

# Paul D. Adams

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

316 papers	76,269 citations	80 h-index	275 g-index
361 ext. papers	89,825 ext. citations	7.8 avg, IF	7.56 L-index

#	Paper	IF	Citations
316	Integration of software tools for integrative modeling of biomolecular systems.. <i>Journal of Structural Biology</i> , <b>2022</b> , 107841	3.4	0
315	Modular automated bottom-up proteomic sample preparation for high-throughput applications.. <i>PLoS ONE</i> , <b>2022</b> , 17, e0264467	3.7	
314	A Synthetic Gene Library Yields a Previously Unknown Glycoside Phosphorylase That Degrades and Assembles Poly-β,3-GlcNAc, Completing the Suite of β-Linked GlcNAc Polysaccharides.. <i>ACS Central Science</i> , <b>2022</b> , 8, 430-440	16.8	0
313	Structural dynamics in the water and proton channels of photosystem II during the S to S transition. <i>Nature Communications</i> , <b>2021</b> , 12, 6531	17.4	6
312	Potent and Selective Covalent Inhibitors of the Papain-like Protease from SARS-CoV-2 <b>2021</b> ,		4
311	Protein identification from electron cryomicroscopy maps by automated model building and side-chain matching. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2021</b> , 77, 457-462	5.5	2
310	Mechanism Across Scales: A Holistic Modeling Framework Integrating Laboratory and Field Studies for Microbial Ecology. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 642422	5.7	4
309	Efficient production of oxidized terpenoids via engineering fusion proteins of terpene synthase and cytochrome P450. <i>Metabolic Engineering</i> , <b>2021</b> , 64, 41-51	9.7	11
308	Engineering <i>Saccharomyces cerevisiae</i> for isoprenol production. <i>Metabolic Engineering</i> , <b>2021</b> , 64, 154-166.	7	7
307	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> , <b>2021</b> , 14, 108	7.8	2
306	A multiplexed nanostructure-initiator mass spectrometry (NIMS) assay for simultaneously detecting glycosyl hydrolase and lignin modifying enzyme activities. <i>Scientific Reports</i> , <b>2021</b> , 11, 11803	4.9	1
305	Reply to Wang et al.: Clear evidence of binding of O <sub>x</sub> 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> , <b>2021</b> , 118,	11.5	3
304	O-/N-/S-Specificity in Glycosyltransferase Catalysis: From Mechanistic Understanding to Engineering. <i>ACS Catalysis</i> , <b>2021</b> , 11, 1810-1815	13.1	10
303	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , <b>2021</b> , 18, 156-164	21.6	22
302	Accurate prediction of protein structures and interactions using a three-track neural network. <i>Science</i> , <b>2021</b> , 373, 871-876	33.3	522
301	Macromolecular refinement of X-ray and cryoelectron microscopy structures with Phenix/OPLS3e for improved structure and ligand quality. <i>Structure</i> , <b>2021</b> , 29, 913-921.e4	5.2	12
300	CERES: a cryo-EM re-refinement system for continuous improvement of deposited models. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2021</b> , 77, 48-61	5.5	3

299	A Global Ramachandran Score Identifies Protein Structures with Unlikely Stereochemistry. <i>Structure</i> , <b>2020</b> , 28, 1249-1258.e2	5.2	23
298	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> , <b>2020</b> , 634, 177-199	1.7	2
297	An iron (II) dependent oxygenase performs the last missing step of plant lysine catabolism. <i>Nature Communications</i> , <b>2020</b> , 11, 2931	17.4	2
296	Response of <i>Pseudomonas putida</i> to Complex, Aromatic-Rich Fractions from Biomass. <i>ChemSusChem</i> , <b>2020</b> , 13, 4455-4467	8.3	9
295	What are the current limits on determination of protonation state using neutron macromolecular crystallography?. <i>Methods in Enzymology</i> , <b>2020</b> , 634, 225-255	1.7	
294	Structure and Function of BorB, the Type II Thioesterase from the Borrelidin Biosynthetic Gene Cluster. <i>Biochemistry</i> , <b>2020</b> , 59, 1630-1639	3.2	4
293	Improved chemistry restraints for crystallographic refinement by integrating the Amber force field into Phenix. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2020</b> , 76, 51-62	5.5	16
292	Density modification of cryo-EM maps. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2020</b> , 76, 912-925	5.5	11
291	Arginine off-kilter: guanidinium is not as planar as restraints denote. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2020</b> , 76, 1159-1166	5.5	2
290	Untangling the sequence of events during the S <sub>1</sub> -S <sub>2</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> , <b>2020</b> , 117, 12624-12635	11.5	65
289	Cryo-EM map interpretation and protein model-building using iterative map segmentation. <i>Protein Science</i> , <b>2020</b> , 29, 87-99	6.3	18
288	Structural Mechanism of Regioselectivity in an Unusual Bacterial Acyl-CoA Dehydrogenase. <i>Journal of the American Chemical Society</i> , <b>2020</b> , 142, 835-846	16.4	3
287	Characterization of a Metal-Resistant Strain With a High Molybdate Affinity ModA From Contaminated Sediments at the Oak Ridge Reservation. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 587127	5.7	4
286	Novel bacterial clade reveals origin of form I Rubisco. <i>Nature Plants</i> , <b>2020</b> , 6, 1158-1166	11.5	13
285	Improvement of cryo-EM maps by density modification. <i>Nature Methods</i> , <b>2020</b> , 17, 923-927	21.6	123
284	Automated "Cells-To-Peptides" Sample Preparation Workflow for High-Throughput, Quantitative Proteomic Assays of Microbes. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 3752-3761	5.6	17
283	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> , <b>2019</b> , 56, 85-96	9.7	25
282	Structural insights into dehydratase substrate selection for the borrelidin and fluvirucin polyketide synthases. <i>Journal of Industrial Microbiology and Biotechnology</i> , <b>2019</b> , 46, 1225-1235	4.2	3

