

# Paul D. Adams

## List of Publications by Year in descending order

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351  
papers

100,900  
citations

4658

85  
h-index

261

299  
g-index

361  
all docs

361  
docs citations

361  
times ranked

71257  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>PHENIX</i> : a comprehensive Python-based system for macromolecular structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 213-221.	2.5	20,564
2	<i>Phaser</i> crystallographic software. <i>Journal of Applied Crystallography</i> , 2007, 40, 658-674.	4.5	17,782
3	Crystallography & NMR System: A New Software Suite for Macromolecular Structure Determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 905-921.	2.5	14,711
4	Towards automated crystallographic structure refinement with <i>phenix.refine</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 352-367.	2.5	4,573
5	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in <i>Phenix</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 861-877.	2.3	4,060
6	PHENIX: building new software for automated crystallographic structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1948-1954.	2.5	3,979
7	Accurate prediction of protein structures and interactions using a three-track neural network. <i>Science</i> , 2021, 373, 871-876.	12.6	2,843
8	MolProbity: More and better reference data for improved all-atom structure validation. <i>Protein Science</i> , 2018, 27, 293-315.	7.6	2,776
9	Real-space refinement in <i>PHENIX</i> for cryo-EM and crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 531-544.	2.3	2,065
10	Iterative model building, structure refinement and density modification with the <i>PHENIX AutoBuild</i> wizard. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 61-69.	2.5	1,319
11	<i>electronic Ligand Builder and Optimization Workbench</i> ( <i>eLBOW</i> ): a tool for ligand coordinate and restraint generation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 1074-1080.	2.5	1,035
12	Structural Basis for Double-Stranded RNA Processing by Dicer. <i>Science</i> , 2006, 311, 195-198.	12.6	860
13	Decision-making in structure solution using Bayesian estimates of map quality: the <i>PHENIX AutoSol</i> wizard. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 582-601.	2.5	804
14	EMRinger: side chain-directed model and map validation for 3D cryo-electron microscopy. <i>Nature Methods</i> , 2015, 12, 943-946.	19.0	799
15	The Phenix software for automated determination of macromolecular structures. <i>Methods</i> , 2011, 55, 94-106.	3.8	764
16	Cross-validated maximum likelihood enhances crystallographic simulated annealing refinement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 5018-5023.	7.1	623
17	New tools for the analysis and validation of cryo-EM maps and atomic models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 814-840.	2.3	575
18	Polder maps: improving OMIT maps by excluding bulk solvent. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 148-157.	2.3	500

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19	<i>iotbx.cif</i> : a comprehensive CIF toolbox. <i>Journal of Applied Crystallography</i> , 2011, 44, 1259-1263.	4.5	487
20	Engineering dynamic pathway regulation using stress-response promoters. <i>Nature Biotechnology</i> , 2013, 31, 1039-1046.	17.5	411
21	A New Generation of Crystallographic Validation Tools for the Protein Data Bank. <i>Structure</i> , 2011, 19, 1395-1412.	3.3	405
22	Structures of the intermediates of Kok <sup>TM</sup> 's photosynthetic water oxidation clock. <i>Nature</i> , 2018, 563, 421-425.	27.8	386
23	Simultaneous Femtosecond X-ray Spectroscopy and Diffraction of Photosystem II at Room Temperature. <i>Science</i> , 2013, 340, 491-495.	12.6	378
24	SPARX, a new environment for Cryo-EM image processing. <i>Journal of Structural Biology</i> , 2007, 157, 47-55.	2.8	356
25	Metabolic engineering of <i>Escherichia coli</i> for limonene and perillyl alcohol production. <i>Metabolic Engineering</i> , 2013, 19, 33-41.	7.0	343
26	Structure of photosystem II and substrate binding at room temperature. <i>Nature</i> , 2016, 540, 453-457.	27.8	323
27	Recent developments in the PHENIX software for automated crystallographic structure determination. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 53-55.	2.4	319
28	A dimerization motif for transmembrane $\alpha$ -helices. <i>Nature Structural Biology</i> , 1994, 1, 157-163.	9.7	294
29	The Computational Crystallography Toolbox: crystallographic algorithms in a reusable software framework. <i>Journal of Applied Crystallography</i> , 2002, 35, 126-136.	4.5	262
30	Joint X-ray and neutron refinement with <i>phenix.refine</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1153-1163.	2.5	259
31	Modelling dynamics in protein crystal structures by ensemble refinement. <i>ELife</i> , 2012, 1, e00311.	6.0	248
32	Improvement of cryo-EM maps by density modification. <i>Nature Methods</i> , 2020, 17, 923-927.	19.0	243
33	Use of knowledge-based restraints in <i>phenix.refine</i> to improve macromolecular refinement at low resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 381-390.	2.5	230
34	Conformational variability in the refined structure of the chaperonin GroEL at 2.8 Å resolution. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 1083-1094.	8.2	219
35	Automated map sharpening by maximization of detail and connectivity. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 545-559.	2.3	218
36	<i>Phaser.MRage</i> : automated molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2276-2286.	2.5	216

