Randy J Read

List of Publications by Year
in descending order

208 papers	98,582 citations	11908 72 h-index	3595 187 g-index
233 all docs	233 docs citations	233 times ranked	73631 citing authors

#	Article	IF	Citations
1	PHENIX: a comprehensive Python-based system for macromolecular structure solution. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 213-221.	2.5	20,564
2	Phasercrystallographic software. Journal of Applied Crystallography, 2007, 40, 658-674.	1.9	17,782
3	Crystallography & NMR System: A New Software Suite for Macromolecular Structure Determination. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 905-921.	2.5	14,711
4	Overview of theCCP4 suite and current developments. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 235-242.	2.5	11,098
5	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
6	PHENIX: building new software for automated crystallographic structure determination. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1948-1954.	2.5	3,979
7	Accurate prediction of protein structures and interactions using a three-track neural network. Science, 2021, 373, 871-876.	6.0	2,843
8	Real-space refinement inPHENIXfor cryo-EM and crystallography. Acta Crystallographica Section D: Structural Biology, 2018, 74, 531-544.	1.1	2,065
9	Likelihood-enhanced fast translation functions. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 458-464.	2.5	1,560
10	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
11	Likelihood-enhanced fast rotation functions. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 432-438.	2.5	1,074
12	Structure of a serpinâ€“protease complex shows inhibition by deformation. Nature, 2000, 407, 923-926.	13.7	1,022
13	Shiga-like toxins are neutralized by tailored multivalent carbohydrate ligands. Nature, 2000, 403, 669-672.	13.7	853
14	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
15	The Phenix software for automated determination of macromolecular structures. Methods, 2011, 55, 94-106.	1.9	764
16	Pushing the boundaries of molecular replacement with maximum likelihood. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1373-1382.	2.5	728
17	Cross-validated maximum likelihood enhances crystallographic simulated annealing refinement. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 5018-5023.	3.3	623
18	Automated Structure Solution with the PHENIX Suite. Methods in Molecular Biology, 2008, 426, 419-435.	0.4	492

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19	Structure of the Shiga-like Toxin I B-Pentamer Complexed with an Analogue of Its Receptor Gb3,. Biochemistry, 1998, 37, 1777-1788.	1.2	416
20	A New Generation of Crystallographic Validation Tools for the Protein Data Bank. Structure, 2011, 19, 1395-1412.	1.6	405
21	The crystal structure of pertussis toxin. Structure, 1994, 2, 45-57.	1.6	338
22	Crystal structure of the cell-binding B oligomer of verotoxin-1 from E. coli. Nature, 1992, 355, 748-750.	13.7	319
23	Recent developments in thePHENIXsoftware for automated crystallographic structure determination. Journal of Synchrotron Radiation, 2004, 11, 53-55.	1.0	319
24	Accumulating Evidence Suggests That Several AB-Toxins Subvert the Endoplasmic Reticulum-Associated Protein Degradation Pathway To Enter Target Cells. Biochemistry, 1997, 36, 11051-11054.	1.2	307
25	High-resolution structure prediction and the crystallographic phase problem. Nature, 2007, 450, 259-264.	13.7	296
26	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	6.0	253
27	Crystal and molecular structures of the complex of Î±-chymotrypsin with its inhibitor Turkey ovomucoid third domain at 1.8 Ã... resolution. Journal of Molecular Biology, 1987, 195, 397-418.	2.0	245
28	Exome sequencing identifies NBEAL2 as the causative gene for gray platelet syndrome. Nature Genetics, 2011, 43, 735-737.	9.4	245
29	Improvement of cryo-EM maps by density modification. Nature Methods, 2020, 17, 923-927.	9.0	243
30	Improved molecular replacement by density- and energy-guided protein structure optimization. Nature, 2011, 473, 540-543.	13.7	226
31	Crystal structure of the CRISPR RNAâ€“guided surveillance complex from Escherichia coli. Science, 2014, 345, 1473-1479.	6.0	226
32	Structure of the complex of Streptomyces griseus protease B and the third domain of the turkey ovomucoid inhibitor at 1.8-.ANG. resolution. Biochemistry, 1983, 22, 4420-4433.	1.2	224
33	How vitronectin binds PAI-1 to modulate fibrinolysis and cell migration. Nature Structural and Molecular Biology, 2003, 10, 541-544.	3.6	217
34	Phaser.MRage: automated molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2276-2286.	2.5	216
35	A multiple-start Monte Carlo docking method. Proteins: Structure, Function and Bioinformatics, 1992, 13, 206-222.	1.5	211
36	Improvement of molecular-replacement models withSculptor. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 303-312.	2.5	207