281	Massively Parallel Fitness Profiling Reveals Multiple Novel Enzymes in Lysine Metabolism. <i>MBio</i> , <b>2019</b> , 10,	7.8	28
280	Methyl ketone production by <i>Pseudomonas putida</i> is enhanced by plant-derived amino acids. <i>Biotechnology and Bioengineering</i> , <b>2019</b> , 116, 1909-1922	4.9	15
279	Cryo_fit: Democratization of flexible fitting for cryo-EM. <i>Journal of Structural Biology</i> , <b>2019</b> , 208, 1-6	3.4	15
278	Iron-sulfur clusters have no right angles. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2019</b> , 75, 16-20	5.5	9
277	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2019</b> , 75, 861-877	5.5	1527
276	A rapid methods development workflow for high-throughput quantitative proteomic applications. <i>PLoS ONE</i> , <b>2019</b> , 14, e0211582	3.7	13
275	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> , <b>2019</b> , 75, 451-454	5.5	32
274	Iron- and aluminium-induced depletion of molybdenum in acidic environments impedes the nitrogen cycle. <i>Environmental Microbiology</i> , <b>2019</b> , 21, 152-163	5.2	10
273	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. <i>MBio</i> , <b>2018</b> , 9,	7.8	37
272	Integrated analysis of isopentenyl pyrophosphate (IPP) toxicity in isoprenoid-producing <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , <b>2018</b> , 47, 60-72	9.7	62
271	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> , <b>2018</b> , 115, 1000-1013	4.9	25
270	Employing a biochemical protecting group for a sustainable indigo dyeing strategy. <i>Nature Chemical Biology</i> , <b>2018</b> , 14, 256-261	11.7	85
269	: a software library for aspherical atom model X-ray scattering factor calculations with CPUs and GPUs. <i>Journal of Applied Crystallography</i> , <b>2018</b> , 51, 193-199	3.8	12
268	Discovery of enzymes for toluene synthesis from anoxic microbial communities. <i>Nature Chemical Biology</i> , <b>2018</b> , 14, 451-457	11.7	28
267	Interactive comparison and remediation of collections of macromolecular structures. <i>Protein Science</i> , <b>2018</b> , 27, 182-194	6.3	10
266	MolProbity: More and better reference data for improved all-atom structure validation. <i>Protein Science</i> , <b>2018</b> , 27, 293-315	6.3	1169
265	Map segmentation, automated model-building and their application to the Cryo-EM Model Challenge. <i>Journal of Structural Biology</i> , <b>2018</b> , 204, 338-343	3.4	5
264	Evaluation system and web infrastructure for the second cryo-EM model challenge. <i>Journal of Structural Biology</i> , <b>2018</b> , 204, 96-108	3.4	9

