

Paul D Adams

List of Publications by Year in descending order

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Version: 2024-02-01

348
papers

105,600
citations

5434

84
h-index

222

305
g-index

383
all docs

383
docs citations

383
times ranked

91231
citing authors

#	ARTICLE	IF	CITATIONS
1	AlphaFold predictions are valuable hypotheses and accelerate but do not replace experimental structure determination. <i>Nature Methods</i> , 2024, 21, 110-116.	19.6	68
2	Environmental stress mediates groundwater microbial community assembly. <i>Nature Microbiology</i> , 2024, 9, 490-501.	13.1	14
3	Universal parameters of bulk-solvent masks. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2024, 80, 194-201.	0.1	0
4	Community recommendations on cryoEM data archiving and validation. <i>IUCr</i> , 2024, 11, 140-151.	2.3	4
5	Structural and biochemical basis for regiospecificity of the flavonoid glycosyltransferase UGT95A1. <i>Journal of Biological Chemistry</i> , 2024, , 107602.	3.5	0
6	Protonation of histidine rings using quantum-mechanical methods. <i>Acta Crystallographica Section D: Structural Biology</i> , 2024, 80, .	2.4	0
7	Likelihood-based interactive local docking into cryo-EM maps in <i>ChimeraX</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2024, 80, .	2.4	0
8	Characterization of lignin degrading enzyme PmdC, which catalyzes a key step in the synthesis of polymer precursor 2-pyrone-4,6-dicarboxylic acid (PDC). <i>Journal of Biological Chemistry</i> , 2024, , 107736.	3.5	0
9	Mechanistic and structural characterization of an iridium-containing cytochrome reveals kinetically relevant cofactor dynamics. <i>Nature Catalysis</i> , 2023, 6, 39-51.	28.3	7
10	<i>In situ</i> ligand restraints from quantum-mechanical methods. <i>Acta Crystallographica Section D: Structural Biology</i> , 2023, 79, 100-110.	2.4	7
11	A Membrane-Associated Light-Harvesting Model is Enabled by Functionalized Assemblies of Gene-Doubled TMV Proteins. <i>Small</i> , 2023, 19, .	11.2	3
12	Accelerating crystal structure determination with iterative <i>AlphaFold</i> prediction. <i>Acta Crystallographica Section D: Structural Biology</i> , 2023, 79, 234-244.	2.4	24
13	Structural and biochemical insight into a modular β -1,4-galactan synthase in plants. <i>Nature Plants</i> , 2023, 9, 486-500.	9.4	4
14	Potent and selective covalent inhibition of the papain-like protease from SARS-CoV-2. <i>Nature Communications</i> , 2023, 14, .	13.2	25
15	Complete integration of carbene-transfer chemistry into biosynthesis. <i>Nature</i> , 2023, 617, 403-408.	36.2	20
16	Efficient structure-factor modeling for crystals with multiple components. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2023, 79, 345-352.	0.1	1
17	Structural evidence for intermediates during O ₂ formation in photosystem II. <i>Nature</i> , 2023, 617, 629-636.	36.2	69
18	Overall protein structure quality assessment using hydrogen-bonding parameters. <i>Acta Crystallographica Section D: Structural Biology</i> , 2023, 79, 684-693.	2.4	3

