

# Hans Hebert

## List of Publications by Year in descending order

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81  
papers

5,294  
citations

126907

33  
h-index

88630

70  
g-index

85  
all docs

85  
docs citations

85  
times ranked

7475  
citing authors

#	ARTICLE	IF	CITATIONS
1	The gut microbiota influences blood-brain barrier permeability in mice. <i>Science Translational Medicine</i> , 2014, 6, 263ra158.	12.4	1,589
2	Bicarbonate and functional CFTR channel are required for proper mucin secretion and link cystic fibrosis with its mucus phenotype. <i>Journal of Experimental Medicine</i> , 2012, 209, 1263-1272.	8.5	292
3	Calcium and pH-dependent packing and release of the gel-forming MUC2 mucin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5645-5650.	7.1	265
4	Biomimetic spinning of artificial spider silk from a chimeric minispidroin. <i>Nature Chemical Biology</i> , 2017, 13, 262-264.	8.0	231
5	Structure of potassium channels. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 3677-3693.	5.4	187
6	The cyclin-dependent kinase 8 module sterically blocks Mediator interactions with RNA polymerase II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15788-15793.	7.1	186
7	Human Microsomal Prostaglandin E Synthase-1. <i>Journal of Biological Chemistry</i> , 2003, 278, 22199-22209.	3.4	153
8	Structural basis for induced formation of the inflammatory mediator prostaglandin E <sub>2</sub> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 11110-11115.	7.1	139
9	Structural Basis for Detoxification and Oxidative Stress Protection in Membranes. <i>Journal of Molecular Biology</i> , 2006, 360, 934-945.	4.2	129
10	Efficient protein production inspired by how spiders make silk. <i>Nature Communications</i> , 2017, 8, 15504.	12.8	102
11	The normal trachea is cleaned by MUC5B mucin bundles from the submucosal glands coated with the MUC5AC mucin. <i>Biochemical and Biophysical Research Communications</i> , 2017, 492, 331-337.	2.1	92
12	STRUCTURE OF THE Na, K PUMP: CRYSTALLIZATION OF PURE MEMBRANE-BOUND Na, K-ATPase AND IDENTIFICATION OF FUNCTIONAL DOMAINS OF THE $\gamma$ -SUBUNIT. <i>Annals of the New York Academy of Sciences</i> , 1982, 402, 207-225.	3.8	89
13	The projection structure of Perfringolysin O ( <i>Clostridium perfringens</i> $\beta$ -toxin). <i>FEBS Letters</i> , 1993, 319, 125-127.	2.8	81
14	Three-dimensional structure of renal Na,K-ATPase from cryo-electron microscopy of two-dimensional crystals 1 Edited by M. F. Moody. <i>Journal of Molecular Biology</i> , 2001, 314, 479-494.	4.2	76
15	Magnetite Nanoparticles Can Be Coupled to Microbubbles to Support Multimodal Imaging. <i>Biomacromolecules</i> , 2012, 13, 1390-1399.	5.4	73
16	Structural basis of recognition and destabilization of the histone H2B ubiquitinated nucleosome by the DOT1L histone H3 Lys79 methyltransferase. <i>Genes and Development</i> , 2019, 33, 620-625.	5.9	73
17	ATP-Induced Conformational Dynamics in the AAA+ Motor Unit of Magnesium Chelatase. <i>Structure</i> , 2010, 18, 354-365.	3.3	70
18	Identification of Key Residues Determining Species Differences in Inhibitor Binding of Microsomal Prostaglandin E Synthase-1*. <i>Journal of Biological Chemistry</i> , 2010, 285, 29254-29261.	3.4	68

