

Thomas C Terwilliger

List of Publications by Year in descending order

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184
papers

58,732
citations

25034

57
h-index

4432

172
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200
all docs

200
docs citations

200
times ranked

54597
citing authors

#	ARTICLE	IF	CITATIONS
1	A monomeric mycobacteriophage immunity repressor utilizes two domains to recognize an asymmetric DNA sequence. <i>Nature Communications</i> , 2022, 13, .	12.8	5
2	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	19.0	73
3	Protein identification from electron cryomicroscopy maps by automated model building and side-chain matching. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 457-462.	2.3	9
4	Engineering an efficient and bright split <i>Corynactis californica</i> green fluorescent protein. <i>Scientific Reports</i> , 2021, 11, 18440.	3.3	2
5	Cryo-EM map interpretation and protein model building using iterative map segmentation. <i>Protein Science</i> , 2020, 29, 87-99.	7.6	27
6	Bottom-up structural proteomics: cryoEM of protein complexes enriched from the cellular milieu. <i>Nature Methods</i> , 2020, 17, 79-85.	19.0	80
7	Improvement of cryo-EM maps by density modification. <i>Nature Methods</i> , 2020, 17, 923-927.	19.0	243
8	Density modification of cryo-EM maps. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 912-925.	2.3	28
9	Bottom-up Structural Proteomics: Cryo-EM of Protein Complexes Enriched from the Cellular Milieu. <i>Biophysical Journal</i> , 2020, 118, 291a.	0.5	0
10	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in <i>Phenix</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 861-877.	2.3	4,060
11	BpeB, a major resistance-nodulation-cell division transporter from <i>Burkholderia cenocepacia</i> : construct design, crystallization and preliminary structural analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 710-716.	0.8	1
12	A fully automatic method yielding initial models from high-resolution cryo-electron microscopy maps. <i>Nature Methods</i> , 2018, 15, 905-908.	19.0	137
13	Map segmentation, automated model-building and their application to the Cryo-EM Model Challenge. <i>Journal of Structural Biology</i> , 2018, 204, 338-343.	2.8	6
14	Automated map sharpening by maximization of detail and connectivity. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 545-559.	2.3	218
15	Real-space refinement in <i>PHENIX</i> for cryo-EM and crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 531-544.	2.3	2,065
16	New tools for the analysis and validation of cryo-EM maps and atomic models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 814-840.	2.3	575
17	Responses to 'Atomic resolution': a badly abused term in structural biology. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 381-383.	2.3	7
18	A genome-wide structure-based survey of nucleotide binding proteins in <i>M. tuberculosis</i> . <i>Scientific Reports</i> , 2017, 7, 12489.	3.3	5

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19	Structural and Biophysical Characterization of the Mycobacterium tuberculosis Protein Rv0577, a Protein Associated with Neutral Red Staining of Virulent Tuberculosis Strains and Homologue of the Streptomyces coelicolor Protein KbpA. <i>Biochemistry</i> , 2017, 56, 4015-4027.	2.5	4
20	Polder maps: improving OMIT maps by excluding bulk solvent. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 148-157.	2.3	500
21	Raw diffraction data preservation and reuse: overview, update on practicalities and metadata requirements. <i>IUCrj</i> , 2017, 4, 87-99.	2.2	34
22	SAD phasing for easy or challenging problems. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a35-a35.	0.1	0
23	Phasing strategies II – molecular replacement. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a391-a391.	0.1	0
24	Model-building using cryo-EM and crystallographic maps. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C1327-C1327.	0.1	0
25	Can I solve my structure by SAD phasing? Planning an experiment, scaling data and evaluating the useful anomalous correlation and anomalous signal. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 359-374.	2.3	29
26	Efficient merging of data from multiple samples for determination of anomalous substructure. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 296-302.	2.3	13
27	Can I solve my structure by SAD phasing? Anomalous signal in SAD phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 346-358.	2.3	31
28	RNA Structure Refinement Using the ERRASER-Phenix Pipeline. <i>Methods in Molecular Biology</i> , 2016, 1320, 269-282.	0.9	24
29	Predicting X-ray diffuse scattering from translation-“libration”-screw structural ensembles. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1657-1667.	2.5	14
30	FEM: feature-enhanced map. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 646-666.	2.5	157
31	A Suite of Engineered GFP Molecules for Oligomeric Scaffolding. <i>Structure</i> , 2015, 23, 1754-1768.	3.3	30
32	X-ray structure determination using low-resolution electron microscopy maps for molecular replacement. <i>Nature Protocols</i> , 2015, 10, 1275-1284.	12.0	22
33	Protein crystallography from the perspective of technology developments. <i>Crystallography Reviews</i> , 2015, 21, 122-153.	1.5	33
34	Macromolecular X-ray structure determination using weak, single-wavelength anomalous data. <i>Nature Methods</i> , 2015, 12, 127-130.	19.0	31
35	Conformational dynamics of a crystalline protein from microsecond-scale molecular dynamics simulations and diffuse X-ray scattering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17887-17892.	7.1	55
36	Continuous mutual improvement of macromolecular structure models in the PDB and of X-ray crystallographic software: the dual role of deposited experimental data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2533-2543.	2.5	29

