Jens P Morth

List of Publications by Year
in descending order

72 papers	4,677 citations	159585 30 h-index	110387 64 g-index
77 all docs	77 docs citations	77 times ranked	5934 citing authors

#	Article	IF	Citations
1	Migraineâ€Associated Mutation in the Na,Kâ€ATPase Leads to Disturbances in Cardiac Metabolism and Reduced Cardiac Function. Journal of the American Heart Association, 2022, 11, e021814.	3.7	9
2	A GH115 Î±-glucuronidase structure reveals dimerization-mediated substrate binding and a proton wire potentially important for catalysis. Acta Crystallographica Section D: Structural Biology, 2022, 78, 658-668.	2.3	2
3	Phospholipids alter activity and stability of mitochondrial membrane-bound ubiquitin ligase MARCH5. Life Science Alliance, 2022, 5, e202101309.	2.8	4
4	Searching for a UV-filter in the eyes of high-flying birds. Scientific Reports, 2021, 11, 273.	3.3	3
5	Substrate binding in the processive cellulase Cel7A: Transition state of complexation and roles of conserved tryptophan residues. Journal of Biological Chemistry, 2020, 295, 1454-1463.	3.4	14
6	Structural and biochemical characterization of a family 7 highly thermostable endoglucanase from the fungus Rasamsonia emersonii. FEBS Journal, 2020, 287, 2577-2596.	4.7	11
7	The extracellular juncture domains in the intimin passenger adopt a constitutively extended conformation inducing restraints to its sphere of action. Scientific Reports, 2020, 10, 21249.	3.3	8
8	SjÃ¶gren syndrome/scleroderma autoantigen 1 is a direct Tankyrase binding partner in cancer cells. Communications Biology, 2020, 3, 123.	4.4	5
9	Physicochemical Characterisation of KEIFâ€"The Intrinsically Disordered N-Terminal Region of Magnesium Transporter A. Biomolecules, 2020, 10, 623.	4.0	5
10	Characterization of the enzymatic activity of the serine protease domain of Factor VII activating protease (FSAP). Scientific Reports, 2019, 9, 18990.	3.3	13
11	Factor VII deficiency: Unveiling the cellular and molecular mechanisms underlying three model alterations of the enzyme catalytic domain. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 660-667.	3.8	11
12	Structural Origin of Metal Specificity in Isatin Hydrolase from Labrenzia aggregata Investigated by Computer Simulations. Chemistry - A European Journal, 2018, 24, 5074-5077.	3.3	4
13	A fundamental catalytic difference between zinc and manganese dependent enzymes revealed in a bacterial isatin hydrolase. Scientific Reports, 2018, 8, 13104.	3.3	10
14	TBC1D5 controls the GTPase cycle of Rab7b. Journal of Cell Science, 2018, 131, .	2.0	32
15	Overview of the membrane-associated RING-CH (MARCH) E3 ligase family. New Biotechnology, 2017, 38, 7-15.	4.4	56
16	The crystal structure of the regulatory domain of the human sodium-driven chloride/bicarbonate exchanger. Scientific Reports, 2017, 7, 12131.	3.3	7
17	Loss-of-activity-mutation in the cardiac chloride-bicarbonate exchanger AE3 causes short QT syndrome. Nature Communications, 2017, 8, 1696.	12.8	88
18	Malonate in the nucleotide-binding site traps human AKAP18Î³/Î´ in a novel conformational state. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 591-597.	0.8	5

