

# Haydyn D T Mertens

## List of Publications by Year in descending order

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Version: 2024-02-01

61  
papers

6,783  
citations

126708

33  
h-index

149479

56  
g-index

67  
all docs

67  
docs citations

67  
times ranked

11669  
citing authors

#	ARTICLE	IF	CITATIONS
1	New developments in the <i>ATSAS</i> program package for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2012, 45, 342-350.	1.9	1,551
2	<i>ATSAS 2.8</i> : a comprehensive data analysis suite for small-angle scattering from macromolecular solutions. <i>Journal of Applied Crystallography</i> , 2017, 50, 1212-1225.	1.9	1,205
3	Advanced ensemble modelling of flexible macromolecules using X-ray solution scattering. <i>IUCr</i> , 2015, 2, 207-217.	1.0	516
4	<i>ATSAS 3.0</i> : expanded functionality and new tools for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2021, 54, 343-355.	1.9	512
5	Structural characterization of proteins and complexes using small-angle X-ray solution scattering. <i>Journal of Structural Biology</i> , 2010, 172, 128-141.	1.3	470
6	A low-background-intensity focusing small-angle X-ray scattering undulator beamline. <i>Journal of Applied Crystallography</i> , 2013, 46, 1670-1680.	1.9	450
7	Structural basis for engagement by complement factor H of C3b on a self surface. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 463-470.	3.6	220
8	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.	3.8	103
9	Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. <i>Nature Microbiology</i> , 2017, 2, 17047.	5.9	102
10	Ammonium hydroxide treatment of A $\beta$ 2 produces an aggregate free solution suitable for biophysical and cell culture characterization. <i>PeerJ</i> , 2013, 1, e73.	0.9	93
11	Sapoin Lipid Nanoparticles: A Highly Versatile and Modular Tool for Membrane Protein Research. <i>Structure</i> , 2018, 26, 345-355.e5.	1.6	69
12	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.	2.0	68
13	Stabilization of Nontoxic A $\beta$ -Oligomers: Insights into the Mechanism of Action of Hydroxyquinolines in Alzheimer's Disease. <i>Journal of Neuroscience</i> , 2015, 35, 2871-2884.	1.7	67
14	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.	3.3	67
15	Structure, topology and function of the translocase of the outer membrane of mitochondria. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 265-274.	2.8	59
16	Cell-free protein synthesis of membrane (1,3)- $\beta$ -d-glucan (curdian) synthase: Co-translational insertion in liposomes and reconstitution in nanodiscs. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 743-757.	1.4	58
17	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.	1.6	58
18	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.	2.5	57

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19	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.	3.3	56
20	A Structural Core Within Apolipoprotein C-II Amyloid Fibrils Identified Using Hydrogen Exchange and Proteolysis. <i>Journal of Molecular Biology</i> , 2007, 366, 1639-1651.	2.0	53
21	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, 105-122.	2.0	51
22	Epsin and Sla2 form assemblies through phospholipid interfaces. <i>Nature Communications</i> , 2018, 9, 328.	5.8	47
23	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.	1.4	46
24	Characterisation of the First Enzymes Committed to Lysine Biosynthesis in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2012, 7, e40318.	1.1	45
25	LabDisk for SAXS: a centrifugal microfluidic sample preparation platform for small-angle X-ray scattering. <i>Lab on A Chip</i> , 2016, 16, 1161-1170.	3.1	44
26	Recognition of Mitochondrial Targeting Sequences by the Import Receptors Tom20 and Tom22. <i>Journal of Molecular Biology</i> , 2011, 405, 804-818.	2.0	43
27	A Flexible Multidomain Structure Drives the Function of the Urokinase-type Plasminogen Activator Receptor (uPAR)*. <i>Journal of Biological Chemistry</i> , 2012, 287, 34304-34315.	1.6	43
28	Structural Analysis of the C-Terminal Region (Modules 18-20) of Complement Regulator Factor H (FH). <i>PLoS ONE</i> , 2012, 7, e32187.	1.1	39
29	Structural Basis for Draxin-Modulated Axon Guidance and Fasciculation by Netrin-1 through DCC. <i>Neuron</i> , 2018, 97, 1261-1267.e4.	3.8	39
30	The CD27L and CTP1L Endolysins Targeting Clostridia Contain a Built-in Trigger and Release Factor. <i>PLoS Pathogens</i> , 2014, 10, e1004228.	2.1	37
31	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, 4882-4893.	1.6	36
32	Signaling ammonium across membranes through an ammonium sensor histidine kinase. <i>Nature Communications</i> , 2018, 9, 164.	5.8	36
33	Structural Model of the Cytosolic Domain of the Plant Ethylene Receptor 1 (ETR1). <i>Journal of Biological Chemistry</i> , 2015, 290, 2644-2658.	1.6	35
34	Small Oligomers of Ribulose-bisphosphate Carboxylase/Oxygenase (Rubisco) Activase Are Required for Biological Activity. <i>Journal of Biological Chemistry</i> , 2013, 288, 20607-20615.	1.6	30
35	Using Mutagenesis and Structural Biology to Map the Binding Site for the <i>Plasmodium falciparum</i> Merozoite Protein PfRh4 on the Human Immune Adherence Receptor. <i>Journal of Biological Chemistry</i> , 2014, 289, 450-463.	1.6	30
36	Structural basis for activation of plasma-membrane Ca <sup>2+</sup> -ATPase by calmodulin. <i>Communications Biology</i> , 2018, 1, 206.	2.0	30