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37	A redox switch in angiotensinogen modulates angiotensin release. Nature, 2010, 468, 108-111.	13.7	191
38	Mutations in FRMD7, a newly identified member of the FERM family, cause X-linked idiopathic congenital nystagmus. Nature Genetics, 2006, 38, 1242-1244.	9.4	180
39	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.	3.3	178
40	Incorporation of Prior Phase Information Strengthens Maximum-Likelihood Structure Refinement. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1285-1294.	2.5	172
41	Experiences with a new translation-function program. Journal of Applied Crystallography, 1987, 20, 517-521.	1.9	165
42	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
43	Structural Basis for Benzothiazinone-Mediated Killing of Mycobacterium tuberculosis. Science Translational Medicine, 2012, 4, 150ra121.	5.8	159
44	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	1.6	159
45	The active conformation of plasminogen activator inhibitor 1, a target for drugs to control fibrinolysis and cell adhesion. Structure, 1999, 7, 111-118.	1.6	152
46	Not your average density. Structure, 1997, 5, 1557-1569.	1.6	147
47	Graphical tools for macromolecular crystallography inPHENIX. Journal of Applied Crystallography, 2012, 45, 581-586.	1.9	139
48	A phased translation function. Journal of Applied Crystallography, 1988, 21, 490-495.	1.9	133
49	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
50	Crystal structure of Pseudomonas aeruginosa PAK pilin suggests a main-chain-dominated mode of receptor binding 1 1Edited by R. Huber. Journal of Molecular Biology, 2000, 299, 1005-1017.	2.0	130
51	Refined crystal structure of Streptomyces griseus trypsin at 1.7 Ã... resolution. Journal of Molecular Biology, 1988, 200, 523-551.	2.0	122
52	A 2.6 Ã¥ structure of a serpin polymer and implications for conformational disease 1 1Edited by R. Huber. Journal of Molecular Biology, 1999, 293, 449-455.	2.0	116
53	Structure of a pertussis toxinâ€“sugar complex as a model for receptor binding. Nature Structural and Molecular Biology, 1994, 1, 591-596.	3.6	107
54	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, 13321-13326.	3.3	105

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55	Automated server predictions in CASP7. Proteins: Structure, Function and Bioinformatics, 2007, 69, 68-82.	1.5	105
56	Using SAD data inPhaser. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 338-344.	2.5	105
57	Refined structure of porcine pepsinogen at 1Â·8 Ã... resolution. Journal of Molecular Biology, 1991, 219, 671-692.	2.0	104
58	Simple algorithm for a maximum-likelihood SAD function. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1220-1228.	2.5	101
59	Critical evaluation of comparative model building of Streptomyces griseus trypsin. Biochemistry, 1984, 23, 6570-6575.	1.2	100
60	Assessment of CASP7 predictions in the high accuracy template-based modeling category. Proteins: Structure, Function and Bioinformatics, 2007, 69, 27-37.	1.5	96
61	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, 365-379.	2.0	95
62	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, 2355-2359.	3.3	91
63	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
64	Insights into Krabbe disease from structures of galactocerebrosidase. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15169-15173.	3.3	87
65	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, 53840-53847.	1.6	85
66	Methylation-state-specific recognition of histones by the MBT repeat protein L3MBTL2. Nucleic Acids Research, 2009, 37, 2204-2210.	6.5	85
67	Crystal Structure of Rab11 in Complex with Rab11 Family Interacting Protein 2. Structure, 2006, 14, 1273-1283.	1.6	82
68	Immunoprophylactic Potential of Cloned Shiga Toxin 2 B Subunit. Journal of Infectious Diseases, 2001, 183, 435-443.	1.9	80
69	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, 4868-4872.	3.3	76
70	Molecular pathology of X linked retinoschisis: mutations interfere with retinoschisin secretion and oligomerisation. British Journal of Ophthalmology, 2006, 90, 81-86.	2.1	76
71	Crystal Structure of Double Helical Hexitol Nucleic Acids. Journal of the American Chemical Society, 2002, 124, 928-933.	6.6	75
72	[7] Model phases: Probabilities and bias. Methods in Enzymology, 1997, 277, 110-128.	0.4	74