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19	Improved joint X-ray and neutron refinement procedure in <i>Phenix</i> . Acta Crystallographica Section D: Structural Biology, 2023, 79, 1079-1093.	2.4	1
20	Integration of software tools for integrative modeling of biomolecular systems. Journal of Structural Biology, 2022, 214, 107841.	2.9	11
21	Modular automated bottom-up proteomic sample preparation for high-throughput applications. PLoS ONE, 2022, 17, e0264467.	2.5	3
22	A Synthetic Gene Library Yields a Previously Unknown Glycoside Phosphorylase That Degrades and Assembles Poly- β -1,3-GlcNAc, Completing the Suite of β -Linked GlcNAc Polysaccharides. ACS Central Science, 2022, 8, 430-440.	12.3	11
23	Improved AlphaFold modeling with implicit experimental information. Nature Methods, 2022, 19, 1376-1382.	19.6	75
24	<i>O</i> -/ <i>N</i> -/ <i>S</i> -Specificity in Glycosyltransferase Catalysis: From Mechanistic Understanding to Engineering. ACS Catalysis, 2021, 11, 1810-1815.	11.7	51
25	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	19.6	87
26	Protein identification from electron cryomicroscopy maps by automated model building and side-chain matching. Acta Crystallographica Section D: Structural Biology, 2021, 77, 457-462.	2.4	10
27	Mechanism Across Scales: A Holistic Modeling Framework Integrating Laboratory and Field Studies for Microbial Ecology. Frontiers in Microbiology, 2021, 12, 642422.	3.6	16
28	Efficient production of oxidized terpenoids via engineering fusion proteins of terpene synthase and cytochrome P450. Metabolic Engineering, 2021, 64, 41-51.	7.1	35
29	Engineering <i>Saccharomyces cerevisiae</i> for isoprenol production. Metabolic Engineering, 2021, 64, 154-166.	7.1	38
30	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> . Biotechnology for Biofuels, 2021, 14, 108.	6.3	13
31	A multiplexed nanostructure-initiator mass spectrometry (NIMS) assay for simultaneously detecting glycosyl hydrolase and lignin modifying enzyme activities. Scientific Reports, 2021, 11, 11803.	3.4	8
32	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. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.6	8
33	Accurate prediction of protein structures and interactions using a three-track neural network. Science, 2021, 373, 871-876.	20.9	3,363
34	Macromolecular refinement of X-ray and cryoelectron microscopy structures with Phenix/OPLS3e for improved structure and ligand quality. Structure, 2021, 29, 913-921.e4.	3.4	31
35	<i>CERES</i> : a cryo-EM re-refinement system for continuous improvement of deposited models. Acta Crystallographica Section D: Structural Biology, 2021, 77, 48-61.	2.4	16
36	Structural dynamics in the water and proton channels of photosystem II during the S2 to S3 transition. Nature Communications, 2021, 12, 6531.	13.2	89

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37	Cryo-EM map interpretation and protein model building using iterative map segmentation. <i>Protein Science</i> , 2020, 29, 87-99.	7.8	28
38	Structural Mechanism of Regioselectivity in an Unusual Bacterial Acyl-CoA Dehydrogenase. <i>Journal of the American Chemical Society</i> , 2020, 142, 835-846.	14.6	12
39	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.	3.6	12
40	Novel bacterial clade reveals origin of form I Rubisco. <i>Nature Plants</i> , 2020, 6, 1158-1166.	9.4	51
41	Improvement of cryo-EM maps by density modification. <i>Nature Methods</i> , 2020, 17, 923-927.	19.6	265
42	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, .	2.0	0
43	A Global Ramachandran Score Identifies Protein Structures with Unlikely Stereochemistry. <i>Structure</i> , 2020, 28, 1249-1258.e2.	3.4	106
44	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.	1.7	8
45	An iron (II) dependent oxygenase performs the last missing step of plant lysine catabolism. <i>Nature Communications</i> , 2020, 11, 2931.	13.2	11
46	Response of <i>Pseudomonas putida</i> to Complex, Aromatic-Rich Fractions from Biomass. <i>ChemSusChem</i> , 2020, 13, 4455-4467.	7.5	24
47	What are the current limits on determination of protonation state using neutron macromolecular crystallography?. <i>Methods in Enzymology</i> , 2020, 634, 225-255.	1.7	0
48	Structure and Function of BorB, the Type II Thioesterase from the Borrelidin Biosynthetic Gene Cluster. <i>Biochemistry</i> , 2020, 59, 1630-1639.	2.6	10
49	Untangling the sequence of events during the S ₂ → S ₃ 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.	7.6	172
50	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.	2.4	31
51	Density modification of cryo-EM maps. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 912-925.	2.4	30
52	Arginine off-kilter: guanidinium is not as planar as restraints denote. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1159-1166.	2.4	9
53	Cryo_fit: Democratization of flexible fitting for cryo-EM. <i>Journal of Structural Biology</i> , 2019, 208, 1-6.	2.9	35
54	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.	3.8	33