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37	A Barley Efflux Transporter Operates in a Na <sup>+</sup> -Dependent Manner, as Revealed by a Multidisciplinary Platform. <i>Plant Cell</i> , 2016, 28, 202-218.	3.1	29
38	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.	1.1	25
39	Small angle X-ray scattering analysis of Cu <sup>2+</sup> -induced oligomers of the Alzheimer's amyloid $\beta$ peptide. <i>Metallomics</i> , 2015, 7, 536-543.	1.0	25
40	Solution Structure of CCP Modules 10 <sup>Å</sup> –12 Illuminates Functional Architecture of the Complement Regulator, Factor H. <i>Journal of Molecular Biology</i> , 2012, 424, 295-312.	2.0	24
41	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, 190-196.	2.9	24
42	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.	1.1	22
43	Death-Associated Protein Kinase Activity Is Regulated by Coupled Calcium/Calmodulin Binding to Two Distinct Sites. <i>Structure</i> , 2016, 24, 851-861.	1.6	21
44	Conformational Analysis of a Genetically Encoded FRET Biosensor by SAXS. <i>Biophysical Journal</i> , 2012, 102, 2866-2875.	0.2	19
45	Restoring structural parameters of lipid mixtures from small-angle X-ray scattering data. <i>Journal of Applied Crystallography</i> , 2021, 54, 169-179.	1.9	17
46	Structural Insights into the Polyphyletic Origins of Glycyl tRNA Synthetases. <i>Journal of Biological Chemistry</i> , 2016, 291, 14430-14446.	1.6	16
47	Structural model of human dUTPase in complex with a novel proteinaceous inhibitor. <i>Scientific Reports</i> , 2018, 8, 4326.	1.6	15
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.	1.6	13
49	Structure of the endocytic adaptor complex reveals the basis for efficient membrane anchoring during clathrin-mediated endocytosis. <i>Nature Communications</i> , 2021, 12, 2889.	5.8	13
50	An automated data processing and analysis pipeline for transmembrane proteins in detergent solutions. <i>Scientific Reports</i> , 2020, 10, 8081.	1.6	12
51	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.	1.6	11
52	Structural role of essential light chains in the apicomplexan glideosome. <i>Communications Biology</i> , 2020, 3, 568.	2.0	10
53	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, 7216-7224.	2.4	5
54	Conformational flexibility of EptA driven by an interdomain helix provides insights for enzyme-substrate recognition. <i>IUCr</i> , 2021, 8, 732-746.	1.0	5

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55	Impact of Fluorinated Ionic Liquids on Human Phenylalanine Hydroxylase—A Potential Drug Delivery System. <i>Nanomaterials</i> , 2022, 12, 893.	1.9	5
56	N-terminal phosphorylation regulates the activity of glycogen synthase kinase 3 from <i>Plasmodium falciparum</i> . <i>Biochemical Journal</i> , 2022, 479, 337-356.	1.7	2
57	Hybrid solution methods for tackling membrane proteins. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a66-a66.	0.0	0
58	Outrunning radiation damage in synchrotron biological small-angle X-ray scattering. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a191-a191.	0.0	0
59	Integrating SEC-SAXS with MALLS/QELS/RI at the EMBL-P12 bioSAXS beamline. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C652-C652.	0.0	0
60	ATSAS 2.8 software for small-angle scattering from macromolecular solutions. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C647-C647.	0.0	0
61	Coflow SEC-SAXS at high flux. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a336-a336.	0.0	0