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37	Substructure search procedures for macromolecular structures. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1966-1973.	2.5	214
38	Crystal structure of a bacterial ribonuclease P RNA. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13392-13397.	7.1	206
39	Taking snapshots of photosynthetic water oxidation using femtosecond X-ray diffraction and spectroscopy. Nature Communications, 2014, 5, 4371.	12.8	206
40	New tools for structure refinement in PHENIX. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s15-s15.	0.3	205
41	Computational searching and mutagenesis suggest a structure for the pentameric transmembrane domain of phospholamban. Nature Structural and Molecular Biology, 1995, 2, 154-162.	8.2	198
42	New applications of simulated annealing in X-ray crystallography and solution NMR. Structure, 1997, 5, 325-336.	3.3	197
43	Structural organization of the pentameric transmembrane alpha-helices of phospholamban, a cardiac ion channel. EMBO Journal, 1994, 13, 4757-4764.	7.8	175
44	Improved low-resolution crystallographic refinement with Phenix and Rosetta. Nature Methods, 2013, 10, 1102-1104.	19.0	175
45	Enhancing fatty acid production by the expression of the regulatory transcription factor FadR. Metabolic Engineering, 2012, 14, 653-660.	7.0	173
46	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. MBio, 2015, 6, e00326-15.	4.1	173
47	Targeted proteomics for metabolic pathway optimization: Application to terpene production. Metabolic Engineering, 2011, 13, 194-203.	7.0	169
48	Nanoflow electrospinning serial femtosecond crystallography. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1584-1587.	2.5	167
49	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
50	Error Rate Comparison during Polymerase Chain Reaction by DNA Polymerase. Molecular Biology International, 2014, 2014, 1-8.	1.7	160
51	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	3.3	159
52	FEM: feature-enhanced map. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 646-666.	2.5	157
53	Shining Light into Black Boxes. Science, 2012, 336, 159-160.	12.6	154
54	A robust bulk-solvent correction and anisotropic scaling procedure. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 850-855.	2.5	153