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73	G-actin provides substrate-specificity to eukaryotic initiation factor 2Î± holophosphatases. ELife, 2015, 4, .	2.8	70
74	The identification of three biologically relevant globotriaosyl ceramide receptor binding sites on the Verotoxin 1 B subunit. Molecular Microbiology, 1999, 32, 953-960.	1.2	68
75	How Changes in Affinity of Corticosteroid-binding Globulin Modulate Free Cortisol Concentration. Journal of Clinical Endocrinology and Metabolism, 2013, 98, 3315-3322.	1.8	68
76	Insights into Hunter syndrome from the structure of iduronate-2-sulfatase. Nature Communications, 2017, 8, 15786.	5.8	68
77	Crystal Structure of the Pertussis Toxinâ€“ATP Complex: A Molecular Sensor. Journal of Molecular Biology, 1996, 258, 661-671.	2.0	67
78	AMPylation targets the rate-limiting step of BiPâ€™s ATPase cycle for its functional inactivation. ELife, 2017, 6, .	2.8	66
79	Implications of AlphaFold2 for crystallographic phasing by molecular replacement. Acta Crystallographica Section D: Structural Biology, 2022, 78, 1-13.	1.1	65
80	The S-to-R Transition of Corticosteroid-Binding Globulin and the Mechanism of Hormone Release. Journal of Molecular Biology, 2008, 380, 244-251.	2.0	64
81	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 597-610.	2.5	60
82	A log-likelihood-gain intensity target for crystallographic phasing that accounts for experimental error. Acta Crystallographica Section D: Structural Biology, 2016, 72, 375-387.	1.1	58
83	Comparison of the B-pentamers of heat-labile enterotoxin and verotoxin-1: two structures with remarkable similarity and dissimilarity. Biochemistry, 1993, 32, 191-198.	1.2	57
84	Evaluation of templateâ€based modeling in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1113-1127.	1.5	56
85	Structural insights into the redox-switch mechanism of the MarR/DUF24-type regulator HypR. Nucleic Acids Research, 2012, 40, 4178-4192.	6.5	54
86	Aerolysin and pertussis toxin share a common receptor-binding domain. EMBO Journal, 1997, 16, 3426-3434.	3.5	51
87	Atomic solvation parameters in the analysis of proteinâ€protein docking results. Protein Science, 1995, 4, 2087-2099.	3.1	50
88	The application of multivariate statistical techniques improves single-wavelength anomalous diffraction phasing. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 22-27.	2.5	49
89	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.	3.3	47
90	Assessing the utility of <scp>CASP14</scp> models for molecular replacement. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1752-1769.	1.5	47

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91	Experimental phasing: best practice and pitfalls. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 458-469.	2.5	45
92	Allosteric Modulation of Hormone Release from Thyroxine and Corticosteroid-binding Globulins. Journal of Biological Chemistry, 2011, 286, 16163-16173.	1.6	45
93	Crystallographic evidence for deviating C3b structure. Nature, 2007, 448, E1-E2.	13.7	44
94	Intensity statistics in the presence of translational noncrystallographic symmetry. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 176-183.	2.5	43
95	Automating crystallographic structure solution and refinement of proteinâ€“ligand complexes. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 144-154.	2.5	43
96	DEMON/ANGEL: a suite of programs to carry out density modification. Journal of Applied Crystallography, 1995, 28, 347-351.	1.9	42
97	Improved estimates of coordinate error for molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2209-2215.	2.5	42
98	Azasugar inhibitors as pharmacological chaperones for Krabbe disease. Chemical Science, 2015, 6, 3075-3086.	3.7	42
99	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, 773-783.	2.0	41
100	A mosquitocidal toxin with a ricin-like cell-binding domain. Nature Structural and Molecular Biology, 1995, 2, 358-359.	3.6	40
101	Automated identification of elemental ions in macromolecular crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1104-1114.	2.5	40
102	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.	1.1	40
103	Structural snapshots illustrate the catalytic cycle of Î²-galactocerebrosidase, the defective enzyme in Krabbe disease. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20479-20484.	3.3	39
104	An oligomeric stateâ€dependent switch in the <scp>ER</scp> enzyme <scp>FICD</scp> regulates <scp>AMP</scp> ylation and de <scp>AMP</scp> ylation of BiP. EMBO Journal, 2019, 38, e102177.	3.5	39
105	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, 253-264.	1.6	38
106	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, 1801-1808.	2.5	38
107	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
108	Model morphing and sequence assignment after molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2244-2250.	2.5	37

