Oleg Y Dmitriev

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The KH domain facilitates the substrate specificity and unwinding processivity of DDX43 helicase. Journal of Biological Chemistry, 2021, 296, 100085.	3.4	15
2	At sixes and sevens: cryptic domain in the metal binding chain of the human copper transporter ATP7A. Biophysical Journal, 2021, 120, 4600-4607.	0.5	3
3	Nanobodies against the metal binding domains of ATP7B as tools to study copper transport in the cell. Metallomics, 2020, 12, 1941-1950.	2.4	0
4	Molecular Architecture of the Copper-Transporting ATPase ATP7B. , 2019, , 33-43.		6
5	The Structure of Metal Binding Domain 1 of the Copper Transporter ATP7B Reveals Mechanism of a Singular Wilson Disease Mutation. Scientific Reports, 2018, 8, 581.	3.3	15
6	Engineered Protein Model of the ATP synthase H+- Channel Shows No Salt Bridge at the Rotor-Stator Interface. Scientific Reports, 2018, 8, 11361.	3.3	4
7	Binding of Copper and Cisplatin to Atox1 Is Mediated by Glutathione through the Formation of Metal–Sulfur Clusters. Biochemistry, 2017, 56, 3129-3141.	2.5	27
8	Dynamics of the metal binding domains and regulation of the human copper transporters ATP7B and ATP7A. IUBMB Life, 2017, 69, 226-235.	3.4	32
9	The metal chaperone Atox1 regulates the activity of the human copper transporter ATP7B by modulating domain dynamics. Journal of Biological Chemistry, 2017, 292, 18169-18177.	3.4	45
10	Nanobodies as Probes for Protein Dynamics in Vitro and in Cells. Journal of Biological Chemistry, 2016, 291, 3767-3775.	3.4	84
11	Interactions between Metal-binding Domains Modulate Intracellular Targeting of Cu(I)-ATPase ATP7B, as Revealed by Nanobody Binding. Journal of Biological Chemistry, 2014, 289, 32682-32693.	3.4	33
12	The use of nanopore analysis for discovering drugs which bind to α-synuclein for treatment of Parkinson's disease. European Journal of Medicinal Chemistry, 2014, 88, 42-54.	5.5	37
13	Copper chaperone Atox1 interacts with the metal-binding domain of Wilson's disease protein in cisplatin detoxification. Biochemical Journal, 2013, 454, 147-156.	3.7	53
14	Molecular Events Initiating Exit of a Copper-transporting ATPase ATP7B from the Trans-Golgi Network. Journal of Biological Chemistry, 2012, 287, 36041-36050.	3.4	53
15	Cellâ€free synthesis of membrane subunits of ATP synthase in phospholipid bicelles: NMR shows subunit <i>a</i> fold similar to the protein in the cell membrane. Protein Science, 2012, 21, 279-288.	7.6	25
16	Mechanism of tumor resistance to cisplatin mediated by the copper transporter ATP7BThis paper is one of a selection of papers published in a Special Issue entitled CSBMCB 53rd Annual Meeting — Membrane Proteins in Health and Disease, and has undergone the Journal's usual peer review process Biochemistry and Cell Biology, 2011, 89, 138-147	2.0	42
17	Difference in Stability of the N-domain Underlies Distinct Intracellular Properties of the E1064A and H1069Q Mutants of Copper-transporting ATPase ATP7B. Journal of Biological Chemistry, 2011, 286, 16355-16362.	3.4	35
18	Interaction with Monomeric Subunit c Drives Insertion of ATP Synthase Subunit a into the Membrane	3.4	11

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19	Cellular copper levels determine the phenotype of the Arg ⁸⁷⁵ variant of ATP7B/Wilson disease protein. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5390-5395.	7.1	47
20	Crystallization and preliminary X-ray studies of the N-domain of the Wilson disease associated protein. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 621-624.	0.7	3
21	The soluble metal-binding domain of the copper transporter ATP7B binds and detoxifies cisplatin. Biochemical Journal, 2009, 419, 51-59.	3.7	60
22	Interaction of transmembrane helices in ATP synthase subunit a in solution as revealed by spin label difference NMR. Biochimica Et Biophysica Acta - Bioenergetics, 2008, 1777, 227-237.	1.0	7
23	Function and Regulation of Human Copper-Transporting ATPases. Physiological Reviews, 2007, 87, 1011-1046.	28.8	679
24	The rigid connecting loop stabilizes hairpin folding of the two helices of the ATP synthase subunit <i>c</i> . Protein Science, 2007, 16, 2118-2122.	7.6	18
25	NMR assignment of the Wilson disease associated protein N-domain. Journal of Biomolecular NMR, 2006, 36, 61-61.	2.8	3
26	Solution structure of the N-domain of Wilson disease protein: Distinct nucleotide-binding environment and effects of disease mutations. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5302-5307.	7.1	107
27	Letter to the Editor: Backbone1H,15N and13C Assignments for the Subunit a of the E.ÂColi ATP Synthase. Journal of Biomolecular NMR, 2004, 29, 439-440.	2.8	7
28	Subunit a of the E. coli ATP synthase: reconstitution and high resolution NMR with protein purified in a mixed polarity solvent. FEBS Letters, 2004, 556, 35-38.	2.8	22
29	Mechanics of coupling proton movements to c -ring rotation in ATP synthase. FEBS Letters, 2003, 555, 29-34.	2.8	138
30	Structure of Ala24/Asp61 → Asp24/Asn61 Substituted Subunit c of Escherichia coli ATP Synthase: Implications for the Mechanism of Proton Transport and Rotary Movement in the Fo Complex. Biochemistry, 2002, 41, 5537-5547.	2.5	19
31	Structural model of the transmembrane Fo rotary sector of H+-transporting ATP synthase derived by solution NMR and intersubunit cross-linking in situ. Biochimica Et Biophysica Acta - Biomembranes, 2002, 1565, 232-245.	2.6	72
32	The oligomeric subunit C rotor in the fo sector of ATP synthase: unresolved questions in our understanding of function. Journal of Bioenergetics and Biomembranes, 2000, 32, 433-439.	2.3	18
33	Structure of the Membrane Domain of Subunit b of theEscherichia coli F0F1 ATP Synthase. Journal of Biological Chemistry, 1999, 274, 15598-15604.	3.4	130
34	Defining the Domain of Binding of F1 Subunit ε with the Polar Loop of F0 Subunit c in theEscherichia coli ATP Synthase. Journal of Biological Chemistry, 1999, 274, 17011-17016.	3.4	55