

# Paul D. Adams

## List of Publications by Year in descending order

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351  
papers

100,900  
citations

5782

84  
h-index

305

299  
g-index

361  
all docs

361  
docs citations

361  
times ranked

78632  
citing authors

#	ARTICLE	IF	CITATIONS
1	Integration of software tools for integrative modeling of biomolecular systems. <i>Journal of Structural Biology</i> , 2022, 214, 107841.	1.3	7
2	Modular automated bottom-up proteomic sample preparation for high-throughput applications. <i>PLoS ONE</i> , 2022, 17, e0264467.	1.1	3
3	A Synthetic Gene Library Yields a Previously Unknown Glycoside Phosphorylase That Degrades and Assembles Poly- $\beta$ -1,3-GlcNAc, Completing the Suite of $\beta$ -Linked GlcNAc Polysaccharides. <i>ACS Central Science</i> , 2022, 8, 430-440.	5.3	7
4	O/N-Specificity in Glycosyltransferase Catalysis: From Mechanistic Understanding to Engineering. <i>ACS Catalysis</i> , 2021, 11, 1810-1815.	5.5	42
5	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	9.0	73
6	Protein identification from electron cryomicroscopy maps by automated model building and side-chain matching. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 457-462.	1.1	9
7	Mechanism Across Scales: A Holistic Modeling Framework Integrating Laboratory and Field Studies for Microbial Ecology. <i>Frontiers in Microbiology</i> , 2021, 12, 642422.	1.5	12
8	Efficient production of oxidized terpenoids via engineering fusion proteins of terpene synthase and cytochrome P450. <i>Metabolic Engineering</i> , 2021, 64, 41-51.	3.6	33
9	Engineering <i>Saccharomyces cerevisiae</i> for isoprenol production. <i>Metabolic Engineering</i> , 2021, 64, 154-166.	3.6	34
10	Experimental and theoretical insights into the effects of pH on catalysis of bond-cleavage by the lignin peroxidase isozyme H8 from <i>Phanerochaete chrysosporium</i> . <i>Biotechnology for Biofuels</i> , 2021, 14, 108.	6.2	10
11	A multiplexed nanostructure-initiator mass spectrometry (NIMS) assay for simultaneously detecting glycosyl hydrolase and lignin modifying enzyme activities. <i>Scientific Reports</i> , 2021, 11, 11803.	1.6	7
12	Reply to Wang et al.: Clear evidence of binding of Ox to the oxygen-evolving complex of photosystem II is best observed in the omit map. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2102342118.	3.3	7
13	Accurate prediction of protein structures and interactions using a three-track neural network. <i>Science</i> , 2021, 373, 871-876.	6.0	2,843
14	Macromolecular refinement of X-ray and cryoelectron microscopy structures with Phenix/OPLS3e for improved structure and ligand quality. <i>Structure</i> , 2021, 29, 913-921.e4.	1.6	29
15	CERES: a cryo-EM re-refinement system for continuous improvement of deposited models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 48-61.	1.1	14
16	Structural dynamics in the water and proton channels of photosystem II during the S2 to S3 transition. <i>Nature Communications</i> , 2021, 12, 6531.	5.8	73
17	Cryo-EM map interpretation and protein model building using iterative map segmentation. <i>Protein Science</i> , 2020, 29, 87-99.	3.1	27
18	Structural Mechanism of Regioselectivity in an Unusual Bacterial Acyl-CoA Dehydrogenase. <i>Journal of the American Chemical Society</i> , 2020, 142, 835-846.	6.6	9