263	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> , <b>2018</b> , 74, 621-631	5.5	4
262	Evaluation of models determined by neutron diffraction and proposed improvements to their validation and deposition. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 800-813	5.5	10
261	Automated map sharpening by maximization of detail and connectivity. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 545-559	5.5	132
260	Real-space refinement in PHENIX for cryo-EM and crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 531-544	5.5	917
259	New tools for the analysis and validation of cryo-EM maps and atomic models. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 814-840	5.5	291
258	A bacterial pioneer produces cellulase complexes that persist through community succession. <i>Nature Microbiology</i> , <b>2018</b> , 3, 99-107	26.6	19
257	Structures of the intermediates of Kokoh photosynthetic water oxidation clock. <i>Nature</i> , <b>2018</b> , 563, 421-425	55.4	261
256	Distribution of evaluation scores for the models submitted to the second cryo-EM model challenge. <i>Data in Brief</i> , <b>2018</b> , 20, 1629-1638	1.2	4
255	Rapid characterization of the activities of lignin-modifying enzymes based on nanostructure-initiator mass spectrometry (NIMS). <i>Biotechnology for Biofuels</i> , <b>2018</b> , 11, 266	7.8	6
254	Renewable production of high density jet fuel precursor sesquiterpenes from. <i>Biotechnology for Biofuels</i> , <b>2018</b> , 11, 285	7.8	24
253	Engineering glycoside hydrolase stability by the introduction of zinc binding. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 702-710	5.5	1
252	A fully automatic method yielding initial models from high-resolution cryo-electron microscopy maps. <i>Nature Methods</i> , <b>2018</b> , 15, 905-908	21.6	82
251	Jungle Express is a versatile repressor system for tight transcriptional control. <i>Nature Communications</i> , <b>2018</b> , 9, 3617	17.4	13
250	Automated flow-based/digital microfluidic platform integrated with onsite electroporation process for multiplex genetic engineering applications <b>2018</b> ,		3
249	Accurate model annotation of a near-atomic resolution cryo-EM map. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 3103-3108	11.5	92
248	Structure of the human TRiC/CCT Subunit 5 associated with hereditary sensory neuropathy. <i>Scientific Reports</i> , <b>2017</b> , 7, 3673	4.9	20
247	Structure of aryl -demethylase offers molecular insight into a catalytic tyrosine-dependent mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E3205-E3214	11.5	21
246	Production of jet fuel precursor monoterpenoids from engineered Escherichia coli. <i>Biotechnology and Bioengineering</i> , <b>2017</b> , 114, 1703-1712	4.9	56

245	On-chip integration of droplet microfluidics and nanostructure-initiator mass spectrometry for enzyme screening. <i>Lab on A Chip</i> , <b>2017</b> , 17, 323-331	7.2	33
244	Plant cell wall glycosyltransferases: High-throughput recombinant expression screening and general requirements for these challenging enzymes. <i>PLoS ONE</i> , <b>2017</b> , 12, e0177591	3.7	15
243	Expression of naturally ionic liquid-tolerant thermophilic cellulases in <i>Aspergillus niger</i> . <i>PLoS ONE</i> , <b>2017</b> , 12, e0189604	3.7	8
242	X-ray diffraction analysis and in vitro characterization of the UAM2 protein from <i>Oryza sativa</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2017</b> , 73, 241-245	1.1	1
241	The Experiment Data Depot: A Web-Based Software Tool for Biological Experimental Data Storage, Sharing, and Visualization. <i>ACS Synthetic Biology</i> , <b>2017</b> , 6, 2248-2259	5.7	34
240	The cryo-electron microscopy structure of human transcription factor IIH. <i>Nature</i> , <b>2017</b> , 549, 414-417	50.4	60
239	Comprehensive in Vitro Analysis of Acyltransferase Domain Exchanges in Modular Polyketide Synthases and Its Application for Short-Chain Ketone Production. <i>ACS Synthetic Biology</i> , <b>2017</b> , 6, 139-147	5.7	71
238	Polder maps: improving OMIT maps by excluding bulk solvent. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2017</b> , 73, 148-157	5.5	335
237	Reply to Kiser: Dioxygen binding in NOV1 crystal structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E6029-E6030	11.5	3
236	Berkeley Screen: a set of 96 solutions for general macromolecular crystallization. <i>Journal of Applied Crystallography</i> , <b>2017</b> , 50, 1352-1358	3.8	6
235	An editor for the generation and customization of geometry restraints. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2017</b> , 73, 123-130	5.5	22
234	Comparative Community Proteomics Demonstrates the Unexpected Importance of Actinobacterial Glycoside Hydrolase Family 12 Protein for Crystalline Cellulose Hydrolysis. <i>MBio</i> , <b>2016</b> , 7,	7.8	12
233	Structure of photosystem II and substrate binding at room temperature. <i>Nature</i> , <b>2016</b> , 540, 453-457	50.4	260
232	Can I solve my structure by SAD phasing? Anomalous signal in SAD phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2016</b> , 72, 346-58	5.5	26
231	A second-generation expression system for tyrosine-sulfated proteins and its application in crop protection. <i>Integrative Biology (United Kingdom)</i> , <b>2016</b> , 8, 542-5	3.7	12
230	A Droplet Microfluidic Platform for Automating Genetic Engineering. <i>ACS Synthetic Biology</i> , <b>2016</b> , 5, 426-33	5.7	46
229	Exploiting the Substrate Promiscuity of Hydroxycinnamoyl-CoA:Shikimate Hydroxycinnamoyl Transferase to Reduce Lignin. <i>Plant and Cell Physiology</i> , <b>2016</b> , 57, 568-79	4.9	54
228	Structural Basis of Stereospecificity in the Bacterial Enzymatic Cleavage of $\beta$ -Aryl Ether Bonds in Lignin. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 5234-46	5.4	27

