Thomas C Terwilliger

List of Publications by Year in Descending Order

181 papers	44,921 citations	56 h-index	200 g-index
200 ext. papers	52,724 ext. citations	8.6 avg, IF	7.4 L-index

#	Paper	IF	Citations
181	Protein identification from electron cryomicroscopy maps by automated model building and side-chain matching. *Acta Crystallographica Section D: Structural Biology*, **2021**, 77, 457-462	5.5	2
180	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. *Nature Methods*, **2021**, 18, 156-164	21.6	22
179	Engineering an efficient and bright split Corynactis californica green fluorescent protein. *Scientific Reports*, **2021**, 11, 18440	4.9	
178	A Comprehensive Review on Mycobacterium tuberculosis Targets and Drug Development from a Structural Perspective **2020**, 545-566		3
177	Density modification of cryo-EM maps. *Acta Crystallographica Section D: Structural Biology*, **2020**, 76, 912-925	5.5	11
176	Cryo-EM map interpretation and protein model-building using iterative map segmentation. *Protein Science*, **2020**, 29, 87-99	6.3	18
175	Bottom-up structural proteomics: cryoEM of protein complexes enriched from the cellular milieu. *Nature Methods*, **2020**, 17, 79-85	21.6	35
174	Improvement of cryo-EM maps by density modification. *Nature Methods*, **2020**, 17, 923-927	21.6	123
173	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. *Acta Crystallographica Section D: Structural Biology*, **2019**, 75, 861-877	5.5	1527
172	Map segmentation, automated model-building and their application to the Cryo-EM Model Challenge. *Journal of Structural Biology*, **2018**, 204, 338-343	3.4	5
171	Automated map sharpening by maximization of detail and connectivity. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 545-559	5.5	132
170	Real-space refinement in PHENIX for cryo-EM and crystallography. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 531-544	5.5	917
169	New tools for the analysis and validation of cryo-EM maps and atomic models. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 814-840	5.5	291
168	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	1.1	
167	A fully automatic method yielding initial models from high-resolution cryo-electron microscopy maps. *Nature Methods*, **2018**, 15, 905-908	21.6	82
166	Responses to "Atomic resolution": a badly abused term in structural biology. *Acta Crystallographica Section D: Structural Biology*, **2017**, 73, 381-383	5.5	5
165	A genome-wide structure-based survey of nucleotide binding proteins in M. tuberculosis. *Scientific Reports*, **2017**, 7, 12489	4.9	4

164	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	3.2	4
163	Polder maps: improving OMIT maps by excluding bulk solvent. *Acta Crystallographica Section D: Structural Biology*, **2017**, 73, 148-157	5.5	335
162	Raw diffraction data preservation and reuse: overview, update on practicalities and metadata requirements. *IUCrJ*, **2017**, 4, 87-99	4.7	24
161	Can I solve my structure by SAD phasing? Anomalous signal in SAD phasing. *Acta Crystallographica Section D: Structural Biology*, **2016**, 72, 346-58	5.5	26
160	RNA Structure Refinement Using the ERRASER-Phenix Pipeline. *Methods in Molecular Biology*, **2016**, 1320, 269-82	1.4	19
159	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, 359-74	5.5	23
158	Efficient merging of data from multiple samples for determination of anomalous substructure. *Acta Crystallographica Section D: Structural Biology*, **2016**, 72, 296-302	5.5	10
157	FEM: feature-enhanced map. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 646-66		113
156	A Suite of Engineered GFP Molecules for Oligomeric Scaffolding. *Structure*, **2015**, 23, 1754-1768	5.2	23
155	X-ray structure determination using low-resolution electron microscopy maps for molecular replacement. *Nature Protocols*, **2015**, 10, 1275-84	18.8	16
154	Protein Crystallography from the Perspective of Technology Developments. *Crystallography Reviews*, **2015**, 21, 122-153	1.3	26
153	Macromolecular X-ray structure determination using weak, single-wavelength anomalous data. *Nature Methods*, **2015**, 12, 127-30	21.6	27
152	Predicting X-ray diffuse scattering from translation-libration-screw structural ensembles. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 1657-67		9
151	Automated identification of elemental ions in macromolecular crystal structures. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 1104-14		27
150	Structural biology. Crystal structure of the CRISPR RNA-guided surveillance complex from Escherichia coli. *Science*, **2014**, 345, 1473-9	33.3	182
149	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, 17887-92	11.5	38
148	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, 2533-43		21
147	Metrics for comparison of crystallographic maps. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 2593-606		22

