Randy J Read

List of Publications by Year in Descending Order

197 papers	77,880 citations	67 h-index	233 g-index
233 ext. papers	89,271 ext. citations	8.7 avg, IF	7.49 L-index

#	Paper	IF	Citations
197	Implications of AlphaFold2 for crystallographic phasing by molecular replacement.. *Acta Crystallographica Section D: Structural Biology*, **2022**, 78, 1-13	5.5	11
196	Crystal structures of BMPRII extracellular domain in binary and ternary receptor complexes with BMP10.. *Nature Communications*, **2022**, 13, 2395	17.4	1
195	Submission of structural biology data for review purposes. *Acta Crystallographica Section F, Structural Biology Communications*, **2021**, 77, 435-436	1.1	
194	Angiotensinogen and the Modulation of Blood Pressure. *Frontiers in Cardiovascular Medicine*, **2021**, 8, 645123	5.4	6
193	Likelihood-based estimation of substructure content from single-wavelength anomalous diffraction (SAD) intensity data. *Acta Crystallographica Section D: Structural Biology*, **2021**, 77, 880-893	5.5	0
192	Phasertng: directed acyclic graphs for crystallographic phasing. *Acta Crystallographica Section D: Structural Biology*, **2021**, 77, 1-10	5.5	6
191	Detection of translational noncrystallographic symmetry in Patterson functions. *Acta Crystallographica Section D: Structural Biology*, **2021**, 77, 131-141	5.5	2
190	Adaptive Cartesian and torsional restraints for interactive model rebuilding. *Acta Crystallographica Section D: Structural Biology*, **2021**, 77, 438-446	5.5	3
189	Accurate prediction of protein structures and interactions using a three-track neural network. *Science*, **2021**, 373, 871-876	33.3	522
188	Assessing the utility of CASP14 models for molecular replacement. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 1752-1769	4.2	18
187	Submission of structural biology data for review purposes. *Acta Crystallographica Section D: Structural Biology*, **2021**, 77, 1477-1478	5.5	0
186	Density modification of cryo-EM maps. *Acta Crystallographica Section D: Structural Biology*, **2020**, 76, 912-925	5.5	11
185	Factors influencing estimates of coordinate error for molecular replacement. *Acta Crystallographica Section D: Structural Biology*, **2020**, 76, 19-27	5.5	4
184	Measuring and using information gained by observing diffraction data. *Acta Crystallographica Section D: Structural Biology*, **2020**, 76, 238-247	5.5	1
183	Three new Co-editors appointed to Acta Crystallographica Section D, Structural Biology. *Acta Crystallographica Section D: Structural Biology*, **2020**, 76, 612	5.5	
182	Improvement of cryo-EM maps by density modification. *Nature Methods*, **2020**, 17, 923-927	21.6	123
181	Evaluation of template-based modeling in CASP13. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1113-1127	4.2	38

180	Evaluation of model refinement in CASP13. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1249-1262	4.2	25
179	Germline mutations in the transcription factor IKZF5 cause thrombocytopenia. *Blood*, **2019**, 134, 2070-2081	16.6	23
178	Coping with strong translational noncrystallographic symmetry and extreme anisotropy in molecular replacement with Phaser: human Rab27a. *Acta Crystallographica Section D: Structural Biology*, **2019**, 75, 342-353	5.5	6
177	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. *Acta Crystallographica Section D: Structural Biology*, **2019**, 75, 455-457	5.5	7
176	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
175	An oligomeric state-dependent switch in the ER enzyme FICD regulates AMPylation and deAMPylation of BiP. *EMBO Journal*, **2019**, 38, e102177	13	18
174	Structural basis for the specificity of renin-mediated angiotensinogen cleavage. *Journal of Biological Chemistry*, **2019**, 294, 2353-2364	5.4	10
173	Measurement of the total angiotensinogen and its reduced and oxidised forms in human plasma using targeted LC-MS/MS. *Analytical and Bioanalytical Chemistry*, **2019**, 411, 427-437	4.4	3
