Paul D. Adams

List of Publications by Year
in descending order

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351 papers	100,900 citations	4942 84 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. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 213-221.	2.5	20,564
2	<i>Phaser</i>crystallographic 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	Towards automated crystallographic structure refinement with <i>phenix.refine</i>. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 352-367.	2.5	4,573
5	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in <i>Phenix</i>. 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	MolProbity: More and better reference data for improved allâ€atom structure validation. Protein Science, 2018, 27, 293-315.	3.1	2,776
9	Real-space refinement in<i>PHENIX</i>for cryo-EM and crystallography. Acta Crystallographica Section D: Structural Biology, 2018, 74, 531-544.	1.1	2,065
10	Iterative model building, structure refinement and density modification with the<i>PHENIX AutoBuild</i>wizard. Acta Crystallographica Section D: Biological Crystallography, 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. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1074-1080.	2.5	1,035
12	Structural Basis for Double-Stranded RNA Processing by Dicer. Science, 2006, 311, 195-198.	6.0	860
13	Decision-making in structure solution using Bayesian estimates of map quality: the<i>PHENIX AutoSol</i>wizard. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 582-601.	2.5	804
14	EMRinger: side chainâ€“directed model and map validation for 3D cryo-electron microscopy. Nature Methods, 2015, 12, 943-946.	9.0	799
15	The Phenix software for automated determination of macromolecular structures. Methods, 2011, 55, 94-106.	1.9	764
16	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
17	New tools for the analysis and validation of cryo-EM maps and atomic models. Acta Crystallographica Section D: Structural Biology, 2018, 74, 814-840.	1.1	575
18	Polder maps: improving OMIT maps by excluding bulk solvent. Acta Crystallographica Section D: Structural Biology, 2017, 73, 148-157.	1.1	500

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19	<i>iotbx.cif</i>: a comprehensive CIF toolbox. Journal of Applied Crystallography, 2011, 44, 1259-1263.	1.9	487
20	Engineering dynamic pathway regulation using stress-response promoters. Nature Biotechnology, 2013, 31, 1039-1046.	9.4	411
21	A New Generation of Crystallographic Validation Tools for the Protein Data Bank. Structure, 2011, 19, 1395-1412.	1.6	405
22	Structures of the intermediates of Kokâ€™s photosynthetic water oxidation clock. Nature, 2018, 563, 421-425.	13.7	386
23	Simultaneous Femtosecond X-ray Spectroscopy and Diffraction of Photosystem II at Room Temperature. Science, 2013, 340, 491-495.	6.0	378
24	SPARX, a new environment for Cryo-EM image processing. Journal of Structural Biology, 2007, 157, 47-55.	1.3	356
25	Metabolic engineering of Escherichia coli for limonene and perillyl alcohol production. Metabolic Engineering, 2013, 19, 33-41.	3.6	343
26	Structure of photosystem II and substrate binding at room temperature. Nature, 2016, 540, 453-457.	13.7	323
27	Recent developments in thePHENIXsoftware for automated crystallographic structure determination. Journal of Synchrotron Radiation, 2004, 11, 53-55.	1.0	319
28	A dimerization motif for transmembrane Î±â€“helices. Nature Structural Biology, 1994, 1, 157-163.	9.7	294
29	TheComputational Crystallography Toolbox: crystallographic algorithms in a reusable software framework. Journal of Applied Crystallography, 2002, 35, 126-136.	1.9	262
30	Joint X-ray and neutron refinement with<i>phenix.refine</i>. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1153-1163.	2.5	259
31	Modelling dynamics in protein crystal structures by ensemble refinement. ELife, 2012, 1, e00311.	2.8	248
32	Improvement of cryo-EM maps by density modification. Nature Methods, 2020, 17, 923-927.	9.0	243