146	Archiving raw crystallographic data. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 2500-1		11
145	1.55 Å resolution X-ray crystal structure of Rv3902c from Mycobacterium tuberculosis. *Acta Crystallographica Section F, Structural Biology Communications*, **2014**, 70, 414-7	1.1	1
144	Automating crystallographic structure solution and refinement of protein-ligand complexes. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 144-54		33
143	Ligand placement based on prior structures: the guided ligand-replacement method. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 134-43		11
142	Subfamily-specific adaptations in the structures of two penicillin-binding proteins from Mycobacterium tuberculosis. *PLoS ONE*, **2014**, 9, e116249	3.7	4
141	Finding non-crystallographic symmetry in density maps of macromolecular structures. *Journal of Structural and Functional Genomics*, **2013**, 14, 91-5		12
140	Crystal structure of AcrB complexed with linezolid at 3.5 Å resolution. *Journal of Structural and Functional Genomics*, **2013**, 14, 71-5		32
139	Improved low-resolution crystallographic refinement with Phenix and Rosetta. *Nature Methods*, **2013**, 10, 1102-4	21.6	137
138	Improved crystallographic structures using extensive combinatorial refinement. *Structure*, **2013**, 21, 1923-30	5.3	15
137	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, 17820-5	11.5	56
136	Advances, interactions, and future developments in the CNS, Phenix, and Rosetta structural biology software systems. *Annual Review of Biophysics*, **2013**, 42, 265-87	21.1	76
135	Model morphing and sequence assignment after molecular replacement. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2244-50		24
134	Split green fluorescent protein as a modular binding partner for protein crystallization. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2513-23		24
133	Improving experimental phases for strong reflections prior to density modification. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2039-49		6
132	A new protein-protein interaction sensor based on tripartite split-GFP association. *Scientific Reports* , **2013**, 3, 2854	4.9	131
131	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	0.1	1
130	Graphical tools for macromolecular crystallography in PHENIX. *Journal of Applied Crystallography*, **2012**, 45, 581-586	3.8	95
129	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		24

128	Towards automated crystallographic structure refinement with phenix.refine. *Acta Crystallographica Section D: Biological Crystallography*, **2012**, 68, 352-67		3236
127	Improved crystallographic models through iterated local density-guided model deformation and reciprocal-space refinement. *Acta Crystallographica Section D: Biological Crystallography*, **2012**, 68, 861-70		33
126	Automatic Fortran to C++ conversion with FABLE. *Source Code for Biology and Medicine*, **2012**, 7, 5	1.9	9
125	phenix.mr_rosetta: molecular replacement and model rebuilding with Phenix and Rosetta. *Journal of Structural and Functional Genomics*, **2012**, 13, 81-90		109
124	Enhancement of crystallization with nucleotide ligands identified by dye-ligand affinity chromatography. *Journal of Structural and Functional Genomics*, **2012**, 13, 71-9		4
123	Chemical shift assignments for Rv0577, a putative glyoxylase associated with virulence from Mycobacterium tuberculosis. *Biomolecular NMR Assignments*, **2012**, 6, 43-6	0.7	4
122	Inaugural structure from the DUF3349 superfamily of proteins, Mycobacterium tuberculosis Rv0543c. *Archives of Biochemistry and Biophysics*, **2011**, 506, 150-6	4.1	6
121	The Phenix software for automated determination of macromolecular structures. *Methods*, **2011**, 55, 94-106	4.6	580
120	Improved molecular replacement by density- and energy-guided protein structure optimization. *Nature*, **2011**, 473, 540-3	50.4	196
119	The TB Structural Genomics Consortium: a decade of progress. *Tuberculosis*, **2011**, 91, 155-72	2.6	33
118	The success of structural genomics. *Journal of Structural and Functional Genomics*, **2011**, 12, 43-4		18
117	Experimental mapping of soluble protein domains using a hierarchical approach. *Nucleic Acids Research*, **2011**, 39, e125	20.1	26
116	A high-throughput immobilized bead screen for stable proteins and multi-protein complexes. *Protein Engineering, Design and Selection*, **2011**, 24, 565-78	1.9	11
115	An extracellular disulfide bond forming protein (DsbF) from Mycobacterium tuberculosis: structural, biochemical, and gene expression analysis. *Journal of Molecular Biology*, **2010**, 396, 1211-26	6.5	20
114	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, 41-9		19
113	Solution structure of Rv2377c-founding member of the MbtH-like protein family. *Tuberculosis*, **2010**, 90, 245-51	2.6	27
112	PHENIX: a comprehensive Python-based system for macromolecular structure solution. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 213-21		16067
111	Rapid chain tracing of polypeptide backbones in electron-density maps. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 285-94		6

