Paul D. Adams

List of Publications by Year
in descending order

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	Integration of software tools for integrative modeling of biomolecular systems. Journal of Structural Biology, 2022, 214, 107841.	2.8	7
2	Modular automated bottom-up proteomic sample preparation for high-throughput applications. PLoS ONE, 2022, 17, e0264467.	2.5	3
3	A Synthetic Gene Library Yields a Previously Unknown Glycoside Phosphorylase That Degrades and Assembles Poly-Î²-1,3-GlcNAc, Completing the Suite of Î²-Linked GlcNAc Polysaccharides. ACS Central Science, 2022, 8, 430-440.	11.3	7
4	*O*-/*N*-/*S*-Specificity in Glycosyltransferase Catalysis: From Mechanistic Understanding to Engineering. ACS Catalysis, 2021, 11, 1810-1815.	11.2	42
5	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	19.0	73
6	Protein identification from electron cryomicroscopy maps by automated model building and side-chain matching. Acta Crystallographica Section D: Structural Biology, 2021, 77, 457-462.	2.3	9
7	Mechanism Across Scales: A Holistic Modeling Framework Integrating Laboratory and Field Studies for Microbial Ecology. Frontiers in Microbiology, 2021, 12, 642422.	3.5	12
8	Efficient production of oxidized terpenoids via engineering fusion proteins of terpene synthase and cytochrome P450. Metabolic Engineering, 2021, 64, 41-51.	7.0	33
9	Engineering Saccharomyces cerevisiae for isoprenol production. Metabolic Engineering, 2021, 64, 154-166.	7.0	34
10	Experimental and theoretical insights into the effects of pH on catalysis of bond-cleavage by the lignin peroxidase isozyme H8 from Phanerochaete chrysosporium. Biotechnology for Biofuels, 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. Scientific Reports, 2021, 11, 11803.	3.3	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. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2102342118.	7.1	7
13	Accurate prediction of protein structures and interactions using a three-track neural network. Science, 2021, 373, 871-876.	12.6	2,843
14	Macromolecular refinement of X-ray and cryoelectron microscopy structures with Phenix/OPLS3e for improved structure and ligand quality. Structure, 2021, 29, 913-921.e4.	3.3	29
15	*CERES*: a cryo-EM re-refinement system for continuous improvement of deposited models. Acta Crystallographica Section D: Structural Biology, 2021, 77, 48-61.	2.3	14
16	Structural dynamics in the water and proton channels of photosystem II during the S2 to S3 transition. Nature Communications, 2021, 12, 6531.	12.8	73
17	Cryoâ€EM map interpretation and protein modelâ€building using iterative map segmentation. Protein Science, 2020, 29, 87-99.	7.6	27
18	Structural Mechanism of Regioselectivity in an Unusual Bacterial Acyl-CoA Dehydrogenase. Journal of the American Chemical Society, 2020, 142, 835-846.	13.7	9

#	Article	IF	Citations
19	Characterization of a Metal-Resistant Bacillus Strain With a High Molybdate Affinity ModA From Contaminated Sediments at the Oak Ridge Reservation. Frontiers in Microbiology, 2020, 11, 587127.	3.5	11
20	Novel bacterial clade reveals origin of form I Rubisco. Nature Plants, 2020, 6, 1158-1166.	9.3	46
21	Improvement of cryo-EM maps by density modification. Nature Methods, 2020, 17, 923-927.	19.0	243
22	Draft Genome Sequence of *Bacillus* sp. Strain EB106-08-02-XG196, Isolated from High-Nitrate-Contaminated Sediment. Microbiology Resource Announcements, 2020, 9, .	0.6	0
23	A Global Ramachandran Score Identifies Protein Structures with Unlikely Stereochemistry. Structure, 2020, 28, 1249-1258.e2.	3.3	86
24	Implementation of the riding hydrogen model in CCTBX to support the next generation of X-ray and neutron joint refinement in Phenix. Methods in Enzymology, 2020, 634, 177-199.	1.0	8
25	An iron (II) dependent oxygenase performs the last missing step of plant lysine catabolism. Nature Communications, 2020, 11, 2931.	12.8	11
26	Response of *Pseudomonas putida* to Complex, Aromatic-Rich Fractions from Biomass. ChemSusChem, 2020, 13, 4455-4467.	6.8	23