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19	Characterization of a Metal-Resistant <i>Bacillus</i> Strain With a High Molybdate Affinity ModA From Contaminated Sediments at the Oak Ridge Reservation. <i>Frontiers in Microbiology</i> , 2020, 11, 587127.	1.5	11
20	Novel bacterial clade reveals origin of form I Rubisco. <i>Nature Plants</i> , 2020, 6, 1158-1166.	4.7	46
21	Improvement of cryo-EM maps by density modification. <i>Nature Methods</i> , 2020, 17, 923-927.	9.0	243
22	Draft Genome Sequence of <i>Bacillus</i> sp. Strain EB106-08-02-XG196, Isolated from High-Nitrate-Contaminated Sediment. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
23	A Global Ramachandran Score Identifies Protein Structures with Unlikely Stereochemistry. <i>Structure</i> , 2020, 28, 1249-1258.e2.	1.6	86
24	Implementation of the riding hydrogen model in CCTBX to support the next generation of X-ray and neutron joint refinement in Phenix. <i>Methods in Enzymology</i> , 2020, 634, 177-199.	0.4	8
25	An iron (II) dependent oxygenase performs the last missing step of plant lysine catabolism. <i>Nature Communications</i> , 2020, 11, 2931.	5.8	11
26	Response of <i>Pseudomonas putida</i> to Complex, Aromatic-Rich Fractions from Biomass. <i>ChemSusChem</i> , 2020, 13, 4455-4467.	3.6	23
27	What are the current limits on determination of protonation state using neutron macromolecular crystallography?. <i>Methods in Enzymology</i> , 2020, 634, 225-255.	0.4	0
28	Structure and Function of BorB, the Type II Thioesterase from the Borrelidin Biosynthetic Gene Cluster. <i>Biochemistry</i> , 2020, 59, 1630-1639.	1.2	10
29	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.	3.3	149
30	Improved chemistry restraints for crystallographic refinement by integrating the Amber force field into <i>Phenix</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 51-62.	1.1	29
31	Density modification of cryo-EM maps. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 912-925.	1.1	28
32	Arginine off-kilter: guanidinium is not as planar as restraints denote. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1159-1166.	1.1	7
33	Cryo_fit: Democratization of flexible fitting for cryo-EM. <i>Journal of Structural Biology</i> , 2019, 208, 1-6.	1.3	30
34	Automated Cells-To-Peptides Sample Preparation Workflow for High-Throughput, Quantitative Proteomic Assays of Microbes. <i>Journal of Proteome Research</i> , 2019, 18, 3752-3761.	1.8	32
35	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.	3.6	46
36	Structural insights into dehydratase substrate selection for the borrelidin and fluvirucin polyketide synthases. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 1225-1235.	1.4	7

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37	Massively Parallel Fitness Profiling Reveals Multiple Novel Enzymes in <i>Pseudomonas putida</i> Lysine Metabolism. MBio, 2019, 10, .	1.8	60
38	Methyl ketone production by <i>Pseudomonas putida</i> is enhanced by plant-derived amino acids. Biotechnology and Bioengineering, 2019, 116, 1909-1922.	1.7	29
39	A rapid methods development workflow for high-throughput quantitative proteomic applications. PLoS ONE, 2019, 14, e0211582.	1.1	17
40	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
41	Iron- and aluminium-induced depletion of molybdenum in acidic environments impedes the nitrogen cycle. Environmental Microbiology, 2019, 21, 152-163.	1.8	22
42	Iron-sulfur clusters have no right angles. Acta Crystallographica Section D: Structural Biology, 2019, 75, 16-20.	1.1	16
43	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
44	Updated validation and deposition tools in the <i>Phenix</i> GUI. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a339-a339.	0.0	0
45	Developing a shared computing and networking infrastructure for the ALS-ENABLE structural biology program at the Advanced Light Source. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a248-a248.	0.0	0
46	Efficient real-space refinement for cryo-EM and crystallography. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e86-e86.	0.0	0
47	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. MBio, 2018, 9, .	1.8	57
48	Integrated analysis of isopentenyl pyrophosphate (IPP) toxicity in isoprenoid-producing <i>Escherichia coli</i> . Metabolic Engineering, 2018, 47, 60-72.	3.6	106
49	Toward industrial production of isoprenoids in <i>Escherichia coli</i> : Lessons learned from CRISPR-Cas9 based optimization of a chromosomally integrated mevalonate pathway. Biotechnology and Bioengineering, 2018, 115, 1000-1013.	1.7	39
50	Employing a biochemical protecting group for a sustainable indigo dyeing strategy. Nature Chemical Biology, 2018, 14, 256-261.	3.9	143
51	<i>DiSCaMB</i> : a software library for aspherical atom model X-ray scattering factor calculations with CPUs and GPUs. Journal of Applied Crystallography, 2018, 51, 193-199.	1.9	24
52	Discovery of enzymes for toluene synthesis from anoxic microbial communities. Nature Chemical Biology, 2018, 14, 451-457.	3.9	47
53	Interactive comparison and remediation of collections of macromolecular structures. Protein Science, 2018, 27, 182-194.	3.1	13
54	MolProbity: More and better reference data for improved all-atom structure validation. Protein Science, 2018, 27, 293-315.	3.1	2,776