110	Rapid model building of beta-sheets in electron-density maps. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 276-84		4
109	Rapid model building of alpha-helices in electron-density maps. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 268-75		20
108	Structure of Rv1848 (UreA), the Mycobacterium tuberculosis urease gamma subunit. *Acta Crystallographica Section F: Structural Biology Communications*, **2010**, 66, 781-6		10
107	Recent developments in phasing and structure refinement for macromolecular crystallography. *Current Opinion in Structural Biology*, **2009**, 19, 566-72	8.1	21
106	Automated, high-throughput platform for protein solubility screening using a split-GFP system. *Journal of Structural and Functional Genomics*, **2009**, 10, 47-55		27
105	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		11
104	Decision-making in structure solution using Bayesian estimates of map quality: the PHENIX AutoSol wizard. *Acta Crystallographica Section D: Biological Crystallography*, **2009**, 65, 582-601		657
103	Lessons from structural genomics. *Annual Review of Biophysics*, **2009**, 38, 371-83	21.1	99
102	Protein production and purification. *Nature Methods*, **2008**, 5, 135-46	21.6	655
101	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, 187-95	1.4	3
100	Iterative model building, structure refinement and density modification with the PHENIX AutoBuild wizard. *Acta Crystallographica Section D: Biological Crystallography*, **2008**, 64, 61-9		1042
99	Iterative-build OMIT maps: map improvement by iterative model building and refinement without model bias. *Acta Crystallographica Section D: Biological Crystallography*, **2008**, 64, 515-24		130
98	Automated structure solution with the PHENIX suite. *Methods in Molecular Biology*, **2008**, 426, 419-35	1.4	421
97	New molecular reporters for rapid protein folding assays. *PLoS ONE*, **2008**, 3, e2387	3.7	38
96	Domain orientation in the inactive response regulator Mycobacterium tuberculosis MtrA provides a barrier to activation. *Biochemistry*, **2007**, 46, 6733-43	3.2	64
95	Ligand identification using electron-density map correlations. *Acta Crystallographica Section D: Biological Crystallography*, **2007**, 63, 101-7		50
94	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. *Acta Crystallographica Section D: Biological Crystallography*, **2007**, 63, 597-610		56
93	RIKEN aids international structural genomics efforts. *Nature*, **2007**, 445, 21	50.4	14