27	What are the current limits on determination of protonation state using neutron macromolecular crystallography?. Methods in Enzymology, 2020, 634, 225-255.	1.0	0
28	Structure and Function of BorB, the Type II Thioesterase from the Borrelidin Biosynthetic Gene Cluster. Biochemistry, 2020, 59, 1630-1639.	2.5	10
29	Untangling the sequence of events during the $S_2 \rightarrow S_3$ 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.	7.1	149
30	Improved chemistry restraints for crystallographic refinement by integrating the Amber force field into *Phenix*. Acta Crystallographica Section D: Structural Biology, 2020, 76, 51-62.	2.3	29
31	Density modification of cryo-EM maps. Acta Crystallographica Section D: Structural Biology, 2020, 76, 912-925.	2.3	28
32	Arginine off-kilter: guanidinium is not as planar as restraints denote. Acta Crystallographica Section D: Structural Biology, 2020, 76, 1159-1166.	2.3	7
33	Cryo_fit: Democratization of flexible fitting for cryo-EM. Journal of Structural Biology, 2019, 208, 1-6.	2.8	30
34	Automated "Cells-To-Peptides" Sample Preparation Workflow for High-Throughput, Quantitative Proteomic Assays of Microbes. Journal of Proteome Research, 2019, 18, 3752-3761.	3.7	32
35	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.	7.0	46
36	Structural insights into dehydratase substrate selection for the borrelidin and fluvirucin polyketide synthases. Journal of Industrial Microbiology and Biotechnology, 2019, 46, 1225-1235.	3.0	7

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37	Massively Parallel Fitness Profiling Reveals Multiple Novel Enzymes in <i>Pseudomonas putida</i> Lysine Metabolism. MBio, 2019, 10, .	4.1	60
38	Methyl ketone production by <i>Pseudomonas putida</i> is enhanced by plant–derived amino acids. Biotechnology and Bioengineering, 2019, 116, 1909-1922.	3.3	29
39	A rapid methods development workflow for high-throughput quantitative proteomic applications. PLoS ONE, 2019, 14, e0211582.	2.5	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.	2.3	46
41	Iron–and aluminium–induced depletion of molybdenum in acidic environments impedes the nitrogen cycle. Environmental Microbiology, 2019, 21, 152-163.	3.8	22
42	Iron–sulfur clusters have no right angles. Acta Crystallographica Section D: Structural Biology, 2019, 75, 16-20.	2.3	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.	2.3	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.	0.1	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.	0.1	0
46	Efficient real-space refinement for cryo-EM and crystallography. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e86-e86.	0.1	0
47	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. MBio, 2018, 9, .	4.1	57
48	Integrated analysis of isopentenyl pyrophosphate (IPP) toxicity in isoprenoid-producing Escherichia coli. Metabolic Engineering, 2018, 47, 60-72.	7.0	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.	3.3	39
50	Employing a biochemical protecting group for a sustainable indigo dyeing strategy. Nature Chemical Biology, 2018, 14, 256-261.	8.0	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.	4.5	24
52	Discovery of enzymes for toluene synthesis from anoxic microbial communities. Nature Chemical Biology, 2018, 14, 451-457.	8.0	47
53	Interactive comparison and remediation of collections of macromolecular structures. Protein Science, 2018, 27, 182-194.	7.6	13
54	MolProbity: More and better reference data for improved all–atom structure validation. Protein Science, 2018, 27, 293-315.	7.6	2,776

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55	A bacterial pioneer produces cellulase complexes that persist through community succession. Nature Microbiology, 2018, 3, 99-107.	13.3	38
56	Structures of the intermediates of Kok's photosynthetic water oxidation clock. Nature, 2018, 563, 421-425.	27.8	386
57	Distribution of evaluation scores for the models submitted to the second cryo-EM model challenge. Data in Brief, 2018, 20, 1629-1638.	1.0	5
