

# Jens P Morth

## List of Publications by Year in descending order

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72  
papers

4,677  
citations

159525

30  
h-index

110317

64  
g-index

77  
all docs

77  
docs citations

77  
times ranked

5934  
citing authors

#	ARTICLE	IF	CITATIONS
1	Migraine-associated Mutation in the Na,K-ATPase Leads to Disturbances in Cardiac Metabolism and Reduced Cardiac Function. <i>Journal of the American Heart Association</i> , 2022, 11, e021814.	1.6	9
2	A GH115 $\pm$ glucuronidase structure reveals dimerization-mediated substrate binding and a proton wire potentially important for catalysis. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 658-668.	1.1	2
3	Phospholipids alter activity and stability of mitochondrial membrane-bound ubiquitin ligase MARCH5. <i>Life Science Alliance</i> , 2022, 5, e202101309.	1.3	4
4	Searching for a UV-filter in the eyes of high-flying birds. <i>Scientific Reports</i> , 2021, 11, 273.	1.6	3
5	Substrate binding in the processive cellulase Cel7A: Transition state of complexation and roles of conserved tryptophan residues. <i>Journal of Biological Chemistry</i> , 2020, 295, 1454-1463.	1.6	14
6	Structural and biochemical characterization of a family 7 highly thermostable endoglucanase from the fungus <i>Rasamsonia emersonii</i> . <i>FEBS Journal</i> , 2020, 287, 2577-2596.	2.2	11
7	The extracellular juncture domains in the intimin passenger adopt a constitutively extended conformation inducing restraints to its sphere of action. <i>Scientific Reports</i> , 2020, 10, 21249.	1.6	8
8	Sjögren syndrome/scleroderma autoantigen 1 is a direct Tankyrase binding partner in cancer cells. <i>Communications Biology</i> , 2020, 3, 123.	2.0	5
9	Physicochemical Characterisation of KEIF <sup>2</sup> The Intrinsically Disordered N-Terminal Region of Magnesium Transporter A. <i>Biomolecules</i> , 2020, 10, 623.	1.8	5
10	Characterization of the enzymatic activity of the serine protease domain of Factor VII activating protease (FSAP). <i>Scientific Reports</i> , 2019, 9, 18990.	1.6	13
11	Factor VII deficiency: Unveiling the cellular and molecular mechanisms underlying three model alterations of the enzyme catalytic domain. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 660-667.	1.8	11
12	Structural Origin of Metal Specificity in Isatin Hydrolase from <i>Labrenzia aggregata</i> Investigated by Computer Simulations. <i>Chemistry - A European Journal</i> , 2018, 24, 5074-5077.	1.7	4
13	A fundamental catalytic difference between zinc and manganese dependent enzymes revealed in a bacterial isatin hydrolase. <i>Scientific Reports</i> , 2018, 8, 13104.	1.6	10
14	TBC1D5 controls the GTPase cycle of Rab7b. <i>Journal of Cell Science</i> , 2018, 131, .	1.2	32
15	Overview of the membrane-associated RING-CH (MARCH) E3 ligase family. <i>New Biotechnology</i> , 2017, 38, 7-15.	2.4	56
16	The crystal structure of the regulatory domain of the human sodium-driven chloride/bicarbonate exchanger. <i>Scientific Reports</i> , 2017, 7, 12131.	1.6	7
17	Loss-of-activity-mutation in the cardiac chloride-bicarbonate exchanger AE3 causes short QT syndrome. <i>Nature Communications</i> , 2017, 8, 1696.	5.8	88
18	Malonate in the nucleotide-binding site traps human AKAP18 $\beta$ in a novel conformational state. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 591-597.	0.4	5