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37	Metrics for comparison of crystallographic maps. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2593-2606.	2.5	29
38	Archiving raw crystallographic data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2500-2501.	2.5	18
39	1.55 Å resolution X-ray crystal structure of Rv3902c from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 414-417.	0.8	1
40	Automated identification of elemental ions in macromolecular crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1104-1114.	2.5	40
41	Crystal structure of the CRISPR RNA-guided surveillance complex from <i>Escherichia coli</i> . <i>Science</i> , 2014, 345, 1473-1479.	12.6	226
42	Combining Crystallographic and Structure-Modeling Approaches in Macromolecular Crystallography. <i>Biophysical Journal</i> , 2014, 106, 34a.	0.5	0
43	Diffuse X-Ray Scattering for Ensemble Modeling of Crystalline Proteins. <i>Biophysical Journal</i> , 2014, 106, 384a.	0.5	0
44	Automating crystallographic structure solution and refinement of protein-ligand complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 144-154.	2.5	43
45	Ligand placement based on prior structures: the guided ligand-replacement method. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 134-143.	2.5	11
46	Subfamily-Specific Adaptations in the Structures of Two Penicillin-Binding Proteins from <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2014, 9, e116249.	2.5	6
47	Improved low-resolution crystallographic refinement with Phenix and Rosetta. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C782-C782.	0.1	0
48	New tools for automated model completion and refinement. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C327-C327.	0.1	0
49	Finding non-crystallographic symmetry in density maps of macromolecular structures. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 91-95.	1.2	15
50	Crystal structure of AcrB complexed with linezolid at 3.5 Å resolution. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 71-75.	1.2	38
51	Improved low-resolution crystallographic refinement with Phenix and Rosetta. <i>Nature Methods</i> , 2013, 10, 1102-1104.	19.0	175
52	Improved Crystallographic Structures Using Extensive Combinatorial Refinement. <i>Structure</i> , 2013, 21, 1923-1930.	3.3	18
53	Crystal structure of <i>Bacillus subtilis</i> GabR, an autorepressor and transcriptional activator of <i>gabT</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17820-17825.	7.1	66
54	Advances, Interactions, and Future Developments in the CNS, Phenix, and Rosetta Structural Biology Software Systems. <i>Annual Review of Biophysics</i> , 2013, 42, 265-287.	10.0	88