92	Functional linkages can reveal protein complexes for structure determination. *Structure*, **2007**, 15, 1079-89	5.2	2
91	The structure and computational analysis of Mycobacterium tuberculosis protein CitE suggest a novel enzymatic function. *Journal of Molecular Biology*, **2007**, 365, 275-83	6.5	31
90	Automated structure determination with phenix. *NATO Science Series Series II, Mathematics, Physics and Chemistry*, **2007**, 101-109		2
89	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*, **2006**, 7, 139-47		5
88	A Toolbox of GFP Technologies. *Imaging & Microscopy*, **2006**, 8, 60-61		
87	Solution structure of the conserved hypothetical protein Rv2302 from Mycobacterium tuberculosis. *Journal of Bacteriology*, **2006**, 188, 5993-6001	3.5	7
86	Functional and structural characterization of a thiol peroxidase from Mycobacterium tuberculosis. *Journal of Molecular Biology*, **2006**, 361, 850-63	6.5	39
85	Automated ligand fitting by core-fragment fitting and extension into density. *Acta Crystallographica Section D: Biological Crystallography*, **2006**, 62, 915-22		75
84	Structure of Mycobacterium tuberculosis RuvA, a protein involved in recombination. *Acta Crystallographica Section F: Structural Biology Communications*, **2006**, 62, 731-4		11
83	Engineering and characterization of a superfolder green fluorescent protein. *Nature Biotechnology*, **2006**, 24, 79-88	44.5	1486
82	Is one solution good enough?. *Nature Structural and Molecular Biology*, **2006**, 13, 184-5; discussion 185	17.6	97
81	Crystal structure of a putative pyridoxine 5Rphosphate oxidase (Rv2607) from Mycobacterium tuberculosis. *Proteins: Structure, Function and Bioinformatics*, **2006**, 62, 563-9	4.2	18
80	Structural and functional features of an NDP kinase from the hyperthermophile crenarchaeon Pyrobaculum aerophilum. *Protein Science*, **2005**, 14, 2562-73	6.3	10
79	Protein tagging and detection with engineered self-assembling fragments of green fluorescent protein. *Nature Biotechnology*, **2005**, 23, 102-7	44.5	599
78	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, 113-9		62
77	Structure of pyrR (Rv1379) from Mycobacterium tuberculosis: a persistence gene and protein drug target. *Acta Crystallographica Section D: Biological Crystallography*, **2005**, 61, 355-64		15
76	Structures and technology for biologists. *Nature Structural and Molecular Biology*, **2004**, 11, 296-7	17.6	14
75	Recent developments in the PHENIX software for automated crystallographic structure determination. *Journal of Synchrotron Radiation*, **2004**, 11, 53-5	2.4	273

74	Mycobacterium tuberculosis RmlC epimerase (Rv3465): a promising drug-target structure in the rhamnose pathway. *Acta Crystallographica Section D: Biological Crystallography*, **2004**, 60, 895-902		29
73	Using prime-and-switch phasing to reduce model bias in molecular replacement. *Acta Crystallographica Section D: Biological Crystallography*, **2004**, 60, 2144-9		59
72	SOLVE and RESOLVE: automated structure solution, density modification and model building. *Journal of Synchrotron Radiation*, **2004**, 11, 49-52	2.4	348
71	SOLVE and RESOLVE: automated structure solution and density modification. *Methods in Enzymology*, **2003**, 374, 22-37	1.7	416
70	Automatic solution of heavy-atom substructures. *Methods in Enzymology*, **2003**, 374, 37-83	1.7	31
69	The crystal structure of the first enzyme in the pantothenate biosynthetic pathway, ketopantoate hydroxymethyltransferase, from M tuberculosis. *Structure*, **2003**, 11, 753-64	5.2	32
68	Binding and reversible denaturation of double-stranded DNA by Ff gene 5 protein. *Biopolymers*, **2003**, 70, 637-48	2.2	7
67	Automated main-chain model building by template matching and iterative fragment extension. *Acta Crystallographica Section D: Biological Crystallography*, **2003**, 59, 38-44		501
66	Automated side-chain model building and sequence assignment by template matching. *Acta Crystallographica Section D: Biological Crystallography*, **2003**, 59, 45-9		88
65	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, 1174-82		63
64	Statistical density modification using local pattern matching. *Acta Crystallographica Section D: Biological Crystallography*, **2003**, 59, 1688-701		23
63	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*, **2002**, 11, 601-13	6.3	5
62	Structural Genomics: Foundation for the Future of Biology?. *Scientific World Journal, The*, **2002**, 2, 5-6	2.2	0
61	Statistical density modification with non-crystallographic symmetry. *Acta Crystallographica Section D: Biological Crystallography*, **2002**, 58, 2082-6		38
60	Rapid automatic NCS identification using heavy-atom substructures. *Acta Crystallographica Section D: Biological Crystallography*, **2002**, 58, 2213-5		20
59	Automated structure solution, density modification and model building. *Acta Crystallographica Section D: Biological Crystallography*, **2002**, 58, 1937-40		243
58	PHENIX: building new software for automated crystallographic structure determination. *Acta Crystallographica Section D: Biological Crystallography*, **2002**, 58, 1948-54		3477
57	Engineering soluble proteins for structural genomics. *Nature Biotechnology*, **2002**, 20, 927-32	44.5	152

