

# Morgan Lawrenz

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11827659/publications.pdf>

Version: 2024-02-01

9  
papers

685  
citations

1040056

9  
h-index

1372567

10  
g-index

10  
all docs

10  
docs citations

10  
times ranked

1063  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cloud-based simulations on Google Exacycle reveal ligand modulation of GPCR activation pathways. <i>Nature Chemistry</i> , 2014, 6, 15-21.	13.6	388
2	Independent-Trajectories Thermodynamic-Integration Free-Energy Changes for Biomolecular Systems: Determinants of H5N1 Avian Influenza Virus Neuraminidase Inhibition by Peramivir. <i>Journal of Chemical Theory and Computation</i> , 2009, 5, 1106-1116.	5.3	87
3	Cloud computing approaches for prediction of ligand binding poses and pathways. <i>Scientific Reports</i> , 2015, 5, 7918.	3.3	54
4	Impact of calcium on N1 influenza neuraminidase dynamics and binding free energy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2523-2532.	2.6	49
5	A network of molecular switches controls the activation of the two-component response regulator NtrC. <i>Nature Communications</i> , 2015, 6, 7283.	12.8	40
6	Thermodynamic integration to predict host-guest binding affinities. <i>Journal of Computer-Aided Molecular Design</i> , 2012, 26, 569-576.	2.9	22
7	Effects of Biomolecular Flexibility on Alchemical Calculations of Absolute Binding Free Energies. <i>Journal of Chemical Theory and Computation</i> , 2011, 7, 2224-2232.	5.3	18
8	Elucidating Ligand-Modulated Conformational Landscape of GPCRs Using Cloud-Computing Approaches. <i>Methods in Enzymology</i> , 2015, 557, 551-572.	1.0	15
9	Independent-Trajectory Thermodynamic Integration: A Practical Guide to Protein-Drug Binding Free Energy Calculations Using Distributed Computing. <i>Methods in Molecular Biology</i> , 2012, 819, 469-486.	0.9	10