Amanda Buyan

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9075225/publications.pdf

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		1478505	1372567	
11	191	6	10	
papers	citations	h-index	g-index	
11	11	11	334	
all docs	docs citations	times ranked	citing authors	

#	Article	IF	CITATIONS
1	Computational studies of Piezo1 yield insights into key lipid–protein interactions, channel activation, and agonist binding. Biophysical Reviews, 2022, 14, 209-219.	3.2	3
2	Initiating Coarse-Grained MD Simulations for Membrane-Bound Proteins. Methods in Molecular Biology, 2022, 2402, 131-141.	0.9	0
3	In pursuit of a selective hepatocellular carcinoma therapeutic agent: Novel thalidomide derivatives with antiproliferative, antimigratory and STAT3 inhibitory properties. European Journal of Medicinal Chemistry, 2021, 217, 113353.	5.5	1
4	Differences in local anaesthetic and antiepileptic binding in the inactivated state of human sodium channel Nav1.4. Biophysical Journal, 2021, 120, 5553-5563.	0.5	4
5	Piezo1 Forms Specific, Functionally Important Interactions with Phosphoinositides and Cholesterol. Biophysical Journal, 2020, 119, 1683-1697.	0.5	60
6	Protonation state of inhibitors determines interaction sites within voltage-gated sodium channels. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3135-E3144.	7.1	38
7	Voltage-Gated Sodium Channel Pharmacology. Advances in Pharmacology, 2017, 79, 255-285.	2.0	4
8	Multiscale Simulations Suggest a Mechanism for the Association of the Dok7 PH Domain with PIP-Containing Membranes. PLoS Computational Biology, 2016, 12, e1005028.	3.2	24
9	Primary and Secondary Dimer Interfaces of the Fibroblast Growth Factor Receptor 3 Transmembrane Domain: Characterization via Multiscale Molecular Dynamics Simulations. Biochemistry, 2014, 53, 323-332.	2.5	24
10	Sidekick for Membrane Simulations: Automated Ensemble Molecular Dynamics Simulations of Transmembrane Helices. Journal of Chemical Theory and Computation, 2014, 10, 2165-2175.	5.3	27
11	ReplicOpter: A replicate optimizer for flexible docking. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3156-3165.	2.6	6