33	Use of knowledge-based restraints in <i>phenix.refine</i> to improve macromolecular refinement at low resolution. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 381-390.	2.5	230
34	Conformational variability in the refined structure of the chaperonin GroEL at 2.8 Ã… resolution. Nature Structural and Molecular Biology, 1995, 2, 1083-1094.	3.6	219
35	Automated map sharpening by maximization of detail and connectivity. Acta Crystallographica Section D: Structural Biology, 2018, 74, 545-559.	1.1	218
36	<i>Phaser.MRage</i>: automated molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 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.	3.3	206
39	Taking snapshots of photosynthetic water oxidation using femtosecond X-ray diffraction and spectroscopy. Nature Communications, 2014, 5, 4371.	5.8	206
40	New tools for structure refinement in<i>PHENIX</i>. 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.	3.6	198
42	New applications of simulated annealing in X-ray crystallography and solution NMR. Structure, 1997, 5, 325-336.	1.6	197
43	Structural organization of the pentameric transmembrane alpha-helices of phospholamban, a cardiac ion channel.. EMBO Journal, 1994, 13, 4757-4764.	3.5	175
44	Improved low-resolution crystallographic refinement with Phenix and Rosetta. Nature Methods, 2013, 10, 1102-1104.	9.0	175
45	Enhancing fatty acid production by the expression of the regulatory transcription factor FadR. Metabolic Engineering, 2012, 14, 653-660.	3.6	173
46	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. MBio, 2015, 6, e00326-15.	1.8	173
47	Targeted proteomics for metabolic pathway optimization: Application to terpene production. Metabolic Engineering, 2011, 13, 194-203.	3.6	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.	1.6	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.	6.0	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 Ligninâ€™s Barrier to Cost-Effective Lignocellulosic Biofuels. Molecules, 2010, 15, 8641-8688.	1.7	151
56	Survey of renewable chemicals produced from lignocellulosic biomass during ionic liquid pretreatment. Biotechnology for Biofuels, 2013, 6, 14.	6.2	151
57	Improved prediction for the structure of the dimeric transmembrane domain of glycophorin A obtained through global searching. , 1996, 26, 257-261.		149
58	Robust indexing for automatic data collection. Journal of Applied Crystallography, 2004, 37, 399-409.	1.9	149
59	Untangling the sequence of events during the S ₂ â†' S ₃ transition in photosystem II and implications for the water oxidation mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12624-12635.	3.3	149
60	Room temperature femtosecond X-ray diffraction of photosystem II microcrystals. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9721-9726.	3.3	144
61	Employing a biochemical protecting group for a sustainable indigo dyeing strategy. Nature Chemical Biology, 2018, 14, 256-261.	3.9	143
62	Experimentally based orientational refinement of membrane protein models: a structure for the Influenza A M2 H + channel 1 1Edited by G. von Heijne. Journal of Molecular Biology, 1999, 286, 951-962.	2.0	141
63	Accurate macromolecular structures using minimal measurements from X-ray free-electron lasers. Nature Methods, 2014, 11, 545-548.	9.0	140
64	Principal component analysis of proteomics (PCAP) as a tool to direct metabolic engineering. Metabolic Engineering, 2015, 28, 123-133.	3.6	140
65	Impact of ionic liquid pretreated plant biomass on Saccharomyces cerevisiae growth and biofuel production. Green Chemistry, 2011, 13, 2743.	4.6	139
66	Graphical tools for macromolecular crystallography in<i>PHENIX</i>. Journal of Applied Crystallography, 2012, 45, 581-586.	1.9	139
67	Generalized X-ray and neutron crystallographic analysis: more accurate and complete structures for biological macromolecules. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 567-573.	2.5	137