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19	Crystal Structure of a Two-domain Fragment of Hepatocyte Growth Factor Activator Inhibitor-1. Journal of Biological Chemistry, 2016, 291, 14340-14355.	3.4	16
20	Data for the co-expression and purification of human recombinant CaMKK2 in complex with calmodulin in Escherichia coli. Data in Brief, 2016, 8, 733-740.	1.0	3
21	Secretion of the Intimin Passenger Domain Is Driven by Protein Folding. Journal of Biological Chemistry, 2016, 291, 20096-20112.	3.4	17
22	Using the fluorescent properties of STO-609 as a tool to assist structure-function analyses of recombinant CaMKK2. Biochemical and Biophysical Research Communications, 2016, 476, 102-107.	2.1	4
23	The magnesium transporter A is activated by cardiolipin and is highly sensitive to free magnesium in vitro. ELife, 2016, 5, .	6.0	40
24	The magnesium transporter A, a bacterial P-type ATPase dependent on cardiolipin and selectively sensitive to free magnesium in vitro. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s48-s48.	0.1	0
25	Structural and biochemical characterization of SjÃ¶gren syndrome/scleroderma autoantigen 1 (SSSCA1). Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s254-s254.	0.1	0
26	Reduced expression of aquaporins in human intestinal mucosa in early stage inflammatory bowel disease. Clinical and Experimental Gastroenterology, 2015, 8, 49.	2.3	62
27	Enzymatic Detection and Quantification Assay of Isatin, a Putative Stress Biomarker in Blood. ACS Chemical Neuroscience, 2015, 6, 1353-1360.	3.5	7
28	A Proton Wire and Water Channel Revealed in the Crystal Structure of Isatin Hydrolase. Journal of Biological Chemistry, 2014, 289, 21351-21359.	3.4	20
29	Cellular Disposal of miR23b by RAB27-Dependent Exosome Release Is Linked to Acquisition of Metastatic Properties. Cancer Research, 2014, 74, 5758-5771.	0.9	237
30	The glia doctrine: Addressing the role of glial cells in healthy brain ageing. Mechanisms of Ageing and Development, 2013, 134, 449-459.	4.6	28
31	Structural Basis and SAR for G007-LK, a Lead Stage 1,2,4-Triazole Based Specific Tankyrase 1/2 Inhibitor. Journal of Medicinal Chemistry, 2013, 56, 3012-3023.	6.4	109
32	The N-terminal cytoplasmic region of NCBE displays features of an intrinsic disordered structure and represents a novel target for specific drug screening. Frontiers in Physiology, 2013, 4, 320.	2.8	2
33	Probing determinants of cyclopiazonic acid sensitivity of bacterial <scp>C</scp>a²⁺â€<scp>ATP</scp>ases. FEBS Journal, 2013, 280, 5441-5449.	4.7	8
34	Ion Pathways in the Sarcoplasmic Reticulum Ca2+-ATPase. Journal of Biological Chemistry, 2013, 288, 10759-10765.	3.4	125
35	Identifying ligand-binding hot spots in proteins using brominated fragments. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1060-1065.	0.7	10
36	Probing determinants of cyclopiazonic acid sensitivity of bacterial Ca2+-ATPases. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s367-s367.	0.3	0

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37	The sensor region of the ubiquitous cytosolic sensor kinase, PdtaS, contains PAS and GAF domain sensing modules. Journal of Structural Biology, 2012, 177, 498-505.	2.8	18
38	Purification, crystallization and preliminary crystallographic studies of a PacL homologue fromListeria monocytogenes. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 424-427.	0.7	5
39	Abstract 3387: Secreted exosomes from cultured bladder cells are enriched for distinct miRNAs detected in circulation of metastatic bladder cancer patients. , 2012, , .		1
40	HiLiDeâ€"Systematic Approach to Membrane Protein Crystallization in Lipid and Detergent. Crystal Growth and Design, 2011, 11, 2098-2106.	3.0	72
41	P-type ATPases at a glance. Journal of Cell Science, 2011, 124, 3917-3917.	2.0	12
42	Crystal structure of a copper-transporting PIB-type ATPase. Nature, 2011, 475, 59-64.	27.8	293
43	Structural insights into the high affinity binding of cardiotonic steroids to the Na+,K+-ATPase. Journal of Structural Biology, 2011, 174, 296-306.	2.8	146
44	A structural overview of the plasma membrane Na+,K+-ATPase and H+-ATPase ion pumps. Nature Reviews Molecular Cell Biology, 2011, 12, 60-70.	37.0	345
45	Crystallization and preliminary structural analysis of theListeria monocytogenesCa²⁺-ATPase LMCA1. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 718-722.	0.7	12
46	Crystal Structure of Plasminogen Activator Inhibitor-1 in an Active Conformation with Normal Thermodynamic Stability*. Journal of Biological Chemistry, 2011, 286, 29709-29717.	3.4	32
47	P-type ATPases at a glance. Journal of Cell Science, 2011, 124, 2515-2519.	2.0	125
48	Characterization of a Listeria monocytogenes Ca2+ Pump. Journal of Biological Chemistry, 2011, 286, 1609-1617.	3.4	37
49	The Plasmodium falciparum Ca2+-ATPase PfATP6: insensitive to artemisinin, but a potential drug target. Biochemical Society Transactions, 2011, 39, 823-831.	3.4	59
50	In and out of the cation pumps: P-Type ATPase structure revisited. Current Opinion in Structural Biology, 2010, 20, 431-439.	5.7	129
51	Ion transport by the sodium pump. Biochimica Et Biophysica Acta - Bioenergetics, 2010, 1797, 26-27.	1.0	0
52	Phosphorylation of the Na⁺,K⁺â€ATPase and the H⁺,K⁺â€ATPase. FEBS Letters, 2010, 584, 2589-2595.	2.8	86
53	Structure determination using poorly diffracting membrane-protein crystals: the H⁺-ATPase and Na⁺,K⁺-ATPase case history. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 309-313.	2.5	15
54	Neurological disease mutations compromise a C-terminal ion pathway in the Na+/K+-ATPase. Nature, 2010, 467, 99-102.	27.8	125