56	The TB structural genomics consortium: providing a structural foundation for drug discovery. *Current Drug Targets Infectious Disorders*, **2002**, 2, 121-41		60
55	Maximum-likelihood density modification using pattern recognition of structural motifs. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 1755-62		129
54	Map-likelihood phasing. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 1763-75		68
53	Solution structure of Pyrobaculum aerophilum DsrC, an archaeal homologue of the gamma subunit of dissimilatory sulfite reductase. *FEBS Journal*, **2001**, 268, 5842-50		32
52	Ff gene 5 protein has a high binding affinity for single-stranded phosphorothioate DNA. *Biochemistry*, **2001**, 40, 2267-75	3.2	12
51	Maximum-likelihood density modification for x-ray crystallography **2000**, 4123, 243		
50	Maximum-likelihood density modification. *Acta Crystallographica Section D: Biological Crystallography*, **2000**, 56, 965-72		1471
49	Structural genomics in North America. *Nature Structural Biology*, **2000**, 7 Suppl, 935-9		77
48	In vivo screening of haloalkane dehalogenase mutants. *Bioorganic and Medicinal Chemistry*, **1999**, 7, 2175-81	3.4	3
47	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, 501-5		44
46	Automated MAD and MIR structure solution. *Acta Crystallographica Section D: Biological Crystallography*, **1999**, 55, 849-61		2761
45	Sigma2R, a reciprocal-space measure of the quality of macromolecular electron-density maps. *Acta Crystallographica Section D: Biological Crystallography*, **1999**, 55, 1174-8		5
44	Reciprocal-space solvent flattening. *Acta Crystallographica Section D: Biological Crystallography*, **1999**, 55, 1863-71		152
43	Evaluation of macromolecular electron-density map quality using the correlation of local r.m.s. density. *Acta Crystallographica Section D: Biological Crystallography*, **1999**, 55, 1872-7		52
42	Rapid protein-folding assay using green fluorescent protein. *Nature Biotechnology*, **1999**, 17, 691-5	44.5	726
41	Exploring structure space. A protein structure initiative. *Genetica*, **1999**, 106, 141-7	1.5	6
40	Haloalkane dehalogenases: structure of a Rhodococcus enzyme. *Biochemistry*, **1999**, 38, 16105-14	3.2	137
39	Structure of translation initiation factor 5A from Pyrobaculum aerophilum at 1.75 A resolution. *Structure*, **1998**, 6, 1207-14	5.2	98

