Brian D Weitzner

List of Publications by Year
in descending order

19	2,403	623734	794594
papers	citations	14 h-index	19 g-index

22	22	22	3800
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. The Biophysicist, 2021, 2, 108-122.	0.3	8
2	Anchor extension: a structure-guided approach to design cyclic peptides targeting enzyme active sites. Nature Communications, 2021, 12, 3384.	12.8	37
3	Integration of the Rosetta suite with the python software stack via reproducible packaging and core programming interfaces for distributed simulation. Protein Science, 2020, 29, 43-51.	7.6	13
4	The influence of proline isomerization on potency and stability of anti-HIV antibody 10E8. Scientific Reports, 2020, 10, 14313.	3.3	12
5	Better together: Elements of successful scientific software development in a distributed collaborative community. PLoS Computational Biology, 2020, 16, e1007507.	3.2	27
6	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
7	A computational method for design of connected catalytic networks in proteins. Protein Science, 2019, 28, 2036-2041.	7.6	28
8	De novo design of potent and selective mimics of IL-2 and IL-15. Nature, 2019, 565, 186-191.	27.8	362
9	RosettaAntibodyDesign (RAbD): A general framework for computational antibody design. PLoS Computational Biology, 2018, 14, e1006112.	3.2	115
10	Modeling and docking of antibody structures with Rosetta. Nature Protocols, 2017, 12, 401-416.	12.0	236
11	I am a United Academic Worker. Science, 2017, 358, 266-266.	12.6	1
12	Accurate Structure Prediction of CDR H3 Loops Enabled by a Novel Structure-Based C-Terminal Constraint. Journal of Immunology, 2017, 198, 505-515.	0.8	43
13	An Integrated Framework Advancing Membrane Protein Modeling and Design. PLoS Computational Biology, 2015, 11, e1004398.	3.2	145
14	The Origin of CDR H3 Structural Diversity. Structure, 2015, 23, 302-311.	3.3	78
15	A Framework to Simplify Combined Sampling Strategies in Rosetta. PLoS ONE, 2015, 10, e0138220.	2.5	10
16	Blind prediction performance of RosettaAntibody 3.0: Grafting, relaxation, kinematic loop modeling, and full CDR optimization. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1611-1623.	2.6	91
17	Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE). PLoS ONE, 2013, 8, e63906.	2.5	348
18	Real-Time PyMOL Visualization for Rosetta and PyRosetta. PLoS ONE, 2011, 6, e21931.	2.5	55

#	Article	IF	Citations
19	Benchmarking and Analysis of Protein Docking Performance in Rosetta v3.2. PLoS ONE, 2011, 6, e22477.	2.5	272