172	computation of the PDB to audit diffraction anisotropy of soluble and membrane proteins. *Data in Brief*, **2018**, 19, 753-757	1.2	1
171	Gyre and gimble: a maximum-likelihood replacement for Patterson correlation refinement. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 279-289	5.5	13
170	On the application of the expected log-likelihood gain to decision making in molecular replacement. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 245-255	5.5	22
169	Real-space refinement in PHENIX for cryo-EM and crystallography. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 531-544	5.5	917
168	Structure and oligomerization of the periplasmic domain of GspL from the type II secretion system of Pseudomonas aeruginosa. *Scientific Reports*, **2018**, 8, 16760	4.9	5
167	Maximum-likelihood determination of anomalous substructures. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 98-105	5.5	3
166	Exploiting distant homologues for phasing through the generation of compact fragments, local fold refinement and partial solution combination. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 290-304	5.5	19
165	Insights into Hunter syndrome from the structure of iduronate-2-sulfatase. *Nature Communications*, **2017**, 8, 15786	17.4	42
164	Ab initio solution of macromolecular crystal structures without direct methods. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 3637-3641	11.5	32
163	How serpins transport hormones and regulate their release. *Seminars in Cell and Developmental Biology*, **2017**, 62, 133-141	7.5	17

162	Responses to 'Atomic resolution': a badly abused term in structural biology. *Acta Crystallographica Section D: Structural Biology*, **2017**, 73, 381-383	5.5	5
161	X-ray diffraction reveals the intrinsic difference in the physical properties of membrane and soluble proteins. *Scientific Reports*, **2017**, 7, 17013	4.9	7
160	Decoding Corticotropin-Releasing Factor Receptor Type 1 Crystal Structures. *Current Molecular Pharmacology*, **2017**, 10, 334-344	3.7	17
159	AMPylation targets the rate-limiting step of BiP's ATPase cycle for its functional inactivation. *ELife*, **2017**, 6,	8.9	43
158	A critical examination of the recently reported crystal structures of the human SMN protein. *Human Molecular Genetics*, **2016**, 25, 4717-4725	5.6	9
157	Structural basis of GM-CSF and IL-2 sequestration by the viral decoy receptor GIF. *Nature Communications*, **2016**, 7, 13228	17.4	11
156	Molecular Mechanism of Z 1-Antitrypsin Deficiency. *Journal of Biological Chemistry*, **2016**, 291, 15674-86	5.4	21
155	A log-likelihood-gain intensity target for crystallographic phasing that accounts for experimental error. *Acta Crystallographica Section D: Structural Biology*, **2016**, 72, 375-87	5.5	48
154	Structure of Gremlin-2 in Complex with GDF5 Gives Insight into DAN-Family-Mediated BMP Antagonism. *Cell Reports*, **2016**, 16, 2077-2086	10.6	22
153	ANS complex of St John's wort PR-10 protein with 28 copies in the asymmetric unit: a fiendish combination of pseudosymmetry with tetartohedral twinning. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 829-43		14
152	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. *Structure*, **2015**, 23, 1156-67	5.2	131
151	Azasugar inhibitors as pharmacological chaperones for Krabbe disease. *Chemical Science*, **2015**, 6, 3075-3086	9.1	36
150	X-ray structure determination using low-resolution electron microscopy maps for molecular replacement. *Nature Protocols*, **2015**, 10, 1275-84	18.8	16
149	Macromolecular X-ray structure determination using weak, single-wavelength anomalous data. *Nature Methods*, **2015**, 12, 127-30	21.6	27
148	Structure of human saposin A at lysosomal pH. *Acta Crystallographica Section F, Structural Biology Communications*, **2015**, 71, 895-900	1.1	7
147	Local error estimates dramatically improve the utility of homology models for solving crystal structures by molecular replacement. *Structure*, **2015**, 23, 397-406	5.2	18
