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List of Publications by Citations

197 papers	77,880 citations	67 h-index	233 g-index
233 ext. papers	89,271 ext. citations	8.7 avg, IF	7.49 L-index

#	Paper	IF	Citations
197	PHENIX: a comprehensive Python-based system for macromolecular structure solution. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 213-21		16067
196	Phaser crystallographic software. *Journal of Applied Crystallography*, **2007**, 40, 658-674	3.8	14212
195	Crystallography & NMR system: A new software suite for macromolecular structure determination. *Acta Crystallographica Section D: Biological Crystallography*, **1998**, 54, 905-21		14106
194	Overview of the CCP4 suite and current developments. *Acta Crystallographica Section D: Biological Crystallography*, **2011**, 67, 235-42		8847
193	PHENIX: building new software for automated crystallographic structure determination. *Acta Crystallographica Section D: Biological Crystallography*, **2002**, 58, 1948-54		3477
192	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. *Acta Crystallographica Section D: Structural Biology*, **2019**, 75, 861-877	5.5	1527
191	Likelihood-enhanced fast translation functions. *Acta Crystallographica Section D: Biological Crystallography*, **2005**, 61, 458-64		1503
190	Iterative model building, structure refinement and density modification with the PHENIX AutoBuild wizard. *Acta Crystallographica Section D: Biological Crystallography*, **2008**, 64, 61-9		1042
189	Likelihood-enhanced fast rotation functions. *Acta Crystallographica Section D: Biological Crystallography*, **2004**, 60, 432-8		1017
188	Real-space refinement in PHENIX for cryo-EM and crystallography. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 531-544	5.5	917
187	Structure of a serpin-protease complex shows inhibition by deformation. *Nature*, **2000**, 407, 923-6	50.4	916
186	Shiga-like toxins are neutralized by tailored multivalent carbohydrate ligands. *Nature*, **2000**, 403, 669-72	50.4	772
185	Pushing the boundaries of molecular replacement with maximum likelihood. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 1373-82		665
184	Decision-making in structure solution using Bayesian estimates of map quality: the PHENIX AutoSol wizard. *Acta Crystallographica Section D: Biological Crystallography*, **2009**, 65, 582-601		657
183	The Phenix software for automated determination of macromolecular structures. *Methods*, **2011**, 55, 94-106	4.6	580
182	Cross-validated maximum likelihood enhances crystallographic simulated annealing refinement. *Proceedings of the National Academy of Sciences of the United States of America*, **1997**, 94, 5018-23	11.5	561
181	Accurate prediction of protein structures and interactions using a three-track neural network. *Science*, **2021**, 373, 871-876	33.3	522

180	Automated structure solution with the PHENIX suite. *Methods in Molecular Biology*, **2008**, 426, 419-35	1.4	421
179	Structure of the shiga-like toxin I B-pentamer complexed with an analogue of its receptor Gb3. *Biochemistry*, **1998**, 37, 1777-88	3.2	377
178	A new generation of crystallographic validation tools for the protein data bank. *Structure*, **2011**, 19, 1395-412	5.2	335
177	The crystal structure of pertussis toxin. *Structure*, **1994**, 2, 45-57	5.2	297
176	Crystal structure of the cell-binding B oligomer of verotoxin-1 from E. coli. *Nature*, **1992**, 355, 748-50	50.4	280
175	Accumulating evidence suggests that several AB-toxins subvert the endoplasmic reticulum-associated protein degradation pathway to enter target cells. *Biochemistry*, **1997**, 36, 11051-4	3.2	278
174	Recent developments in the PHENIX software for automated crystallographic structure determination. *Journal of Synchrotron Radiation*, **2004**, 11, 53-5	2.4	273
173	High-resolution structure prediction and the crystallographic phase problem. *Nature*, **2007**, 450, 259-64	50.4	262
172	Crystal and molecular structures of the complex of alpha-chymotrypsin with its inhibitor turkey ovomucoid third domain at 1.8 A resolution. *Journal of Molecular Biology*, **1987**, 195, 397-418	6.5	235
171	Exome sequencing identifies NBEAL2 as the causative gene for gray platelet syndrome. *Nature Genetics*, **2011**, 43, 735-7	36.3	224
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166	A multiple-start Monte Carlo docking method. *Proteins: Structure, Function and Bioinformatics*, **1992**, 13, 206-22	4.2	187
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164	A redox switch in angiotensinogen modulates angiotensin release. *Nature*, **2010**, 468, 108-11	50.4	171
163	Improvement of molecular-replacement models with Sculptor. *Acta Crystallographica Section D: Biological Crystallography*, **2011**, 67, 303-12		167

162	Inactive conformation of the serpin alpha(1)-antichymotrypsin indicates two-stage insertion of the reactive loop: implications for inhibitory function and conformational disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 67-72	11.5	166
161	Incorporation of prior phase information strengthens maximum-likelihood structure refinement. *Acta Crystallographica Section D: Biological Crystallography*, **1998**, 54, 1285-94		158
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159	Not your average density. *Structure*, **1997**, 5, 1557-69	5.2	142
158	Mutations in FRMD7, a newly identified member of the FERM family, cause X-linked idiopathic congenital nystagmus. *Nature Genetics*, **2006**, 38, 1242-4	36.3	137
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155	Iterative-build OMIT maps: map improvement by iterative model building and refinement without model bias. *Acta Crystallographica Section D: Biological Crystallography*, **2008**, 64, 515-24		130
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152	Improvement of cryo-EM maps by density modification. *Nature Methods*, **2020**, 17, 923-927	21.6	123
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142	Structure of a pertussis toxin-sugar complex as a model for receptor binding. *Nature Structural and Molecular Biology*, **1994**, 1, 591-6	17.6	94
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31	Flawed methods in COVID-19: Attacks the 1-Beta Chain of Hemoglobin and Captures the Porphyrin to Inhibit Human Heme Metabolism		4
30	Factors influencing estimates of coordinate error for molecular replacement. *Acta Crystallographica Section D: Structural Biology*, **2020**, 76, 19-27	5.5	4
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