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55	Model morphing and sequence assignment after molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2244-2250.	2.5	37
56	Split green fluorescent protein as a modular binding partner for protein crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2513-2523.	2.5	29
57	Improving experimental phases for strong reflections prior to density modification. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2039-2049.	2.5	7
58	A New Protein-Protein Interaction Sensor Based on Tripartite Split-GFP Association. <i>Scientific Reports</i> , 2013, 3, 2854.	3.3	190
59	Model-Building and Reduction of Model Bias in Electron Density Maps. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2013, , 193-203.	0.5	1
60	Using <i>PHASER</i> for phasing in conjunction with wide-convergence refinement and model building techniques. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s40-s40.	0.3	2
61	Automatic Fortran to C++ conversion with FABLE. <i>Source Code for Biology and Medicine</i> , 2012, 7, 5.	1.7	15
62	phenix.mr_rosetta: molecular replacement and model rebuilding with Phenix and Rosetta. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 81-90.	1.2	131
63	Enhancement of crystallization with nucleotide ligands identified by dye-ligand affinity chromatography. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 71-79.	1.2	5
64	Chemical shift assignments for Rv0577, a putative glyoxylase associated with virulence from <i>Mycobacterium tuberculosis</i> . <i>Biomolecular NMR Assignments</i> , 2012, 6, 43-46.	0.8	5
65	Graphical tools for macromolecular crystallography in <i>PHENIX</i> . <i>Journal of Applied Crystallography</i> , 2012, 45, 581-586.	4.5	139
66	Application of DEN refinement and automated model building to a difficult case of molecular-replacement phasing: the structure of a putative succinyl-diaminopimelate desuccinylase from <i>Corynebacterium glutamicum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 391-403.	2.5	26
67	Towards automated crystallographic structure refinement with <i>phenix.refine</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 352-367.	2.5	4,573
68	Improved crystallographic models through iterated local density-guided model deformation and reciprocal-space refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 861-870.	2.5	37
69	Inaugural structure from the DUF3349 superfamily of proteins, <i>Mycobacterium tuberculosis</i> Rv0543c. <i>Archives of Biochemistry and Biophysics</i> , 2011, 506, 150-156.	3.0	6
70	The Phenix software for automated determination of macromolecular structures. <i>Methods</i> , 2011, 55, 94-106.	3.8	764
71	Improved molecular replacement by density- and energy-guided protein structure optimization. <i>Nature</i> , 2011, 473, 540-543.	27.8	226
72	The TB Structural Genomics Consortium: A decade of progress. <i>Tuberculosis</i> , 2011, 91, 155-172.	1.9	39

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73	The success of structural genomics. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 43-44.	1.2	20
74	Experimental mapping of soluble protein domains using a hierarchical approach. <i>Nucleic Acids Research</i> , 2011, 39, e125-e125.	14.5	29
75	A high-throughput immobilized bead screen for stable proteins and multi-protein complexes. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 565-578.	2.1	12
76	The optimization of in vitro high-throughput chemical lysis of <i>Escherichia coli</i> . Application to ACP domain of the polyketide synthase ppsC from <i>Mycobacterium tuberculosis</i> . <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 41-49.	1.2	19
77	Solution structure of Rv2377c-founding member of the Mbth-like protein family. <i>Tuberculosis</i> , 2010, 90, 245-251.	1.9	37
78	<i>PHENIX</i> : a comprehensive Python-based system for macromolecular structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 213-221.	2.5	20,564
79	Rapid chain tracing of polypeptide backbones in electron-density maps. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 285-294.	2.5	6
80	Rapid model building of β -sheets in electron-density maps. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 276-284.	2.5	4
81	Rapid model building of α -helices in electron-density maps. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 268-275.	2.5	25
82	Structure of Rv1848 (UreA), the <i>Mycobacterium tuberculosis</i> urease β subunit. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 781-786.	0.7	10
83	An Extracellular Disulfide Bond Forming Protein (DsbF) from <i>Mycobacterium tuberculosis</i> : Structural, Biochemical, and Gene Expression Analysis. <i>Journal of Molecular Biology</i> , 2010, 396, 1211-1226.	4.2	23
84	Recent developments in phasing and structure refinement for macromolecular crystallography. <i>Current Opinion in Structural Biology</i> , 2009, 19, 566-572.	5.7	23
85	Automated, high-throughput platform for protein solubility screening using a split-GFP system. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 47-55.	1.2	32
86	Analysis of nucleoside-binding proteins by ligand-specific elution from dye resin: application to <i>Mycobacterium tuberculosis</i> aldehyde dehydrogenases. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 291-301.	1.2	13
87	Decision-making in structure solution using Bayesian estimates of map quality: the <i>PHENIX</i> AutoSol wizard. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 582-601.	2.5	804
88	Independent tyrosyl contributions to the CD of Ff gene 5 protein and the distinctive effects of Y41H and Y41F mutants on protein-protein cooperative interactions. <i>Protein Science</i> , 2009, 11, 601-613.	7.6	5
89	Lessons from Structural Genomics. <i>Annual Review of Biophysics</i> , 2009, 38, 371-383.	10.0	115
90	Iterative model building, structure refinement and density modification with the <i>PHENIX</i> AutoBuild wizard. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 61-69.	2.5	1,319

