

Jared Adolf-Bryfogle

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1718287/publications.pdf>

Version: 2024-02-01

13
papers

1,178
citations

932766

10
h-index

1058022

14
g-index

20
all docs

20
docs citations

20
times ranked

1834
citing authors

#	ARTICLE	IF	CITATIONS
1	Toward complete rational control over protein structure and function through computational design. <i>Current Opinion in Structural Biology</i> , 2021, 66, 170-177.	2.6	13
2	CoV3D: a database of high resolution coronavirus protein structures. <i>Nucleic Acids Research</i> , 2021, 49, D282-D287.	6.5	58
3	Biochemical and structural characterization of two cif-like epoxide hydrolases from <i>Burkholderia cenocepacia</i> . <i>Current Research in Structural Biology</i> , 2021, 3, 72-84.	1.1	2
4	Modeling Immunity with Rosetta: Methods for Antibody and Antigen Design. <i>Biochemistry</i> , 2021, 60, 825-846.	1.2	24
5	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. <i>The Biophysicist</i> , 2021, 2, 108-122.	0.1	8
6	Development and Evaluation of GlycanDock: A Protein-Glycoligand Docking Refinement Algorithm in Rosetta. <i>Journal of Physical Chemistry B</i> , 2021, 125, 6807-6820.	1.2	12
7	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. <i>Nature Communications</i> , 2021, 12, 6947.	5.8	16
8	Better together: Elements of successful scientific software development in a distributed collaborative community. <i>PLoS Computational Biology</i> , 2020, 16, e1007507.	1.5	27
9	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	9.0	513
10	Automatically Fixing Errors in Glycoprotein Structures with Rosetta. <i>Structure</i> , 2019, 27, 134-139.e3.	1.6	93
11	Modeling and docking of antibody structures with Rosetta. <i>Nature Protocols</i> , 2017, 12, 401-416.	5.5	236
12	Residue-centric modeling and design of saccharide and glycoconjugate structures. <i>Journal of Computational Chemistry</i> , 2017, 38, 276-287.	1.5	41
13	PyIgClassify: a database of antibody CDR structural classifications. <i>Nucleic Acids Research</i> , 2015, 43, D432-D438.	6.5	105