68	A fully automatic method yielding initial models from high-resolution cryo-electron microscopy maps. Nature Methods, 2018, 15, 905-908.	9.0	137
69	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
70	Role of the Â-phosphate of ATP in triggering protein folding by GroEL-GroES: function, structure and energetics. EMBO Journal, 2003, 22, 4877-4887.	3.5	130
71	Metabolic engineering for the high-yield production of isoprenoid-based C5 alcohols in E. coli. Scientific Reports, 2015, 5, 11128.	1.6	125
72	Coupling of receptor conformation and ligand orientation determine graded activity. Nature Chemical Biology, 2010, 6, 837-843.	3.9	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. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19103-19107.	3.3	113
74	<i>phenix.model_vs_data</i>: a high-level tool for the calculation of crystallographic model and data statistics. Journal of Applied Crystallography, 2010, 43, 669-676.	1.9	112
75	Accurate model annotation of a near-atomic resolution cryo-EM map. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3103-3108.	3.3	111
76	Exploring the Structural Dynamics of the E.coli Chaperonin GroEL Using Translation-libration-screw Crystallographic Refinement of Intermediate States. Journal of Molecular Biology, 2004, 342, 229-245.	2.0	109
77	Integrated analysis of isopentenyl pyrophosphate (IPP) toxicity in isoprenoid-producing Escherichia coli. Metabolic Engineering, 2018, 47, 60-72.	3.6	106
78	An atomic model of brome mosaic virus using direct electron detection and real-space optimization. Nature Communications, 2014, 5, 4808.	5.8	105
79	Comprehensive <i>in Vitro</i> Analysis of Acyltransferase Domain Exchanges in Modular Polyketide Synthases and Its Application for Short-Chain Ketone Production. ACS Synthetic Biology, 2017, 6, 139-147.	1.9	100
80	Automated ligand fitting by core-fragment fitting and extension into density. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 915-922.	2.5	98
81	Crystallographic model quality at a glance. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 297-300.	2.5	95
82	The protein structure initiative structural genomics knowledgebase. Nucleic Acids Research, 2009, 37, D365-D368.	6.5	94
83	Use of a New Label, 13Cî—»18O, in the Determination of a Structural Model of Phospholamban in a Lipid Bilayer. Spatial Restraints Resolve the Ambiguity Arising from Interpretations of Mutagenesis Data. Journal of Molecular Biology, 2000, 300, 677-685.	2.0	92
84	Correlation analysis of targeted proteins and metabolites to assess and engineer microbial isopentenol production. Biotechnology and Bioengineering, 2014, 111, 1648-1658.	1.7	89
85	The cryo-electron microscopy structure of human transcription factor IIH. Nature, 2017, 549, 414-417.	13.7	89
86	Thermoascus aurantiacus is a promising source of enzymes for biomass deconstruction under thermophilic conditions. Biotechnology for Biofuels, 2012, 5, 54.	6.2	88
87	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
88	High-resolution structure of RNase P protein from Thermotoga maritima. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7497-7502.	3.3	87
89	A Global Ramachandran Score Identifies Protein Structures with Unlikely Stereochemistry. Structure, 2020, 28, 1249-1258.e2.	1.6	86
90	Recent developments for the efficient crystallographic refinement of macromolecular structures. Current Opinion in Structural Biology, 1998, 8, 606-611.	2.6	83

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91	X-Ray Crystallographic and Kinetic Studies of Human Sorbitol Dehydrogenase. Structure, 2003, 11, 1071-1085.	1.6	83
92	Three Novel Rice Genes Closely Related to the ArabidopsisIRX9, IRX9L, and IRX14 Genes and Their Roles in Xylan Biosynthesis. Frontiers in Plant Science, 2013, 4, 83.	1.7	83
93	Surprises and pitfalls arising from (pseudo)symmetry. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 99-107.	2.5	81