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109	Structure of Gremlin-2 in Complex with GDF5 Gives Insight into DAN-Family-Mediated BMP Antagonism. Cell Reports, 2016, 16, 2077-2086.	2.9	37
110	Swiveling Domain Mechanism in Pyruvate Phosphate Dikinase[,]. Biochemistry, 2007, 46, 14845-14853.	1.2	36
111	Macromolecular X-ray structure determination using weak, single-wavelength anomalous data. Nature Methods, 2015, 12, 127-130.	9.0	31
112	Phenylalanine 30 plays an important role in receptor binding of verotoxin-1. Molecular Microbiology, 1996, 19, 891-899.	1.2	30
113	Extending the limits of molecular replacement through combined simulated annealing and maximum-likelihood refinement. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 181-190.	2.5	30
114	Molecular Mechanism of Z Î±1-Antitrypsin Deficiency. Journal of Biological Chemistry, 2016, 291, 15674-15686.	1.6	30
115	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.	1.1	30
116	Germline mutations in the transcription factor IKZF5 cause thrombocytopenia. Blood, 2019, 134, 2070-2081.	0.6	29
117	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.	6.6	28
118	Evaluation of model refinement in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1249-1262.	1.5	28
119	Density modification of cryo-EM maps. Acta Crystallographica Section D: Structural Biology, 2020, 76, 912-925.	1.1	28
120	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
121	Decoding Corticotropin-Releasing Factor Receptor Type 1 Crystal Structures. Current Molecular Pharmacology, 2017, 10, 334-344.	0.7	25
122	Temperature-responsive release of thyroxine and its environmental adaptation in Australians. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20132747.	1.2	24
123	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, 471-480.	2.5	24
124	[3] Noncrystallographic symmetry averaging in phase refinement and extension. Methods in Enzymology, 1997, 277, 18-53.	0.4	23
125	Critical evaluation of the research docking program for the CASP2 challenge. Proteins: Structure, Function and Bioinformatics, 1997, 29, 205-209.	1.5	23
126	Detecting outliers in non-redundant diffraction data. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1759-1764.	2.5	23

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127	Recent developments in phasing and structure refinement for macromolecular crystallography. Current Opinion in Structural Biology, 2009, 19, 566-572.	2.6	23
128	Novel Pentameric Structure of the Diarrhea-Inducing Region of the Rotavirus Enterotoxigenic Protein NSP4. Journal of Virology, 2011, 85, 12721-12732.	1.5	23
129	X-ray structure determination using low-resolution electron microscopy maps for molecular replacement. Nature Protocols, 2015, 10, 1275-1284.	5.5	22
130	Modeling the Carbohydrate-Binding Specificity of Pig Edema Toxin. Biochemistry, 1998, 37, 1789-1799.	1.2	21
131	Domain definition and target classification for CASP7. Proteins: Structure, Function and Bioinformatics, 2007, 69, 10-18.	1.5	21
132	Structural basis for the specificity of renin-mediated angiotensinogen cleavage. Journal of Biological Chemistry, 2019, 294, 2353-2364.	1.6	21
133	Local Error Estimates Dramatically Improve the Utility of Homology Models for Solving Crystal Structures by Molecular Replacement. Structure, 2015, 23, 397-406.	1.6	19
134	How serpins transport hormones and regulate their release. Seminars in Cell and Developmental Biology, 2017, 62, 133-141.	2.3	19
135	Case-controlled structure validation. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 140-147.	2.5	17
136	As MAD as can be. Structure, 1996, 4, 11-14.	1.6	16
137	Adaptive Cartesian and torsional restraints for interactive model rebuilding. Acta Crystallographica Section D: Structural Biology, 2021, 77, 438-446.	1.1	16
138	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, 829-843.	2.5	15
139	Structural basis of GM-CSF and IL-2 sequestration by the viral decoy receptor GIF. Nature Communications, 2016, 7, 13228.	5.8	15
140	Toxins. Current Opinion in Structural Biology, 1993, 3, 853-860.	2.6	14
141	Gyreandgimble: a maximum-likelihood replacement for Patterson correlation refinement. Acta Crystallographica Section D: Structural Biology, 2018, 74, 279-289.	1.1	14
142	Monte Carlo algorithms for docking to proteins. Supramolecular Chemistry, 1995, 6, 135-140.	1.5	13
143	A critical examination of the recently reported crystal structures of the human SMN protein. Human Molecular Genetics, 2016, 25, ddw298.	1.4	13
144	X-ray diffraction reveals the intrinsic difference in the physical properties of membrane and soluble proteins. Scientific Reports, 2017, 7, 17013.	1.6	13