146	G-actin provides substrate-specificity to eukaryotic initiation factor 2holophosphatases. *ELife*, **2015**, 4,	8.9	47
145	Automated identification of elemental ions in macromolecular crystal structures. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 1104-14		27

144	Structural biology. Crystal structure of the CRISPR RNA-guided surveillance complex from Escherichia coli. *Science*, **2014**, 345, 1473-9	33.3	182
143	Transcriptional diversity during lineage commitment of human blood progenitors. *Science*, **2014**, 345, 1251033	33.3	187
142	Likelihood-based molecular-replacement solution for a highly pathological crystal with tetartohedral twinning and sevenfold translational noncrystallographic symmetry. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 471-80		20
141	Temperature-responsive release of thyroxine and its environmental adaptation in Australians. *Proceedings of the Royal Society B: Biological Sciences*, **2014**, 281, 20132747	4.4	11
140	Automating crystallographic structure solution and refinement of protein-ligand complexes. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 144-54		33
139	Towards engineering hormone-binding globulins as drug delivery agents. *PLoS ONE*, **2014**, 9, e113402	3.7	11
138	How changes in affinity of corticosteroid-binding globulin modulate free cortisol concentration. *Journal of Clinical Endocrinology and Metabolism*, **2013**, 98, 3315-22	5.6	51
137	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
136	Structural snapshots illustrate the catalytic cycle of β-galactocerebrosidase, the defective enzyme in Krabbe disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 20479-84	11.5	30
135	Intensity statistics in the presence of translational noncrystallographic symmetry. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 176-83		34
134	Model morphing and sequence assignment after molecular replacement. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2244-50		24
133	Phaser.MRage: automated molecular replacement. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2276-86		144
132	Improved estimates of coordinate error for molecular replacement. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2209-15		33
131	Improving experimental phases for strong reflections prior to density modification. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2039-49		6
130	Extending the Reach of Molecular Replacement. *NATO Science for Peace and Security Series A: Chemistry and Biology*, **2013**, 113-122	0.1	
129	Graphical tools for macromolecular crystallography in PHENIX. *Journal of Applied Crystallography*, **2012**, 45, 581-586	3.8	95
128	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
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	Structural basis for benzothiazinone-mediated killing of Mycobacterium tuberculosis. *Science Translational Medicine*, **2012**, 4, 150ra121	17.5	123
125	Severe diffraction anisotropy, rotational pseudosymmetry and twinning complicate the refinement of a pentameric coiled-coil structure of NSP4 of rotavirus. *Acta Crystallographica Section D: Biological Crystallography*, **2012**, 68, 1541-8		5
124	A new pentameric structure of rotavirus NSP4 revealed by molecular replacement. *Acta Crystallographica Section D: Biological Crystallography*, **2012**, 68, 57-61		7
123	phenix.mr_rosetta: molecular replacement and model rebuilding with Phenix and Rosetta. *Journal of Structural and Functional Genomics*, **2012**, 13, 81-90		109
122	Structural insights into the redox-switch mechanism of the MarR/DUF24-type regulator HypR. *Nucleic Acids Research*, **2012**, 40, 4178-92	20.1	49
121	Exome sequencing identifies NBEAL2 as the causative gene for gray platelet syndrome. *Nature Genetics*, **2011**, 43, 735-7	36.3	224
120	The Phenix software for automated determination of macromolecular structures. *Methods*, **2011**, 55, 94-106	4.6	580