94	<i>Web-Ice</i>: integrated data collection and analysis for macromolecular crystallography. Journal of Applied Crystallography, 2008, 41, 176-184.	1.9	81
95	A Versatile Microfluidic Device for Automating Synthetic Biology. ACS Synthetic Biology, 2015, 4, 1151-1164.	1.9	81
96	Production of jet fuel precursor monoterpenoids from engineered <i>Escherichia coli</i>. Biotechnology and Bioengineering, 2017, 114, 1703-1712.	1.7	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. Journal of Molecular Biology, 2004, 335, 233-245.	2.0	80
98	Label-free in situ imaging of lignification in the cell wall of low lignin transgenic Populus trichocarpa. Planta, 2009, 230, 589-597.	1.6	80
99	Identification of a Sphingolipid Î±-Glucuronosyltransferase That Is Essential for Pollen Function in<i>Arabidopsis</i>Â Â Â. Plant Cell, 2014, 26, 3314-3325.	3.1	80
100	Bulk-solvent and overall scaling revisited: faster calculations, improved results. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 625-634.	2.5	79
101	Analytics for Metabolic Engineering. Frontiers in Bioengineering and Biotechnology, 2015, 3, 135.	2.0	79
102	Transmembrane signal transduction of the Î±IIbÎ²3 integrin. Protein Science, 2009, 11, 1800-1812.	3.1	78
103	Phylogenomically Guided Identification of Industrially Relevant GH1 Î²-Glucosidases through DNA Synthesis and Nanostructure-Initiator Mass Spectrometry. ACS Chemical Biology, 2014, 9, 2082-2091.	1.6	78
104	Exploiting the Substrate Promiscuity of Hydroxycinnamoyl-CoA:Shikimate Hydroxycinnamoyl Transferase to Reduce Lignin. Plant and Cell Physiology, 2016, 57, 568-579.	1.5	78
105	Structure of a Three-Domain Sesquiterpene Synthase: A Prospective Target for Advanced Biofuels Production. Structure, 2011, 19, 1876-1884.	1.6	76
106	Structural basis of light chain amyloidogenicity: comparison of the thermodynamic properties, fibrillogenic potential and tertiary structural features of four VÎ»6 proteins. Journal of Molecular Recognition, 2004, 17, 323-331.	1.1	73
107	Characterizing Strain Variation in Engineered E.Âcoli Using a Multi-Omics-Based Workflow. Cell Systems, 2016, 2, 335-346.	2.9	73
108	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	9.0	73

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109	Structural dynamics in the water and proton channels of photosystem II during the S2 to S3 transition. Nature Communications, 2021, 12, 6531.	5.8	73
110	A droplet-to-digital (D2D) microfluidic device for single cell assays. Lab on A Chip, 2015, 15, 225-236.	3.1	70
111	Molecular Dynamics Applied to X-ray Structure Refinement. Accounts of Chemical Research, 2002, 35, 404-412.	7.6	68
112	Validated near-atomic resolution structure of bacteriophage epsilon15 derived from cryo-EM and modeling. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12301-12306.	3.3	68
113	STRUCTURAL PERSPECTIVES OF PHOSPHOLAMBAN, A HELICAL TRANSMEMBRANE PENTAMER. Annual Review of Biophysics and Biomolecular Structure, 1997, 26, 157-179.	18.3	67
114	The plant glycosyltransferase clone collection for functional genomics. Plant Journal, 2014, 79, 517-529.	2.8	67
115	Crystal structure of DNA sequence specificity subunit of a type I restriction-modification enzyme and its functional implications. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3248-3253.	3.3	66
116	Crystal Structures of a Group II Chaperonin Reveal the Open and Closed States Associated with the Protein Folding Cycle. Journal of Biological Chemistry, 2010, 285, 27958-27966.	1.6	66
117	Biochemical characterization and crystal structure of endoglucanase Cel5A from the hyperthermophilic Thermotoga maritima. Journal of Structural Biology, 2010, 172, 372-379.	1.3	65
118	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. Journal of Structural and Functional Genomics, 2011, 12, 45-54.	1.2	65
119	Addition of a carbohydrate-binding module enhances cellulase penetration into cellulose substrates. Biotechnology for Biofuels, 2013, 6, 93.	6.2	63