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19	Bri2 BRICHOS client specificity and chaperone activity are governed by assembly state. <i>Nature Communications</i> , 2017, 8, 2081.	12.8	67
20	Two-dimensional crystals of membrane-bound gastric H,K-ATPase. <i>FEBS Letters</i> , 1992, 299, 159-162.	2.8	55
21	Single-particle cryoelectron microscopy analysis reveals the HIV-1 spike as a tripod structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18844-18849.	7.1	55
22	Huntingtin <sup>TM</sup> 's spherical solenoid structure enables polyglutamine tract-dependent modulation of its structure and function. <i>ELife</i> , 2016, 5, e11184.	6.0	52
23	Granule-stored MUC5B mucins are packed by the non-covalent formation of N-terminal head-to-head tetramers. <i>Journal of Biological Chemistry</i> , 2018, 293, 5746-5754.	3.4	50
24	Projection structure at 8 Å resolution of the melibiose permease, an Na-sugar co-transporter from <i>Escherichia coli</i> . <i>EMBO Journal</i> , 2002, 21, 3569-3574.	7.8	44
25	A New Cryo-EM Single-Particle Ab Initio Reconstruction Method Visualizes Secondary Structure Elements in an ATP-Fueled AAA+ Motor. <i>Journal of Molecular Biology</i> , 2008, 375, 934-947.	4.2	44
26	On the interplay of shell structure with low- and high-frequency mechanics of multifunctional magnetic microbubbles. <i>Soft Matter</i> , 2014, 10, 214-226.	2.7	44
27	Crystalline layers and three-dimensional structure of <i>Staphylococcus aureus</i> $\alpha$ -toxin. <i>Journal of Molecular Biology</i> , 1990, 214, 299-306.	4.2	43
28	Structural modelling of the DNAJB6 oligomeric chaperone shows a peptide-binding cleft lined with conserved S/T-residues at the dimer interface. <i>Scientific Reports</i> , 2018, 8, 5199.	3.3	43
29	Transmembrane topology of FRO2, a ferric chelate reductase from <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2006, 62, 215-221.	3.9	42
30	Augmentation of Bri2 molecular chaperone activity against amyloid- $\beta^2$ reduces neurotoxicity in mouse hippocampus in vitro. <i>Communications Biology</i> , 2020, 3, 32.	4.4	42
31	The 3.0 Å... projection structure of microsomal glutathione transferase as determined by electron crystallography of p 21212 two-dimensional crystals. <i>Journal of Molecular Biology</i> , 1997, 271, 751-758.	4.2	40
32	Aldehyde-alcohol dehydrogenase forms a high-order spirosome architecture critical for its activity. <i>Nature Communications</i> , 2019, 10, 4527.	12.8	39
33	Intestinal MUC2 Mucin Supramolecular Topology by Packing and Release Resting on D3 Domain Assembly. <i>Journal of Molecular Biology</i> , 2014, 426, 2567-2579.	4.2	36
34	The projection structure of the membrane protein microsomal glutathione transferase at 3 Å... resolution as determined from two-dimensional hexagonal crystals. <i>Journal of Molecular Biology</i> , 1999, 288, 243-253.	4.2	34
35	Peptide Anchor for Folate-Targeted Liposomal Delivery. <i>Biomacromolecules</i> , 2015, 16, 2904-2910.	5.4	34
36	Location of Substrate Binding Sites within the Integral Membrane Protein Microsomal Glutathione Transferase-1. <i>Biochemistry</i> , 2007, 46, 2812-2822.	2.5	33

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37	A spiderinâ€derived solubility tag enables controlled aggregation of a designed amyloid protein. FEBS Journal, 2018, 285, 1873-1885.	4.7	32
38	Cryo-EM Reveals Promoter DNA Binding and Conformational Flexibility of the General Transcription Factor TFIID. Structure, 2009, 17, 1442-1452.	3.3	31
39	Microsomal glutathione transferase 1 exhibits one-third-of-the-sites-reactivity towards glutathione. Archives of Biochemistry and Biophysics, 2009, 487, 42-48.	3.0	31
40	Cryoâ€EM structure of native human uromodulin, a zona pellucida module polymer. EMBO Journal, 2020, 39, e106807.	7.8	31
41	Subunit arrangement in the dodecameric chloroplast small heat shock protein Hsp21. Protein Science, 2011, 20, 291-301.	7.6	29
42	Liposome and protein based stealth nanoparticles. Faraday Discussions, 2013, 166, 417.	3.2	26
43	Size controlled protein nanoemulsions for active targeting of folate receptor positive cells. Colloids and Surfaces B: Biointerfaces, 2015, 135, 90-98.	5.0	26
44	Molecular Architecture of Yeast Chromatin Assembly Factor 1. Scientific Reports, 2016, 6, 26702.	3.3	26
45	The structure of membrane associated proteins in eicosanoid and glutathione metabolism as determined by electron crystallography. Current Opinion in Structural Biology, 2007, 17, 396-404.	5.7	25
46	Exploring the activity of tobacco etch virus protease in detergent solutions. Analytical Biochemistry, 2008, 382, 69-71.	2.4	25
47	Structural model of dodecameric heat-shock protein Hsp21: Flexible N-terminal arms interact with client proteins while C-terminal tails maintain the dodecamer and chaperone activity. Journal of Biological Chemistry, 2017, 292, 8103-8121.	3.4	24
48	The Polyglutamine Expansion at the N-Terminal of Huntingtin Protein Modulates the Dynamic Configuration and Phosphorylation of the C-Terminal HEAT Domain. Structure, 2020, 28, 1035-1050.e8.	3.3	24
49	RNA activationâ€independent DNA targeting of the Type III CRISPRâ€Cas system by a Csm complex. EMBO Reports, 2017, 18, 826-840.	4.5	23
50	Three-dimensional structure of renal Na,K-ATPase determined from two-dimensional membrane crystals of the p1 form. Journal of Structural Biology, 1988, 100, 86-93.	0.8	20
51	Crocus-derived compounds alter the aggregation pathway of Alzheimerâ€™s Disease - associated beta amyloid protein. Scientific Reports, 2020, 10, 18150.	3.3	18
52	Integrative Structural Investigation on the Architecture of Human Importin4_Histone H3/H4_Asf1a Complex and Its Histone H3 Tail Binding. Journal of Molecular Biology, 2018, 430, 822-841.	4.2	17
53	Recombinant Bri3 BRICHOS domain is a molecular chaperone with effect against amyloid formation and non-fibrillar protein aggregation. Scientific Reports, 2020, 10, 9817.	3.3	16
54	Turning of the receptor-binding domains opens up the murine leukaemia virus Env for membrane fusion. EMBO Journal, 2008, 27, 2799-2808.	7.8	15

