Jared Adolf-Bryfogle

List of Publications by Year
in descending order

13	1,178	933447 10	1058476 14
papers	citations	h-index	g-index

20	20	20	1834
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Toward complete rational control over protein structure and function through computational design. Current Opinion in Structural Biology, 2021, 66, 170-177.	5.7	13
2	CoV3D: a database of high resolution coronavirus protein structures. Nucleic Acids Research, 2021, 49, D282-D287.	14.5	58
3	Biochemical and structural characterization of two cif-like epoxide hydrolases from Burkholderia cenocepacia. Current Research in Structural Biology, 2021, 3, 72-84.	2.2	2
4	Modeling Immunity with Rosetta: Methods for Antibody and Antigen Design. Biochemistry, 2021, 60, 825-846.	2.5	24
5	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. The Biophysicist, 2021, 2, 108-122.	0.3	8
6	Development and Evaluation of GlycanDock: A Proteinâ€“Glycoligand Docking Refinement Algorithm in Rosetta. Journal of Physical Chemistry B, 2021, 125, 6807-6820.	2.6	12
7	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. Nature Communications, 2021, 12, 6947.	12.8	16
8	Better together: Elements of successful scientific software development in a distributed collaborative community. PLoS Computational Biology, 2020, 16, e1007507.	3.2	27
9	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
10	Automatically Fixing Errors in Glycoprotein Structures with Rosetta. Structure, 2019, 27, 134-139.e3.	3.3	93
11	Modeling and docking of antibody structures with Rosetta. Nature Protocols, 2017, 12, 401-416.	12.0	236
12	Residueâ€centric modeling and design of saccharide and glycoconjugate structures. Journal of Computational Chemistry, 2017, 38, 276-287.	3.3	41
13	PyIgClassify: a database of antibody CDR structural classifications. Nucleic Acids Research, 2015, 43, D432-D438.	14.5	105