Andrew Leaver-Fay

List of Publications by Year
in descending order

16	4,617	687363 13	940533 16
papers	citations	h-index	g-index

16	16	16	6080
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Rosetta3. Methods in Enzymology, 2011, 487, 545-574.	1.0	1,620
2	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. Journal of Chemical Theory and Computation, 2017, 13, 3031-3048.	5.3	1,032
3	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
4	RosettaScripts: A Scripting Language Interface to the Rosetta Macromolecular Modeling Suite. PLoS ONE, 2011, 6, e20161.	2.5	506
5	Generation of bispecific IgG antibodies by structure-based design of an orthogonal Fab interface. Nature Biotechnology, 2014, 32, 191-198.	17.5	210
6	Combined Covalent-Electrostatic Model of Hydrogen Bonding Improves Structure Prediction with Rosetta. Journal of Chemical Theory and Computation, 2015, 11, 609-622.	5.3	204
7	Scientific Benchmarks for Guiding Macromolecular Energy Function Improvement. Methods in Enzymology, 2013, 523, 109-143.	1.0	195
8	A Generic Program for Multistate Protein Design. PLoS ONE, 2011, 6, e20937.	2.5	88
9	Foldit Standalone: a video game-derived protein structure manipulation interface using Rosetta. Bioinformatics, 2017, 33, 2765-2767.	4.1	77
10	Computationally Designed Bispecific Antibodies using Negative State Repertoires. Structure, 2016, 24, 641-651.	3.3	54
11	SwiftLib: rapid degenerate-codon-library optimization through dynamic programming. Nucleic Acids Research, 2015, 43, e34-e34.	14.5	53
12	Better together: Elements of successful scientific software development in a distributed collaborative community. PLoS Computational Biology, 2020, 16, e1007507.	3.2	27
13	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. Nature Communications, 2021, 12, 6947.	12.8	16
14	A cyber-linked undergraduate research experience in computational biomolecular structure prediction and design. PLoS Computational Biology, 2017, 13, e1005837.	3.2	12
15	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. The Biophysicist, 2021, 2, 108-122.	0.3	8
16	Comparative Analysis of Sulfoniumâ˜Ï€, Ammoniumâ˜Ï€, and Sulfurâ˜Ï€ Interactions and Relevance to SAM-Dependent Methyltransferases. Journal of the American Chemical Society, 2022, 144, 2535-2545.	13.7	2