58	Rapid characterization of the activities of lignin-modifying enzymes based on nanostructure-initiator mass spectrometry (NIMS). Biotechnology for Biofuels, 2018, 11, 266.	6.2	14
59	Renewable production of high density jet fuel precursor sesquiterpenes from Escherichia coli. Biotechnology for Biofuels, 2018, 11, 285.	6.2	43
60	Engineering glycoside hydrolase stability by the introduction of zinc binding. Acta Crystallographica Section D: Structural Biology, 2018, 74, 702-710.	2.3	1
61	A fully automatic method yielding initial models from high-resolution cryo-electron microscopy maps. Nature Methods, 2018, 15, 905-908.	19.0	137
62	Jungle Express is a versatile repressor system for tight transcriptional control. Nature Communications, 2018, 9, 3617.	12.8	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. Journal of Structural Biology, 2018, 204, 338-343.	2.8	6
65	Evaluation system and web infrastructure for the second cryo-EM model challenge. Journal of Structural Biology, 2018, 204, 96-108.	2.8	11
66	From deep TLS validation to ensembles of atomic models built from elemental motions. II. Analysis of TLS refinement results by explicit interpretation. Acta Crystallographica Section D: Structural Biology, 2018, 74, 621-631.	2.3	7
67	Improved chemistry restraints for crystallographic refinement by integrating Amber molecular mechanics in Phenix. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a145-a145.	0.1	2
68	Evaluation of models determined by neutron diffraction and proposed improvements to their validation and deposition. Acta Crystallographica Section D: Structural Biology, 2018, 74, 800-813.	2.3	15
69	Automated map sharpening by maximization of detail and connectivity. Acta Crystallographica Section D: Structural Biology, 2018, 74, 545-559.	2.3	218
70	Real-space refinement in *PHENIX* for cryo-EM and crystallography. Acta Crystallographica Section D: Structural Biology, 2018, 74, 531-544.	2.3	2,065
71	New tools for the analysis and validation of cryo-EM maps and atomic models. Acta Crystallographica Section D: Structural Biology, 2018, 74, 814-840.	2.3	575
72	Polder maps: improving OMIT maps for ligand building and validation. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a308-a308.	0.1	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.	0.1	0
74	High-throughput protein–ligand complex structure solution with Phenix. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a445-a445.	0.1	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.	7.1	111
78	Structure of the human TRiC/CCT Subunit 5 associated with hereditary sensory neuropathy. Scientific Reports, 2017, 7, 3673.	3.3	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.	7.1	24
80	Production of jet fuel precursor monoterpenoids from engineered <i>Escherichia coli</i>. Biotechnology and Bioengineering, 2017, 114, 1703-1712.	3.3	81
81	On-chip integration of droplet microfluidics and nanostructure-initiator mass spectrometry for enzyme screening. Lab on A Chip, 2017, 17, 323-331.	6.0	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.	3.8	45
83	The cryo-electron microscopy structure of human transcription factor IIH. Nature, 2017, 549, 414-417.	27.8	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.	3.8	100
85	Polder maps: improving OMIT maps for ligand building and validation. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C48-C48.	0.1	0
86	Polder maps: improving OMIT maps by excluding bulk solvent. Acta Crystallographica Section D: Structural Biology, 2017, 73, 148-157.	2.3	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.	7.1	4
88	Plant cell wall glycosyltransferases: High-throughput recombinant expression screening and general requirements for these challenging enzymes. PLoS ONE, 2017, 12, e0177591.	2.5	21
89	Expression of naturally ionic liquid-tolerant thermophilic cellulases in Aspergillus niger. PLoS ONE, 2017, 12, e0189604.	2.5	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.	0.8	1