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55	Dead-end complex, lipid interactions and catalytic mechanism of microsomal glutathione transferase 1, an electron crystallography and mutagenesis investigation. <i>Scientific Reports</i> , 2017, 7, 7897.	3.3	14
56	Structure analysis of fibrinogen by electron microscopy and image processing. <i>Journal of Structural Biology</i> , 1988, 98, 312-319.	0.8	13
57	Structure of two-dimensional crystals of membrane-bound Na,K-ATPase as analyzed by correlation averaging. <i>Journal of Ultrastructure Research</i> , 1985, 92, 28-35.	1.1	12
58	Coexistence of different forms of Na,K-ATPase in two-dimensional membrane crystals. <i>FEBS Letters</i> , 1990, 268, 83-87.	2.8	11
59	Renal Na,K-ATPase Structure from Cryo-Electron Microscopy of Two-Dimensional Crystals. <i>Annals of the New York Academy of Sciences</i> , 2003, 986, 9-16.	3.8	10
60	Shell thickness determination of polymer-shelled microbubbles using transmission electron microscopy. <i>Micron</i> , 2016, 85, 39-43.	2.2	9
61	Assembly of two-dimensional membrane crystals of Na,K-ATPase. <i>Journal of Structural Biology</i> , 1988, 99, 234-243.	0.8	8
62	Cryo-electron microscope analysis of frozen-hydrated crystals of Na, K-ATPase.. <i>Acta Histochemica Et Cytochemica</i> , 1992, 25, 279-285.	1.6	8
63	Structural and Functional Analysis of Calcium Ion Mediated Binding of 5-Lipoxygenase to Nanodiscs. <i>PLoS ONE</i> , 2016, 11, e0152116.	2.5	8
64	Evaluation of scanners and CCD cameras for high-resolution TEM of protein crystals and single particles. , 2000, 49, 292-300.		7
65	Investigation of the elimination process of a multimodal polymer-shelled contrast agent in rats using ultrasound and transmission electron microscopy. <i>Biomedical Spectroscopy and Imaging</i> , 2015, 4, 81-93.	1.2	7
66	Method to Visualize and Analyze Membrane Interacting Proteins by Transmission Electron Microscopy. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	7
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73	CryoEM: a crystals to single particles round-trip. Current Opinion in Structural Biology, 2019, 58, 59-67.	5.7	4
74	A Novel N-terminal Region to Chromodomain in CHD7 is Required for the Efficient Remodeling Activity. Journal of Molecular Biology, 2021, 433, 167114.	4.2	4
75	Two-Dimensional Crystallization and Electron Crystallography of MAPEG Proteins. Methods in Enzymology, 2005, 401, 161-168.	1.0	3
76	Free RCK Arrangement in KcsA, a Putative Escherichia coli Potassium Channel, as Suggested by Electron Crystallography. Structure, 2015, 23, 199-205.	3.3	3
77	Two-Dimensional Crystallization Procedure, from Protein Expression to Sample Preparation. BioMed Research International, 2015, 2015, 1-10.	1.9	2
78	Structures of apolipoprotein A-I in high density lipoprotein generated by electron microscopy and biased simulations. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 2726-2738.	2.4	2
79	Electron Crystallography of a Small Membrane-Bound Enzyme, Microsomal Glutathione Transferase. Microscopy and Microanalysis, 2000, 6, 232-233.	0.4	0
80	Two-Dimensional Crystallization of Biological Macromolecules. , 2009, , 95-111.		0
81	Structural properties of functional HDL and variants of apoA-I. FASEB Journal, 2012, 26, 997.5.	0.5	0