Thomas C Terwilliger

List of Publications by Year
in descending order

184	58,732	28736 57	5102 172
papers	citations	h-index	g-index

200	200	200	60167
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A monomeric mycobacteriophage immunity repressor utilizes two domains to recognize an asymmetric DNA sequence. Nature Communications, 2022, 13, .	5.8	5
2	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	9.0	73
3	Protein identification from electron cryomicroscopy maps by automated model building and side-chain matching. Acta Crystallographica Section D: Structural Biology, 2021, 77, 457-462.	1.1	9
4	Engineering an efficient and bright split Corynactis californica green fluorescent protein. Scientific Reports, 2021, 11, 18440.	1.6	2
5	Cryoâ€EM map interpretation and protein modelâ€building using iterative map segmentation. Protein Science, 2020, 29, 87-99.	3.1	27
6	Bottom-up structural proteomics: cryoEM of protein complexes enriched from the cellular milieu. Nature Methods, 2020, 17, 79-85.	9.0	80
7	Improvement of cryo-EM maps by density modification. Nature Methods, 2020, 17, 923-927.	9.0	243
8	Density modification of cryo-EM maps. Acta Crystallographica Section D: Structural Biology, 2020, 76, 912-925.	1.1	28
9	Bottom-up Structural Proteomics: Cryo-EM of Protein Complexes Enriched from the Cellular Milieu. Biophysical Journal, 2020, 118, 291a.	0.2	0
10	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. Acta Crystallographica Section D: Structural Biology, 2019, 75, 861-877.	1.1	4,060
11	BpeB, a major resistance-nodulation-cell division transporter from Burkholderia cenocepacia: construct design, crystallization and preliminary structural analysis. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 710-716.	0.4	1
12	A fully automatic method yielding initial models from high-resolution cryo-electron microscopy maps. Nature Methods, 2018, 15, 905-908.	9.0	137
13	Map segmentation, automated model-building and their application to the Cryo-EM Model Challenge. Journal of Structural Biology, 2018, 204, 338-343.	1.3	6
14	Automated map sharpening by maximization of detail and connectivity. Acta Crystallographica Section D: Structural Biology, 2018, 74, 545-559.	1.1	218
15	Real-space refinement inPHENIXfor cryo-EM and crystallography. Acta Crystallographica Section D: Structural Biology, 2018, 74, 531-544.	1.1	2,065
16	New tools for the analysis and validation of cryo-EM maps and atomic models. Acta Crystallographica Section D: Structural Biology, 2018, 74, 814-840.	1.1	575
17	Responses to`Atomic resolution': a badly abused term in structural biology. Acta Crystallographica Section D: Structural Biology, 2017, 73, 381-383.	1.1	7
18	A genome-wide structure-based survey of nucleotide binding proteins in M. tuberculosis. Scientific Reports, 2017, 7, 12489.	1.6	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. Biochemistry, 2017, 56, 4015-4027.	1.2	4
20	Polder maps: improving OMIT maps by excluding bulk solvent. Acta Crystallographica Section D: Structural Biology, 2017, 73, 148-157.	1.1	500
21	Raw diffraction data preservation and reuse: overview, update on practicalities and metadata requirements. IUCrJ, 2017, 4, 87-99.	1.0	34
22	SAD phasing for easy or challenging problems. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a35-a35.	0.0	0
23	Phasing strategies II â€“ molecular replacement. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a391-a391.	0.0	0
24	Model-building using cryo-EM and crystallographic maps. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C1327-C1327.	0.0	0
25	Can I solve my structure by SAD phasing? Planning an experiment, scaling data and evaluating the useful anomalous correlation and anomalous signal. Acta Crystallographica Section D: Structural Biology, 2016, 72, 359-374.	1.1	29
26	Efficient merging of data from multiple samples for determination of anomalous substructure. Acta Crystallographica Section D: Structural Biology, 2016, 72, 296-302.	1.1	13
27	Can I solve my structure by SAD phasing? Anomalous signal in SAD phasing. Acta Crystallographica Section D: Structural Biology, 2016, 72, 346-358.	1.1	31
28	RNA Structure Refinement Using the ERRASER-Phenix Pipeline. Methods in Molecular Biology, 2016, 1320, 269-282.	0.4	24
29	Predicting X-ray diffuse scattering from translationâ€“librationâ€“screw structural ensembles. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1657-1667.	2.5	14
30	FEM: feature-enhanced map. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 646-666.	2.5	157
31	A Suite of Engineered GFP Molecules for Oligomeric Scaffolding. Structure, 2015, 23, 1754-1768.	1.6	30
32	X-ray structure determination using low-resolution electron microscopy maps for molecular replacement. Nature Protocols, 2015, 10, 1275-1284.	5.5	22
33	Protein crystallography from the perspective of technology developments. Crystallography Reviews, 2015, 21, 122-153.	0.4	33
34	Macromolecular X-ray structure determination using weak, single-wavelength anomalous data. Nature Methods, 2015, 12, 127-130.	9.0	31
35	Conformational dynamics of a crystalline protein from microsecond-scale molecular dynamics simulations and diffuse X-ray scattering. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17887-17892.	3.3	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. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2533-2543.	2.5	29

