

# 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	A Novel N-terminal Region to Chromodomain in CHD7 is Required for the Efficient Remodeling Activity. <i>Journal of Molecular Biology</i> , 2021, 433, 167114.	4.2	4
2	The Polyglutamine Expansion at the N-Terminal of Huntingtin Protein Modulates the Dynamic Configuration and Phosphorylation of the C-Terminal HEAT Domain. <i>Structure</i> , 2020, 28, 1035-1050.e8.	3.3	24
3	Crocus-derived compounds alter the aggregation pathway of Alzheimer's Disease - associated beta amyloid protein. <i>Scientific Reports</i> , 2020, 10, 18150.	3.3	18
4	Recombinant Bri3 BRICHOS domain is a molecular chaperone with effect against amyloid formation and non-fibrillar protein aggregation. <i>Scientific Reports</i> , 2020, 10, 9817.	3.3	16
5	Arachidonic acid promotes the binding of 5-lipoxygenase on nanodiscs containing 5-lipoxygenase activating protein in the absence of calcium-ions. <i>PLoS ONE</i> , 2020, 15, e0228607.	2.5	5
6	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
7	Cryo-EM structure of native human uromodulin, a zona pellucida module polymer. <i>EMBO Journal</i> , 2020, 39, e106807.	7.8	31
8	Aldehyde-alcohol dehydrogenase forms a high-order spirosome architecture critical for its activity. <i>Nature Communications</i> , 2019, 10, 4527.	12.8	39
9	CryoEM: a crystals to single particles round-trip. <i>Current Opinion in Structural Biology</i> , 2019, 58, 59-67.	5.7	4
10	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
11	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
12	A spidroin-derived solubility tag enables controlled aggregation of a designed amyloid protein. <i>FEBS Journal</i> , 2018, 285, 1873-1885.	4.7	32
13	Integrative Structural Investigation on the Architecture of Human Importin4_Histone H3/H4_Asf1a Complex and Its Histone H3 Tail Binding. <i>Journal of Molecular Biology</i> , 2018, 430, 822-841.	4.2	17
14	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
15	Biomimetic spinning of artificial spider silk from a chimeric minispidroin. <i>Nature Chemical Biology</i> , 2017, 13, 262-264.	8.0	231
16	Efficient protein production inspired by how spiders make silk. <i>Nature Communications</i> , 2017, 8, 15504.	12.8	102
17	RNA activation-independent DNA targeting of the Type III CRISPR-Cas system by a Csm complex. <i>EMBO Reports</i> , 2017, 18, 826-840.	4.5	23
18	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. <i>Journal of Biological Chemistry</i> , 2017, 292, 8103-8121.	3.4	24

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19	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
20	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
21	Structures of apolipoprotein A-I in high density lipoprotein generated by electron microscopy and biased simulations. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2726-2738.	2.4	2
22	Bri2 BRICHOS client specificity and chaperone activity are governed by assembly state. <i>Nature Communications</i> , 2017, 8, 2081.	12.8	67
23	Method to Visualize and Analyze Membrane Interacting Proteins by Transmission Electron Microscopy. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	7
24	Structural and Functional Analysis of Calcium Ion Mediated Binding of 5-Lipoxygenase to Nanodiscs. <i>PLoS ONE</i> , 2016, 11, e0152116.	2.5	8
25	Molecular Architecture of Yeast Chromatin Assembly Factor 1. <i>Scientific Reports</i> , 2016, 6, 26702.	3.3	26
26	Shell thickness determination of polymer-shelled microbubbles using transmission electron microscopy. <i>Micron</i> , 2016, 85, 39-43.	2.2	9
27	Huntingtin's spherical solenoid structure enables polyglutamine tract-dependent modulation of its structure and function. <i>ELife</i> , 2016, 5, e11184.	6.0	52
28	A Refined Single-Particle Reconstruction Procedure to Process Two-Dimensional Crystal Images from Transmission Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2015, 21, 876-885.	0.4	5
29	Two-Dimensional Crystallization Procedure, from Protein Expression to Sample Preparation. <i>BioMed Research International</i> , 2015, 2015, 1-10.	1.9	2
30	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
31	Free RCK Arrangement in Kch, a Putative Escherichia coli Potassium Channel, as Suggested by Electron Crystallography. <i>Structure</i> , 2015, 23, 199-205.	3.3	3
32	Peptide Anchor for Folate-Targeted Liposomal Delivery. <i>Biomacromolecules</i> , 2015, 16, 2904-2910.	5.4	34
33	Size controlled protein nanoemulsions for active targeting of folate receptor positive cells. <i>Colloids and Surfaces B: Biointerfaces</i> , 2015, 135, 90-98.	5.0	26
34	Structure of potassium channels. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 3677-3693.	5.4	187
35	The gut microbiota influences blood-brain barrier permeability in mice. <i>Science Translational Medicine</i> , 2014, 6, 263ra158.	12.4	1,589
36	The projection structure of Kch, a putative potassium channel in Escherichia coli, by electron crystallography. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 237-243.	2.6	6