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91	Berkeley Screen: a set of 96 solutions for general macromolecular crystallization. Journal of Applied Crystallography, 2017, 50, 1352-1358.	4.5	11
92	An editor for the generation and customization of geometry restraints. Acta Crystallographica Section D: Structural Biology, 2017, 73, 123-130.	2.3	27
93	Phasing strategies II â€" molecular replacement. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a391-a391.	0.1	0
94	Model-building using cryo-EM and crystallographic maps. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C1327-C1327.	0.1	0
95	Video tutorials for the <i>Phenix</i> software suite. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C1134-C1134.	0.1	0
96	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.	7.1	50
97	Can I solve my structure by SAD phasing? Planning an experiment, scaling data and evaluating the useful anomalous correlation and anomalous signal. Acta Crystallographica Section D: Structural Biology, 2016, 72, 359-374.	2.3	29
98	No observable conformational changes in PSII. Nature, 2016, 533, E1-E2.	27.8	40
99	Nonâ€invasive imaging of cellulose microfibril orientation within plant cell walls by polarized Raman microspectroscopy. Biotechnology and Bioengineering, 2016, 113, 82-90.	3.3	21
100	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.	3.4	44
101	Characterizing Strain Variation in Engineered E.Âcoli Using a Multi-Omics-Based Workflow. Cell Systems, 2016, 2, 335-346.	6.2	73
102	Comparative Community Proteomics Demonstrates the Unexpected Importance of Actinobacterial Glycoside Hydrolase Family 12 Protein for Crystalline Cellulose Hydrolysis. MBio, 2016, 7, .	4.1	17
103	Structure of photosystem II and substrate binding at room temperature. Nature, 2016, 540, 453-457.	27.8	323
104	Can I solve my structure by SAD phasing? Anomalous signal in SAD phasing. Acta Crystallographica Section D: Structural Biology, 2016, 72, 346-358.	2.3	31
105	A second-generation expression system for tyrosine-sulfated proteins and its application in crop protection. Integrative Biology (United Kingdom), 2016, 8, 542-545.	1.3	23
106	A Droplet Microfluidic Platform for Automating Genetic Engineering. ACS Synthetic Biology, 2016, 5, 426-433.	3.8	63
107	Exploiting the Substrate Promiscuity of Hydroxycinnamoyl-CoA:Shikimate Hydroxycinnamoyl Transferase to Reduce Lignin. Plant and Cell Physiology, 2016, 57, 568-579.	3.1	78
108	Structural Basis of Stereospecificity in the Bacterial Enzymatic Cleavage of Î²-Aryl Ether Bonds in Lignin. Journal of Biological Chemistry, 2016, 291, 5234-5246.	3.4	40

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109	A new default restraint library for the protein backbone in *Phenix*: a conformation-dependent geometry goes mainstream. Acta Crystallographica Section D: Structural Biology, 2016, 72, 176-179.	2.3	39
110	Improved ligand geometries in crystallographic refinement using *AFITT* in *PHENIX*. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1062-1072.	2.3	29
111	New bulk-solvent model improves model-to-data fit and facilitates map interpretation. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s22-s22.	0.1	0
112	Predicting X-ray diffuse scattering from translation–libration–screw structural ensembles. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1657-1667.	2.5	14
113	Analytics for Metabolic Engineering. Frontiers in Bioengineering and Biotechnology, 2015, 3, 135.	4.1	79
114	Development of a High Throughput Platform for Screening Glycoside Hydrolases Based on Oxime-NIMS. Frontiers in Bioengineering and Biotechnology, 2015, 3, 153.	4.1	14
115	Use of Nanostructure-Initiator Mass Spectrometry to Deduce Selectivity of Reaction in Glycoside Hydrolases. Frontiers in Bioengineering and Biotechnology, 2015, 3, 165.	4.1	6
116	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. MBio, 2015, 6, e00326-15.	4.1	173
117	The Berkeley Center for Structural Biology at the Advanced Light Source. Synchrotron Radiation News, 2015, 28, 22-27.	0.8	2