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55	Supramolecular Self-Assembled Chaos: Polyphenolic Lignin's Barrier to Cost-Effective Lignocellulosic Biofuels. <i>Molecules</i> , 2010, 15, 8641-8688.	3.8	151
56	Survey of renewable chemicals produced from lignocellulosic biomass during ionic liquid pretreatment. <i>Biotechnology for Biofuels</i> , 2013, 6, 14.	6.2	151
57	Improved prediction for the structure of the dimeric transmembrane domain of glycophorin A obtained through global searching. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 26, 257-261.	2.6	149
58	Robust indexing for automatic data collection. <i>Journal of Applied Crystallography</i> , 2004, 37, 399-409.	4.5	149
59	Untangling the sequence of events during the S <sub>2</sub> → S <sub>3</sub> transition in photosystem II and implications for the water oxidation mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12624-12635.	7.1	149
60	Room temperature femtosecond X-ray diffraction of photosystem II microcrystals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9721-9726.	7.1	144
61	Employing a biochemical protecting group for a sustainable indigo dyeing strategy. <i>Nature Chemical Biology</i> , 2018, 14, 256-261.	8.0	143
62	Experimentally based orientational refinement of membrane protein models: a structure for the Influenza A M2 H <sub>3</sub> channel 1. Edited by G. von Heijne. <i>Journal of Molecular Biology</i> , 1999, 286, 951-962.	4.2	141
63	Accurate macromolecular structures using minimal measurements from X-ray free-electron lasers. <i>Nature Methods</i> , 2014, 11, 545-548.	19.0	140
64	Principal component analysis of proteomics (PCAP) as a tool to direct metabolic engineering. <i>Metabolic Engineering</i> , 2015, 28, 123-133.	7.0	140
65	Impact of ionic liquid pretreated plant biomass on <i>Saccharomyces cerevisiae</i> growth and biofuel production. <i>Green Chemistry</i> , 2011, 13, 2743.	9.0	139
66	Graphical tools for macromolecular crystallography in <i>PHENIX</i> . <i>Journal of Applied Crystallography</i> , 2012, 45, 581-586.	4.5	139
67	Generalized X-ray and neutron crystallographic analysis: more accurate and complete structures for biological macromolecules. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 567-573.	2.5	137
68	A fully automatic method yielding initial models from high-resolution cryo-electron microscopy maps. <i>Nature Methods</i> , 2018, 15, 905-908.	19.0	137
69	phenix.mr_rosetta: molecular replacement and model rebuilding with Phenix and Rosetta. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 81-90.	1.2	131
70	Role of the γ-phosphate of ATP in triggering protein folding by GroEL-GroES: function, structure and energetics. <i>EMBO Journal</i> , 2003, 22, 4877-4887.	7.8	130
71	Metabolic engineering for the high-yield production of isoprenoid-based C <sub>5</sub> alcohols in <i>E. coli</i> . <i>Scientific Reports</i> , 2015, 5, 11128.	3.3	125
72	Coupling of receptor conformation and ligand orientation determine graded activity. <i>Nature Chemical Biology</i> , 2010, 6, 837-843.	8.0	121

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73	Energy-dispersive X-ray emission spectroscopy using an X-ray free-electron laser in a shot-by-shot mode. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19103-19107.	7.1	113
74	<i>phenix.model_vs_data</i> : a high-level tool for the calculation of crystallographic model and data statistics. <i>Journal of Applied Crystallography</i> , 2010, 43, 669-676.	4.5	112
75	Accurate model annotation of a near-atomic resolution cryo-EM map. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3103-3108.	7.1	111
76	Exploring the Structural Dynamics of the E.coli Chaperonin GroEL Using Translation-libration-screw Crystallographic Refinement of Intermediate States. <i>Journal of Molecular Biology</i> , 2004, 342, 229-245.	4.2	109
77	Integrated analysis of isopentenyl pyrophosphate (IPP) toxicity in isoprenoid-producing <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2018, 47, 60-72.	7.0	106
78	An atomic model of brome mosaic virus using direct electron detection and real-space optimization. <i>Nature Communications</i> , 2014, 5, 4808.	12.8	105
79	Comprehensive <i>in Vitro</i> Analysis of Acyltransferase Domain Exchanges in Modular Polyketide Synthases and Its Application for Short-Chain Ketone Production. <i>ACS Synthetic Biology</i> , 2017, 6, 139-147.	3.8	100
80	Automated ligand fitting by core-fragment fitting and extension into density. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 915-922.	2.5	98
81	Crystallographic model quality at a glance. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 297-300.	2.5	95
82	The protein structure initiative structural genomics knowledgebase. <i>Nucleic Acids Research</i> , 2009, 37, D365-D368.	14.5	94
83	Use of a New Label, $^{13}\text{C}\rightarrow^{18}\text{O}$ , in the Determination of a Structural Model of Phospholamban in a Lipid Bilayer. Spatial Restraints Resolve the Ambiguity Arising from Interpretations of Mutagenesis Data. <i>Journal of Molecular Biology</i> , 2000, 300, 677-685.	4.2	92
84	Correlation analysis of targeted proteins and metabolites to assess and engineer microbial isopentenol production. <i>Biotechnology and Bioengineering</i> , 2014, 111, 1648-1658.	3.3	89
85	The cryo-electron microscopy structure of human transcription factor IIH. <i>Nature</i> , 2017, 549, 414-417.	27.8	89
86	<i>Thermoascus aurantiacus</i> is a promising source of enzymes for biomass deconstruction under thermophilic conditions. <i>Biotechnology for Biofuels</i> , 2012, 5, 54.	6.2	88
87	Advances, Interactions, and Future Developments in the CNS, Phenix, and Rosetta Structural Biology Software Systems. <i>Annual Review of Biophysics</i> , 2013, 42, 265-287.	10.0	88
88	High-resolution structure of RNase P protein from <i>Thermotoga maritima</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7497-7502.	7.1	87
89	A Global Ramachandran Score Identifies Protein Structures with Unlikely Stereochemistry. <i>Structure</i> , 2020, 28, 1249-1258.e2.	3.3	86
90	Recent developments for the efficient crystallographic refinement of macromolecular structures. <i>Current Opinion in Structural Biology</i> , 1998, 8, 606-611.	5.7	83

