 1132-1136.	2.6	9
97	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> , 2005, 62, 292-296.	2.6	6
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, 387-391.	2.6	18
99	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, 392-395.	2.6	16
100	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, 474-478.	2.6	11
101	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, 213-217.	2.6	35
102	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, 768-771.	2.6	20
103	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, 1078-1081.	2.6	21
104	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.	2.6	8
105	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, 404-408.	2.6	28
106	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, 167-170.	2.6	29
107	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, 171-175.	2.6	14
108	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, 611-614.	2.6	27

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109	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, 607-610.	2.6	8
110	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, 615-618.	2.6	6
111	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, 629-633.	2.6	9
112	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, 619-624.	2.6	2
113	Crystal structure of an $\hat{I}\pm/\hat{I}^2$ serine hydrolase (YDR428C) from <i>Saccharomyces cerevisiae</i> at 1.85 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 755-758.	2.6	11
114	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, 801-805.	2.6	6
115	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, 806-809.	2.6	7
116	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, 759-763.	2.6	17
117	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, 810-813.	2.6	17
118	Crystal structure of uronate isomerase (TM0064) from <i>Thermotoga maritima</i> at 2.85 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 142-145.	2.6	8
119	Crystal structure of $\hat{I}^3$ -glutamyl phosphate reductase (TM0293) from <i>Thermotoga maritima</i> at 2.0 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 157-161.	2.6	17
120	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> , 2003, 54, 174-177.	2.6	32
121	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, 142-145.	2.6	50
122	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> , 2002, 50, 371-374.	2.6	8
123	Statistical properties of hyperbolic systems with tangential singularities. <i>Nonlinearity</i> , 2001, 14, 1393-1410.	1.4	1
124	Kinematic Vibrational Entropy Assessment and Analysis of SARS CoV-2 Main Protease. <i>Journal of Chemical Information and Modeling</i> , 0, , .	5.4	2