38	Scission of DNA at a preselected sequence using a single-strand-specific chemical nuclease. *Chemistry and Biology*, **1998**, 5, 283-92		20
37	Class-directed structure determination: foundation for a protein structure initiative. *Protein Science* , **1998**, 7, 1851-6	6.3	81
36	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 --> Phe substitutions. *Biochemistry*, **1998**, 37, 7463-77	3.2	26
35	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	2	4
34	Direct Methods, and the use of Synchrotron Radiation for Macromolecular Crystallography **1998**, 445-450		
33	[30] Multiwavelength anomalous diffraction phasing of macromolecular structures: Analysis of MAD data as single isomorphous replacement with anomalous scattering data using the MADMRG program. *Methods in Enzymology*, **1997**, 276, 530-537	1.7	37
32	Analyses of the stability and function of three surface mutants (R82C, K69H, and L32R) of the gene V protein from Ff phage by X-ray crystallography. *Protein Science*, **1997**, 6, 771-80	6.3	11
31	Raman spectroscopy of the Ff gene V protein and complexes with poly(dA): nonspecific DNA recognition and binding. *Biochemistry*, **1996**, 35, 9603-9	3.2	19
30	Gene V protein dimerization and cooperativity of binding of poly(dA). *Biochemistry*, **1996**, 35, 16652-64	3.2	19
29	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, 148-59	6.5	20
28	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		6
27	Relationship between in vivo activity and in vitro measures of function and stability of a protein. *Biochemistry*, **1995**, 34, 11970-8	3.2	19
26	Circular dichroism spectroscopy of three tyrosine-to-phenylalanine substitutions of fd gene 5 protein. *Biochemistry*, **1995**, 34, 12854-65	3.2	14
25	Engineering the stability and function of gene V protein. *Advances in Protein Chemistry*, **1995**, 46, 177-215		14
24	MAD phasing: Bayesian estimates of F(A). *Acta Crystallographica Section D: Biological Crystallography*, **1994**, 50, 11-6		22
23	In vivo characterization of mutants of the bacteriophage f1 gene V protein isolated by saturation mutagenesis. *Journal of Molecular Biology*, **1994**, 236, 556-71	6.5	45
22	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	3.2	26
21	Repacking protein interiors. *Trends in Biotechnology*, **1991**, 9, 59-63	15.1	18

20	Approaches to predicting effects of single amino acid substitutions on the function of a protein. *Biochemistry*, **1991**, 30, 6230-40	3.2	14
19	Reversible denaturation of the gene V protein of bacteriophage f1. *Biochemistry*, **1991**, 30, 2772-82	3.2	45
18	Isolation and in vitro characterization of temperature-sensitive mutants of the bacteriophage f1 gene V protein. *Journal of Molecular Biology*, **1991**, 219, 257-75	6.5	16
17	Construction of a synthetic variant of the bacteriophage f1 gene V by assembling oligodeoxynucleotides corresponding to only one strand of DNA. *Gene*, **1988**, 71, 41-7	3.8	12
16	Simple and highly efficient site-specific mutagenesis, by ligation of an oligodeoxyribonucleotide into gapped heteroduplex DNA in which the template strand contains deoxyuridine. *Gene*, **1988**, 69, 317-24	3.8	11
15	Isomorphous replacement: effects of errors on the phase probability distribution. *Acta Crystallographica Section A: Foundations and Advances*, **1987**, 43, 6-13		19
14	Generalized method of determining heavy-atom positions using the difference Patterson function. *Acta Crystallographica Section A: Foundations and Advances*, **1987**, 43, 1-5		103
13	Unbiased three-dimensional refinement of heavy-atom parameters by correlation of origin-removed Patterson functions. *Acta Crystallographica Section A: Foundations and Advances*, **1983**, 39, 813-817		134
12	Rapid determination of [guanidino-15N]arginine in plasma with gas chromatography--mass spectrometry: application to human metabolic studies. *Analytical Biochemistry*, **1983**, 131, 75-82	3.1	20
11	Hydrophobic moments and protein structure. *Faraday Symposia of the Chemical Society*, **1982**, 17, 109		363
10	The helical hydrophobic moment: a measure of the amphiphilicity of a helix. *Nature*, **1982**, 299, 371-4	50.4	895
9	Gas chromatography-mass spectrometry determination of [15N]ammonia enrichment in blood and urine. *Analytical Biochemistry*, **1981**, 114, 125-30	3.1	28
8	Structural studies of bee melittin. *Biophysical Journal*, **1980**, 32, 252-4	2.9	21
7	Improving AlphaFold modeling using implicit information from experimental density maps		2
6	Density modification of cryo-EM maps		2
5	Automated map sharpening by maximization of detail and connectivity		6
4	Real-space refinement in Phenix for cryo-EM and crystallography		8
3	A fully automatic method yielding initial models from high-resolution electron cryo-microscopy maps		4