120	A Droplet Microfluidic Platform for Automating Genetic Engineering. ACS Synthetic Biology, 2016, 5, 426-433.	1.9	63
121	Identification and Characterization of a Golgi-Localized UDP-Xylose Transporter Family from Arabidopsis. Plant Cell, 2015, 27, 1218-1227.	3.1	61
122	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 597-610.	2.5	60
123	Understanding changes in lignin of Panicum virgatum and Eucalyptus globulus as a function of ionic liquid pretreatment. Bioresource Technology, 2012, 126, 156-161.	4.8	60
124	Massively Parallel Fitness Profiling Reveals Multiple Novel Enzymes in <i>Pseudomonas putida</i> Lysine Metabolism. MBio, 2019, 10, .	1.8	60
125	On macromolecular refinement at subatomic resolution with interatomic scatterers. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 1194-1197.	2.5	59
126	Averaged kick maps: less noise, more signalâ€¦and probably less bias. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 921-931.	2.5	59

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127	Ligand identification using electron-density map correlations. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 101-107.	2.5	57
128	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. MBio, 2018, 9, .	1.8	57
129	A Peptide-Based Method for 13C Metabolic Flux Analysis in Microbial Communities. PLoS Computational Biology, 2014, 10, e1003827.	1.5	56
130	Understanding the impact of ionic liquid pretreatment on cellulose and lignin via thermochemical analysis. Biomass and Bioenergy, 2013, 54, 276-283.	2.9	55
131	Conformational dynamics of a crystalline protein from microsecond-scale molecular dynamics simulations and diffuse X-ray scattering. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17887-17892.	3.3	55
132	Production of anteiso-branched fatty acids in Escherichia coli; next generation biofuels with improved cold-flow properties. Metabolic Engineering, 2014, 26, 111-118.	3.6	55
133	Manipulation of the carbon storage regulator system for metabolite remodeling and biofuel production in Escherichia coli. Microbial Cell Factories, 2012, 11, 79.	1.9	53
134	Structure and mechanism of NOV1, a resveratrol-cleaving dioxygenase. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14324-14329.	3.3	50
135	Automatic multiple-zone rigid-body refinement with a large convergence radius. Journal of Applied Crystallography, 2009, 42, 607-615.	1.9	49
136	Analysis of plant nucleotide sugars by hydrophilic interaction liquid chromatography and tandem mass spectrometry. Analytical Biochemistry, 2014, 448, 14-22.	1.1	49
137	Multifunctional cellulase catalysis targeted by fusion to different carbohydrate-binding modules. Biotechnology for Biofuels, 2015, 8, 220.	6.2	49
138	On the handling of atomic anisotropic displacement parameters. Journal of Applied Crystallography, 2002, 35, 477-480.	1.9	48
139	Glycoside Hydrolases from a targeted Compost Metagenome, activity-screening and functional characterization. BMC Biotechnology, 2012, 12, 38.	1.7	48
140	Numerically stable algorithms for the computation of reduced unit cells. Acta Crystallographica Section A: Foundations and Advances, 2004, 60, 1-6.	0.3	47
141	Discovery of enzymes for toluene synthesis from anoxic microbial communities. Nature Chemical Biology, 2018, 14, 451-457.	3.9	47
142	<i>TLS</i>from fundamentals to practice. Crystallography Reviews, 2013, 19, 230-270.	0.4	46
143	Optimization of the IPP-bypass mevalonate pathway and fed-batch fermentation for the production of isoprenol in Escherichia coli. Metabolic Engineering, 2019, 56, 85-96.	3.6	46
144	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). Acta Crystallographica Section D: Structural Biology, 2019, 75, 451-454.	1.1	46

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145	Novel bacterial clade reveals origin of form I Rubisco. Nature Plants, 2020, 6, 1158-1166.	4.7	46
146	A targeted proteomics toolkit for high-throughput absolute quantification of Escherichia coli proteins. Metabolic Engineering, 2014, 26, 48-56.	3.6	45