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91	X-Ray Crystallographic and Kinetic Studies of Human Sorbitol Dehydrogenase. <i>Structure</i> , 2003, 11, 1071-1085.	3.3	83
92	Three Novel Rice Genes Closely Related to the Arabidopsis IRX9, IRX9L, and IRX14 Genes and Their Roles in Xylan Biosynthesis. <i>Frontiers in Plant Science</i> , 2013, 4, 83.	3.6	83
93	Surprises and pitfalls arising from (pseudo)symmetry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 99-107.	2.5	81
94	Web-Ice: integrated data collection and analysis for macromolecular crystallography. <i>Journal of Applied Crystallography</i> , 2008, 41, 176-184.	4.5	81
95	A Versatile Microfluidic Device for Automating Synthetic Biology. <i>ACS Synthetic Biology</i> , 2015, 4, 1151-1164.	3.8	81
96	Production of jet fuel precursor monoterpenoids from engineered <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2017, 114, 1703-1712.	3.3	81
97	Crystal Structures of the Rhodococcus Proteasome with and without its Pro-peptides: Implications for the Role of the Pro-peptide in Proteasome Assembly. <i>Journal of Molecular Biology</i> , 2004, 335, 233-245.	4.2	80
98	Label-free in situ imaging of lignification in the cell wall of low lignin transgenic <i>Populus trichocarpa</i> . <i>Planta</i> , 2009, 230, 589-597.	3.2	80
99	Identification of a Sphingolipid $\beta$ -Glucuronosyltransferase That Is Essential for Pollen Function in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 3314-3325.	6.6	80
100	Bulk-solvent and overall scaling revisited: faster calculations, improved results. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 625-634.	2.5	79
101	Analytics for Metabolic Engineering. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 135.	4.1	79
102	Transmembrane signal transduction of the $\beta$ 2 integrin. <i>Protein Science</i> , 2009, 11, 1800-1812.	7.6	78
103	Phylogenomically Guided Identification of Industrially Relevant GH1 $\beta$ -Glucosidases through DNA Synthesis and Nanostructure-Initiator Mass Spectrometry. <i>ACS Chemical Biology</i> , 2014, 9, 2082-2091.	3.4	78
104	Exploiting the Substrate Promiscuity of Hydroxycinnamoyl-CoA:Shikimate Hydroxycinnamoyl Transferase to Reduce Lignin. <i>Plant and Cell Physiology</i> , 2016, 57, 568-579.	3.1	78
105	Structure of a Three-Domain Sesquiterpene Synthase: A Prospective Target for Advanced Biofuels Production. <i>Structure</i> , 2011, 19, 1876-1884.	3.3	76
106	Structural basis of light chain amyloidogenicity: comparison of the thermodynamic properties, fibrillogenic potential and tertiary structural features of four $\beta$ 2-microglobulin proteins. <i>Journal of Molecular Recognition</i> , 2004, 17, 323-331.	2.1	73
107	Characterizing Strain Variation in Engineered <i>E. coli</i> Using a Multi-Omics-Based Workflow. <i>Cell Systems</i> , 2016, 2, 335-346.	6.2	73
108	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	19.0	73