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145	Towards Engineering Hormone-Binding Globulins as Drug Delivery Agents. PLoS ONE, 2014, 9, e113402.	1.1	13
146	Preliminary crystallographic studies of glycosomal glyceraldehyde phosphate dehydrogenase from Trypanosoma brucei brucei. Journal of Molecular Biology, 1987, 194, 573-575.	2.0	12
147	Structure and oligomerization of the periplasmic domain of GspL from the type II secretion system of Pseudomonas aeruginosa. Scientific Reports, 2018, 8, 16760.	1.6	12
148	Monte Carlo docking with ubiquitin. Protein Science, 1995, 4, 885-899.	3.1	11
149	Structure of human saposin A at lysosomal pH. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 895-900.	0.4	11
150	Angiotensinogen and the Modulation of Blood Pressure. Frontiers in Cardiovascular Medicine, 2021, 8, 645123.	1.1	11
151	Phasertng: directed acyclic graphs for crystallographic phasing. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1-10.	1.1	10
152	Multiple-Start Monte Carlo Docking of Flexible Ligands. , 1994, , 71-108.		10
153	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Acta Crystallographica Section D: Structural Biology, 2019, 75, 455-457.	1.1	10
154	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, 1541-1548.	2.5	9
155	A new pentameric structure of rotavirus NSP4 revealed by molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 57-61.	2.5	9
156	Crystallization and preliminary X-ray crystallographic analysis of verotoxin-1 B-subunit. Journal of Molecular Biology, 1991, 221, 729-731.	2.0	8
157	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. IUCrJ, 2019, 6, 341-343.	1.0	8
158	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.	1.1	8
159	CRLF3 plays a key role in the final stage of platelet genesis and is a potential therapeutic target for thrombocythemia. Blood, 2022, 139, 2227-2239.	0.6	8
160	Purification, Crystallization and Preliminary X-ray Analysis of Murine Interleukin-5. Journal of Molecular Biology, 1994, 241, 269-272.	2.0	7
161	Improving experimental phases for strong reflections prior to density modification. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2039-2049.	2.5	7
162	Responses to`Atomic resolution': a badly abused term in structural biology. Acta Crystallographica Section D: Structural Biology, 2017, 73, 381-383.	1.1	7

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163	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.	1.9	7
164	Factors influencing estimates of coordinate error for molecular replacement. Acta Crystallographica Section D: Structural Biology, 2020, 76, 19-27.	1.1	6
165	Crystal structures of BMPRII extracellular domain in binary and ternary receptor complexes with BMP10. Nature Communications, 2022, 13, 2395.	5.8	6
166	New ways of looking at experimental phasing. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1891-1902.	2.5	5
167	Solving Serpin Crystal Structures. Methods in Enzymology, 2011, 501, 49-61.	0.4	5
168	Detection of translational noncrystallographic symmetry in Patterson functions. Acta Crystallographica Section D: Structural Biology, 2021, 77, 131-141.	1.1	5
169	Likelihood-based molecular replacement in phaser. NATO Science Series Series II, Mathematics, Physics and Chemistry, 2007, , 91-100.	0.1	5
170	Maximum-likelihood determination of anomalous substructures. Acta Crystallographica Section D: Structural Biology, 2018, 74, 98-105.	1.1	4
171	Critical evaluation of the research docking program for the CASP2 challenge. Proteins: Structure, Function and Bioinformatics, 1997, 29, 205-209.	1.5	4
172	Automated structure determination with phenix. NATO Science Series Series II, Mathematics, Physics and Chemistry, 2007, , 101-109.	0.1	4
173	Au courant computation of the PDB to audit diffraction anisotropy of soluble and membrane proteins. Data in Brief, 2018, 19, 753-757.	0.5	3
174	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 321-323.	0.4	3
175	Measuring and using information gained by observing diffraction data. Acta Crystallographica Section D: Structural Biology, 2020, 76, 238-247.	1.1	3
176	Submission of structural biology data for review purposes. IUCrJ, 2022, 9, 1-2.	1.0	3
177	Fragment-based modeling of NAD binding to the catalytic subunits of diphtheria and pertussis toxins. , 1998, 31, 282-298.		2
178	From Poor Resolution to Rich Insight. Structure, 2010, 18, 664-665.	1.6	2
179	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
180	Strengthening molecular replacement with maximum likelihood in Beast. Crystallography Reviews, 2003, 9, 33-41.	0.4	1