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91	Iterative-build OMIT maps: map improvement by iterative model building and refinement without model bias. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 515-524.	2.5	165
92	Automated Structure Solution with the PHENIX Suite. <i>Methods in Molecular Biology</i> , 2008, 426, 419-435.	0.9	492
93	Protein production and purification. <i>Nature Methods</i> , 2008, 5, 135-146.	19.0	763
94	From No Expression to High-Level Soluble Expression in <i>Escherichia coli</i> by Screening a Library of the Target Proteins with Randomized N-Termini. <i>Methods in Molecular Biology</i> , 2008, 426, 187-195.	0.9	3
95	New Molecular Reporters for Rapid Protein Folding Assays. <i>PLoS ONE</i> , 2008, 3, e2387.	2.5	40
96	Policies in Structural Genomics/ Structural Proteomics. , 2008, , 539-566.		1
97	The Structure and Computational Analysis of <i>Mycobacterium tuberculosis</i> Protein CitE Suggest a Novel Enzymatic Function. <i>Journal of Molecular Biology</i> , 2007, 365, 275-283.	4.2	37
98	Domain Orientation in the Inactive Response Regulator <i>Mycobacterium tuberculosis</i> MtrA Provides a Barrier to Activation. <i>Biochemistry</i> , 2007, 46, 6733-6743.	2.5	76
99	Ligand identification using electron-density map correlations. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 101-107.	2.5	57
100	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 597-610.	2.5	60
101	RIKEN aids international structural genomics efforts. <i>Nature</i> , 2007, 445, 21-21.	27.8	14
102	Functional Linkages Can Reveal Protein Complexes for Structure Determination. <i>Structure</i> , 2007, 15, 1079-1089.	3.3	2
103	An automated high-throughput screening method for the identification of high-yield, soluble protein variants using cell-free expression and systematic truncation. <i>Journal of Structural and Functional Genomics</i> , 2007, 7, 139-147.	1.2	7
104	Automated structure determination with phenix. <i>NATO Science Series Series II, Mathematics, Physics and Chemistry</i> , 2007, , 101-109.	0.1	4
105	Functional and Structural Characterization of a Thiol Peroxidase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2006, 361, 850-863.	4.2	58
106	Automated ligand fitting by core-fragment fitting and extension into density. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 915-922.	2.5	98
107	Structure of <i>Mycobacterium tuberculosis</i> RuvA, a protein involved in recombination. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 731-734.	0.7	12
108	Engineering and characterization of a superfolder green fluorescent protein. <i>Nature Biotechnology</i> , 2006, 24, 79-88.	17.5	1,949

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109	Is one solution good enough?. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 184-185.	8.2	110
110	A Toolbox of GFP Technologies. <i>Imaging & Microscopy</i> , 2006, 8, 60-61.	0.1	0
111	Solution Structure of the Conserved Hypothetical Protein Rv2302 from <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , 2006, 188, 5993-6001.	2.2	7
112	Structural and functional features of an NDP kinase from the hyperthermophile crenarchaeon <i>Pyrobaculum aerophilum</i> . <i>Protein Science</i> , 2005, 14, 2562-2573.	7.6	12
113	Protein tagging and detection with engineered self-assembling fragments of green fluorescent protein. <i>Nature Biotechnology</i> , 2005, 23, 102-107.	17.5	781
114	Recent Advances in GFP Folding Reporter and Split-GFP Solubility Reporter Technologies. Application to Improving the Folding and Solubility of Recalcitrant Proteins from <i>Mycobacterium tuberculosis</i> . <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 113-119.	1.2	65
115	Structure of <i>pyrR</i> (Rv1379) from <i>Mycobacterium tuberculosis</i> : a persistence gene and protein drug target. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 355-364.	2.5	17
116	Crystal structure of a putative pyridoxine 5 α -phosphate oxidase (Rv2607) from <i>Mycobacterium tuberculosis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 563-569.	2.6	19
117	Structures and technology for biologists. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 296-297.	8.2	17
118	Recent developments in the PHENIX software for automated crystallographic structure determination. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 53-55.	2.4	319
119	<i>Mycobacterium tuberculosis</i> RmlC epimerase (Rv3465): a promising drug-target structure in the rhamnose pathway. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 895-902.	2.5	34
120	Using prime-and-switch phasing to reduce model bias in molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2144-2149.	2.5	62
121	SOLVE and RESOLVE: automated structure solution, density modification and model building. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 49-52.	2.4	387
122	The Crystal Structure of the First Enzyme in the Pantothenate Biosynthetic Pathway, Ketopantoate Hydroxymethyltransferase, from <i>M. tuberculosis</i> . <i>Structure</i> , 2003, 11, 753-764.	3.3	38
123	Binding and reversible denaturation of double-stranded DNA by Ff gene 5 protein. <i>Biopolymers</i> , 2003, 70, 637-648.	2.4	9
124	Automated main-chain model building by template matching and iterative fragment extension. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 38-44.	2.5	528
125	Automated side-chain model building and sequence assignment by template matching. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 45-49.	2.5	94
126	Improving macromolecular atomic models at moderate resolution by automated iterative model building, statistical density modification and refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1174-1182.	2.5	69