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37	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
38	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
39	Liposome and protein based stealth nanoparticles. <i>Faraday Discussions</i> , 2013, 166, 417.	3.2	26
40	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
41	Magnetite Nanoparticles Can Be Coupled to Microbubbles to Support Multimodal Imaging. <i>Biomacromolecules</i> , 2012, 13, 1390-1399.	5.4	73
42	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
43	Structural properties of functional HDL and variants of apoA $\epsilon$ . <i>FASEB Journal</i> , 2012, 26, 997.5.	0.5	0
44	Subunit arrangement in the dodecameric chloroplast small heat shock protein Hsp21. <i>Protein Science</i> , 2011, 20, 291-301.	7.6	29
45	ATP-Induced Conformational Dynamics in the AAA+ Motor Unit of Magnesium Chelatase. <i>Structure</i> , 2010, 18, 354-365.	3.3	70
46	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
47	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
48	Cryo-EM Reveals Promoter DNA Binding and Conformational Flexibility of the General Transcription Factor TFIID. <i>Structure</i> , 2009, 17, 1442-1452.	3.3	31
49	Two-Dimensional Crystallization of Biological Macromolecules. , 2009, , 95-111.		0
50	Assembly of Kch, a putative potassium channel from <i>Escherichia coli</i> . <i>Journal of Structural Biology</i> , 2009, 168, 288-293.	2.8	4
51	Microsomal glutathione transferase 1 exhibits one-third-of-the-sites-reactivity towards glutathione. <i>Archives of Biochemistry and Biophysics</i> , 2009, 487, 42-48.	3.0	31
52	Exploring the activity of tobacco etch virus protease in detergent solutions. <i>Analytical Biochemistry</i> , 2008, 382, 69-71.	2.4	25
53	Turning of the receptor-binding domains opens up the murine leukaemia virus Env for membrane fusion. <i>EMBO Journal</i> , 2008, 27, 2799-2808.	7.8	15
54	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

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55	Structural basis for induced formation of the inflammatory mediator prostaglandin E <sub>2</sub> . Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11110-11115.	7.1	139
56	Location of Substrate Binding Sites within the Integral Membrane Protein Microsomal Glutathione Transferase-1. Biochemistry, 2007, 46, 2812-2822.	2.5	33
57	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
58	Structural Basis for Detoxification and Oxidative Stress Protection in Membranes. Journal of Molecular Biology, 2006, 360, 934-945.	4.2	129
59	Transmembrane topology of FRO2, a ferric chelate reductase from Arabidopsis thaliana. Plant Molecular Biology, 2006, 62, 215-221.	3.9	42
60	The cyclin-dependent kinase 8 module sterically blocks Mediator interactions with RNA polymerase II. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15788-15793.	7.1	186
61	Two-Dimensional Crystallization and Electron Crystallography of MAPEG Proteins. Methods in Enzymology, 2005, 401, 161-168.	1.0	3
62	Renal Na,K-ATPase Structure from Cryo-Electron Microscopy of Two-Dimensional Crystals. Annals of the New York Academy of Sciences, 2003, 986, 9-16.	3.8	10
63	Human Microsomal Prostaglandin E Synthase-1. Journal of Biological Chemistry, 2003, 278, 22199-22209.	3.4	153
64	Projection structure at 8 Å resolution of the melibiose permease, an Na-sugar co-transporter from Escherichia coli. EMBO Journal, 2002, 21, 3569-3574.	7.8	44
65	Three-dimensional structure of renal Na,K-ATPase from cryo-electron microscopy of two-dimensional crystals 1 Edited by M. F. Moody. Journal of Molecular Biology, 2001, 314, 479-494.	4.2	76
66	Evaluation of scanners and CCD cameras for high-resolution TEM of protein crystals and single particles. , 2000, 49, 292-300.		7
67	Electron Crystallography of a Small Membrane-Bound Enzyme, Microsomal Glutathione Transferase. Microscopy and Microanalysis, 2000, 6, 232-233.	0.4	0
68	The projection structure of the membrane protein microsomal glutathione transferase at 3 Å... resolution as determined from two-dimensional hexagonal crystals. Journal of Molecular Biology, 1999, 288, 243-253.	4.2	34
69	The 3.0 Å... projection structure of microsomal glutathione transferase as determined by electron crystallography of p 21212 two-dimensional crystals. Journal of Molecular Biology, 1997, 271, 751-758.	4.2	40
70	The projection structure of Perfringolysin O (Clostridium perfringens $\phi$ -toxin). FEBS Letters, 1993, 319, 125-127.	2.8	81
71	Cryo-electron microscope analysis of frozen-hydrated crystals of Na, K-ATPase.. Acta Histochemica Et Cytochemica, 1992, 25, 279-285.	1.6	8
72	Two-dimensional crystals of membrane-bound gastric H,K-ATPase. FEBS Letters, 1992, 299, 159-162.	2.8	55

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73	Crystalline layers and three-dimensional structure of Staphylococcus aureus $\beta$ -toxin. Journal of Molecular Biology, 1990, 214, 299-306.	4.2	43
74	Coexistence of different forms of Na,K-ATPase in two-dimensional membrane crystals. FEBS Letters, 1990, 268, 83-87.	2.8	11
75	Structure analysis of fibrinogen by electron microscopy and image processing. Journal of Structural Biology, 1988, 98, 312-319.	0.8	13
76	Digitization of electron micrographs: A comparison of three different types of scanners. Journal of Electron Microscopy Technique, 1988, 8, 381-388.	1.1	4
77	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
78	Assembly of two-dimensional membrane crystals of Na,K-ATPase. Journal of Structural Biology, 1988, 99, 234-243.	0.8	8
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