

Alexander Krah

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

739
citations

687363

13
h-index

552781

26
g-index

28
all docs

28
docs citations

28
times ranked

622
citing authors

#	ARTICLE	IF	CITATIONS
1	Microscopic rotary mechanism of ion translocation in the Fo complex of ATP synthases. <i>Nature Chemical Biology</i> , 2010, 6, 891-899.	8.0	142
2	Structure of the c10 ring of the yeast mitochondrial ATP synthase in the open conformation. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 485-491.	8.2	116
3	Complete Ion-Coordination Structure in the Rotor Ring of Na ⁺ -Dependent F-ATP Synthases. <i>Journal of Molecular Biology</i> , 2009, 391, 498-507.	4.2	98
4	A New Type of Na ⁺ -Driven ATP Synthase Membrane Rotor with a Two-Carboxylate Ion-Coupling Motif. <i>PLoS Biology</i> , 2013, 11, e1001596.	5.6	61
5	Structural and energetic basis for H ⁺ versus Na ⁺ binding selectivity in ATP synthase Fo rotors. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 763-772.	1.0	58
6	On the Structure of the Proton-Binding Site in the Fo Rotor of Chloroplast ATP Synthases. <i>Journal of Molecular Biology</i> , 2010, 395, 20-27.	4.2	43
7	Extending the Martini Coarse-Grained Force Field to N-Glycans. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 3864-3883.	5.4	30
8	Insights into the regulatory function of the É 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
9	On the Question of Hydronium Binding to ATP-Synthase Membrane Rotors. <i>Biophysical Journal</i> , 2010, 99, L53-L55.	0.5	19
10	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
11	Insights into the ion-coupling mechanism in the MATE transporter NorM-VC. <i>Physical Biology</i> , 2017, 14, 045009.	1.8	16
12	On the ion coupling mechanism of the MATE transporter ClbM. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183137.	2.6	16
13	G117C MelB, a mutant melibiose permease with a changed conformational equilibrium. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 2508-2516.	2.6	15
14	On the ATP binding site of the Îµ subunit from bacterial F-type ATP synthases. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 332-340.	1.0	14
15	The structural basis of a high affinity ATP binding Îµ subunit from a bacterial ATP synthase. <i>PLoS ONE</i> , 2017, 12, e0177907.	2.5	13
16	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
17	On the Mg ²⁺ binding site of the Îµ subunit from bacterial F-type ATP synthases. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2015, 1847, 1101-1112.	1.0	9
18	A role for loop G in the Î²1 strand in GABA _A receptor activation. <i>Journal of Physiology</i> , 2016, 594, 5555-5571.	2.9	7

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19	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
20	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
21	An Alternative HIV-1 Non-Nucleoside Reverse Transcriptase Inhibition Mechanism: Targeting the p51 Subunit. <i>Molecules</i> , 2020, 25, 5902.	3.8	5
22	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
23	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
24	How Ligand Binding Affects the Dynamical Transition Temperature in Proteins. <i>ChemPhysChem</i> , 2020, 21, 916-926.	2.1	3
25	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
26	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
27	1P149 The Mg ²⁺ binding site of the ATP synthase $\hat{\mu}$ subunit from <i>Bacillus subtilis</i> derived by Molecular Dynamics simulations(11.Molecular motor,Poster,The 51st Annual Meeting of the Tj ETQq1 1 0.784314orgBT /Overlock 10		
28	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 ETQq0 001rgBT /Overlock 10		