119	Improved molecular replacement by density- and energy-guided protein structure optimization. *Nature*, **2011**, 473, 540-3	50.4	196
118	A new generation of crystallographic validation tools for the protein data bank. *Structure*, **2011**, 19, 1395-412	5.2	335
117	Overview of the CCP4 suite and current developments. *Acta Crystallographica Section D: Biological Crystallography*, **2011**, 67, 235-42		8847
116	Improvement of molecular-replacement models with Sculptor. *Acta Crystallographica Section D: Biological Crystallography*, **2011**, 67, 303-12		167
115	Using SAD data in Phaser. *Acta Crystallographica Section D: Biological Crystallography*, **2011**, 67, 338-44		90
114	Solving serpin crystal structures. *Methods in Enzymology*, **2011**, 501, 49-61	1.7	3
113	Novel pentameric structure of the diarrhea-inducing region of the rotavirus enterotoxigenic protein NSP4. *Journal of Virology*, **2011**, 85, 12721-32	6.6	21
112	Allosteric modulation of hormone release from thyroxine and corticosteroid-binding globulins. *Journal of Biological Chemistry*, **2011**, 286, 16163-73	5.4	39
111	Insights into Krabbe disease from structures of galactocerebrosidase. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 15169-73	11.5	63
110	A redox switch in angiotensinogen modulates angiotensin release. *Nature*, **2010**, 468, 108-11	50.4	171
109	From poor resolution to rich insight. *Structure*, **2010**, 18, 664-5	5.2	1

108	PHENIX: a comprehensive Python-based system for macromolecular structure solution. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 213-21		16067
107	Experimental phasing: best practice and pitfalls. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 458-69		35
106	Recent developments in phasing and structure refinement for macromolecular crystallography. *Current Opinion in Structural Biology*, **2009**, 19, 566-72	8.1	21
105	Case-controlled structure validation. *Acta Crystallographica Section D: Biological Crystallography*, **2009**, 65, 140-7		15
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	Methylation-state-specific recognition of histones by the MBT repeat protein L3MBTL2. *Nucleic Acids Research*, **2009**, 37, 2204-10	20.1	77
102	The S-to-R transition of corticosteroid-binding globulin and the mechanism of hormone release. *Journal of Molecular Biology*, **2008**, 380, 244-51	6.5	57
101	Iterative model building, structure refinement and density modification with the PHENIX AutoBuild wizard. *Acta Crystallographica Section D: Biological Crystallography*, **2008**, 64, 61-9		1042
100	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
99	Automated structure solution with the PHENIX suite. *Methods in Molecular Biology*, **2008**, 426, 419-35	1.4	421
98	Swiveling domain mechanism in pyruvate phosphate dikinase. *Biochemistry*, **2007**, 46, 14845-53	3.2	29
97	Phaser crystallographic software. *Journal of Applied Crystallography*, **2007**, 40, 658-674	3.8	14212
96	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. *Acta Crystallographica Section D: Biological Crystallography*, **2007**, 63, 597-610		56
95	Assessment of CASP7 predictions in the high accuracy template-based modeling category. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69 Suppl 8, 27-37	4.2	86
94	Domain definition and target classification for CASP7. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69 Suppl 8, 10-8	4.2	19
93	Automated server predictions in CASP7. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69 Suppl 8, 68-82	4.2	95
92	Crystallography: crystallographic evidence for deviating C3b structure. *Nature*, **2007**, 448, E1-2; discussion E2-3	50.4	33
91	High-resolution structure prediction and the crystallographic phase problem. *Nature*, **2007**, 450, 259-64	50.4	262

90	Likelihood-based experimental phasing in phaser. *NATO Science Series Series II, Mathematics, Physics and Chemistry*, **2007**, 67-77		
