

Tao Jiang

List of Publications by Year in descending order

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papers

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#	ARTICLE	IF	CITATIONS
1	Characterization of Lipid-Protein Interactions and Lipid-Mediated Modulation of Membrane Protein Function through Molecular Simulation. <i>Chemical Reviews</i> , 2019, 119, 6086-6161.	47.7	176
2	Lipids and ions traverse the membrane by the same physical pathway in the nhTMEM16 scramblase. <i>ELife</i> , 2017, 6, .	6.0	85
3	A network of phosphatidylinositol 4,5-bisphosphate binding sites regulates gating of the Ca ²⁺ -activated Cl ⁻ channel ANO1 (TMEM16A). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19952-19962.	7.1	48
4	Revealing an outward-facing open conformational state in a CLC Cl ⁻ /H ⁺ exchange transporter. <i>ELife</i> , 2016, 5, .	6.0	43
5	Molecular Basis for Differential Anion Binding and Proton Coupling in the Cl ⁻ /H ⁺ Exchanger CLC-ec1. <i>Journal of the American Chemical Society</i> , 2016, 138, 3066-3075.	13.7	36
6	A CLC-ec1 mutant reveals global conformational change and suggests a unifying mechanism for the CLC Cl ⁻ /H ⁺ transport cycle. <i>ELife</i> , 2020, 9, .	6.0	34
7	Microscopic view of lipids and their diverse biological functions. <i>Current Opinion in Structural Biology</i> , 2018, 51, 177-186.	5.7	26
8	Computational Dissection of Membrane Transport at a Microscopic Level. <i>Trends in Biochemical Sciences</i> , 2020, 45, 202-216.	7.5	21
9	Microscopic Characterization of Membrane Transporter Function by In Silico Modeling and Simulation. <i>Methods in Enzymology</i> , 2016, 578, 373-428.	1.0	8
10	A Microscopic View of the Mechanisms of Active Transport Across the Cellular Membrane. <i>Annual Reports in Computational Chemistry</i> , 2014, 10, 77-125.	1.7	4
11	Characterizing an Intermediate State Between Inactive and Active States of RecA. <i>Biophysical Journal</i> , 2012, 102, 282a.	0.5	1
12	Nucleotide and DNA-Induced Structural Transitions and the Coupling Between ATP and DNA Binding Sites in RecA. <i>Biophysical Journal</i> , 2011, 100, 239a-240a.	0.5	0
13	Coupling of Anion Selectivity and Proton Transport in CLC-ec1. <i>Biophysical Journal</i> , 2013, 104, 627a.	0.5	0
14	An Outward-Facing Open Conformational State in a CLC Transporter. <i>Biophysical Journal</i> , 2016, 110, 178a.	0.5	0
15	Functional Characterization of Calcium-activated Phospholipid Scramblase Activity of nhTMEM16. <i>Biophysical Journal</i> , 2016, 110, 179a-180a.	0.5	0
16	Identification of the Ion Conduction Pathway in a TMEM16 Scramblase. <i>Biophysical Journal</i> , 2017, 112, 276a.	0.5	0
17	Identification of Cardiolipin Binding Sites on Membrane Proteins using an Accelerated Computational Membrane Model. <i>Biophysical Journal</i> , 2018, 114, 460a-461a.	0.5	0
18	Lipids and Ions Traverse the Membrane by the Same Physical Pathway in the nhTMEM16 Scramblase. <i>Biophysical Journal</i> , 2018, 114, 149a.	0.5	0

#	ARTICLE	IF	CITATIONS
19	Elucidating Conformational Changes Underlying the Conversion of TMEM16A Mutants from Anion Channels to Scramblases. <i>Biophysical Journal</i> , 2019, 116, 221a.	0.5	0
20	A Network of PIP2 Binding Sites Regulate Gating of the Calcium-Activated Chloride Channel TMEM16A. <i>Biophysical Journal</i> , 2020, 118, 555a-556a.	0.5	0
21	Investigating Conformational Changes to Understand the Transport Mechanism of CLC Chloride/Proton Antiporters. <i>Biophysical Journal</i> , 2020, 118, 443a.	0.5	0
22	Effects of PIP2 Binding to its Different Binding Sites on ANO1 Function. <i>Biophysical Journal</i> , 2020, 118, 419a.	0.5	0