

List of Publications by Citations

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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
3 <sup>16</sup>	PHENIX: a comprehensive Python-based system for macromolecular structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2010</b> , 66, 213-21		16067
3 <sup>15</sup>	Phaser crystallographic software. <i>Journal of Applied Crystallography</i> , <b>2007</b> , 40, 658-674	3.8	14212
3 <sup>14</sup>	Crystallography & NMR system: A new software suite for macromolecular structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1998</b> , 54, 905-21		14106
3 <sup>13</sup>	PHENIX: building new software for automated crystallographic structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2002</b> , 58, 1948-54		3477
3 <sup>12</sup>	Towards automated crystallographic structure refinement with phenix.refine. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 352-67		3236
3 <sup>11</sup>	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
3 <sup>10</sup>	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
3 <sup>09</sup>	Iterative model building, structure refinement and density modification with the PHENIX AutoBuild wizard. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2008</b> , 64, 61-9		1042
3 <sup>08</sup>	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
3 <sup>07</sup>	Structural basis for double-stranded RNA processing by Dicer. <i>Science</i> , <b>2006</b> , 311, 195-8	33.3	729
3 <sup>06</sup>	electronic Ligand Builder and Optimization Workbench (eLBOW): a tool for ligand coordinate and restraint generation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 1074-80		712
3 <sup>05</sup>	Decision-making in structure solution using Bayesian estimates of map quality: the PHENIX AutoSol wizard. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 582-601		657
3 <sup>04</sup>	The Phenix software for automated determination of macromolecular structures. <i>Methods</i> , <b>2011</b> , 55, 94-106	4.6	580
3 <sup>03</sup>	Cross-validated maximum likelihood enhances crystallographic simulated annealing refinement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1997</b> , 94, 5018-23	11.5	561
3 <sup>02</sup>	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
3 <sup>01</sup>	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
3 <sup>00</sup>	Engineering dynamic pathway regulation using stress-response promoters. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 1039-46	44.5	338

299	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
298	A new generation of crystallographic validation tools for the protein data bank. <i>Structure</i> , <b>2011</b> , 19, 1395-1412	5.4	335
297	Simultaneous femtosecond X-ray spectroscopy and diffraction of photosystem II at room temperature. <i>Science</i> , <b>2013</b> , 340, 491-5	33.3	334
296	SPARX, a new environment for Cryo-EM image processing. <i>Journal of Structural Biology</i> , <b>2007</b> , 157, 47-55	3.4	327
295	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
294	Metabolic engineering of <i>Escherichia coli</i> for limonene and perillyl alcohol production. <i>Metabolic Engineering</i> , <b>2013</b> , 19, 33-41	9.7	281
293	A dimerization motif for transmembrane alpha-helices. <i>Nature Structural Biology</i> , <b>1994</b> , 1, 157-63		278
292	Recent developments in the PHENIX software for automated crystallographic structure determination. <i>Journal of Synchrotron Radiation</i> , <b>2004</b> , 11, 53-5	2.4	273
291	Structures of the intermediates of KokK photosynthetic water oxidation clock. <i>Nature</i> , <b>2018</b> , 563, 421-425	5.4	261
290	Structure of photosystem II and substrate binding at room temperature. <i>Nature</i> , <b>2016</b> , 540, 453-457	50.4	260
289	Conformational variability in the refined structure of the chaperonin GroEL at 2.8 Å resolution. <i>Nature Structural and Molecular Biology</i> , <b>1995</b> , 2, 1083-94	17.6	207
288	New tools for structure refinement in PHENIX. <i>Acta Crystallographica Section A: Foundations and Advances</i> , <b>2010</b> , 66, s15-s15		199
287	Joint X-ray and neutron refinement with phenix.refine. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2010</b> , 66, 1153-63		193
286	Substructure search procedures for macromolecular structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2003</b> , 59, 1966-73		187
285	Crystal structure of a bacterial ribonuclease P RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 13392-7	11.5	186
284	Computational searching and mutagenesis suggest a structure for the pentameric transmembrane domain of phospholamban. <i>Nature Structural and Molecular Biology</i> , <b>1995</b> , 2, 154-62	17.6	186
283	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
282	New applications of simulated annealing in X-ray crystallography and solution NMR. <i>Structure</i> , <b>1997</b> , 5, 325-36	5.2	183