89	Likelihood-based molecular replacement in phaser. *NATO Science Series Series II, Mathematics, Physics and Chemistry*, **2007**, 91-100		5
88	Automated structure determination with phenix. *NATO Science Series Series II, Mathematics, Physics and Chemistry*, **2007**, 101-109		2
87	Crystal structure of rab11 in complex with rab11 family interacting protein 2. *Structure*, **2006**, 14, 1273-83	5.2	72
86	Molecular pathology of X linked retinoschisis: mutations interfere with retinoschisin secretion and oligomerisation. *British Journal of Ophthalmology*, **2006**, 90, 81-6	5.5	64
85	Structural mechanism for the carriage and release of thyroxine in the blood. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 13321-6	11.5	94
84	Mutations in FRMD7, a newly identified member of the FERM family, cause X-linked idiopathic congenital nystagmus. *Nature Genetics*, **2006**, 38, 1242-4	36.3	137
83	Liberating crystallographers. *Structure*, **2005**, 13, 1236-7	5.2	
82	Likelihood-enhanced fast translation functions. *Acta Crystallographica Section D: Biological Crystallography*, **2005**, 61, 458-64		1503
81	Solution structure of the Kaposi's sarcoma-associated herpesvirus K3 N-terminal domain reveals a Novel E2-binding C4HC3-type RING domain. *Journal of Biological Chemistry*, **2004**, 279, 53840-7	5.4	77
80	Recent developments in the PHENIX software for automated crystallographic structure determination. *Journal of Synchrotron Radiation*, **2004**, 11, 53-5	2.4	273
79	The application of multivariate statistical techniques improves single-wavelength anomalous diffraction phasing. *Acta Crystallographica Section D: Biological Crystallography*, **2004**, 60, 22-7		48
78	Likelihood-enhanced fast rotation functions. *Acta Crystallographica Section D: Biological Crystallography*, **2004**, 60, 432-8		1017
77	Simple algorithm for a maximum-likelihood SAD function. *Acta Crystallographica Section D: Biological Crystallography*, **2004**, 60, 1220-8		90
76	Pushing the boundaries of molecular replacement with maximum likelihood. Erratum. *Acta Crystallographica Section D: Biological Crystallography*, **2003**, 59, 404-404		2
75	New ways of looking at experimental phasing. *Acta Crystallographica Section D: Biological Crystallography*, **2003**, 59, 1891-902		5
74	Application of the complex multivariate normal distribution to crystallographic methods with insights into multiple isomorphous replacement phasing. *Acta Crystallographica Section D: Biological Crystallography*, **2003**, 59, 1801-8		35
73	How vitronectin binds PAI-1 to modulate fibrinolysis and cell migration. *Nature Structural and Molecular Biology*, **2003**, 10, 541-4	17.6	187

72	Strengthening molecular replacement with maximum likelihood in Beast. *Crystallography Reviews*, **2003**, 9, 33-41	1.3	1
71	PHENIX: building new software for automated crystallographic structure determination. *Acta Crystallographica Section D: Biological Crystallography*, **2002**, 58, 1948-54		3477
70	Crystal structure of double helical hexitol nucleic acids. *Journal of the American Chemical Society*, **2002**, 124, 928-33	16.4	67
69	Pushing the boundaries of molecular replacement with maximum likelihood. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 1373-82		665
68	Immunoprophylactic potential of cloned Shiga toxin 2 B subunit. *Journal of Infectious Diseases*, **2001**, 183, 435-43	7	72
67	Different structural requirements for plasminogen activator inhibitor 1 (PAI-1) during latency transition and proteinase inhibition as evidenced by phage-displayed hypermutated PAI-1 libraries. *Journal of Molecular Biology*, **2001**, 305, 773-83	6.5	36
66	Shiga-like toxins are neutralized by tailored multivalent carbohydrate ligands. *Nature*, **2000**, 403, 669-72	50.4	772
65	Structure of a serpin-protease complex shows inhibition by deformation. *Nature*, **2000**, 407, 923-6	50.4	916