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55	A bacterial pioneer produces cellulase complexes that persist through community succession. <i>Nature Microbiology</i> , 2018, 3, 99-107.	5.9	38
56	Structures of the intermediates of Kokâ€™s photosynthetic water oxidation clock. <i>Nature</i> , 2018, 563, 421-425.	13.7	386
57	Distribution of evaluation scores for the models submitted to the second cryo-EM model challenge. <i>Data in Brief</i> , 2018, 20, 1629-1638.	0.5	5
58	Rapid characterization of the activities of lignin-modifying enzymes based on nanostructure-initiator mass spectrometry (NIMS). <i>Biotechnology for Biofuels</i> , 2018, 11, 266.	6.2	14
59	Renewable production of high density jet fuel precursor sesquiterpenes from <i>Escherichia coli</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 285.	6.2	43
60	Engineering glycoside hydrolase stability by the introduction of zinc binding. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 702-710.	1.1	1
61	A fully automatic method yielding initial models from high-resolution cryo-electron microscopy maps. <i>Nature Methods</i> , 2018, 15, 905-908.	9.0	137
62	Jungle Express is a versatile repressor system for tight transcriptional control. <i>Nature Communications</i> , 2018, 9, 3617.	5.8	33
63	Automated flow-based/digital microfluidic platform integrated with onsite electroporation process for multiplex genetic engineering applications. , 2018, , .		5
64	Map segmentation, automated model-building and their application to the Cryo-EM Model Challenge. <i>Journal of Structural Biology</i> , 2018, 204, 338-343.	1.3	6
65	Evaluation system and web infrastructure for the second cryo-EM model challenge. <i>Journal of Structural Biology</i> , 2018, 204, 96-108.	1.3	11
66	From deep TLS validation to ensembles of atomic models built from elemental motions. II. Analysis of TLS refinement results by explicit interpretation. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 621-631.	1.1	7
67	Improved chemistry restraints for crystallographic refinement by integrating Amber molecular mechanics in Phenix. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a145-a145.	0.0	2
68	Evaluation of models determined by neutron diffraction and proposed improvements to their validation and deposition. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 800-813.	1.1	15
69	Automated map sharpening by maximization of detail and connectivity. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 545-559.	1.1	218
70	Real-space refinement in PHENIX for cryo-EM and crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 531-544.	1.1	2,065
71	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.	1.1	575
72	Polder maps: improving OMIT maps for ligand building and validation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a308-a308.	0.0	0

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73	The collaborative crystallography program at the Advanced Light Source. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a431-a431.	0.0	0
74	High-throughput protein-ligand complex structure solution with Phenix. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a445-a445.	0.0	0
75	Self-assembled gold nanoparticle film for nanostructure-initiator mass spectrometry with passive on-line salt fractionation. , 2017, , .		0
76	Parallel microarraying of microfluidic droplets for high-throughput integration with matrix-assisted laser desorption ionization mass spectrometry. , 2017, , .		0
77	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
78	Structure of the human TRiC/CCT Subunit 5 associated with hereditary sensory neuropathy. Scientific Reports, 2017, 7, 3673.	1.6	31
79	Structure of aryl O-demethylase offers molecular insight into a catalytic tyrosine-dependent mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3205-E3214.	3.3	24
80	Production of jet fuel precursor monoterpenoids from engineered <i>Escherichia coli</i> . Biotechnology and Bioengineering, 2017, 114, 1703-1712.	1.7	81
81	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
82	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
83	The cryo-electron microscopy structure of human transcription factor IIH. Nature, 2017, 549, 414-417.	13.7	89
84	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
85	Polder maps: improving OMIT maps for ligand building and validation. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C48-C48.	0.0	0
86	Polder maps: improving OMIT maps by excluding bulk solvent. Acta Crystallographica Section D: Structural Biology, 2017, 73, 148-157.	1.1	500
87	Reply to Kiser: Dioxygen binding in NOV1 crystal structures. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6029-E6030.	3.3	4
88	Plant cell wall glycosyltransferases: High-throughput recombinant expression screening and general requirements for these challenging enzymes. PLoS ONE, 2017, 12, e0177591.	1.1	21
89	Expression of naturally ionic liquid-tolerant thermophilic cellulases in <i>Aspergillus niger</i> . PLoS ONE, 2017, 12, e0189604.	1.1	13
90	X-ray diffraction analysis and <i>in vitro</i> characterization of the UAM2 protein from <i>Oryza sativa</i> . Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 241-245.	0.4	1