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55	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.	7.1	47
56	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.	3.0	7
57	Massively Parallel Fitness Profiling Reveals Multiple Novel Enzymes in <i>Pseudomonas putida</i> Lysine Metabolism. <i>MBio</i> , 2019, 10, .	4.4	60
58	Methyl ketone production by <i>Pseudomonas putida</i> is enhanced by plant-derived amino acids. <i>Biotechnology and Bioengineering</i> , 2019, 116, 1909-1922.	3.5	30
59	A rapid methods development workflow for high-throughput quantitative proteomic applications. <i>PLoS ONE</i> , 2019, 14, e0211582.	2.5	17
60	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.	2.4	53
61	Federating Structural Models and Data: Outcomes from A Workshop on Archiving Integrative Structures. <i>Structure</i> , 2019, 27, 1745-1759.	3.4	40
62	Iron- and aluminium-induced depletion of molybdenum in acidic environments impedes the nitrogen cycle. <i>Environmental Microbiology</i> , 2019, 21, 152-163.	3.9	23
63	Iron-sulfur clusters have no right angles. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 16-20.	2.4	16
64	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.	2.4	4,722
65	Updated validation and deposition tools in the <i>Phenix</i> GUI. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2019, 75, a339-a339.	0.1	0
66	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. <i>MBio</i> , 2018, 9, .	4.4	58
67	Integrated analysis of isopentenyl pyrophosphate (IPP) toxicity in isoprenoid-producing <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2018, 47, 60-72.	7.1	118
68	Toward industrial production of isoprenoids in <i>Escherichia coli</i> : Lessons learned from CRISPR-Cas9 based optimization of a chromosomally integrated mevalonate pathway. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1000-1013.	3.5	41
69	Employing a biochemical protecting group for a sustainable indigo dyeing strategy. <i>Nature Chemical Biology</i> , 2018, 14, 256-261.	8.0	156
70	<i>DiSCaMB</i> : a software library for aspherical atom model X-ray scattering factor calculations with CPUs and GPUs. <i>Journal of Applied Crystallography</i> , 2018, 51, 193-199.	4.9	27
71	Discovery of enzymes for toluene synthesis from anoxic microbial communities. <i>Nature Chemical Biology</i> , 2018, 14, 451-457.	8.0	47
72	Interactive comparison and remediation of collections of macromolecular structures. <i>Protein Science</i> , 2018, 27, 182-194.	7.8	14

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73	MolProbity: More and better reference data for improved all-atom structure validation. <i>Protein Science</i> , 2018, 27, 293-315.	7.8	3,117
74	A bacterial pioneer produces cellulase complexes that persist through community succession. <i>Nature Microbiology</i> , 2018, 3, 99-107.	13.1	39
75	Structures of the intermediates of Kokorin's photosynthetic water oxidation clock. <i>Nature</i> , 2018, 563, 421-425.	36.2	423
76	Distribution of evaluation scores for the models submitted to the second cryo-EM model challenge. <i>Data in Brief</i> , 2018, 20, 1629-1638.	1.1	5
77	Rapid characterization of the activities of lignin-modifying enzymes based on nanostructure-initiator mass spectrometry (NIMS). <i>Biotechnology for Biofuels</i> , 2018, 11, 266.	6.3	14
78	Renewable production of high density jet fuel precursor sesquiterpenes from <i>Escherichia coli</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 285.	6.3	48
79	Engineering glycoside hydrolase stability by the introduction of zinc binding. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 702-710.	2.4	1
80	A fully automatic method yielding initial models from high-resolution cryo-electron microscopy maps. <i>Nature Methods</i> , 2018, 15, 905-908.	19.6	144
81	Jungle Express is a versatile repressor system for tight transcriptional control. <i>Nature Communications</i> , 2018, 9, 3617.	13.2	34
82	Automated flow-based/digital microfluidic platform integrated with onsite electroporation process for multiplex genetic engineering applications. , 2018, , .		5
83	Map segmentation, automated model-building and their application to the Cryo-EM Model Challenge. <i>Journal of Structural Biology</i> , 2018, 204, 338-343.	2.9	6
84	Evaluation system and web infrastructure for the second cryo-EM model challenge. <i>Journal of Structural Biology</i> , 2018, 204, 96-108.	2.9	12
85	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.	2.4	8
86	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.	0.1	2
87	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.	2.4	15
88	Automated map sharpening by maximization of detail and connectivity. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 545-559.	2.4	240
89	Real-space refinement in PHENIX for cryo-EM and crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 531-544.	2.4	2,342
90	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.	2.4	629