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55	A systematic approach to membrane protein crystallization in bilayers. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s14-s14.	0.3	2
56	Crystallographic analysis reveals a unique lidocaine binding site on human serum albumin. Journal of Structural Biology, 2010, 171, 353-360.	2.8	93
57	The structure of the Na ⁺ ,K ⁺ -ATPase and mapping of isoform differences and disease-related mutations. Philosophical Transactions of the Royal Society B: Biological Sciences, 2009, 364, 217-227.	4.0	78
58	The C Terminus of Na+,K+-ATPase Controls Na+ Affinity on Both Sides of the Membrane through Arg935. Journal of Biological Chemistry, 2009, 284, 18715-18725.	3.4	49
59	Cyclopiazonic Acid Is Complexed to a Divalent Metal Ion When Bound to the Sarcoplasmic Reticulum Ca2+-ATPase. Journal of Biological Chemistry, 2009, 284, 13513-13518.	3.4	90
60	P-type ATPases as drug targets: Tools for medicine and science. Biochimica Et Biophysica Acta - Bioenergetics, 2009, 1787, 207-220.	1.0	129
61	Molecular Insights Into The Modulation Of Sodium Binding Affinity And Voltage Sensitivity Of The Sodium-Potassium Pump From Molecular Dynamics Simulations, Electrophysiology And Structure. Biophysical Journal, 2009, 96, 210a.	0.5	0
62	X-ray crystallographic studies of the pig renal Na+,K+-ATPase. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, s30-s30.	0.3	0
63	The structure of the Ca2+-ATPase bound to cyclopiazonic acid reveals a complexed divalent ion. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, s150-s150.	0.3	0
64	Identification and Function of a Cytoplasmic K+ Site of the Na+, K+-ATPase. Journal of Biological Chemistry, 2008, 283, 27982-27990.	3.4	34
65	Twoâ€Component Systems of Mycobacterium tuberculosisâ€"Structureâ€Based Approaches. Methods in Enzymology, 2007, 423, 479-501.	1.0	15
66	Crystal structure of the plasma membrane proton pump. Nature, 2007, 450, 1111-1114.	27.8	359
67	The structural basis of calcium transport by the calcium pump. Nature, 2007, 450, 1036-1042.	27.8	419
68	Crystal structure of the sodiumâ€"potassium pump. Nature, 2007, 450, 1043-1049.	27.8	789
69	Membrane's Eleven: heavy-atom derivatives of membrane-protein crystals. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 877-882.	2.5	14
70	Structural and Functional Aspects of the Sensor Histidine Kinase PrrB from Mycobacterium tuberculosis. Structure, 2006, 14, 275-285.	3.3	41
71	A novel two-component system found inMycobacterium tuberculosis. FEBS Letters, 2005, 579, 4145-4148.	2.8	36
72	The Crystal and Solution Structure of a Putative Transcriptional Antiterminator from Mycobacterium tuberculosis. Structure, 2004, 12, 1595-1605.	3.3	42