118	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. Nature Structural and Molecular Biology, 2015, 22, 433-434.	8.2	40
119	Multifunctional cellulase catalysis targeted by fusion to different carbohydrate-binding modules. Biotechnology for Biofuels, 2015, 8, 220.	6.2	49
120	Programming new geometry restraints: parallelity of atomic groups. Journal of Applied Crystallography, 2015, 48, 1130-1141.	4.5	13
121	Principal component analysis of proteomics (PCAP) as a tool to direct metabolic engineering. Metabolic Engineering, 2015, 28, 123-133.	7.0	140
122	Metabolic engineering for the high-yield production of isoprenoid-based C5 alcohols in E. coli. Scientific Reports, 2015, 5, 11128.	3.3	125
123	Identification and Characterization of a Golgi-Localized UDP-Xylose Transporter Family from Arabidopsis. Plant Cell, 2015, 27, 1218-1227.	6.6	61
124	FEM: feature-enhanced map. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 646-666.	2.5	157
125	A Versatile Microfluidic Device for Automating Synthetic Biology. ACS Synthetic Biology, 2015, 4, 1151-1164.	3.8	81
126	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	3.3	159

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127	Indexing amyloid peptide diffraction from serial femtosecond crystallography: new algorithms for sparse patterns. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 357-366.	2.5	18
128	Using support vector machines to improve elemental ion identification in macromolecular crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1147-1158.	2.5	4
129	Standard Flow Liquid Chromatography for Shotgun Proteomics in Bioenergy Research. Frontiers in Bioengineering and Biotechnology, 2015, 3, 44.	4.1	44
130	EMRinger: side chainâ€"directed model and map validation for 3D cryo-electron microscopy. Nature Methods, 2015, 12, 943-946.	19.0	799
131	Macromolecular X-ray structure determination using weak, single-wavelength anomalous data. Nature Methods, 2015, 12, 127-130.	19.0	31
132	A droplet-to-digital (D2D) microfluidic device for single cell assays. Lab on A Chip, 2015, 15, 225-236.	6.0	70
133	From deep TLS validation to ensembles of atomic models built from elemental motions. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1668-1683.	2.5	14
134	Macromolecular crystallographic estructure refinement. Arbor, 2015, 191, a219.	0.3	3
135	Cellulosic Biomass Pretreatment and Sugar Yields as a Function of Biomass Particle Size. PLoS ONE, 2014, 9, e100836.	2.5	19
136	Development of a Native Escherichia coli Induction System for Ionic Liquid Tolerance. PLoS ONE, 2014, 9, e101115.	2.5	31
137	Understanding the Role of Histidine in the GHSxG Acyltransferase Active Site Motif: Evidence for Histidine Stabilization of the Malonyl-Enzyme Intermediate. PLoS ONE, 2014, 9, e109421.	2.5	10
138	Pressure stabilizer for reproducible picoinjection in droplet microfluidic systems. Lab on A Chip, 2014, 14, 4533-4539.	6.0	34
139	A Peptide-Based Method for 13C Metabolic Flux Analysis in Microbial Communities. PLoS Computational Biology, 2014, 10, e1003827.	3.2	56
140	An atomic model of brome mosaic virus using direct electron detection and real-space optimization. Nature Communications, 2014, 5, 4808.	12.8	105
141	Structural and Biochemical Studies of Actin in Complex with Synthetic Macrolide Tail Analogues. ChemMedChem, 2014, 9, 2286-2293.	3.2	20
142	Conformationâ€dependent backbone geometry restraints set a new standard for protein crystallographic refinement. FEBS Journal, 2014, 281, 4061-4071.	4.7	36
143	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.	7.1	55
144	Error Rate Comparison during Polymerase Chain Reaction by DNA Polymerase. Molecular Biology International, 2014, 2014, 1-8.	1.7	160

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145	Improved crystal orientation and physical properties from single-shot XFEL stills. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3299-3309.	2.5	38
146	Metrics for comparison of crystallographic maps. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2593-2606.	2.5	29
