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List of Publications by Year
in descending order

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61 papers	5,318 citations	172457 29 h-index	138484 58 g-index
62 all docs	62 docs citations	62 times ranked	4713 citing authors

#	Article	IF	Citations
1	Structure and Mechanism of the Lactose Permease of Escherichia coli. Science, 2003, 301, 610-615.	12.6	1,390
2	The Crystal Structure of a Sodium Galactose Transporter Reveals Mechanistic Insights into Na ⁺ /Sugar Symport. Science, 2008, 321, 810-814.	12.6	515
3	The crystal structure of mouse VDAC1 at 2.3 â„« 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
4	The structure of the ubiquinol oxidase from Escherichia coli and its ubiquinone binding site. Nature Structural Biology, 2000, 7, 910-917.	9.7	354
5	Structure and function of Na+-symporters with inverted repeats. Current Opinion in Structural Biology, 2009, 19, 425-432.	5.7	198
6	The mechanism of sodium and substrate release from the binding pocket of vSGLT. Nature, 2010, 468, 988-991.	27.8	197
7	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
8	The 3D structures of VDAC represent a native conformation. Trends in Biochemical Sciences, 2010, 35, 514-521.	7.5	115
9	The Crystal Structure of the Primary Ca2+ Sensor of the Na+/Ca2+ Exchanger Reveals a Novel Ca2+ Binding Motif*. Journal of Biological Chemistry, 2006, 281, 21577-21581.	3.4	107
10	Lactose permease as a paradigm for membrane transport proteins (Review). Molecular Membrane Biology, 2004, 21, 227-236.	2.0	106
11	The second Ca ²⁺ -binding domain of the Na ⁺ â€“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
12	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
13	The lactose permease of Escherichia coli: overall structure, the sugarâ€binding site and the alternating access model for transport. FEBS Letters, 2003, 555, 96-101.	2.8	92
14	Structure-guided simulations illuminate the mechanism of ATP transport through VDAC1. Nature Structural and Molecular Biology, 2014, 21, 626-632.	8.2	87
15	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
16	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
17	The Electrostatics of VDAC: Implications for Selectivity and Gating. Journal of Molecular Biology, 2010, 396, 580-592.	4.2	81
18	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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19	Affixing N-terminal Î±-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
20	Substrate-bound outward-open structure of a Na+-coupled sialic acid symporter reveals a new Na+ site. Nature Communications, 2018, 9, 1753.	12.8	62
21	Photoaffinity labeling with cholesterol analogues precisely maps a cholesterol-binding site in voltage-dependent anion channel-1. Journal of Biological Chemistry, 2017, 292, 9294-9304.	3.4	54
22	Bridging the gap between structure and kinetics of human SGLT1. American Journal of Physiology - Cell Physiology, 2012, 302, C1293-C1305.	4.6	51
23	Structure of cytochrome c oxidase: a comparison of the bacterial and mitochondrial enzymes. BBA - Proteins and Proteomics, 2001, 1544, 1-9.	2.1	47
24	Bridging the gap: A GFPâ€based strategy for overexpression and purification of membrane proteins with intra and extracellular Câ€termini. Protein Science, 2010, 19, 868-880.	7.6	45
25	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
26	Water Permeation through the Sodium-Dependent Galactose Cotransporter vSGLT. Biophysical Journal, 2010, 99, L56-L58.	0.5	41
27	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
28	A lower affinity to cytosolic proteins reveals VDAC3 isoform-specific role in mitochondrial biology. Journal of General Physiology, 2020, 152, .	1.9	36
29	Structural features and lipid binding domain of tubulin on biomimetic mitochondrial membranes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3622-E3631.	7.1	35
30	MicroED structure of lipid-embedded mammalian mitochondrial voltage-dependent anion channel. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32380-32385.	7.1	35
31	Conformational transitions of the sodium-dependent sugar transporter, vSGLT. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2742-E2751.	7.1	33
32	A large Rab GTPase encoded by CRACR2A is a component of subsynaptic vesicles that transmit T cell activation signals. Science Signaling, 2016, 9, ra31.	3.6	29
33	Assessing the role of residue E73 and lipid headgroup charge in VDAC1 voltage gating. Biochimica Et Biophysica Acta - Bioenergetics, 2019, 1860, 22-29.	1.0	27
34	ABCB10 exports mitochondrial biliverdin, driving metabolic maladaptation in obesity. Science Translational Medicine, 2021, 13, .	12.4	27
35	Structure and Functional Analysis of a Ca2+ Sensor Mutant of the Na+/Ca2+ Exchanger. Journal of Biological Chemistry, 2009, 284, 14688-14692.	3.4	26
36	Protonation state of glutamate 73 regulates the formation of a specific dimeric association of mVDAC1. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E172-E179.	7.1	26