64	A mutant Shiga-like toxin IIe bound to its receptor Gb(3): structure of a group II Shiga-like toxin with altered binding specificity. *Structure*, **2000**, 8, 253-64	5.2	32
63	Inactive conformation of the serpin alpha(1)-antichymotrypsin indicates two-stage insertion of the reactive loop: implications for inhibitory function and conformational disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 67-72	11.5	166
62	Crystal structure of Pseudomonas aeruginosa PAK pilin suggests a main-chain-dominated mode of receptor binding. *Journal of Molecular Biology*, **2000**, 299, 1005-17	6.5	120
61	Extending the limits of molecular replacement through combined simulated annealing and maximum-likelihood refinement. *Acta Crystallographica Section D: Biological Crystallography*, **1999**, 55, 181-90		27
60	Detecting outliers in non-redundant diffraction data. *Acta Crystallographica Section D: Biological Crystallography*, **1999**, 55, 1759-64		20
59	The identification of three biologically relevant globotriaosyl ceramide receptor binding sites on the Verotoxin 1 B subunit. *Molecular Microbiology*, **1999**, 32, 953-60	4.1	58
58	The active conformation of plasminogen activator inhibitor 1, a target for drugs to control fibrinolysis and cell adhesion. *Structure*, **1999**, 7, 111-8	5.2	136
57	A 2.6 A structure of a serpin polymer and implications for conformational disease. *Journal of Molecular Biology*, **1999**, 293, 449-55	6.5	108
56	Fragment-based modeling of NAD binding to the catalytic subunits of diphtheria and pertussis toxins **1998**, 31, 282-298		2
55	Crystallography & NMR system: A new software suite for macromolecular structure determination. *Acta Crystallographica Section D: Biological Crystallography*, **1998**, 54, 905-21		14106

54	Incorporation of prior phase information strengthens maximum-likelihood structure refinement. *Acta Crystallographica Section D: Biological Crystallography*, **1998**, 54, 1285-94		158
53	Structure of the shiga-like toxin I B-pentamer complexed with an analogue of its receptor Gb3. *Biochemistry*, **1998**, 37, 1777-88	3.2	377
52	Modeling the carbohydrate-binding specificity of pig edema toxin. *Biochemistry*, **1998**, 37, 1789-99	3.2	19
51	Molecular Docking with a View: The Integration of a Monte Carlo Docking Program into a Virtual Reality Environment **1998**, 309-322		
50	Noncrystallographic symmetry averaging in phase refinement and extension. *Methods in Enzymology*, **1997**, 277, 18-53	1.7	12
49	[Model phases: probabilities and bias. *Methods in Enzymology*, **1997**, 277, 110-28	1.7	54
48	Accumulating evidence suggests that several AB-toxins subvert the endoplasmic reticulum-associated protein degradation pathway to enter target cells. *Biochemistry*, **1997**, 36, 11051-4	3.2	278
47	Cross-validated maximum likelihood enhances crystallographic simulated annealing refinement. *Proceedings of the National Academy of Sciences of the United States of America*, **1997**, 94, 5018-23	11.5	561
46	Not your average density. *Structure*, **1997**, 5, 1557-69	5.2	142
45	Aerolysin and pertussis toxin share a common receptor-binding domain. *EMBO Journal*, **1997**, 16, 3426-34	4.3	47
44	Critical evaluation of the research docking program for the CASP2 challenge. *Proteins: Structure, Function and Bioinformatics*, **1997**, 29, 205-209	4.2	22
43	Critical evaluation of the research docking program for the CASP2 challenge. *Proteins: Structure, Function and Bioinformatics*, **1997**, 29, 205-209	4.2	4
42	Crystal structure of the pertussis toxin-ATP complex: a molecular sensor. *Journal of Molecular Biology*, **1996**, 258, 661-71	6.5	56
41	As MAD as can be. *Structure*, **1996**, 4, 11-4	5.2	15
40	Phenylalanine 30 plays an important role in receptor binding of verotoxin-1. *Molecular Microbiology* , **1996**, 19, 891-9	4.1	24
39	Structural Insights into Pertussis Toxin Action. *Molecular Biology Intelligence Unit*, **1996**, 191-216		
38	Monte Carlo docking with ubiquitin. *Protein Science*, **1995**, 4, 885-99	6.3	9