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109	Structural dynamics in the water and proton channels of photosystem II during the S2 to S3 transition. <i>Nature Communications</i> , 2021, 12, 6531.	12.8	73
110	A droplet-to-digital (D2D) microfluidic device for single cell assays. <i>Lab on A Chip</i> , 2015, 15, 225-236.	6.0	70
111	Molecular Dynamics Applied to X-ray Structure Refinement. <i>Accounts of Chemical Research</i> , 2002, 35, 404-412.	15.6	68
112	Validated near-atomic resolution structure of bacteriophage epsilon15 derived from cryo-EM and modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12301-12306.	7.1	68
113	STRUCTURAL PERSPECTIVES OF PHOSPHOLAMBAN, A HELICAL TRANSMEMBRANE PENTAMER. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1997, 26, 157-179.	18.3	67
114	The plant glycosyltransferase clone collection for functional genomics. <i>Plant Journal</i> , 2014, 79, 517-529.	5.7	67
115	Crystal structure of DNA sequence specificity subunit of a type I restriction-modification enzyme and its functional implications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3248-3253.	7.1	66
116	Crystal Structures of a Group II Chaperonin Reveal the Open and Closed States Associated with the Protein Folding Cycle. <i>Journal of Biological Chemistry</i> , 2010, 285, 27958-27966.	3.4	66
117	Biochemical characterization and crystal structure of endoglucanase Cel5A from the hyperthermophilic <i>Thermotoga maritima</i> . <i>Journal of Structural Biology</i> , 2010, 172, 372-379.	2.8	65
118	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 45-54.	1.2	65
119	Addition of a carbohydrate-binding module enhances cellulase penetration into cellulose substrates. <i>Biotechnology for Biofuels</i> , 2013, 6, 93.	6.2	63
120	A Droplet Microfluidic Platform for Automating Genetic Engineering. <i>ACS Synthetic Biology</i> , 2016, 5, 426-433.	3.8	63
121	Identification and Characterization of a Golgi-Localized UDP-Xylose Transporter Family from <i>Arabidopsis</i> . <i>Plant Cell</i> , 2015, 27, 1218-1227.	6.6	61
122	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 597-610.	2.5	60
123	Understanding changes in lignin of <i>Panicum virgatum</i> and <i>Eucalyptus globulus</i> as a function of ionic liquid pretreatment. <i>Bioresource Technology</i> , 2012, 126, 156-161.	9.6	60
124	Massively Parallel Fitness Profiling Reveals Multiple Novel Enzymes in <i>Pseudomonas putida</i> Lysine Metabolism. <i>MBio</i> , 2019, 10, .	4.1	60
125	On macromolecular refinement at subatomic resolution with interatomic scatterers. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1194-1197.	2.5	59
126	Averaged kick maps: less noise, more signal and probably less bias. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 921-931.	2.5	59