#	Article	IF	Citations
37	Metrics for comparison of crystallographic maps. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2593-2606.	2.5	29
38	Archiving raw crystallographic data. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2500-2501.	2.5	18
39	1.55â€…Ã… resolution X-ray crystal structure of Rv3902c fromMycobacterium tuberculosis. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 414-417.	0.4	1
40	Automated identification of elemental ions in macromolecular crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1104-1114.	2.5	40
41	Crystal structure of the CRISPR RNAâ€“guided surveillance complex from Escherichia coli. Science, 2014, 345, 1473-1479.	6.0	226
42	Combining Crystallographic and Structure-Modeling Approaches in Macromolecular Crystallography. Biophysical Journal, 2014, 106, 34a.	0.2	0
43	Diffuse X-Ray Scattering for Ensemble Modeling of Crystalline Proteins. Biophysical Journal, 2014, 106, 384a.	0.2	0
44	Automating crystallographic structure solution and refinement of proteinâ€“ligand complexes. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 144-154.	2.5	43
45	Ligand placement based on prior structures: the guided ligand-replacement method. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 134-143.	2.5	11
46	Subfamily-Specific Adaptations in the Structures of Two Penicillin-Binding Proteins from Mycobacterium tuberculosis. PLoS ONE, 2014, 9, e116249.	1.1	6
47	Improved low-resolution crystallographic refinement with Phenix and Rosetta. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C782-C782.	0.0	0
48	New tools for automated model completion and refinement. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C327-C327.	0.0	0
49	Finding non-crystallographic symmetry in density maps of macromolecular structures. Journal of Structural and Functional Genomics, 2013, 14, 91-95.	1.2	15
50	Crystal structure of AcrB complexed with linezolid at 3.5ÂÃ… resolution. Journal of Structural and Functional Genomics, 2013, 14, 71-75.	1.2	38
51	Improved low-resolution crystallographic refinement with Phenix and Rosetta. Nature Methods, 2013, 10, 1102-1104.	9.0	175
52	Improved Crystallographic Structures Using Extensive Combinatorial Refinement. Structure, 2013, 21, 1923-1930.	1.6	18
53	Crystal structure of Bacillus subtilis GabR, an autorepressor and transcriptional activator of gabT. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17820-17825.	3.3	66
54	Advances, Interactions, and Future Developments in the CNS, Phenix, and Rosetta Structural Biology Software Systems. Annual Review of Biophysics, 2013, 42, 265-287.	4.5	88

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55	Model morphing and sequence assignment after molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2244-2250.	2.5	37
56	Split green fluorescent protein as a modular binding partner for protein crystallization. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2513-2523.	2.5	29
57	Improving experimental phases for strong reflections prior to density modification. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2039-2049.	2.5	7
58	A New Protein-Protein Interaction Sensor Based on Tripartite Split-GFP Association. Scientific Reports, 2013, 3, 2854.	1.6	190
59	Model-Building and Reduction of Model Bias in Electron Density Maps. NATO Science for Peace and Security Series A: Chemistry and Biology, 2013, , 193-203.	0.5	1
60	UsingPHASERfor phasing in conjunction with wide-convergence refinement and model building techniques. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s40-s40.	0.3	2
61	Automatic Fortran to C++ conversion with FABLE. Source Code for Biology and Medicine, 2012, 7, 5.	1.7	15
62	phenix.mr_rosetta: molecular replacement and model rebuilding with Phenix and Rosetta. Journal of Structural and Functional Genomics, 2012, 13, 81-90.	1.2	131
63	Enhancement of crystallization with nucleotide ligands identified by dye-ligand affinity chromatography. Journal of Structural and Functional Genomics, 2012, 13, 71-79.	1.2	5
64	Chemical shift assignments for Rv0577, a putative glyoxylase associated with virulence from Mycobacterium tuberculosis. Biomolecular NMR Assignments, 2012, 6, 43-46.	0.4	5
65	Graphical tools for macromolecular crystallography inPHENIX. Journal of Applied Crystallography, 2012, 45, 581-586.	1.9	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 Corynebacterium glutamicum. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 391-403.	2.5	26
67	Towards automated crystallographic structure refinement with phenix.refine. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 352-367.	2.5	4,573
68	Improved crystallographic models through iterated local density-guided model deformation and reciprocal-space refinement. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 861-870.	2.5	37
69	Inaugural structure from the DUF3349 superfamily of proteins, Mycobacterium tuberculosis Rv0543c. Archives of Biochemistry and Biophysics, 2011, 506, 150-156.	1.4	6
70	The Phenix software for automated determination of macromolecular structures. Methods, 2011, 55, 94-106.	1.9	764
71	Improved molecular replacement by density- and energy-guided protein structure optimization. Nature, 2011, 473, 540-543.	13.7	226
72	The TB Structural Genomics Consortium: A decade of progress. Tuberculosis, 2011, 91, 155-172.	0.8	39

