

Jeff Abramson

List of Publications by Year in descending order

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61
papers

5,318
citations

172457

29
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138484

58
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62
all docs

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docs citations

62
times ranked

4713
citing authors

#	ARTICLE	IF	CITATIONS
1	Function Trumps Form in Two Sugar Symporters, LacY and vSGLT. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3572.	4.1	4
2	Genotype–phenotype correlations and novel molecular insights into the DHX30-associated neurodevelopmental disorders. <i>Genome Medicine</i> , 2021, 13, 90.	8.2	16
3	ABCB10 exports mitochondrial biliverdin, driving metabolic maladaptation in obesity. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	27
4	Functional and structural analyses of novel Smith-Kingsmore Syndrome-Associated MTOR variants reveal potential new mechanisms and predictors of pathogenicity. <i>PLoS Genetics</i> , 2021, 17, e1009651.	3.5	9
5	MicroED structure of lipid-embedded mammalian mitochondrial voltage-dependent anion channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32380-32385.	7.1	35
6	Protein structure reveals how a malaria parasite imports a wide range of sugars. <i>Nature</i> , 2020, 578, 220-221.	27.8	4
7	Charge Reduction of Membrane Proteins in Native Mass Spectrometry Using Alkali Metal Acetate Salts. <i>Analytical Chemistry</i> , 2020, 92, 6622-6630.	6.5	8
8	A lower affinity to cytosolic proteins reveals VDAC3 isoform-specific role in mitochondrial biology. <i>Journal of General Physiology</i> , 2020, 152, .	1.9	36
9	Multiple neurosteroid and cholesterol binding sites in voltage-dependent anion channel-1 determined by photo-affinity labeling. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2019, 1864, 1269-1279.	2.4	26
10	Assessing the role of residue E73 and lipid headgroup charge in VDAC1 voltage gating. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2019, 1860, 22-29.	1.0	27
11	Protonation state of glutamate 73 regulates the formation of a specific dimeric association of mVDAC1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E172-E179.	7.1	26
12	Conformational transitions of the sodium-dependent sugar transporter, vSGLT. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2742-E2751.	7.1	33
13	Harnessing photoinduced electron transfer to optically determine protein sub-nanoscale atomic distances. <i>Nature Communications</i> , 2018, 9, 4738.	12.8	23
14	Substrate-bound outward-open structure of a Na ⁺ -coupled sialic acid symporter reveals a new Na ⁺ site. <i>Nature Communications</i> , 2018, 9, 1753.	12.8	62
15	Click Chemistry Reagent for Identification of Sites of Covalent Ligand Incorporation in Integral Membrane Proteins. <i>Analytical Chemistry</i> , 2017, 89, 2636-2644.	6.5	20
16	Photoaffinity labeling with cholesterol analogues precisely maps a cholesterol-binding site in voltage-dependent anion channel-1. <i>Journal of Biological Chemistry</i> , 2017, 292, 9294-9304.	3.4	54
17	Structural features and lipid binding domain of tubulin on biomimetic mitochondrial membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3622-E3631.	7.1	35
18	An Assessment of How VDAC Structures Have Impacted Our Understanding of Their Function. <i>Biological and Medical Physics Series</i> , 2017, , 141-160.	0.4	4

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19	Stochastic steps in secondary active sugar transport. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3960-6.	7.1	38
20	A large Rab GTPase encoded by <i>CRACR2A</i> is a component of subsynaptic vesicles that transmit T cell activation signals. Science Signaling, 2016, 9, ra31.	3.6	29
21	Identification of a Second Substrate-binding Site in Solute-Sodium Symporters. Journal of Biological Chemistry, 2015, 290, 127-141.	3.4	18
22	DYRK1A haploinsufficiency causes a new recognizable syndrome with microcephaly, intellectual disability, speech impairment, and distinct facies. European Journal of Human Genetics, 2015, 23, 1473-1481.	2.8	101
23	High Resolution Structure and Double Electron-Electron Resonance of the Zebrafish Voltage-dependent Anion Channel 2 Reveal an Oligomeric Population. Journal of Biological Chemistry, 2014, 289, 12566-12577.	3.4	116
24	Structural Determinants of Water Permeation through the Sodium-Galactose Transporter vSGLT. Biophysical Journal, 2014, 106, 1280-1289.	0.5	25
25	Structure-guided simulations illuminate the mechanism of ATP transport through VDAC1. Nature Structural and Molecular Biology, 2014, 21, 626-632.	8.2	87
26	Structures of the Prokaryotic Galactose Transporter vSGLT and Their Implications on Alternating Access Mechanism in Human SGLT1. Springer Series in Biophysics, 2014, , 59-78.	0.4	0
27	Watch Water Flow. Science, 2013, 340, 1294-1295.	12.6	13
28	Bridging the gap between structure and kinetics of human SGLT1. American Journal of Physiology - Cell Physiology, 2012, 302, C1293-C1305.	4.6	51
29	Affixing N-terminal α -Helix to the Wall of the Voltage-dependent Anion Channel Does Not Prevent Its Voltage Gating. Journal of Biological Chemistry, 2012, 287, 11437-11445.	3.4	70
30	Characterization and Purification of a Na ⁺ /Ca ²⁺ Exchanger from an Archaeobacterium. Journal of Biological Chemistry, 2012, 287, 8652-8659.	3.4	13
31	It's All in the Symmetry. Science, 2012, 335, 669-670.	12.6	8
32	High-throughput Crystallization of Membrane Proteins Using the Lipidic Bicelle Method. Journal of Visualized Experiments, 2012, , e3383.	0.3	23
33	Crystal structure of lactose permease in complex with an affinity inactivator yields unique insight into sugar recognition. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9361-9366.	7.1	84
34	The 3D structures of VDAC represent a native conformation. Trends in Biochemical Sciences, 2010, 35, 514-521.	7.5	115
35	Bridging the gap: A GFP-based strategy for overexpression and purification of membrane proteins with intra and extracellular C-termini. Protein Science, 2010, 19, 868-880.	7.6	45
36	The mechanism of sodium and substrate release from the binding pocket of vSGLT. Nature, 2010, 468, 988-991.	27.8	197

