Han Wen

List of Publications by Year
in descending order

13	253	1163117 8	1199594 12
papers	citations	h-index	g-index

14	14	14	367
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Molecular mechanisms underlying menthol binding and activation of TRPM8 ion channel. Nature Communications, 2020, 11, 3790.	12.8	54
2	Heat activation mechanism of TRPV1: New insights from molecular dynamics simulation. Temperature, 2019, 6, 120-131.	3.0	34
3	Probing the Structural Dynamics of the NMDA Receptor Activation by Coarse-Grained Modeling. Biophysical Journal, 2017, 112, 2589-2601.	0.5	33
4	Decrypting the Heat Activation Mechanism of TRPV1 Channel by Molecular Dynamics Simulation. Biophysical Journal, 2018, 114, 40-52.	0.5	30
5	A survey of coarse-grained methods for modeling protein conformational transitions. Current Opinion in Structural Biology, 2017, 42, 24-30.	5.7	22
6	Toward elucidating the heat activation mechanism of the TRPV1 channel gating by molecular dynamics simulation. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1938-1949.	2.6	21
7	Pathogenic mechanism of a catecholaminergic polymorphic ventricular tachycardia causing-mutation in cardiac calcium release channel RyR2. Journal of Molecular and Cellular Cardiology, 2018, 117, 26-35.	1.9	21
8	Congenital myopathyâ€related mutations in tropomyosin disrupt regulatory function through altered actin affinity and tropomodulin binding. FEBS Journal, 2019, 286, 1877-1893.	4.7	14
9	Cross-subunit interactions that stabilize open states mediate gating in NMDA receptors. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	10
10	RNANetMotif: Identifying sequence-structure RNA network motifs in RNA-protein binding sites. PLoS Computational Biology, 2022, 18, e1010293.	3.2	9
11	Investigating dual Ca²⁺ modulation of the ryanodine receptor 1 by molecular dynamics simulation. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1528-1539.	2.6	4
12	Predicting lipid and ligand binding sites in TRPV1 channel by molecular dynamics simulation and machine learning. Proteins: Structure, Function and Bioinformatics, 2021, 89, 966-977.	2.6	1
13	Molecular dynamics simulation of tropomyosin bound to actins/myosin in the closed and open states. Proteins: Structure, Function and Bioinformatics, 2019, 87, 805-814.	2.6	0