147	Structure of the OsSERK2 leucine-rich repeat extracellular domain. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3080-3086.	2.5	16
148	Accurate macromolecular structures using minimal measurements from X-ray free-electron lasers. Nature Methods, 2014, 11, 545-548.	19.0	140
149	Correlation analysis of targeted proteins and metabolites to assess and engineer microbial isopentenol production. Biotechnology and Bioengineering, 2014, 111, 1648-1658.	3.3	89
150	Rapid Kinetic Characterization of Glycosyl Hydrolases Based on Oxime Derivatization and Nanostructure-Initiator Mass Spectrometry (NIMS). ACS Chemical Biology, 2014, 9, 1470-1479.	3.4	36
151	CRYO-EM Atomic Model of Brome Mosaic Virus Derived from Direct Electron Detection Images and a Real-Space Model Optimization Protocol. Biophysical Journal, 2014, 106, 600a.	0.5	2
152	Analysis of plant nucleotide sugars by hydrophilic interaction liquid chromatography and tandem mass spectrometry. Analytical Biochemistry, 2014, 448, 14-22.	2.4	49
153	Production of anteiso-branched fatty acids in Escherichia coli; next generation biofuels with improved cold-flow properties. Metabolic Engineering, 2014, 26, 111-118.	7.0	55
154	<i>In Vitro</i> Analysis of Carboxyacyl Substrate Tolerance in the Loading and First Extension Modules of Borrelidin Polyketide Synthase. Biochemistry, 2014, 53, 5975-5977.	2.5	21
155	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.	6.6	80
156	Automated identification of elemental ions in macromolecular crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1104-1114.	2.5	40
157	Phylogenomically Guided Identification of Industrially Relevant GH1 Î²-Glucosidases through DNA Synthesis and Nanostructure-Initiator Mass Spectrometry. ACS Chemical Biology, 2014, 9, 2082-2091.	3.4	78
158	Constructing Tailored Isoprenoid Products by Structure-Guided Modification of Geranylgeranyl Reductase. Structure, 2014, 22, 1028-1036.	3.3	28
159	A targeted proteomics toolkit for high-throughput absolute quantification of Escherichia coli proteins. Metabolic Engineering, 2014, 26, 48-56.	7.0	45
160	Taking snapshots of photosynthetic water oxidation using femtosecond X-ray diffraction and spectroscopy. Nature Communications, 2014, 5, 4371.	12.8	206
161	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.	3.1	42
162	Combining Crystallographic and Structure-Modeling Approaches in Macromolecular Crystallography. Biophysical Journal, 2014, 106, 34a.	0.5	0

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163	The plant glycosyltransferase clone collection for functional genomics. Plant Journal, 2014, 79, 517-529.	5.7	67
164	Diffuse X-Ray Scattering for Ensemble Modeling of Crystalline Proteins. Biophysical Journal, 2014, 106, 384a.	0.5	0
165	Automating crystallographic structure solution and refinement of protein–ligand complexes. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 144-154.	2.5	43
166	Ligand placement based on prior structures: the guided ligand-replacement method. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 134-143.	2.5	11
167	Flexible torsion-angle noncrystallographic symmetry restraints for improved macromolecular structure refinement. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1346-1356.	2.5	19
168	Addition of a carbohydrate-binding module enhances cellulase penetration into cellulose substrates. Biotechnology for Biofuels, 2013, 6, 93.	6.2	63
169	Application of targeted proteomics and biological parts assembly in E. coli to optimize the biosynthesis of an anti-malarial drug precursor, amorpha-4,11-diene. Chemical Engineering Science, 2013, 103, 21-28.	3.8	14
170	Understanding the impact of ionic liquid pretreatment on cellulose and lignin via thermochemical analysis. Biomass and Bioenergy, 2013, 54, 276-283.	5.7	55
171	Metabolic engineering of Escherichia coli for limonene and perillyl alcohol production. Metabolic Engineering, 2013, 19, 33-41.	7.0	343
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