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19	Crystal Structure of a Two-domain Fragment of Hepatocyte Growth Factor Activator Inhibitor-1. <i>Journal of Biological Chemistry</i> , 2016, 291, 14340-14355.	1.6	16
20	Data for the co-expression and purification of human recombinant CaMKK2 in complex with calmodulin in <i>Escherichia coli</i> . <i>Data in Brief</i> , 2016, 8, 733-740.	0.5	3
21	Secretion of the Intimin Passenger Domain Is Driven by Protein Folding. <i>Journal of Biological Chemistry</i> , 2016, 291, 20096-20112.	1.6	17
22	Using the fluorescent properties of STO-609 as a tool to assist structure-function analyses of recombinant CaMKK2. <i>Biochemical and Biophysical Research Communications</i> , 2016, 476, 102-107.	1.0	4
23	The magnesium transporter A is activated by cardiolipin and is highly sensitive to free magnesium in vitro. <i>ELife</i> , 2016, 5, .	2.8	40
24	The magnesium transporter A, a bacterial P-type ATPase dependent on cardiolipin and selectively sensitive to free magnesium in vitro. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s48-s48.	0.0	0
25	Structural and biochemical characterization of Sjögren syndrome/scleroderma autoantigen 1 (SSSCA1). <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s254-s254.	0.0	0
26	Reduced expression of aquaporins in human intestinal mucosa in early stage inflammatory bowel disease. <i>Clinical and Experimental Gastroenterology</i> , 2015, 8, 49.	1.0	62
27	Enzymatic Detection and Quantification Assay of Isatin, a Putative Stress Biomarker in Blood. <i>ACS Chemical Neuroscience</i> , 2015, 6, 1353-1360.	1.7	7
28	A Proton Wire and Water Channel Revealed in the Crystal Structure of Isatin Hydrolase. <i>Journal of Biological Chemistry</i> , 2014, 289, 21351-21359.	1.6	20
29	Cellular Disposal of miR23b by RAB27-Dependent Exosome Release Is Linked to Acquisition of Metastatic Properties. <i>Cancer Research</i> , 2014, 74, 5758-5771.	0.4	237
30	The glia doctrine: Addressing the role of glial cells in healthy brain ageing. <i>Mechanisms of Ageing and Development</i> , 2013, 134, 449-459.	2.2	28
31	Structural Basis and SAR for G007-LK, a Lead Stage 1,2,4-Triazole Based Specific Tankyrase 1/2 Inhibitor. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 3012-3023.	2.9	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. <i>Frontiers in Physiology</i> , 2013, 4, 320.	1.3	2
33	Probing determinants of cyclopiazonic acid sensitivity of bacterial $\text{Ca}^{2+}$ -ATPases. <i>FEBS Journal</i> , 2013, 280, 5441-5449.	2.2	8
34	Ion Pathways in the Sarcoplasmic Reticulum $\text{Ca}^{2+}$ -ATPase. <i>Journal of Biological Chemistry</i> , 2013, 288, 10759-10765.	1.6	125
35	Identifying ligand-binding hot spots in proteins using brominated fragments. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1060-1065.	0.7	10
36	Probing determinants of cyclopiazonic acid sensitivity of bacterial $\text{Ca}^{2+}$ -ATPases. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s367-s367.	0.3	0

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37	The sensor region of the ubiquitous cytosolic sensor kinase, PtdaS, contains PAS and GAF domain sensing modules. <i>Journal of Structural Biology</i> , 2012, 177, 498-505.	1.3	18
38	Purification, crystallization and preliminary crystallographic studies of a PacL homologue from <i>Listeria monocytogenes</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 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	HiLiDe – Systematic Approach to Membrane Protein Crystallization in Lipid and Detergent. <i>Crystal Growth and Design</i> , 2011, 11, 2098-2106.	1.4	72
41	P-type ATPases at a glance. <i>Journal of Cell Science</i> , 2011, 124, 3917-3917.	1.2	12
42	Crystal structure of a copper-transporting PIB-type ATPase. <i>Nature</i> , 2011, 475, 59-64.	13.7	293
43	Structural insights into the high affinity binding of cardiotonic steroids to the Na <sup>+</sup> ,K <sup>+</sup> -ATPase. <i>Journal of Structural Biology</i> , 2011, 174, 296-306.	1.3	146
44	A structural overview of the plasma membrane Na <sup>+</sup> ,K <sup>+</sup> -ATPase and H <sup>+</sup> -ATPase ion pumps. <i>Nature Reviews Molecular Cell Biology</i> , 2011, 12, 60-70.	16.1	345
45	Crystallization and preliminary structural analysis of the <i>Listeria monocytogenes</i> Ca <sup>2+</sup> -ATPase LMCA1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 718-722.	0.7	12
46	Crystal Structure of Plasminogen Activator Inhibitor-1 in an Active Conformation with Normal Thermodynamic Stability*. <i>Journal of Biological Chemistry</i> , 2011, 286, 29709-29717.	1.6	32
47	P-type ATPases at a glance. <i>Journal of Cell Science</i> , 2011, 124, 2515-2519.	1.2	125
48	Characterization of a <i>Listeria monocytogenes</i> Ca <sup>2+</sup> Pump. <i>Journal of Biological Chemistry</i> , 2011, 286, 1609-1617.	1.6	37
49	The <i>Plasmodium falciparum</i> Ca <sup>2+</sup> -ATPase PfATP6: insensitive to artemisinin, but a potential drug target. <i>Biochemical Society Transactions</i> , 2011, 39, 823-831.	1.6	59
50	In and out of the cation pumps: P-Type ATPase structure revisited. <i>Current Opinion in Structural Biology</i> , 2010, 20, 431-439.	2.6	129
51	Ion transport by the sodium pump. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 26-27.	0.5	0
52	Phosphorylation of the Na <sup>+</sup> ,K <sup>+</sup> -ATPase and the H <sup>+</sup> ,K <sup>+</sup> -ATPase. <i>FEBS Letters</i> , 2010, 584, 2589-2595.	1.3	86
53	Structure determination using poorly diffracting membrane-protein crystals: the H <sup>+</sup> -ATPase and Na <sup>+</sup> ,K <sup>+</sup> -ATPase case history. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 309-313.	2.5	15
54	Neurological disease mutations compromise a C-terminal ion pathway in the Na <sup>+</sup> /K <sup>+</sup> -ATPase. <i>Nature</i> , 2010, 467, 99-102.	13.7	125

