

Inga HÃ¶nelt

List of Publications by Year in descending order

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27
papers

1,293
citations

394421

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docs citations

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times ranked

1739
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular Mechanisms for Bacterial Potassium Homeostasis. <i>Journal of Molecular Biology</i> , 2021, 433, 166968.	4.2	57
2	Deciphering ion transport and ATPase coupling in the intersubunit tunnel of KdpFABC. <i>Nature Communications</i> , 2021, 12, 5098.	12.8	10
3	Regulation of lipid saturation without sensing membrane fluidity. <i>Nature Communications</i> , 2020, 11, 756.	12.8	105
4	Structural basis of proton-coupled potassium transport in the KUP family. <i>Nature Communications</i> , 2020, 11, 626.	12.8	60
5	Two Ways To Convert a Low-Affinity Potassium Channel to High Affinity: Control of <i>Bacillus subtilis</i> KtrCD by Glutamate. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	20
6	Membrane Protein Solubilization and Quality Control: An Example of a Primary Active Transporter. <i>Methods in Molecular Biology</i> , 2020, 2127, 93-103.	0.9	1
7	How RCK domains regulate gating of K ⁺ channels. <i>Biological Chemistry</i> , 2019, 400, 1303-1322.	2.5	14
8	A channel profile report of the unusual K ⁺ channel KtrB. <i>Journal of General Physiology</i> , 2019, 151, 1357-1368.	1.9	13
9	Sustained sensing in potassium homeostasis: Cyclic di-AMP controls potassium uptake by KimA at the levels of expression and activity. <i>Journal of Biological Chemistry</i> , 2019, 294, 9605-9614.	3.4	66
10	Native mass spectrometry goes more native: investigation of membrane protein complexes directly from SMALPs. <i>Chemical Communications</i> , 2018, 54, 13702-13705.	4.1	44
11	Cryo-EM structures of KdpFABC suggest a K ⁺ transport mechanism via two inter-subunit half-channels. <i>Nature Communications</i> , 2018, 9, 4971.	12.8	38
12	Activation of the Unfolded Protein Response by Lipid Bilayer Stress. <i>Molecular Cell</i> , 2017, 67, 673-684.e8.	9.7	252
13	The Synergetic Effects of Combining Structural Biology and EPR Spectroscopy on Membrane Proteins. <i>Crystals</i> , 2017, 7, 117.	2.2	5
14	Helical jackknives control the gates of the double-pore K ⁺ uptake system KtrAB. <i>ELife</i> , 2017, 6, .	6.0	23
15	Functional diversity of the superfamily of K ⁺ transporters to meet various requirements. <i>Biological Chemistry</i> , 2015, 396, 1003-1014.	2.5	42
16	Low Affinity and Slow Na ⁺ Binding Precedes High Affinity Aspartate Binding in the Secondary-active Transporter GltPh. <i>Journal of Biological Chemistry</i> , 2015, 290, 15962-15972.	3.4	42
17	Glutamine synthetase 2 is not essential for biosynthesis of compatible solutes in <i>Halobacillus halophilus</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 168.	3.5	2
18	Crystal structure of a substrate-free aspartate transporter. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1224-1226.	8.2	83

#	ARTICLE	IF	CITATIONS
19	Unsynchronised subunit motion in single trimeric sodium-coupled aspartate transporters. <i>Nature</i> , 2013, 502, 119-123.	27.8	122
20	Substrate-Induced Conformational Changes in the S-Component ThiT from an Energy Coupling Factor Transporter. <i>Structure</i> , 2013, 21, 861-867.	3.3	29
21	Conformational heterogeneity of the aspartate transporter GltPh. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 210-214.	8.2	101
22	Bioenergetics of the Moderately Halophilic Bacterium <i>Halobacillus halophilus</i> : Composition and Regulation of the Respiratory Chain. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3839-3846.	3.1	9
23	Molecular Mechanisms of Adaptation of the Moderately Halophilic Bacterium <i>Halobacillus halophilus</i> to Its Environment. <i>Life</i> , 2013, 3, 234-243.	2.4	38
24	KtrB, a member of the superfamily of K ⁺ transporters. <i>European Journal of Cell Biology</i> , 2011, 90, 696-704.	3.6	19
25	Gain of Function Mutations in Membrane Region M2C2 of KtrB Open a Gate Controlling K ⁺ Transport by the KtrAB System from <i>Vibrio alginolyticus</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 10318-10327.	3.4	27
26	Membrane Region M2C2 in Subunit KtrB of the K ⁺ Uptake System KtrAB from <i>Vibrio alginolyticus</i> Forms a Flexible Gate Controlling K ⁺ Flux. <i>Journal of Biological Chemistry</i> , 2010, 285, 28210-28219.	3.4	29
27	ATP Binding to the KTN/RCK Subunit KtrA from the K ⁺ -uptake System KtrAB of <i>Vibrio alginolyticus</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 14018-14027.	3.4	39