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91	Polder maps: improving OMIT maps for ligand building and validation. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a308-a308.	0.1	0
92	The collaborative crystallography program at the Advanced Light Source. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a431-a431.	0.1	0
93	High-throughput protein-ligand complex structure solution with Phenix. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a445-a445.	0.1	0
94	Self-assembled gold nanoparticle film for nanostructure-initiator mass spectrometry with passive on-line salt fractionation. , 2017, , .		0
95	Parallel microarraying of microfluidic droplets for high-throughput integration with matrix-assisted laser desorption ionization mass spectrometry. , 2017, , .		0
96	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.	7.6	112
97	Structure of the human TRiC/CCT Subunit 5 associated with hereditary sensory neuropathy. Scientific Reports, 2017, 7, 3673.	3.4	34
98	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.	7.6	24
99	Production of jet fuel precursor monoterpenoids from engineered <i>Escherichia coli</i> . Biotechnology and Bioengineering, 2017, 114, 1703-1712.	3.5	85
100	On-chip integration of droplet microfluidics and nanostructure-initiator mass spectrometry for enzyme screening. Lab on A Chip, 2017, 17, 323-331.	6.1	46
101	The Experiment Data Depot: A Web-Based Software Tool for Biological Experimental Data Storage, Sharing, and Visualization. ACS Synthetic Biology, 2017, 6, 2248-2259.	4.0	46
102	The cryo-electron microscopy structure of human transcription factor IIH. Nature, 2017, 549, 414-417.	36.2	90
103	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.	4.0	103
104	Polder maps: improving OMIT maps for ligand building and validation. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C48-C48.	0.1	0
105	Polder maps: improving OMIT maps by excluding bulk solvent. Acta Crystallographica Section D: Structural Biology, 2017, 73, 148-157.	2.4	538
106	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.	7.6	4
107	Plant cell wall glycosyltransferases: High-throughput recombinant expression screening and general requirements for these challenging enzymes. PLoS ONE, 2017, 12, e0177591.	2.5	22
108	Expression of naturally ionic liquid-tolerant thermophilic cellulases in <i>Aspergillus niger</i> . PLoS ONE, 2017, 12, e0189604.	2.5	13

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109	X-ray diffraction analysis and <i>in vitro</i> characterization of the UAM2 protein from <i>Oryza sativa</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 241-245.	0.9	1
110	Berkeley Screen: a set of 96 solutions for general macromolecular crystallization. <i>Journal of Applied Crystallography</i> , 2017, 50, 1352-1358.	4.9	15
111	An editor for the generation and customization of geometry restraints. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 123-130.	2.4	29
112	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.	7.6	56
113	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.	2.4	29
114	Outcome of the First wwPDB/CCDC/D3R Ligand Validation Workshop. <i>Structure</i> , 2016, 24, 502-508.	3.4	64
115	No observable conformational changes in PSII. <i>Nature</i> , 2016, 533, E1-E2.	36.2	42
116	Non-invasive imaging of cellulose microfibril orientation within plant cell walls by polarized Raman microspectroscopy. <i>Biotechnology and Bioengineering</i> , 2016, 113, 82-90.	3.5	25
117	Structural and Biochemical Characterization of the Early and Late Enzymes in the Lignin β^2 -Aryl Ether Cleavage Pathway from <i>Sphingobium</i> sp. SYK-6. <i>Journal of Biological Chemistry</i> , 2016, 291, 10228-10238.	3.5	44
118	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	75
119	Comparative Community Proteomics Demonstrates the Unexpected Importance of Actinobacterial Glycoside Hydrolase Family 12 Protein for Crystalline Cellulose Hydrolysis. <i>MBio</i> , 2016, 7, .	4.4	18
120	Structure of photosystem II and substrate binding at room temperature. <i>Nature</i> , 2016, 540, 453-457.	36.2	334
121	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.	2.4	32
122	Volatile components and sensory characteristics of Thai traditional fermented shrimp pastes during fermentation periods. <i>Journal of Food Science and Technology</i> , 2016, 53, 1399-1410.	2.8	31
123	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.	1.3	25
124	A Droplet Microfluidic Platform for Automating Genetic Engineering. <i>ACS Synthetic Biology</i> , 2016, 5, 426-433.	4.0	65
125	Exploiting the Substrate Promiscuity of Hydroxycinnamoyl-CoA:Shikimate Hydroxycinnamoyl Transferase to Reduce Lignin. <i>Plant and Cell Physiology</i> , 2016, 57, 568-579.	3.2	81
126	Structural Basis of Stereospecificity in the Bacterial Enzymatic Cleavage of β^2 -Aryl Ether Bonds in Lignin. <i>Journal of Biological Chemistry</i> , 2016, 291, 5234-5246.	3.5	41