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55	A systematic approach to membrane protein crystallization in bilayers. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s14-s14.	0.3	2
56	Crystallographic analysis reveals a unique lidocaine binding site on human serum albumin. <i>Journal of Structural Biology</i> , 2010, 171, 353-360.	1.3	93
57	The structure of the Na <sup>+</sup> ,K <sup>+</sup> -ATPase and mapping of isoform differences and disease-related mutations. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 217-227.	1.8	78
58	The C Terminus of Na <sup>+</sup> ,K <sup>+</sup> -ATPase Controls Na <sup>+</sup> Affinity on Both Sides of the Membrane through Arg935. <i>Journal of Biological Chemistry</i> , 2009, 284, 18715-18725.	1.6	49
59	Cyclopiazonic Acid Is Complexed to a Divalent Metal Ion When Bound to the Sarcoplasmic Reticulum Ca <sup>2+</sup> -ATPase. <i>Journal of Biological Chemistry</i> , 2009, 284, 13513-13518.	1.6	90
60	P-type ATPases as drug targets: Tools for medicine and science. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2009, 1787, 207-220.	0.5	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. <i>Biophysical Journal</i> , 2009, 96, 210a.	0.2	0
62	X-ray crystallographic studies of the pig renal Na <sup>+</sup> ,K <sup>+</sup> -ATPase. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s30-s30.	0.3	0
63	The structure of the Ca <sup>2+</sup> -ATPase bound to cyclopiazonic acid reveals a complexed divalent ion. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s150-s150.	0.3	0
64	Identification and Function of a Cytoplasmic K <sup>+</sup> Site of the Na <sup>+</sup> , K <sup>+</sup> -ATPase. <i>Journal of Biological Chemistry</i> , 2008, 283, 27982-27990.	1.6	34
65	Two-Component Systems of <i>Mycobacterium tuberculosis</i> —Structure-Based Approaches. <i>Methods in Enzymology</i> , 2007, 423, 479-501.	0.4	15
66	Crystal structure of the plasma membrane proton pump. <i>Nature</i> , 2007, 450, 1111-1114.	13.7	359
67	The structural basis of calcium transport by the calcium pump. <i>Nature</i> , 2007, 450, 1036-1042.	13.7	419
68	Crystal structure of the sodium-potassium pump. <i>Nature</i> , 2007, 450, 1043-1049.	13.7	789
69	Membrane's Eleven: heavy-atom derivatives of membrane-protein crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 877-882.	2.5	14
70	Structural and Functional Aspects of the Sensor Histidine Kinase PrrB from <i>Mycobacterium tuberculosis</i> . <i>Structure</i> , 2006, 14, 275-285.	1.6	41
71	A novel two-component system found in <i>Mycobacterium tuberculosis</i> . <i>FEBS Letters</i> , 2005, 579, 4145-4148.	1.3	36
72	The Crystal and Solution Structure of a Putative Transcriptional Antiterminator from <i>Mycobacterium tuberculosis</i> . <i>Structure</i> , 2004, 12, 1595-1605.	1.6	42