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73	The success of structural genomics. Journal of Structural and Functional Genomics, 2011, 12, 43-44.	1.2	20
74	Experimental mapping of soluble protein domains using a hierarchical approach. Nucleic Acids Research, 2011, 39, e125-e125.	6.5	29
75	A high-throughput immobilized bead screen for stable proteins and multi-protein complexes. Protein Engineering, Design and Selection, 2011, 24, 565-578.	1.0	12
76	The optimization of in vitro high-throughput chemical lysis of Escherichia coli. Application to ACP domain of the polyketide synthase ppsC from Mycobacterium tuberculosis. Journal of Structural and Functional Genomics, 2010, 11, 41-49.	1.2	19
77	Solution structure of Rv2377c-founding member of the MbtH-like protein family. Tuberculosis, 2010, 90, 245-251.	0.8	37
78	PHENIX: a comprehensive Python-based system for macromolecular structure solution. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 213-221.	2.5	20,564
79	Rapid chain tracing of polypeptide backbones in electron-density maps. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 285-294.	2.5	6
80	Rapid model building of Î²-sheets in electron-density maps. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 276-284.	2.5	4
81	Rapid model building of Î±-helices in electron-density maps. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 268-275.	2.5	25
82	Structure of Rv1848 (UreA), theMycobacterium tuberculosisurease Î³ subunit. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 781-786.	0.7	10
83	An Extracellular Disulfide Bond Forming Protein (DsbF) from Mycobacterium tuberculosis: Structural, Biochemical, and Gene Expression Analysis. Journal of Molecular Biology, 2010, 396, 1211-1226.	2.0	23
84	Recent developments in phasing and structure refinement for macromolecular crystallography. Current Opinion in Structural Biology, 2009, 19, 566-572.	2.6	23
85	Automated, high-throughput platform for protein solubility screening using a split-GFP system. Journal of Structural and Functional Genomics, 2009, 10, 47-55.	1.2	32
86	Analysis of nucleoside-binding proteins by ligand-specific elution from dye resin: application to Mycobacterium tuberculosis aldehyde dehydrogenases. Journal of Structural and Functional Genomics, 2009, 10, 291-301.	1.2	13
87	Decision-making in structure solution using Bayesian estimates of map quality: thePHENIX AutoSolwizard. Acta Crystallographica Section D: Biological Crystallography, 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. Protein Science, 2009, 11, 601-613.	3.1	5
89	Lessons from Structural Genomics. Annual Review of Biophysics, 2009, 38, 371-383.	4.5	115
90	Iterative model building, structure refinement and density modification with thePHENIX AutoBuildwizard. Acta Crystallographica Section D: Biological Crystallography, 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. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 515-524.	2.5	165
92	Automated Structure Solution with the PHENIX Suite. Methods in Molecular Biology, 2008, 426, 419-435.	0.4	492
93	Protein production and purification. Nature Methods, 2008, 5, 135-146.	9.0	763
94	From No Expression to High-Level Soluble Expression in Escherichia coli by Screening a Library of the Target Proteins with Randomized N-Termini. Methods in Molecular Biology, 2008, 426, 187-195.	0.4	3
95	New Molecular Reporters for Rapid Protein Folding Assays. PLoS ONE, 2008, 3, e2387.	1.1	40
96	Policies in Structural Genomics/ Structural Proteomics. , 2008, , 539-566.		1
97	The Structure and Computational Analysis of Mycobacterium tuberculosis Protein CitE Suggest a Novel Enzymatic Function. Journal of Molecular Biology, 2007, 365, 275-283.	2.0	37
98	Domain Orientation in the Inactive Response RegulatorMycobacterium tuberculosisMtrA Provides a Barrier to Activationâ€,â€¡. Biochemistry, 2007, 46, 6733-6743.	1.2	76
99	Ligand identification using electron-density map correlations. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 101-107.	2.5	57
100	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 597-610.	2.5	60
101	RIKEN aids international structural genomics efforts. Nature, 2007, 445, 21-21.	13.7	14
102	Functional Linkages Can Reveal Protein Complexes for Structure Determination. Structure, 2007, 15, 1079-1089.	1.6	2
103	An automated high-throughput screening method for the identification of high-yield, soluble protein variants using cell-free expression and systematic truncation. Journal of Structural and Functional Genomics, 2007, 7, 139-147.	1.2	7
104	Automated structure determination with phenix. NATO Science Series Series II, Mathematics, Physics and Chemistry, 2007, , 101-109.	0.1	4
105	Functional and Structural Characterization of a Thiol Peroxidase from Mycobacterium tuberculosis. Journal of Molecular Biology, 2006, 361, 850-863.	2.0	58
106	Automated ligand fitting by core-fragment fitting and extension into density. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 915-922.	2.5	98
107	Structure ofMycobacterium tuberculosisRuvA, a protein involved in recombination. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 731-734.	0.7	12
108	Engineering and characterization of a superfolder green fluorescent protein. Nature Biotechnology, 2006, 24, 79-88.	9.4	1,949