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37	Water Permeation through the Sodium-Dependent Galactose Cotransporter vSGLT. Biophysical Journal, 2010, 99, L56-L58.	0.5	41
38	Fluorescence Detection of Heavy Atom Labeling (FD-HAL): A rapid method for identifying covalently modified cysteine residues by phasing atoms. Journal of Structural Biology, 2010, 171, 82-87.	2.8	11
39	The Electrostatics of VDAC: Implications for Selectivity and Gating. Journal of Molecular Biology, 2010, 396, 580-592.	4.2	81
40	Post-translational Modifications of Integral Membrane Proteins Resolved by Top-down Fourier Transform Mass Spectrometry with Collisionally Activated Dissociation. Molecular and Cellular Proteomics, 2010, 9, 791-803.	3.8	86
41	Crystal packing analysis of murine VDAC1 crystals in a lipidic environment reveals novel insights on oligomerization and orientation. Channels, 2009, 3, 167-170.	2.8	42
42	Chapter 5 Practical Aspects of Membrane Proteins Crystallization in Bicelles. Current Topics in Membranes, 2009, 63, 109-125.	0.9	12
43	Structure and Functional Analysis of a Ca ²⁺ Sensor Mutant of the Na ⁺ /Ca ²⁺ Exchanger. Journal of Biological Chemistry, 2009, 284, 14688-14692.	3.4	26
44	Structure and function of Na ⁺ -symporters with inverted repeats. Current Opinion in Structural Biology, 2009, 19, 425-432.	5.7	198
45	Ca ²⁺ regulation of the Na ⁺ /Ca ²⁺ exchanger. FASEB Journal, 2009, 23, 698.1.	0.5	0
46	The Crystal Structure of a Sodium Galactose Transporter Reveals Mechanistic Insights into Na ⁺ /Sugar Symport. Science, 2008, 321, 810-814.	12.6	515
47	The crystal structure of mouse VDAC1 at 2.3 Å resolution reveals mechanistic insights into metabolite gating. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17742-17747.	7.1	488
48	How Does Regulatory Ca ²⁺ Regulate the Na ⁺ -Ca ²⁺ Exchanger?. Channels, 2007, 1, 397-399.	2.8	13
49	The second Ca ²⁺ -binding domain of the Na ⁺ Ca ²⁺ exchanger is essential for regulation: Crystal structures and mutational analysis. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18467-18472.	7.1	103
50	What We Know about the Structure of NCX1 and How It Relates to Its Function. Annals of the New York Academy of Sciences, 2007, 1099, 1-6.	3.8	15
51	The Crystal Structure of the Primary Ca ²⁺ Sensor of the Na ⁺ /Ca ²⁺ Exchanger Reveals a Novel Ca ²⁺ Binding Motif*. Journal of Biological Chemistry, 2006, 281, 21577-21581.	3.4	107
52	Structural Analysis of Murine Voltage Dependent Anion Channel (VDAC) 1. FASEB Journal, 2006, 20, .	0.5	0
53	Lactose permease as a paradigm for membrane transport proteins (Review). Molecular Membrane Biology, 2004, 21, 227-236.	2.0	106
54	Structural comparison of lactose permease and the glycerol-3-phosphate antiporter: members of the major facilitator superfamily. Current Opinion in Structural Biology, 2004, 14, 413-419.	5.7	80

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55	Structure and Mechanism of the Lactose Permease of <i>Escherichia coli</i> . <i>Science</i> , 2003, 301, 610-615.	12.6	1,390
56	The lactose permease of <i>Escherichia coli</i> : overall structure, the sugar-binding site and the alternating access model for transport. <i>FEBS Letters</i> , 2003, 555, 96-101.	2.8	92
57	Structure and function of quinone binding membrane proteins. <i>Advances in Protein Chemistry</i> , 2003, 63, 151-176.	4.4	4
58	Structure of cytochrome c oxidase: a comparison of the bacterial and mitochondrial enzymes. <i>BBA - Proteins and Proteomics</i> , 2001, 1544, 1-9.	2.1	47
59	Purification, crystallization and preliminary crystallographic studies of an integral membrane protein, cytochrome <i>b</i> ₃ ubiquinol oxidase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1076-1078.	2.5	10
60	The structure of the ubiquinol oxidase from <i>Escherichia coli</i> and its ubiquinone binding site. <i>Nature Structural Biology</i> , 2000, 7, 910-917.	9.7	354
61	Fusion protein approach to improve the crystal quality of cytochrome <i>b</i> ₃ ubiquinol oxidase from <i>Escherichia coli</i> . <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2000, 1459, 449-455.	1.0	14