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91	Berkeley Screen: a set of 96 solutions for general macromolecular crystallization. <i>Journal of Applied Crystallography</i> , 2017, 50, 1352-1358.	1.9	11
92	An editor for the generation and customization of geometry restraints. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 123-130.	1.1	27
93	Phasing strategies II – molecular replacement. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a391-a391.	0.0	0
94	Model-building using cryo-EM and crystallographic maps. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C1327-C1327.	0.0	0
95	Video tutorials for the <i>Phenix</i> software suite. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C1134-C1134.	0.0	0
96	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.	3.3	50
97	Can I solve my structure by SAD phasing? Planning an experiment, scaling data and evaluating the useful anomalous correlation and anomalous signal. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 359-374.	1.1	29
98	No observable conformational changes in PSII. <i>Nature</i> , 2016, 533, E1-E2.	13.7	40
99	Noninvasive imaging of cellulose microfibril orientation within plant cell walls by polarized Raman microspectroscopy. <i>Biotechnology and Bioengineering</i> , 2016, 113, 82-90.	1.7	21
100	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.	1.6	44
101	Characterizing Strain Variation in Engineered <i>E. coli</i> Using a Multi-Omics-Based Workflow. <i>Cell Systems</i> , 2016, 2, 335-346.	2.9	73
102	Comparative Community Proteomics Demonstrates the Unexpected Importance of Actinobacterial Glycoside Hydrolase Family 12 Protein for Crystalline Cellulose Hydrolysis. <i>MBio</i> , 2016, 7, .	1.8	17
103	Structure of photosystem II and substrate binding at room temperature. <i>Nature</i> , 2016, 540, 453-457.	13.7	323
104	Can I solve my structure by SAD phasing? Anomalous signal in SAD phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 346-358.	1.1	31
105	A second-generation expression system for tyrosine-sulfated proteins and its application in crop protection. <i>Integrative Biology (United Kingdom)</i> , 2016, 8, 542-545.	0.6	23
106	A Droplet Microfluidic Platform for Automating Genetic Engineering. <i>ACS Synthetic Biology</i> , 2016, 5, 426-433.	1.9	63
107	Exploiting the Substrate Promiscuity of Hydroxycinnamoyl-CoA:Shikimate Hydroxycinnamoyl Transferase to Reduce Lignin. <i>Plant and Cell Physiology</i> , 2016, 57, 568-579.	1.5	78
108	Structural Basis of Stereospecificity in the Bacterial Enzymatic Cleavage of $\beta^2$ -Aryl Ether Bonds in Lignin. <i>Journal of Biological Chemistry</i> , 2016, 291, 5234-5246.	1.6	40

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109	A new default restraint library for the protein backbone in <i>Phenix</i> : a conformation-dependent geometry goes mainstream. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 176-179.	1.1	39
110	Improved ligand geometries in crystallographic refinement using <i>AFITT</i> in <i>PHENIX</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1062-1072.	1.1	29
111	New bulk-solvent model improves model-to-data fit and facilitates map interpretation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s22-s22.	0.0	0
112	Predicting X-ray diffuse scattering from translation-“libration”-screw structural ensembles. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1657-1667.	2.5	14
113	Analytics for Metabolic Engineering. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 135.	2.0	79
114	Development of a High Throughput Platform for Screening Glycoside Hydrolases Based on Oxime-NIMS. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 153.	2.0	14
115	Use of Nanostructure-Initiator Mass Spectrometry to Deduce Selectivity of Reaction in Glycoside Hydrolases. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 165.	2.0	6
116	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. <i>MBio</i> , 2015, 6, e00326-15.	1.8	173
117	The Berkeley Center for Structural Biology at the Advanced Light Source. <i>Synchrotron Radiation News</i> , 2015, 28, 22-27.	0.2	2
118	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 433-434.	3.6	40
119	Multifunctional cellulase catalysis targeted by fusion to different carbohydrate-binding modules. <i>Biotechnology for Biofuels</i> , 2015, 8, 220.	6.2	49
120	Programming new geometry restraints: parallelity of atomic groups. <i>Journal of Applied Crystallography</i> , 2015, 48, 1130-1141.	1.9	13
121	Principal component analysis of proteomics (PCAP) as a tool to direct metabolic engineering. <i>Metabolic Engineering</i> , 2015, 28, 123-133.	3.6	140
122	Metabolic engineering for the high-yield production of isoprenoid-based C5 alcohols in <i>E. coli</i> . <i>Scientific Reports</i> , 2015, 5, 11128.	1.6	125
123	Identification and Characterization of a Golgi-Localized UDP-Xylose Transporter Family from <i>Arabidopsis</i> . <i>Plant Cell</i> , 2015, 27, 1218-1227.	3.1	61
124	FEM: feature-enhanced map. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 646-666.	2.5	157
125	A Versatile Microfluidic Device for Automating Synthetic Biology. <i>ACS Synthetic Biology</i> , 2015, 4, 1151-1164.	1.9	81
126	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	1.6	159



