Ian W Davis

List of Publications by Year in Descending Order

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