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37	Multiple neurosteroid and cholesterol binding sites in voltage-dependent anion channel-1 determined by photo-affinity labeling. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2019, 1864, 1269-1279.	2.4	26
38	Structural Determinants of Water Permeation through the Sodium-Galactose Transporter vSGLT. Biophysical Journal, 2014, 106, 1280-1289.	0.5	25
39	High-throughput Crystallization of Membrane Proteins Using the Lipidic Bicelle Method. Journal of Visualized Experiments, 2012, , e3383.	0.3	23
40	Harnessing photoinduced electron transfer to optically determine protein sub-nanoscale atomic distances. Nature Communications, 2018, 9, 4738.	12.8	23
41	Click Chemistry Reagent for Identification of Sites of Covalent Ligand Incorporation in Integral Membrane Proteins. Analytical Chemistry, 2017, 89, 2636-2644.	6.5	20
42	Identification of a Second Substrate-binding Site in Solute-Sodium Symporters. Journal of Biological Chemistry, 2015, 290, 127-141.	3.4	18
43	Genotypeâ€“phenotype correlations and novel molecular insights into the DHX30-associated neurodevelopmental disorders. Genome Medicine, 2021, 13, 90.	8.2	16
44	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
45	Fusion protein approach to improve the crystal quality of cytochrome bo3 ubiquinol oxidase from Escherichia coli. Biochimica Et Biophysica Acta - Bioenergetics, 2000, 1459, 449-455.	1.0	14
46	How Does Regulatory Ca²⁺Regulate the Na⁺-Ca²⁺Exchanger?. Channels, 2007, 1, 397-399.	2.8	13
47	Characterization and Purification of a Na+/Ca2+ Exchanger from an Archaebacterium. Journal of Biological Chemistry, 2012, 287, 8652-8659.	3.4	13
48	Watch Water Flow. Science, 2013, 340, 1294-1295.	12.6	13
49	Chapter 5 Practical Aspects of Membrane Proteins Crystallization in Bicelles. Current Topics in Membranes, 2009, 63, 109-125.	0.9	12
50	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
51	Purification, crystallization and preliminary crystallographic studies of an integral membrane protein, cytochromebo3ubiquinol oxidase fromEscherichia coli. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1076-1078.	2.5	10
52	Functional and structural analyses of novel Smith-Kingsmore Syndrome-Associated MTOR variants reveal potential new mechanisms and predictors of pathogenicity. PLoS Genetics, 2021, 17, e1009651.	3.5	9
53	It's All in the Symmetry. Science, 2012, 335, 669-670.	12.6	8
54	Charge Reduction of Membrane Proteins in Native Mass Spectrometry Using Alkali Metal Acetate Salts. Analytical Chemistry, 2020, 92, 6622-6630.	6.5	8

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55	Structure and function of qiuinone binding membrane proteins. Advances in Protein Chemistry, 2003, 63, 151-176.	4.4	4
56	An Assessment of How VDAC Structures Have Impacted Our Understanding of Their Function. Biological and Medical Physics Series, 2017, , 141-160.	0.4	4
57	Protein structure reveals how a malaria parasite imports a wide range of sugars. Nature, 2020, 578, 220-221.	27.8	4
58	Function Trumps Form in Two Sugar Symporters, LacY and vSGLT. International Journal of Molecular Sciences, 2021, 22, 3572.	4.1	4
59	Structural Analysis of Murine Voltage Dependent Anion Channel (VDAC) 1. FASEB Journal, 2006, 20, .	0.5	0
60	Ca 2+ regulation of the Na + /Ca 2+ exchanger. FASEB Journal, 2009, 23, 698.1.	0.5	0
61	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