

Haydyn D T Mertens

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

56

papers

4,911

citations

28

h-index

67

g-index

67

ext. papers

6,057

ext. citations

6.2

avg, IF

5.58

L-index

#	Paper	IF	Citations
56	Impact of Fluorinated Ionic Liquids on Human Phenylalanine Hydroxylase-A Potential Drug Delivery System.. <i>Nanomaterials</i> , 2022 , 12,	5.4	2
55	Structure of the endocytic adaptor complex reveals the basis for efficient membrane anchoring during clathrin-mediated endocytosis. <i>Nature Communications</i> , 2021 , 12, 2889	17.4	5
54	Restoring structural parameters of lipid mixtures from small-angle X-ray scattering data. <i>Journal of Applied Crystallography</i> , 2021 , 54, 169-179	3.8	6
53	: expanded functionality and new tools for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2021 , 54, 343-355	3.8	120
52	Conformational flexibility of EptA driven by an interdomain helix provides insights for enzyme-substrate recognition. <i>IUCrJ</i> , 2021 , 8, 732-746	4.7	0
51	An automated data processing and analysis pipeline for transmembrane proteins in detergent solutions. <i>Scientific Reports</i> , 2020 , 10, 8081	4.9	9
50	Unfolding of monomeric lipoprotein lipase by ANGPTL4: Insight into the regulation of plasma triglyceride metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 4337-4346	11.5	28
49	Structural role of essential light chains in the apicomplexan glideosome. <i>Communications Biology</i> , 2020 , 3, 568	6.7	6
48	Structure of full-length wild-type human phenylalanine hydroxylase by small angle X-ray scattering reveals substrate-induced conformational stability. <i>Scientific Reports</i> , 2019 , 9, 13615	4.9	8
47	Did evolution create a flexible ligand-binding cavity in the urokinase receptor through deletion of a plesiotypic disulfide bond?. <i>Journal of Biological Chemistry</i> , 2019 , 294, 7403-7418	5.4	9
46	Structure of the lipoprotein lipase-GPIHBP1 complex that mediates plasma triglyceride hydrolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 1723-1732	11.5	43
45	Structural Basis for Draxin-Modulated Axon Guidance and Fasciculation by Netrin-1 through DCC. <i>Neuron</i> , 2018 , 97, 1261-1267.e4	13.9	24
44	Epsin and Sla2 form assemblies through phospholipid interfaces. <i>Nature Communications</i> , 2018 , 9, 328	17.4	26
43	Structure, Function, and Biosynthetic Origin of Octapeptin Antibiotics Active against Extensively Drug-Resistant Gram-Negative Bacteria. <i>Cell Chemical Biology</i> , 2018 , 25, 380-391.e5	8.2	44
42	Sapoin Lipid Nanoparticles: A Highly Versatile and Modular Tool for Membrane Protein Research. <i>Structure</i> , 2018 , 26, 345-355.e5	5.2	40
41	Signaling ammonium across membranes through an ammonium sensor histidine kinase. <i>Nature Communications</i> , 2018 , 9, 164	17.4	22
40	Structural model of human dUTPase in complex with a novel proteinaceous inhibitor. <i>Scientific Reports</i> , 2018 , 8, 4326	4.9	9

39	Structural basis for activation of plasma-membrane Ca-ATPase by calmodulin. <i>Communications Biology</i> , 2018 , 1, 206	6.7	20
38	Conformational States of ABC Transporter MsbA in a Lipid Environment Investigated by Small-Angle Scattering Using Stealth Carrier Nanodiscs. <i>Structure</i> , 2018 , 26, 1072-1079.e4	5.2	44
37	Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. <i>Nature Microbiology</i> , 2017 , 2, 17047	26.6	74
36	Combining NMR and small angle X-ray scattering for the study of biomolecular structure and dynamics. <i>Archives of Biochemistry and Biophysics</i> , 2017 , 628, 33-41	4.1	28
35	: a comprehensive data analysis suite for small-angle scattering from macromolecular solutions. <i>Journal of Applied Crystallography</i> , 2017 , 50, 1212-1225	3.8	775
34	Structural Insights into the Polyphyletic Origins of Glycyl tRNA Synthetases. <i>Journal of Biological Chemistry</i> , 2016 , 291, 14430-46	5.4	9
33	Death-Associated Protein Kinase Activity Is Regulated by Coupled Calcium/Calmodulin Binding to Two Distinct Sites. <i>Structure</i> , 2016 , 24, 851-61	5.2	12
32	Crystal Structure of the CTP1L Endolysin Reveals How Its Activity Is Regulated by a Secondary Translation Product. <i>Journal of Biological Chemistry</i> , 2016 , 291, 4882-93	5.4	29
31	A Barley Efflux Transporter Operates in a Na ⁺ -Dependent Manner, as Revealed by a Multidisciplinary Platform. <i>Plant Cell</i> , 2016 , 28, 202-18	11.6	22
30	LabDisk for SAXS: a centrifugal microfluidic sample preparation platform for small-angle X-ray scattering. <i>Lab on A Chip</i> , 2016 , 16, 1161-70	7.2	34
29	Stabilization of nontoxic A β oligomers: insights into the mechanism of action of hydroxyquinolines in Alzheimer's disease. <i>Journal of Neuroscience</i> , 2015 , 35, 2871-84	6.6	56
28	Structural model of the cytosolic domain of the plant ethylene receptor 1 (ETR1). <i>Journal of Biological Chemistry</i> , 2015 , 290, 2644-58	5.4	23
27	Small angle X-ray scattering analysis of Cu(2+)-induced oligomers of the Alzheimer's amyloid β peptide. <i>Metallomics</i> , 2015 , 7, 536-43	4.5	19
26	Alpha-synuclein oligomers and fibrils originate in two distinct conformer pools: a small angle X-ray scattering and ensemble optimisation modelling study. <i>Molecular BioSystems</i> , 2015 , 11, 190-6		22
25	Advanced ensemble modelling of flexible macromolecules using X-ray solution scattering. <i>IUCrJ</i> , 2015 , 2, 207-17	4.7	353
24	The crystal structure of netrin-1 in complex with DCC reveals the bifunctionality of netrin-1 as a guidance cue. <i>Neuron</i> , 2014 , 83, 839-849	13.9	72
23	Measuring the molecular dimensions of wine tannins: comparison of small-angle X-ray scattering, gel-permeation chromatography and mean degree of polymerization. <i>Journal of Agricultural and Food Chemistry</i> , 2014 , 62, 7216-24	5.7	5
22	Using mutagenesis and structural biology to map the binding site for the Plasmodium falciparum merozoite protein PfRh4 on the human immune adherence receptor. <i>Journal of Biological Chemistry</i> , 2014 , 289, 450-63	5.4	23