37	Atomic solvation parameters in the analysis of protein-protein docking results. *Protein Science*, **1995**, 4, 2087-99	6.3	44

36	A mosquitocidal toxin with a ricin-like cell-binding domain. *Nature Structural and Molecular Biology*, **1995**, 2, 358-9	17.6	35
35	Monte Carlo algorithms for docking to proteins. *Supramolecular Chemistry*, **1995**, 6, 135-140	1.8	10
34	DEMON/ANGEL: a suite of programs to carry out density modification. *Journal of Applied Crystallography*, **1995**, 28, 347-351	3.8	30
33	Structure of a pertussis toxin-sugar complex as a model for receptor binding. *Nature Structural and Molecular Biology*, **1994**, 1, 591-6	17.6	94
32	The crystal structure of pertussis toxin. *Structure*, **1994**, 2, 45-57	5.2	297
31	Purification, crystallization and preliminary X-ray analysis of murine interleukin-5. *Journal of Molecular Biology*, **1994**, 241, 269-72	6.5	6
30	Multiple-Start Monte Carlo Docking of Flexible Ligands **1994**, 71-108		10
29	Comparison of the B-pentamers of heat-labile enterotoxin and verotoxin-1: two structures with remarkable similarity and dissimilarity. *Biochemistry*, **1993**, 32, 191-8	3.2	52
28	Toxins. *Current Opinion in Structural Biology*, **1993**, 3, 853-860	8.1	14
27	Structure of glycosomal glyceraldehyde-3-phosphate dehydrogenase from Trypanosoma brucei determined from Laue data. *Proceedings of the National Academy of Sciences of the United States of America*, **1993**, 90, 2355-9	11.5	82
26	A multiple-start Monte Carlo docking method. *Proteins: Structure, Function and Bioinformatics*, **1992** , 13, 206-22	4.2	187
25	Crystal structure of the cell-binding B oligomer of verotoxin-1 from E. coli. *Nature*, **1992**, 355, 748-50	50.4	280
24	Crystallization and preliminary X-ray crystallographic analysis of verotoxin-1 B-subunit. *Journal of Molecular Biology*, **1991**, 221, 729-31	6.5	8
23	Refined structure of porcine pepsinogen at 1.8 A resolution. *Journal of Molecular Biology*, **1991**, 219, 671-92	6.5	96
22	X-ray structure of lipoamide dehydrogenase from Azotobacter vinelandii determined by a combination of molecular and isomorphous replacement techniques. *Journal of Molecular Biology*, **1989**, 206, 365-79	6.5	86
21	A phased translation function. *Journal of Applied Crystallography*, **1988**, 21, 490-495	3.8	103
20	Refined crystal structure of Streptomyces griseus trypsin at 1.7 A resolution. *Journal of Molecular Biology*, **1988**, 200, 523-51	6.5	109
19	Crystal and molecular structures of the complex of alpha-chymotrypsin with its inhibitor turkey ovomucoid third domain at 1.8 A resolution. *Journal of Molecular Biology*, **1987**, 195, 397-418	6.5	235

18	Preliminary crystallographic studies of glycosomal glyceraldehyde phosphate dehydrogenase from Trypanosoma brucei brucei. *Journal of Molecular Biology*, **1987**, 194, 573-5	6.5	12
17	Experiences with a new translation-function program. *Journal of Applied Crystallography*, **1987**, 20, 517-528	3.8	125
16	Critical evaluation of comparative model building of Streptomyces griseus trypsin. *Biochemistry*, **1984**, 23, 6570-5	3.2	94
15	Structure of the complex of Streptomyces griseus protease B and the third domain of the turkey ovomucoid inhibitor at 1.8-A resolution. *Biochemistry*, **1983**, 22, 4420-33	3.2	210
14	Refined crystal structure of the molecular complex of Streptomyces griseus protease B, a serine protease, with the third domain of the ovomucoid inhibitor from turkey. *Proceedings of the National Academy of Sciences of the United States of America*, **1982**, 79, 4868-72	11.5	67
13	Crystal and molecular structure of [tris(4,5-diisopropylimidazol-2-yl)phosphine]dichlorozinc(II)-bis[N,N-dimethylformamide]. *Journal of the American Chemical Society*, **1981**, 103, 6947-6952	16.4	20
12	Improving AlphaFold modeling using implicit information from experimental density maps		2
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