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127	Statistical density modification using local pattern matching. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1688-1701.	2.5	24
128	SOLVE and RESOLVE: Automated Structure Solution and Density Modification. Methods in Enzymology, 2003, 374, 22-37.	1.0	450
129	Automatic Solution of Heavy-Atom Substructures. Methods in Enzymology, 2003, 374, 37-83.	1.0	34
130	The TB Structural Genomics Consortium: Providing a Structural Foundation for Drug Discovery. Current Drug Targets Infectious Disorders, 2002, 2, 121-141.	2.1	66
131	Structural Genomics: Foundation for the Future of Biology?. Scientific World Journal, The, 2002, 2, 5-6.	2.1	1
132	Statistical density modification with non-crystallographic symmetry. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 2082-2086.	2.5	40
133	Rapid automatic NCS identification using heavy-atom substructures. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 2213-2215.	2.5	21
134	Automated structure solution, density modification and model building. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1937-1940.	2.5	252
135	PHENIX: building new software for automated crystallographic structure determination. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1948-1954.	2.5	3,979
136	Engineering soluble proteins for structural genomics. Nature Biotechnology, 2002, 20, 927-932.	17.5	174
137	Ff Gene 5 Protein Has a High Binding Affinity for Single-Stranded Phosphorothioate DNA. Biochemistry, 2001, 40, 2267-2275.	2.5	12
138	Maximum-likelihood density modification using pattern recognition of structural motifs. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1755-1762.	2.5	133
139	Map-likelihood phasing. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1763-1775.	2.5	69
140	Solution structure of <i>Pyrobaculum aerophilum</i> DsrC, an archaeal homologue of the gamma subunit of dissimilatory sulfite reductase. FEBS Journal, 2001, 268, 5842-5850.	0.2	37
141	Maximum-likelihood density modification for x-ray crystallography. , 2000, 4123, 243.		0
142	Maximum-likelihood density modification. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 965-972.	2.5	1,548
143	Structural genomics in North America. , 2000, 7, 935-939.		92
144	In vivo screening of haloalkane dehalogenase mutants. Bioorganic and Medicinal Chemistry, 1999, 7, 2175-2181.	3.0	4

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145	Discrimination of solvent from protein regions in native Fourier as a means of evaluating heavy-atom solutions in the MIR and MAD methods. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 501-505.	2.5	46
146	Automated MAD and MIR structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 849-861.	2.5	2,855
147	$\chi^2 R$, a reciprocal-space measure of the quality of macromolecular electron-density maps. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1174-1178.	2.5	6
148	Reciprocal-space solvent flattening. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1863-1871.	2.5	154
149	Evaluation of macromolecular electron-density map quality using the correlation of local r.m.s. density. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1872-1877.	2.5	53
150	Rapid protein-folding assay using green fluorescent protein. <i>Nature Biotechnology</i> , 1999, 17, 691-695.	17.5	840
151	Exploring structure space. A protein structure initiative. , 1999, 106, 141-147.		7
152	Haloalkane Dehalogenases: Structure of a Rhodococcus Enzyme. <i>Biochemistry</i> , 1999, 38, 16105-16114.	2.5	150
153	Structure of translation initiation factor 5A from <i>Pyrobaculum aerophilum</i> at 1.75 Å resolution. <i>Structure</i> , 1998, 6, 1207-1214.	3.3	109
154	Scission of DNA at a preselected sequence using a single-strand-specific chemical nuclease. <i>Chemistry and Biology</i> , 1998, 5, 283-292.	6.0	20
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