281	Modelling dynamics in protein crystal structures by ensemble refinement. <i>ELife</i> , <b>2012</b> , 1, e00311	8.9	176
280	The Computational Crystallography Toolbox: crystallographic algorithms in a reusable software framework. <i>Journal of Applied Crystallography</i> , <b>2002</b> , 35, 126-136	3.8	167
279	Use of knowledge-based restraints in phenix.refine to improve macromolecular refinement at low resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 381-90		156
278	Structural organization of the pentameric transmembrane alpha-helices of phospholamban, a cardiac ion channel.. <i>EMBO Journal</i> , <b>1994</b> , 13, 4757-4764	13	154
277	Targeted proteomics for metabolic pathway optimization: application to terpene production. <i>Metabolic Engineering</i> , <b>2011</b> , 13, 194-203	9.7	151
276	Nanoflow electrospinning serial femtosecond crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 1584-7		146
275	Phaser.MRage: automated molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 2276-86		144
274	Improved prediction for the structure of the dimeric transmembrane domain of glycophorin A obtained through global searching. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1996</b> , 26, 257-61	4.2	141
273	A robust bulk-solvent correction and anisotropic scaling procedure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2005</b> , 61, 850-5		138
272	Improved low-resolution crystallographic refinement with Phenix and Rosetta. <i>Nature Methods</i> , <b>2013</b> , 10, 1102-4	21.6	137
271	Experimentally based orientational refinement of membrane protein models: A structure for the Influenza A M2 H+ channel. <i>Journal of Molecular Biology</i> , <b>1999</b> , 286, 951-62	6.5	136
270	Room temperature femtosecond X-ray diffraction of photosystem II microcrystals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 9721-6	11.5	135
269	Enhancing fatty acid production by the expression of the regulatory transcription factor FadR. <i>Metabolic Engineering</i> , <b>2012</b> , 14, 653-60	9.7	132
268	Survey of renewable chemicals produced from lignocellulosic biomass during ionic liquid pretreatment. <i>Biotechnology for Biofuels</i> , <b>2013</b> , 6, 14	7.8	132
267	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
266	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , <b>2015</b> , 23, 1156-67	5.2	131
265	Iterative-build OMIT maps: map improvement by iterative model building and refinement without model bias. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2008</b> , 64, 515-24		130
264	Robust indexing for automatic data collection. <i>Journal of Applied Crystallography</i> , <b>2004</b> , 37, 399-409	3.8	129

263	Research priorities. Shining light into black boxes. <i>Science</i> , <b>2012</b> , 336, 159-60	33.3	125
262	Generalized X-ray and neutron crystallographic analysis: more accurate and complete structures for biological macromolecules. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 567-73		123
261	Improvement of cryo-EM maps by density modification. <i>Nature Methods</i> , <b>2020</b> , 17, 923-927	21.6	123
260	Error Rate Comparison during Polymerase Chain Reaction by DNA Polymerase. <i>Molecular Biology International</i> , <b>2014</b> , 2014, 287430		121
259	Impact of ionic liquid pretreated plant biomass on <i>Saccharomyces cerevisiae</i> growth and biofuel production. <i>Green Chemistry</i> , <b>2011</b> , 13, 2743	10	120
258	iotbx.cif: a comprehensive CIF toolbox. <i>Journal of Applied Crystallography</i> , <b>2011</b> , 44, 1259-1263	3.8	120
257	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
256	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
255	FEM: feature-enhanced map. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 646-66		113
254	Natural bacterial communities serve as quantitative geochemical biosensors. <i>MBio</i> , <b>2015</b> , 6, e00326-15	7.8	113
253	Supramolecular self-assembled chaos: polyphenolic lignin as a barrier to cost-effective lignocellulosic biofuels. <i>Molecules</i> , <b>2010</b> , 15, 8641-88	4.8	110
252	Role of the gamma-phosphate of ATP in triggering protein folding by GroEL-GroES: function, structure and energetics. <i>EMBO Journal</i> , <b>2003</b> , 22, 4877-87	13	110
251	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
250	phenix.mr_rosetta: molecular replacement and model rebuilding with Phenix and Rosetta. <i>Journal of Structural and Functional Genomics</i> , <b>2012</b> , 13, 81-90		109
249	Coupling of receptor conformation and ligand orientation determine graded activity. <i>Nature Chemical Biology</i> , <b>2010</b> , 6, 837-43	11.7	102
248	Energy-dispersive X-ray emission spectroscopy using an X-ray free-electron laser in a shot-by-shot mode. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 19103-7	11.5	98
247	Graphical tools for macromolecular crystallography in PHENIX. <i>Journal of Applied Crystallography</i> , <b>2012</b> , 45, 581-586	3.8	95
246	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