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127	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.	2.4	39
128	Improved ligand geometries in crystallographic refinement using <i>AFIT</i> in <i>PHENIX</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1062-1072.	2.4	30
129	From deep TLS validation to ensembles of atomic models built from elemental motions. Addenda and corrigendum. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1073-1075.	2.4	3
130	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.	0.1	0
131	Predicting X-ray diffuse scattering from translation-“libration”-screw structural ensembles. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1657-1667.	2.4	14
132	Analytics for Metabolic Engineering. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 135.	4.2	80
133	Development of a High Throughput Platform for Screening Glycoside Hydrolases Based on Oxime-NIMS. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 153.	4.2	15
134	Use of Nanostructure-Initiator Mass Spectrometry to Deduce Selectivity of Reaction in Glycoside Hydrolases. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 165.	4.2	6
135	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. <i>MBio</i> , 2015, 6, e00326-15.	4.4	179
136	The Berkeley Center for Structural Biology at the Advanced Light Source. <i>Synchrotron Radiation News</i> , 2015, 28, 22-27.	1.0	2
137	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.	8.1	41
138	Multifunctional cellulase catalysis targeted by fusion to different carbohydrate-binding modules. <i>Biotechnology for Biofuels</i> , 2015, 8, 220.	6.3	52
139	Programming new geometry restraints: parallelity of atomic groups. <i>Journal of Applied Crystallography</i> , 2015, 48, 1130-1141.	4.9	14
140	Principal component analysis of proteomics (PCAP) as a tool to direct metabolic engineering. <i>Metabolic Engineering</i> , 2015, 28, 123-133.	7.1	143
141	Metabolic engineering for the high-yield production of isoprenoid-based C5 alcohols in <i>E. coli</i> . <i>Scientific Reports</i> , 2015, 5, 11128.	3.4	128
142	Identification and Characterization of a Golgi-Localized UDP-Xylose Transporter Family from <i>Arabidopsis</i> . <i>Plant Cell</i> , 2015, 27, 1218-1227.	6.7	64
143	FEM: feature-enhanced map. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 646-666.	2.4	160
144	A Versatile Microfluidic Device for Automating Synthetic Biology. <i>ACS Synthetic Biology</i> , 2015, 4, 1151-1164.	4.0	84

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145	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	3.4	163
146	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.	2.4	20
147	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.	2.4	5
148	Standard Flow Liquid Chromatography for Shotgun Proteomics in Bioenergy Research. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 44.	4.2	44
149	EMRinger: side chain-directed model and map validation for 3D cryo-electron microscopy. <i>Nature Methods</i> , 2015, 12, 943-946.	19.6	845
150	Macromolecular X-ray structure determination using weak, single-wavelength anomalous data. <i>Nature Methods</i> , 2015, 12, 127-130.	19.6	33
151	A droplet-to-digital (D2D) microfluidic device for single cell assays. <i>Lab on A Chip</i> , 2015, 15, 225-236.	6.1	73
152	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.	2.4	14
153	Macromolecular crystallographic structure refinement. <i>Arbor</i> , 2015, 191, a219.	0.3	3
154	Cellulosic Biomass Pretreatment and Sugar Yields as a Function of Biomass Particle Size. <i>PLoS ONE</i> , 2014, 9, e100836.	2.5	19
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