227	A new default restraint library for the protein backbone in Phenix: a conformation-dependent geometry goes mainstream. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2016</b> , 72, 176-9	5.5	27
226	Improved ligand geometries in crystallographic refinement using AFITT in PHENIX. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2016</b> , 72, 1062-72	5.5	22
225	Structure and mechanism of NOV1, a resveratrol-cleaving dioxygenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 14324-14329	11.5	40
224	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> , <b>2016</b> , 72, 359-74	5.5	23
223	No observable conformational changes in PSII. <i>Nature</i> , <b>2016</b> , 533, E1-2	50.4	31
222	Non-invasive imaging of cellulose microfibril orientation within plant cell walls by polarized Raman microspectroscopy. <i>Biotechnology and Bioengineering</i> , <b>2016</b> , 113, 82-90	4.9	17
221	Structural and Biochemical Characterization of the Early and Late Enzymes in the Lignin Aryl Ether Cleavage Pathway from <i>Sphingobium</i> sp. SYK-6. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 10228-38	5.4	36
220	Characterizing Strain Variation in Engineered <i>E. coli</i> Using a Multi-Omics-Based Workflow. <i>Cell Systems</i> , <b>2016</b> , 2, 335-46	10.6	59
219	Metabolic engineering for the high-yield production of isoprenoid-based C <sub>15</sub> alcohols in <i>E. coli</i> . <i>Scientific Reports</i> , <b>2015</b> , 5, 11128	4.9	109
218	Identification and Characterization of a Golgi-Localized UDP-Xylose Transporter Family from <i>Arabidopsis</i> . <i>Plant Cell</i> , <b>2015</b> , 27, 1218-27	11.6	46
217	FEM: feature-enhanced map. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 646-66		113
216	A Versatile Microfluidic Device for Automating Synthetic Biology. <i>ACS Synthetic Biology</i> , <b>2015</b> , 4, 1151-64	5.7	57
215	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , <b>2015</b> , 23, 1156-67	5.2	131
214	Indexing amyloid peptide diffraction from serial femtosecond crystallography: new algorithms for sparse patterns. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 357-66		12
213	Using support vector machines to improve elemental ion identification in macromolecular crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 1147-58		4
212	Standard flow liquid chromatography for shotgun proteomics in bioenergy research. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2015</b> , 3, 44	5.8	33
211	EMRinger: side chain-directed model and map validation for 3D cryo-electron microscopy. <i>Nature Methods</i> , <b>2015</b> , 12, 943-6	21.6	523
210	Macromolecular X-ray structure determination using weak, single-wavelength anomalous data. <i>Nature Methods</i> , <b>2015</b> , 12, 127-30	21.6	27



