

Alexander Krah

List of Publications by Year in descending order

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papers

739
citations

687363

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all docs

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28
times ranked

622
citing authors

#	ARTICLE	IF	CITATIONS
1	Bridging the N-terminal and middle domains in FliG of the flagellar rotor. <i>Current Research in Structural Biology</i> , 2022, 4, 59-67.	2.2	2
2	A second shell residue modulates a conserved ATP-binding site with radically different affinities for ATP. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 129766.	2.4	4
3	On the ion coupling mechanism of the MATE transporter ClbM. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183137.	2.6	16
4	Extending the Martini Coarse-Grained Force Field to <i>N</i> -Glycans. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 3864-3883.	5.4	30
5	Characterizing the Hydration Properties of Proton Binding Sites in the ATP Synthase c-Rings of <i>Bacillus</i> Species. <i>Journal of Physical Chemistry B</i> , 2020, 124, 7176-7183.	2.6	5
6	An Alternative HIV-1 Non-Nucleoside Reverse Transcriptase Inhibition Mechanism: Targeting the p51 Subunit. <i>Molecules</i> , 2020, 25, 5902.	3.8	5
7	How Ligand Binding Affects the Dynamical Transition Temperature in Proteins. <i>ChemPhysChem</i> , 2020, 21, 916-926.	2.1	3
8	The Molecular Basis for Purine Binding Selectivity in the Bacterial ATP Synthase $\hat{\mu}$ Subunit. <i>ChemBioChem</i> , 2020, 21, 3249-3254.	2.6	5
9	Insights into water accessible pathways and the inactivation mechanism of proton translocation by the membrane-embedded domain of V-type ATPases. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2019, 1861, 1004-1010.	2.6	10
10	Insights into the regulatory function of the $\hat{\epsilon}$ subunit from bacterial F-type ATP synthases: a comparison of structural, biochemical and biophysical data. <i>Open Biology</i> , 2018, 8, 170275.	3.6	21
11	Single mutations in the $\hat{\mu}$ subunit from thermophilic <i>Bacillus</i> PS3 generate a high binding affinity site for ATP. <i>PeerJ</i> , 2018, 6, e5505.	2.0	3
12	Insights into the ion-coupling mechanism in the MATE transporter NorM-VC. <i>Physical Biology</i> , 2017, 14, 045009.	1.8	16
13	Predicted Structures of the Proton-Bound Membrane-Embedded Rotor Rings of the <i>Saccharomyces cerevisiae</i> and <i>Escherichia coli</i> ATP Synthases. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3297-3307.	2.6	6
14	The structural basis of a high affinity ATP binding $\hat{\mu}$ subunit from a bacterial ATP synthase. <i>PLoS ONE</i> , 2017, 12, e0177907.	2.5	13
15	A role for loop C in the $\hat{\tau}1$ strand in GABA _A receptor activation. <i>Journal of Physiology</i> , 2016, 594, 5555-5571.	2.9	7
16	On the ATP binding site of the $\hat{\mu}$ subunit from bacterial F-type ATP synthases. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 332-340.	1.0	14
17	On the Mg ²⁺ binding site of the $\hat{\mu}$ subunit from bacterial F-type ATP synthases. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2015, 1847, 1101-1112.	1.0	9
18	Linking structural features from mitochondrial and bacterial F-type ATP synthases to their distinct mechanisms of ATPase inhibition. <i>Progress in Biophysics and Molecular Biology</i> , 2015, 119, 94-102.	2.9	18

#	ARTICLE	IF	CITATIONS
19	1P148 Molecular mechanism of the epsilon subunit from F-type ATP synthases studied by Molecular Dynamics simulations(11. Molecular motor,Poster,The 52nd Annual Meeting of the Biophysical Society) Tj ETQq1 10017843140rgBT /Ove		
20	A New Type of Na ⁺ -Driven ATP Synthase Membrane Rotor with a Two-Carboxylate Ion-Coupling Motif. PLoS Biology, 2013, 11, e1001596.	5.6	61
21	1P149 The Mg ²⁺ binding site of the ATP synthase $\hat{\mu}$ subunit from Bacillus subtilis derived by Molecular Dynamics simulations(11.Molecular motor,Poster,The 51st Annual Meeting of the) Tj ETQq1 1 0.7843140rgBT /Overlock 10		
22	Structure of the c10 ring of the yeast mitochondrial ATP synthase in the open conformation. Nature Structural and Molecular Biology, 2012, 19, 485-491.	8.2	116
23	G117C MelB, a mutant melibiose permease with a changed conformational equilibrium. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 2508-2516.	2.6	15
24	Structural and energetic basis for H ⁺ versus Na ⁺ binding selectivity in ATP synthase Fo rotors. Biochimica Et Biophysica Acta - Bioenergetics, 2010, 1797, 763-772.	1.0	58
25	Microscopic rotary mechanism of ion translocation in the Fo complex of ATP synthases. Nature Chemical Biology, 2010, 6, 891-899.	8.0	142
26	On the Question of Hydronium Binding to ATP-Synthase Membrane Rotors. Biophysical Journal, 2010, 99, L53-L55.	0.5	19
27	On the Structure of the Proton-Binding Site in the Fo Rotor of Chloroplast ATP Synthases. Journal of Molecular Biology, 2010, 395, 20-27.	4.2	43
28	Complete Ion-Coordination Structure in the Rotor Ring of Na ⁺ -Dependent F-ATP Synthases. Journal of Molecular Biology, 2009, 391, 498-507.	4.2	98