245	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
244	phenix.model_vs_data: a high-level tool for the calculation of crystallographic model and data statistics. <i>Journal of Applied Crystallography</i> , <b>2010</b> , 43, 669-676	3.8	91
243	Use of a new label, (13)O, in the determination of a structural model of phospholamban in a lipid bilayer. Spatial restraints resolve the ambiguity arising from interpretations of mutagenesis data. <i>Journal of Molecular Biology</i> , <b>2000</b> , 300, 677-85	6.5	91
242	Exploring the structural dynamics of the E.coli chaperonin GroEL using translation-libration-screw crystallographic refinement of intermediate states. <i>Journal of Molecular Biology</i> , <b>2004</b> , 342, 229-45	6.5	88
241	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
240	Crystallographic model quality at a glance. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 297-300		84
239	High-resolution structure of RNase P protein from <i>Thermotoga maritima</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 7497-502	11.5	83
238	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
237	The protein structure initiative structural genomics knowledgebase. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D365-8	20.1	80
236	Recent developments for the efficient crystallographic refinement of macromolecular structures. <i>Current Opinion in Structural Biology</i> , <b>1998</b> , 8, 606-11	8.1	80
235	Advances, interactions, and future developments in the CNS, Phenix, and Rosetta structural biology software systems. <i>Annual Review of Biophysics</i> , <b>2013</b> , 42, 265-87	21.1	76
234	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
233	Automated ligand fitting by core-fragment fitting and extension into density. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2006</b> , 62, 915-22		75
232	Crystal structures of the <i>Rhodococcus</i> proteasome with and without its pro-peptides: implications for the role of the pro-peptide in proteasome assembly. <i>Journal of Molecular Biology</i> , <b>2004</b> , 335, 233-45	6.5	74
231	Transmembrane signal transduction of the alpha(IIb)beta(3) integrin. <i>Protein Science</i> , <b>2002</b> , 11, 1800-12	6.3	73
230	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
229	X-ray crystallographic and kinetic studies of human sorbitol dehydrogenase. <i>Structure</i> , <b>2003</b> , 11, 1071-85	5.2	71
228	Label-free in situ imaging of lignification in the cell wall of low lignin transgenic <i>Populus trichocarpa</i> . <i>Planta</i> , <b>2009</b> , 230, 589-97	4.7	70

227	Surprises and pitfalls arising from (pseudo)symmetry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2008</b> , 64, 99-107		70
226	Web-Ice: integrated data collection and analysis for macromolecular crystallography. <i>Journal of Applied Crystallography</i> , <b>2008</b> , 41, 176-184	3.8	70
225	Structure of a three-domain sesquiterpene synthase: a prospective target for advanced biofuels production. <i>Structure</i> , <b>2011</b> , 19, 1876-84	5.2	68
224	Untangling the sequence of events during the S-K 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
223	Structural perspectives of phospholamban, a helical transmembrane pentamer. <i>Annual Review of Biophysics and Biomolecular Structure</i> , <b>1997</b> , 26, 157-79		64
222	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
221	Crystal structures of a group II chaperonin reveal the open and closed states associated with the protein folding cycle. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 27958-66	5.4	61
220	Crystal structure of DNA sequence specificity subunit of a type I restriction-modification enzyme and its functional implications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 3248-53	11.5	61
219	The cryo-electron microscopy structure of human transcription factor IIH. <i>Nature</i> , <b>2017</b> , 549, 414-417	50.4	60
218	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. <i>Journal of Structural and Functional Genomics</i> , <b>2011</b> , 12, 45-54		60
217	Structural basis of light chain amyloidogenicity: comparison of the thermodynamic properties, fibrillogenic potential and tertiary structural features of four Vlambda6 proteins. <i>Journal of Molecular Recognition</i> , <b>2004</b> , 17, 323-31	2.6	60
216	Identification of a sphingolipid glucuronosyltransferase that is essential for pollen function in <i>Arabidopsis</i> . <i>Plant Cell</i> , <b>2014</b> , 26, 3314-25	11.6	59
215	Analytics for Metabolic Engineering. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2015</b> , 3, 135	5.8	59
214	<i>Thermoascus aurantiacus</i> is a promising source of enzymes for biomass deconstruction under thermophilic conditions. <i>Biotechnology for Biofuels</i> , <b>2012</b> , 5, 54	7.8	59
213	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
212	Validated near-atomic resolution structure of bacteriophage epsilon15 derived from cryo-EM and modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 12301-6	11.5	58
211	Molecular dynamics applied to X-ray structure refinement. <i>Accounts of Chemical Research</i> , <b>2002</b> , 35, 404-413	14.3	58
210	A Versatile Microfluidic Device for Automating Synthetic Biology. <i>ACS Synthetic Biology</i> , <b>2015</b> , 4, 1151-64	5.7	57