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109	Is one solution good enough?. Nature Structural and Molecular Biology, 2006, 13, 184-185.	3.6	110
110	A Toolbox of GFP Technologies. Imaging & Microscopy, 2006, 8, 60-61.	0.1	0
111	Solution Structure of the Conserved Hypothetical Protein Rv2302 from Mycobacterium tuberculosis. Journal of Bacteriology, 2006, 188, 5993-6001.	1.0	7
112	Structural and functional features of an NDP kinase from the hyperthermophile crenarchaeonPyrobaculum aerophilum. Protein Science, 2005, 14, 2562-2573.	3.1	12
113	Protein tagging and detection with engineered self-assembling fragments of green fluorescent protein. Nature Biotechnology, 2005, 23, 102-107.	9.4	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 Mycobacterium tuberculosis. Journal of Structural and Functional Genomics, 2005, 6, 113-119.	1.2	65
115	Structure of pyrR (Rv1379) fromMycobacterium tuberculosis: a persistence gene and protein drug target. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 355-364.	2.5	17
116	Crystal structure of a putative pyridoxine 5â€²-phosphate oxidase (Rv2607) from Mycobacterium tuberculosis. Proteins: Structure, Function and Bioinformatics, 2005, 62, 563-569.	1.5	19
117	Structures and technology for biologists. Nature Structural and Molecular Biology, 2004, 11, 296-297.	3.6	17
118	Recent developments in thePHENIXsoftware for automated crystallographic structure determination. Journal of Synchrotron Radiation, 2004, 11, 53-55.	1.0	319
119	Mycobacterium tuberculosisRmlC epimerase (Rv3465): a promising drug-target structure in the rhamnose pathway. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 895-902.	2.5	34
120	Using prime-and-switch phasing to reduce model bias in molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2144-2149.	2.5	62
121	SOLVE and RESOLVE: automated structure solution, density modification and model building. Journal of Synchrotron Radiation, 2004, 11, 49-52.	1.0	387
122	The Crystal Structure of the First Enzyme in the Pantothenate Biosynthetic Pathway, Ketopantoate Hydroxymethyltransferase, from M. tuberculosis. Structure, 2003, 11, 753-764.	1.6	38
123	Binding and reversible denaturation of double-stranded DNA by Ff gene 5 protein. Biopolymers, 2003, 70, 637-648.	1.2	9
124	Automated main-chain model building by template matching and iterative fragment extension. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 38-44.	2.5	528
125	Automated side-chain model building and sequence assignment by template matching. Acta Crystallographica Section D: Biological Crystallography, 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. Acta Crystallographica Section D: Biological Crystallography, 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.	0.4	450
129	Automatic Solution of Heavy-Atom Substructures. Methods in Enzymology, 2003, 374, 37-83.	0.4	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.	0.8	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.	9.4	174
137	Ff Gene 5 Protein Has a High Binding Affinity for Single-Stranded Phosphorothioate DNA. Biochemistry, 2001, 40, 2267-2275.	1.2	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 Pyrobaculum aerophilum 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.	1.4	4

