

Jason W Labonte

List of Publications by Year in descending order

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18
papers

2,195
citations

759233

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docs citations

24
times ranked

2956
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Basis for Peptide Substrate Specificities of Glycosyltransferase GalNAc-T2. ACS Catalysis, 2021, 11, 2977-2991.	11.2	4
2	Computationally designed peptide macrocycle inhibitors of New Delhi metallo- β -lactamase 1. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	41
3	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. The Biophysicist, 2021, 2, 108-122.	0.3	8
4	Development and Evaluation of GlycanDock: A Protein-Glycoligand Docking Refinement Algorithm in Rosetta. Journal of Physical Chemistry B, 2021, 125, 6807-6820.	2.6	12
5	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
6	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. Nature Communications, 2021, 12, 6947.	12.8	16
7	Novel sampling strategies and a coarse-grained score function for docking homomers, flexible heteromers, and oligosaccharides using Rosetta in CAPRI rounds 37-45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 973-985.	2.6	15
8	Computational design of mixed chirality peptide macrocycles with internal symmetry. Protein Science, 2020, 29, 2433-2445.	7.6	16
9	Better together: Elements of successful scientific software development in a distributed collaborative community. PLoS Computational Biology, 2020, 16, e1007507.	3.2	27
10	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
11	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
12	Residue-centric modeling and design of saccharide and glycoconjugate structures. Journal of Computational Chemistry, 2017, 38, 276-287.	3.3	41
13	Molecular Determinants for Protein Stabilization by Insertional Fusion to a Thermophilic Host Protein. ChemBioChem, 2015, 16, 2392-2402.	2.6	12
14	A Comprehensive, High-Resolution Map of a Gene's Fitness Landscape. Molecular Biology and Evolution, 2014, 31, 1581-1592.	8.9	291
15	Active Site Comparisons and Catalytic Mechanisms of the Hot Dog Superfamily. Chemical Reviews, 2013, 113, 2182-2204.	47.7	43
16	Extending RosettaDock with water, sugar, and pH for prediction of complex structures and affinities for CAPRI rounds 20-27. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2201-2209.	2.6	22
17	Adding Diverse Noncanonical Backbones to Rosetta: Enabling Peptidomimetic Design. PLoS ONE, 2013, 8, e67051.	2.5	59
18	Engineering the synthetic potential of β -lactam synthetase and the importance of catalytic loop dynamics. MedChemComm, 2012, 3, 960.	3.4	6