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127	Indexing amyloid peptide diffraction from serial femtosecond crystallography: new algorithms for sparse patterns. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 357-366.	2.5	18
128	Using support vector machines to improve elemental ion identification in macromolecular crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1147-1158.	2.5	4
129	Standard Flow Liquid Chromatography for Shotgun Proteomics in Bioenergy Research. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 44.	2.0	44
130	EMRinger: side chain-directed model and map validation for 3D cryo-electron microscopy. <i>Nature Methods</i> , 2015, 12, 943-946.	9.0	799
131	Macromolecular X-ray structure determination using weak, single-wavelength anomalous data. <i>Nature Methods</i> , 2015, 12, 127-130.	9.0	31
132	A droplet-to-digital (D2D) microfluidic device for single cell assays. <i>Lab on A Chip</i> , 2015, 15, 225-236.	3.1	70
133	From deep TLS validation to ensembles of atomic models built from elemental motions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1668-1683.	2.5	14
134	Macromolecular crystallographic structure refinement. <i>Arbor</i> , 2015, 191, a219.	0.1	3
135	Cellulosic Biomass Pretreatment and Sugar Yields as a Function of Biomass Particle Size. <i>PLoS ONE</i> , 2014, 9, e100836.	1.1	19
136	Development of a Native <i>Escherichia coli</i> Induction System for Ionic Liquid Tolerance. <i>PLoS ONE</i> , 2014, 9, e101115.	1.1	31
137	Understanding the Role of Histidine in the GHSxG Acyltransferase Active Site Motif: Evidence for Histidine Stabilization of the Malonyl-Enzyme Intermediate. <i>PLoS ONE</i> , 2014, 9, e109421.	1.1	10
138	Pressure stabilizer for reproducible picoinjection in droplet microfluidic systems. <i>Lab on A Chip</i> , 2014, 14, 4533-4539.	3.1	34
139	A Peptide-Based Method for <sup>13</sup> C Metabolic Flux Analysis in Microbial Communities. <i>PLoS Computational Biology</i> , 2014, 10, e1003827.	1.5	56
140	An atomic model of brome mosaic virus using direct electron detection and real-space optimization. <i>Nature Communications</i> , 2014, 5, 4808.	5.8	105
141	Structural and Biochemical Studies of Actin in Complex with Synthetic Macrolide Tail Analogues. <i>ChemMedChem</i> , 2014, 9, 2286-2293.	1.6	20
142	Conformation-dependent backbone geometry restraints set a new standard for protein crystallographic refinement. <i>FEBS Journal</i> , 2014, 281, 4061-4071.	2.2	36
143	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.	3.3	55
144	Error Rate Comparison during Polymerase Chain Reaction by DNA Polymerase. <i>Molecular Biology International</i> , 2014, 2014, 1-8.	1.7	160

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145	Improved crystal orientation and physical properties from single-shot XFEL stills. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3299-3309.	2.5	38
146	Metrics for comparison of crystallographic maps. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2593-2606.	2.5	29
147	Structure of the OsSERK2 leucine-rich repeat extracellular domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3080-3086.	2.5	16
148	Accurate macromolecular structures using minimal measurements from X-ray free-electron lasers. <i>Nature Methods</i> , 2014, 11, 545-548.	9.0	140
149	Correlation analysis of targeted proteins and metabolites to assess and engineer microbial isopentenol production. <i>Biotechnology and Bioengineering</i> , 2014, 111, 1648-1658.	1.7	89
150	Rapid Kinetic Characterization of Glycosyl Hydrolases Based on Oxime Derivatization and Nanostructure-Initiator Mass Spectrometry (NIMS). <i>ACS Chemical Biology</i> , 2014, 9, 1470-1479.	1.6	36
151	CRYO-EM Atomic Model of Brome Mosaic Virus Derived from Direct Electron Detection Images and a Real-Space Model Optimization Protocol. <i>Biophysical Journal</i> , 2014, 106, 600a.	0.2	2
152	Analysis of plant nucleotide sugars by hydrophilic interaction liquid chromatography and tandem mass spectrometry. <i>Analytical Biochemistry</i> , 2014, 448, 14-22.	1.1	49
153	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.	3.6	55
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