21	The CD27L and CTP1L endolysins targeting Clostridia contain a built-in trigger and release factor. <i>PLoS Pathogens</i> , 2014 , 10, e1004228	7.6	34
20	Cell-free protein synthesis of membrane (1,3)- β -D-glucan (curdlan) synthase: co-translational insertion in liposomes and reconstitution in nanodiscs. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013 , 1828, 743-57	3.8	52
19	Small oligomers of ribulose-bisphosphate carboxylase/oxygenase (Rubisco) activase are required for biological activity. <i>Journal of Biological Chemistry</i> , 2013 , 288, 20607-15	5.4	25
18	A low-background-intensity focusing small-angle X-ray scattering undulator beamline. <i>Journal of Applied Crystallography</i> , 2013 , 46, 1670-1680	3.8	374
17	From knock-out phenotype to three-dimensional structure of a promising antibiotic target from <i>Streptococcus pneumoniae</i> . <i>PLoS ONE</i> , 2013 , 8, e83419	3.7	21
16	Ammonium hydroxide treatment of A β produces an aggregate free solution suitable for biophysical and cell culture characterization. <i>PeerJ</i> , 2013 , 1, e73	3.1	72
15	New developments in the program package for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2012 , 45, 342-350	3.8	1316
14	Solution structure of CCP modules 10-12 illuminates functional architecture of the complement regulator, factor H. <i>Journal of Molecular Biology</i> , 2012 , 424, 295-312	6.5	22
13	The PHD and chromo domains regulate the ATPase activity of the human chromatin remodeler CHD4. <i>Journal of Molecular Biology</i> , 2012 , 422, 3-17	6.5	51
12	Conformational analysis of a genetically encoded FRET biosensor by SAXS. <i>Biophysical Journal</i> , 2012 , 102, 2866-75	2.9	17
11	Structural analysis of the C-terminal region (modules 18-20) of complement regulator factor H (FH). <i>PLoS ONE</i> , 2012 , 7, e32187	3.7	31
10	Lack of evidence from studies of soluble protein fragments that Knops blood group polymorphisms in complement receptor-type 1 are driven by malaria. <i>PLoS ONE</i> , 2012 , 7, e34820	3.7	20
9	Characterisation of the first enzymes committed to lysine biosynthesis in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2012 , 7, e40318	3.7	39
8	A flexible multidomain structure drives the function of the urokinase-type plasminogen activator receptor (uPAR). <i>Journal of Biological Chemistry</i> , 2012 , 287, 34304-15	5.4	40
7	Recognition of mitochondrial targeting sequences by the import receptors Tom20 and Tom22. <i>Journal of Molecular Biology</i> , 2011 , 405, 804-18	6.5	42
6	Structural basis for engagement by complement factor H of C3b on a self surface. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 463-70	17.6	184
5	Structural characterization of proteins and complexes using small-angle X-ray solution scattering. <i>Journal of Structural Biology</i> , 2010 , 172, 128-41	3.4	406
4	The central portion of factor H (modules 10-15) is compact and contains a structurally deviant CCP module. <i>Journal of Molecular Biology</i> , 2010 , 395, 105-22	6.5	44

3	Structure, topology and function of the translocase of the outer membrane of mitochondria. <i>Plant Physiology and Biochemistry</i> , 2008 , 46, 265-74	5.4	51
2	A structural core within apolipoprotein C-II amyloid fibrils identified using hydrogen exchange and proteolysis. <i>Journal of Molecular Biology</i> , 2007 , 366, 1639-51	6.5	47
1	Structural role of essential light chains in the apicomplexan glideosome		2