#	Article	IF	Citations
181	Expanding beyond biological crystallography. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1-1.	1.1	1
182	Likelihood-based estimation of substructure content from single-wavelength anomalous diffraction (SAD) intensity data. Acta Crystallographica Section D: Structural Biology, 2021, 77, 880-893.	1.1	1
183	Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Journal of Applied Crystallography, 2019, 52, 495-497.	1.9	1
184	Phaser.Voyager: data-guided model generation and visualization. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e182-e182.	0.0	1
185	Submission of structural biology data for review purposes. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1477-1478.	1.1	1
186	Liberating Crystallographers. Structure, 2005, 13, 1236-1237.	1.6	0
187	Combining Crystallographic and Structure-Modeling Approaches in Macromolecular Crystallography. Biophysical Journal, 2014, 106, 34a.	0.2	0
188	Likelihood-based experimental phasing in phaser. NATO Science Series Series II, Mathematics, Physics and Chemistry, 2007, , 67-77.	0.1	0
189	Phasing by SAD and molecular replacement inPHASER. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s6-s6.	0.3	0
190	Angiotensinogen adjusts its shape to complex with renin and modulate blood pressure. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s30-s30.	0.3	0
191	Extending the Reach of Molecular Replacement. NATO Science for Peace and Security Series A: Chemistry and Biology, 2013, , 113-122.	0.5	0
192	Improved estimates of coordinate error for molecular replacement. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s297-s297.	0.3	0
193	Phasing crystals with single atoms: a century of progress. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s3-s3.	0.3	0
194	Structural Insights into Pertussis Toxin Action. Molecular Biology Intelligence Unit, 1996, , 191-216.	0.2	0
195	Coping with translational non-crystallographic symmetry in molecular replacement. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C319-C319.	0.0	0
196	Modulated protein crystal structure with 28 molecules in the asymmetric unit. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C779-C779.	0.0	0
197	Structural snapshots of GALC: The Krabbe Disease enzyme. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C451-C451.	0.0	0
198	Likelihood-based molecular replacement model pruning inPhaser. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s163-s163.	0.0	0

#	Article	IF	Citations
199	Phasing strategies II â€“ molecular replacement. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a391-a391.	0.0	0
200	On the information content of X-ray diffraction data. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a301-a301.	0.0	0
201	Solving X-ray crystal structures with cryo-EM reconstructions. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e150-e150.	0.0	0
202	The expected log-likelihood gain for decision making in molecular replacement. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e411-e411.	0.0	0
203	Dealing with modulated macromolecular structures with translational non-crystallographic symmetry. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e197-e197.	0.0	0
204	Efficient real-space refinement for cryo-EM and crystallography. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e86-e86.	0.0	0
205	A new 3D reflection data viewer based on NGL. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e165-e165.	0.0	0
206	New Section Editor of Acta Cryst. D. Acta Crystallographica Section D: Structural Biology, 2020, 76, 702-702.	1.1	0
207	Three new Co-editors appointed to Acta Crystallographica Section D, Structural Biology. Acta Crystallographica Section D: Structural Biology, 2020, 76, 612-612.	1.1	0
208	Submission of structural biology data for review purposes. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 435-436.	0.4	0