Jason W Labonte

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3790200/publications.pdf

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18	2,195	759233 12	839539 18
papers	citations	h-index	g-index

24	24	24	2956
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
3	A Comprehensive, High-Resolution Map of a Geneâ€™s Fitness Landscape. Molecular Biology and Evolution, 2014, 31, 1581-1592.	8.9	291
4	Adding Diverse Noncanonical Backbones to Rosetta: Enabling Peptidomimetic Design. PLoS ONE, 2013, 8, e67051.	2.5	59
5	Active Site Comparisons and Catalytic Mechanisms of the Hot Dog Superfamily. Chemical Reviews, 2013, 113, 2182-2204.	47.7	43
6	Residueâ€centric modeling and design of saccharide and glycoconjugate structures. Journal of Computational Chemistry, 2017, 38, 276-287.	3.3	41
7	Computationally designed peptide macrocycle inhibitors of New Delhi metallo-Î²-lactamase 1. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	41
8	Better together: Elements of successful scientific software development in a distributed collaborative community. PLoS Computational Biology, 2020, 16, e1007507.	3.2	27
9	Extending RosettaDock with water, sugar, and pH for prediction of complex structures and affinities for CAPRI rounds 20â€“27. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2201-2209.	2.6	22
10	Computational design of mixed chirality peptide macrocycles with internal symmetry. Protein Science, 2020, 29, 2433-2445.	7.6	16
11	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. Nature Communications, 2021, 12, 6947.	12.8	16
12	Novel sampling strategies and a coarseâ€grained score function for docking homomers, flexible heteromers, and oligosaccharides using Rosetta in CAPRI rounds 37â€“45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 973-985.	2.6	15
13	Molecular Determinants for Protein Stabilization by Insertional Fusion to a Thermophilic Host Protein. ChemBioChem, 2015, 16, 2392-2402.	2.6	12
14	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
15	Shotgun scanning glycomutagenesis: A simple and efficient strategy for constructing and characterizing neoglycoproteins. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	9
16	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. The Biophysicist, 2021, 2, 108-122.	0.3	8
17	Engineering the synthetic potential of Î²-lactam synthetase and the importance of catalytic loop dynamics. MedChemComm, 2012, 3, 960.	3.4	6
18	Structural Basis for Peptide Substrate Specificities of Glycosyltransferase GalNAc-T2. ACS Catalysis, 2021, 11, 2977-2991.	11.2	4