209	A droplet-to-digital (D2D) microfluidic device for single cell assays. <i>Lab on A Chip</i> , <b>2015</b> , 15, 225-36	7.2	53
208	Predicting X-ray diffuse scattering from translation-libration-screw structural ensembles. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 1657-67		9
207	Analytics for Metabolic Engineering. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2015</b> , 3, 135	5.8	59
206	Development of a High Throughput Platform for Screening Glycoside Hydrolases Based on Oxime-NIMS. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2015</b> , 3, 153	5.8	14
205	Use of Nanostructure-Initiator Mass Spectrometry to Deduce Selectivity of Reaction in Glycoside Hydrolases. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2015</b> , 3, 165	5.8	4
204	Natural bacterial communities serve as quantitative geochemical biosensors. <i>MBio</i> , <b>2015</b> , 6, e00326-15	7.8	113
203	The Berkeley Center for Structural Biology at the Advanced Light Source. <i>Synchrotron Radiation News</i> , <b>2015</b> , 28, 22-27	0.6	2
202	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. <i>Nature Structural and Molecular Biology</i> , <b>2015</b> , 22, 433-4	17.6	26
201	Multifunctional cellulase catalysis targeted by fusion to different carbohydrate-binding modules. <i>Biotechnology for Biofuels</i> , <b>2015</b> , 8, 220	7.8	38
200	Programming new geometry restraints: parallelity of atomic groups. <i>Journal of Applied Crystallography</i> , <b>2015</b> , 48, 1130-1141	3.8	10
199	Principal component analysis of proteomics (PCAP) as a tool to direct metabolic engineering. <i>Metabolic Engineering</i> , <b>2015</b> , 28, 123-133	9.7	118
198	From deep TLS validation to ensembles of atomic models built from elemental motions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 1668-83		11
197	Macromolecular crystallographic structure refinement. <i>Arbor</i> , <b>2015</b> , 191, a219	0.2	3
196	Accurate macromolecular structures using minimal measurements from X-ray free-electron lasers. <i>Nature Methods</i> , <b>2014</b> , 11, 545-8	21.6	118
195	Correlation analysis of targeted proteins and metabolites to assess and engineer microbial isopentenol production. <i>Biotechnology and Bioengineering</i> , <b>2014</b> , 111, 1648-58	4.9	75
194	Rapid kinetic characterization of glycosyl hydrolases based on oxime derivatization and nanostructure-initiator mass spectrometry (NIMS). <i>ACS Chemical Biology</i> , <b>2014</b> , 9, 1470-9	4.9	30
193	Analysis of plant nucleotide sugars by hydrophilic interaction liquid chromatography and tandem mass spectrometry. <i>Analytical Biochemistry</i> , <b>2014</b> , 448, 14-22	3.1	40
192	Production of anteiso-branched fatty acids in Escherichia coli; next generation biofuels with improved cold-flow properties. <i>Metabolic Engineering</i> , <b>2014</b> , 26, 111-118	9.7	45



191	In vitro analysis of carboxyacyl substrate tolerance in the loading and first extension modules of borrelidin polyketide synthase. <i>Biochemistry</i> , <b>2014</b> , 53, 5975-7	3.2	18
190	Identification of a sphingolipid $\beta$ -glucuronosyltransferase that is essential for pollen function in Arabidopsis. <i>Plant Cell</i> , <b>2014</b> , 26, 3314-25	11.6	59
189	Automated identification of elemental ions in macromolecular crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 1104-14		27
188	Phylogenomically guided identification of industrially relevant GH1 $\beta$ -glucosidases through DNA synthesis and nanostructure-initiator mass spectrometry. <i>ACS Chemical Biology</i> , <b>2014</b> , 9, 2082-91	4.9	45
187	Constructing tailored isoprenoid products by structure-guided modification of geranylgeranyl reductase. <i>Structure</i> , <b>2014</b> , 22, 1028-36	5.2	23
186	A targeted proteomics toolkit for high-throughput absolute quantification of Escherichia coli proteins. <i>Metabolic Engineering</i> , <b>2014</b> , 26, 48-56	9.7	41
185	Taking snapshots of photosynthetic water oxidation using femtosecond X-ray diffraction and spectroscopy. <i>Nature Communications</i> , <b>2014</b> , 5, 4371	17.4	184
184	Biochemical and structural studies of NADH-dependent FabG used to increase the bacterial production of fatty acids under anaerobic conditions. <i>Applied and Environmental Microbiology</i> , <b>2014</b> , 80, 497-505	4.8	34
183	The plant glycosyltransferase clone collection for functional genomics. <i>Plant Journal</i> , <b>2014</b> , 79, 517-29	6.9	44
182	Cellulosic biomass pretreatment and sugar yields as a function of biomass particle size. <i>PLoS ONE</i> , <b>2014</b> , 9, e100836	3.7	17
181	Development of a native Escherichia coli induction system for ionic liquid tolerance. <i>PLoS ONE</i> , <b>2014</b> , 9, e101115	3.7	30
180	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> , <b>2014</b> , 9, e109421	3.7	7
179	Pressure stabilizer for reproducible picoinjection in droplet microfluidic systems. <i>Lab on A Chip</i> , <b>2014</b> , 14, 4533-9	7.2	27
178	A peptide-based method for $^{13}\text{C}$ Metabolic Flux Analysis in microbial communities. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003827	5	43
177	An atomic model of brome mosaic virus using direct electron detection and real-space optimization. <i>Nature Communications</i> , <b>2014</b> , 5, 4808	17.4	95
176	Structural and biochemical studies of actin in complex with synthetic macrolide tail analogues. <i>ChemMedChem</i> , <b>2014</b> , 9, 2286-93	3.7	15
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