209	Bulk-solvent and overall scaling revisited: faster calculations, improved results. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 625-34		57
208	Production of jet fuel precursor monoterpenoids from engineered <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , <b>2017</b> , 114, 1703-1712	4.9	56
207	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2007</b> , 63, 597-610		56
206	Understanding changes in lignin of <i>Panicum virgatum</i> and <i>Eucalyptus globulus</i> as a function of ionic liquid pretreatment. <i>Bioresource Technology</i> , <b>2012</b> , 126, 156-61	11	55
205	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
204	Three Novel Rice Genes Closely Related to the Arabidopsis IRX9, IRX9L, and IRX14 Genes and Their Roles in Xylan Biosynthesis. <i>Frontiers in Plant Science</i> , <b>2013</b> , 4, 83	6.2	54
203	Biochemical characterization and crystal structure of endoglucanase Cel5A from the hyperthermophilic <i>Thermotoga maritima</i> . <i>Journal of Structural Biology</i> , <b>2010</b> , 172, 372-9	3.4	54
202	Averaged kick maps: less noise, more signal... and probably less bias. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 921-31		54
201	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
200	Addition of a carbohydrate-binding module enhances cellulase penetration into cellulose substrates. <i>Biotechnology for Biofuels</i> , <b>2013</b> , 6, 93	7.8	51
199	Ligand identification using electron-density map correlations. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2007</b> , 63, 101-7		50
198	On macromolecular refinement at subatomic resolution with interatomic scatterers. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2007</b> , 63, 1194-7		49
197	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
196	A Droplet Microfluidic Platform for Automating Genetic Engineering. <i>ACS Synthetic Biology</i> , <b>2016</b> , 5, 426-33	5.7	46
195	Understanding the impact of ionic liquid pretreatment on cellulose and lignin via thermochemical analysis. <i>Biomass and Bioenergy</i> , <b>2013</b> , 54, 276-283	5.3	46
194	Glycoside hydrolases from a targeted compost metagenome, activity-screening and functional characterization. <i>BMC Biotechnology</i> , <b>2012</b> , 12, 38	3.5	46
193	Production of anteiso-branched fatty acids in <i>Escherichia coli</i> ; next generation biofuels with improved cold-flow properties. <i>Metabolic Engineering</i> , <b>2014</b> , 26, 111-118	9.7	45
192	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



191	The plant glycosyltransferase clone collection for functional genomics. <i>Plant Journal</i> , <b>2014</b> , 79, 517-29	6.9	44
190	A peptide-based method for <sup>13</sup> C Metabolic Flux Analysis in microbial communities. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003827	5	43
189	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
188	Manipulation of the carbon storage regulator system for metabolite remodeling and biofuel production in Escherichia coli. <i>Microbial Cell Factories</i> , <b>2012</b> , 11, 79	6.4	41
187	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
186	Addressing the need for alternative transportation fuels: the Joint BioEnergy Institute. <i>ACS Chemical Biology</i> , <b>2008</b> , 3, 17-20	4.9	40
185	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
184	Multifunctional cellulase catalysis targeted by fusion to different carbohydrate-binding modules. <i>Biotechnology for Biofuels</i> , <b>2015</b> , 8, 220	7.8	38
183	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> , <b>2014</b> , 111, 17887-92	11.5	38
182	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. <i>MBio</i> , <b>2018</b> , 9,	7.8	37
181	Automatic multiple-zone rigid-body refinement with a large convergence radius. <i>Journal of Applied Crystallography</i> , <b>2009</b> , 42, 607-615	3.8	37
180	Improving the accuracy of macromolecular structure refinement at 7 Å resolution. <i>Structure</i> , <b>2012</b> , 20, 957-66	5.2	36
179	On the handling of atomic anisotropic displacement parameters. <i>Journal of Applied Crystallography</i> , <b>2002</b> , 35, 477-480	3.8	36
178	Structural and Biochemical Characterization of the Early and Late Enzymes in the Lignin Aryl Ether Cleavage Pathway from Sphingobium sp. SYK-6. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 10228-38	5.4	36
177	Droplet-based microfluidic platform for heterogeneous enzymatic assays. <i>Lab on A Chip</i> , <b>2013</b> , 13, 1817-22	7.2	35
176	From soil to structure, a novel dimeric βglucosidase belonging to glycoside hydrolase family 3 isolated from compost using metagenomic analysis. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 14985-92	5.4	35
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174	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

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