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145	Discrimination of solvent from protein regions in native Fouriers as a means of evaluating heavy-atom solutions in the MIR and MAD methods. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 501-505.	2.5	46
146	Automated MAD and MIR structure solution. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 849-861.	2.5	2,855
147	Ïƒ2 R , a reciprocal-space measure of the quality of macromolecular electron-density maps. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1174-1178.	2.5	6
148	Reciprocal-space solvent flattening. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1863-1871.	2.5	154
149	Evaluation of macromolecular electron-density map quality using the correlation of local r.m.s. density. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1872-1877.	2.5	53
150	Rapid protein-folding assay using green fluorescent protein. Nature Biotechnology, 1999, 17, 691-695.	9.4	840
151	Exploring structure space. A protein structure initiative. , 1999, 106, 141-147.		7
152	Haloalkane Dehalogenases:Â Structure of aRhodococcusEnzymeâ€,â€¡. Biochemistry, 1999, 38, 16105-16114.	1.2	150
153	Structure of translation initiation factor 5A from Pyrobaculum aerophilum at 1.75 Ã¥ resolution. Structure, 1998, 6, 1207-1214.	1.6	109
154	Scission of DNA at a preselected sequence using a single-strand-specific chemical nuclease. Chemistry and Biology, 1998, 5, 283-292.	6.2	20
155	Classâ€directed structure determination: Foundation for a protein structure initiative. Protein Science, 1998, 7, 1851-1856.	3.1	89
156	Circular Dichroism and Electron Microscopy of a Core Y61F Mutant of the F1 Gene 5 Single-Stranded DNA-Binding Protein and Theoretical Analysis of CD Spectra of Four Tyr â†' Phe Substitutionsâ€. Biochemistry, 1998, 37, 7463-7477.	1.2	27
157	A Nondenaturing Purification Scheme for the DNA-Binding Domain of Poly(ADP-Ribose) Polymerase, a Structure-Specific DNA-Binding Protein. Protein Expression and Purification, 1998, 14, 79-86.	0.6	5
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159	Analyses of the stability and function of three surface mutants (R82C, K69H, and L32R) of the gene V protein from Ff phage by Xâ€ray crystallography. Protein Science, 1997, 6, 771-780.	3.1	13
160	Raman Spectroscopy of theFfGene V Protein and Complexes with Poly(dA):Â Nonspecific DNA Recognition and Bindingâ€. Biochemistry, 1996, 35, 9603-9609.	1.2	22
161	Gene V Protein Dimerization and Cooperativity of Binding to Poly(dA)â€. Biochemistry, 1996, 35, 16652-16664.	1.2	21
162	Context Dependence of Mutational Effects in a Protein: The Crystal Structures of the V35I, I47V and V35I/I47V Gene V Protein Core Mutants. Journal of Molecular Biology, 1996, 259, 148-159.	2.0	21

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163	Electrospray ionization with high performance fourier transform ion cyclotron resonance mass spectrometry for the study of noncovalent biomolecular complexes. Techniques in Protein Chemistry, 1996, , 13-22.	0.3	6
164	Engineering the Stability and Function of Gene V Protein. Advances in Protein Chemistry, 1995, 46, 177-215.	4.4	16
165	Relationship between in Vivo Activity and in Vitro Measures of Function and Stability of a Protein. Biochemistry, 1995, 34, 11970-11978.	1.2	22
166	Circular Dichroism Spectroscopy of Three Tyrosine-to-Phenylalanine Substitutions of fd Gene 5 Protein. Biochemistry, 1995, 34, 12854-12865.	1.2	16
167	MAD phasing: Bayesian estimates ofFA. Acta Crystallographica Section D: Biological Crystallography, 1994, 50, 11-16.	2.5	26
168	In Vivo Characterization of Mutants of the Bacteriophage f1 Gene V Protein Isolated by Saturation Mutagenesis. Journal of Molecular Biology, 1994, 236, 556-571.	2.0	52
169	Crystal Structures of Y41H and Y41F Mutants of Gene V Protein from Ff Phage Suggest Possible Protein-Protein Interactions in the GVP-ssDNA Complex. Biochemistry, 1994, 33, 7768-7778.	1.2	31
170	Approaches to predicting effects of single amino acid substitutions on the function of a protein. Biochemistry, 1991, 30, 6230-6240.	1.2	17
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172	Isolation and in vitro characterization of temperature-sensitive mutants of the bacteriophage f1 gene V protein. Journal of Molecular Biology, 1991, 219, 257-275.	2.0	21
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174	Construction of a synthetic variant of the bacteriophage f1 gene V by assembling oligodeoxy-nucleotides corresponding to only one strand of DNA. Gene, 1988, 71, 41-47.	1.0	12
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