

Ian W Davis

List of Publications by Citations

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Version: 2024-04-23

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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.

14
papers

25,576
citations

12
h-index

14
g-index

14
ext. papers

29,222
ext. citations

6.8
avg, IF

6.01
L-index

#	Paper	IF	Citations
14	PHENIX: a comprehensive Python-based system for macromolecular structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010 , 66, 213-21		16067
13	Structure validation by Calpha geometry: phi,psi and Cbeta deviation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 50, 437-50	4.2	3522
12	MolProbity: all-atom contacts and structure validation for proteins and nucleic acids. <i>Nucleic Acids Research</i> , 2007 , 35, W375-83	20.1	3030
11	ROSETTA3: an object-oriented software suite for the simulation and design of macromolecules. <i>Methods in Enzymology</i> , 2011 , 487, 545-74	1.7	1216
10	MOLPROBITY: structure validation and all-atom contact analysis for nucleic acids and their complexes. <i>Nucleic Acids Research</i> , 2004 , 32, W615-9	20.1	816
9	RosettaLigand docking with full ligand and receptor flexibility. <i>Journal of Molecular Biology</i> , 2009 , 385, 381-92	6.5	309
8	The backrub motion: how protein backbone shrugs when a sidechain dances. <i>Structure</i> , 2006 , 14, 265-74	5.2	197
7	Scientific benchmarks for guiding macromolecular energy function improvement. <i>Methods in Enzymology</i> , 2013 , 523, 109-43	1.7	164
6	KING (Kinemage, Next Generation): a versatile interactive molecular and scientific visualization program. <i>Protein Science</i> , 2009 , 18, 2403-9	6.3	129
5	Blind docking of pharmaceutically relevant compounds using RosettaLigand. <i>Protein Science</i> , 2009 , 18, 1998-2002	6.3	60
4	A test of enhancing model accuracy in high-throughput crystallography. <i>Journal of Structural and Functional Genomics</i> , 2005 , 6, 1-11		43
3	KinImmerse: Macromolecular VR for NMR ensembles. <i>Source Code for Biology and Medicine</i> , 2009 , 4, 3	1.9	17
2	POWRS: position-sensitive motif discovery. <i>PLoS ONE</i> , 2012 , 7, e40373	3.7	6
1	Expression Elements Derived From Plant Sequences Provide Effective Gene Expression Regulation and New Opportunities for Plant Biotechnology Traits. <i>Frontiers in Plant Science</i> , 2021 , 12, 712179	6.2	