147	The Experiment Data Depot: A Web-Based Software Tool for Biological Experimental Data Storage, Sharing, and Visualization. ACS Synthetic Biology, 2017, 6, 2248-2259.	1.9	45
148	Addressing the Need for Alternative Transportation Fuels: The Joint BioEnergy Institute. ACS Chemical Biology, 2008, 3, 17-20.	1.6	44
149	Standard Flow Liquid Chromatography for Shotgun Proteomics in Bioenergy Research. Frontiers in Bioengineering and Biotechnology, 2015, 3, 44.	2.0	44
150	Structural and Biochemical Characterization of the Early and Late Enzymes in the Lignin Î²-Aryl Ether Cleavage Pathway from Sphingobium sp. SYK-6. Journal of Biological Chemistry, 2016, 291, 10228-10238.	1.6	44
151	On-chip integration of droplet microfluidics and nanostructure-initiator mass spectrometry for enzyme screening. Lab on A Chip, 2017, 17, 323-331.	3.1	44
152	Intensity statistics in the presence of translational noncrystallographic symmetry. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 176-183.	2.5	43
153	Renewable production of high density jet fuel precursor sesquiterpenes from Escherichia coli. Biotechnology for Biofuels, 2018, 11, 285.	6.2	43
154	Automating crystallographic structure solution and refinement of proteinâ€“ligand complexes. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 144-154.	2.5	43
155	Raman imaging of cell wall polymers in Arabidopsis thaliana. Biochemical and Biophysical Research Communications, 2010, 395, 521-523.	1.0	42
156	Droplet-based microfluidic platform for heterogeneous enzymatic assays. Lab on A Chip, 2013, 13, 1817.	3.1	42
157	From Soil to Structure, a Novel Dimeric Î²-Glucosidase Belonging to Glycoside Hydrolase Family 3 Isolated from Compost Using Metagenomic Analysis. Journal of Biological Chemistry, 2013, 288, 14985-14992.	1.6	42
158	Biochemical and Structural Studies of NADH-Dependent FabG Used To Increase the Bacterial Production of Fatty Acids under Anaerobic Conditions. Applied and Environmental Microbiology, 2014, 80, 497-505.	1.4	42
159	<i>O</i>-/<i>N</i>-/<i>S</i>-Specificity in Glycosyltransferase Catalysis: From Mechanistic Understanding to Engineering. ACS Catalysis, 2021, 11, 1810-1815.	5.5	42
160	Automated identification of elemental ions in macromolecular crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1104-1114.	2.5	40
161	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. Nature Structural and Molecular Biology, 2015, 22, 433-434.	3.6	40
162	No observable conformational changes in PSII. Nature, 2016, 533, E1-E2.	13.7	40

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163	Structural Basis of Stereospecificity in the Bacterial Enzymatic Cleavage of Î²-Aryl Ether Bonds in Lignin. Journal of Biological Chemistry, 2016, 291, 5234-5246.	1.6	40
164	Tracing Determinants of Dual Substrate Specificity in Glycoside Hydrolase Family 5. Journal of Biological Chemistry, 2012, 287, 25335-25343.	1.6	39
165	Toward industrial production of isoprenoids in <i>Escherichia coli</i>: Lessons learned from CRISPRâ€Cas9 based optimization of a chromosomally integrated mevalonate pathway. Biotechnology and Bioengineering, 2018, 115, 1000-1013.	1.7	39
166	A new default restraint library for the protein backbone in<i>Phenix</i>: a conformation-dependent geometry goes mainstream. Acta Crystallographica Section D: Structural Biology, 2016, 72, 176-179.	1.1	39
167	Improved crystal orientation and physical properties from single-shot XFEL stills. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3299-3309.	2.5	38
168	A bacterial pioneer produces cellulase complexes that persist through community succession. Nature Microbiology, 2018, 3, 99-107.	5.9	38
169	Improving the Accuracy of Macromolecular Structure Refinement at 7ÂÅ… Resolution. Structure, 2012, 20, 957-966.	1.6	37
170	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
171	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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