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127	Ligand identification using electron-density map correlations. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 101-107.	2.5	57
128	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. <i>MBio</i> , 2018, 9, .	4.1	57
129	A Peptide-Based Method for <sup>13</sup> C Metabolic Flux Analysis in Microbial Communities. <i>PLoS Computational Biology</i> , 2014, 10, e1003827.	3.2	56
130	Understanding the impact of ionic liquid pretreatment on cellulose and lignin via thermochemical analysis. <i>Biomass and Bioenergy</i> , 2013, 54, 276-283.	5.7	55
131	Conformational dynamics of a crystalline protein from microsecond-scale molecular dynamics simulations and diffuse X-ray scattering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17887-17892.	7.1	55
132	Production of anteiso-branched fatty acids in <i>Escherichia coli</i> ; next generation biofuels with improved cold-flow properties. <i>Metabolic Engineering</i> , 2014, 26, 111-118.	7.0	55
133	Manipulation of the carbon storage regulator system for metabolite remodeling and biofuel production in <i>Escherichia coli</i> . <i>Microbial Cell Factories</i> , 2012, 11, 79.	4.0	53
134	Structure and mechanism of NOV1, a resveratrol-cleaving dioxygenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14324-14329.	7.1	50
135	Automatic multiple-zone rigid-body refinement with a large convergence radius. <i>Journal of Applied Crystallography</i> , 2009, 42, 607-615.	4.5	49
136	Analysis of plant nucleotide sugars by hydrophilic interaction liquid chromatography and tandem mass spectrometry. <i>Analytical Biochemistry</i> , 2014, 448, 14-22.	2.4	49
137	Multifunctional cellulase catalysis targeted by fusion to different carbohydrate-binding modules. <i>Biotechnology for Biofuels</i> , 2015, 8, 220.	6.2	49
138	On the handling of atomic anisotropic displacement parameters. <i>Journal of Applied Crystallography</i> , 2002, 35, 477-480.	4.5	48
139	Glycoside Hydrolases from a targeted Compost Metagenome, activity-screening and functional characterization. <i>BMC Biotechnology</i> , 2012, 12, 38.	3.3	48
140	Numerically stable algorithms for the computation of reduced unit cells. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2004, 60, 1-6.	0.3	47
141	Discovery of enzymes for toluene synthesis from anoxic microbial communities. <i>Nature Chemical Biology</i> , 2018, 14, 451-457.	8.0	47
142	<i>i&gt;TLS&lt;/i&gt; from fundamentals to practice. <i>Crystallography Reviews</i>, 2013, 19, 230-270.</i>	1.5	46
143	Optimization of the IPP-bypass mevalonate pathway and fed-batch fermentation for the production of isoprenol in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2019, 56, 85-96.	7.0	46
144	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 451-454.	2.3	46

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145	Novel bacterial clade reveals origin of form I Rubisco. <i>Nature Plants</i> , 2020, 6, 1158-1166.	9.3	46
146	A targeted proteomics toolkit for high-throughput absolute quantification of <i>Escherichia coli</i> proteins. <i>Metabolic Engineering</i> , 2014, 26, 48-56.	7.0	45
147	The Experiment Data Depot: A Web-Based Software Tool for Biological Experimental Data Storage, Sharing, and Visualization. <i>ACS Synthetic Biology</i> , 2017, 6, 2248-2259.	3.8	45
148	Addressing the Need for Alternative Transportation Fuels: The Joint BioEnergy Institute. <i>ACS Chemical Biology</i> , 2008, 3, 17-20.	3.4	44
149	Standard Flow Liquid Chromatography for Shotgun Proteomics in Bioenergy Research. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 44.	4.1	44
150	Structural and Biochemical Characterization of the Early and Late Enzymes in the Lignin $\beta^2$ -Aryl Ether Cleavage Pathway from <i>Sphingobium</i> sp. SYK-6. <i>Journal of Biological Chemistry</i> , 2016, 291, 10228-10238.	3.4	44
151	On-chip integration of droplet microfluidics and nanostructure-initiator mass spectrometry for enzyme screening. <i>Lab on A Chip</i> , 2017, 17, 323-331.	6.0	44
152	Intensity statistics in the presence of translational noncrystallographic symmetry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 176-183.	2.5	43
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