Andrew Leaver-Fay

List of Publications by Year in Descending Order

15 papers	2,889 citations	12 h-index	16 g-index
16 ext. papers	3,829 ext. citations	10.1 avg, IF	4.03 L-index

#	Paper	IF	Citations
15	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. *Nature Communications*, **2021**, 12, 6947	17.4	0
14	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design.. *The Biophysicist*, **2021**, 2, 108-122	1	1
13	Better together: Elements of successful scientific software development in a distributed collaborative community. *PLoS Computational Biology*, **2020**, 16, e1007507	5	15
12	Macromolecular modeling and design in Rosetta: recent methods and frameworks. *Nature Methods*, **2020**, 17, 665-680	21.6	165
11	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. *Journal of Chemical Theory and Computation*, **2017**, 13, 3031-3048	6.4	486
10	Foldit Standalone: a video game-derived protein structure manipulation interface using Rosetta. *Bioinformatics*, **2017**, 33, 2765-2767	7.2	44
9	A cyber-linked undergraduate research experience in computational biomolecular structure prediction and design. *PLoS Computational Biology*, **2017**, 13, e1005837	5	7
8	Computationally Designed Bispecific Antibodies using Negative State Repertoires. *Structure*, **2016**, 24, 641-651	5.2	41
7	SwiftLib: rapid degenerate-codon-library optimization through dynamic programming. *Nucleic Acids Research*, **2015**, 43, e34	20.1	38
6	Combined covalent-electrostatic model of hydrogen bonding improves structure prediction with Rosetta. *Journal of Chemical Theory and Computation*, **2015**, 11, 609-22	6.4	163
5	Generation of bispecific IgG antibodies by structure-based design of an orthogonal Fab interface. *Nature Biotechnology*, **2014**, 32, 191-8	44.5	164
4	Scientific benchmarks for guiding macromolecular energy function improvement. *Methods in Enzymology*, **2013**, 523, 109-43	1.7	164
3	ROSETTA3: an object-oriented software suite for the simulation and design of macromolecules. *Methods in Enzymology*, **2011**, 487, 545-74	1.7	1216
2	RosettaScripts: a scripting language interface to the Rosetta macromolecular modeling suite. *PLoS ONE*, **2011**, 6, e20161	3.7	311
1	A generic program for multistate protein design. *PLoS ONE*, **2011**, 6, e20937	3.7	74