# Hans Hebert

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 81 papers | 5,294 citations | 126708 33 h-index | 88477 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. Journal of Molecular Biology, 2021, 433, 167114. | 2.0 | 4 |
| 2 | 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. | 1.6 | 24 |
| 3 | Crocus-derived compounds alter the aggregation pathway of Alzheimerâ€™s Disease - associated beta amyloid protein. Scientific Reports, 2020, 10, 18150. | 1.6 | 18 |
| 4 | Recombinant Bri3 BRICHOS domain is a molecular chaperone with effect against amyloid formation and non-fibrillar protein aggregation. Scientific Reports, 2020, 10, 9817. | 1.6 | 16 |
| 5 | Arachidonic acid promotes the binding of 5-lipoxygenase on nanodiscs containing 5-lipoxygenase activating protein in the absence of calcium-ions. PLoS ONE, 2020, 15, e0228607. | 1.1 | 5 |
| 6 | Augmentation of Bri2 molecular chaperone activity against amyloid-Î² reduces neurotoxicity in mouse hippocampus in vitro. Communications Biology, 2020, 3, 32. | 2.0 | 42 |
| 7 | Cryoâ€EM structure of native human uromodulin, a zona pellucida module polymer. EMBO Journal, 2020, 39, e106807. | 3.5 | 31 |
| 8 | Aldehyde-alcohol dehydrogenase forms a high-order spirosome architecture critical for its activity. Nature Communications, 2019, 10, 4527. | 5.8 | 39 |
| 9 | CryoEM: a crystals to single particles round-trip. Current Opinion in Structural Biology, 2019, 58, 59-67. | 2.6 | 4 |
| 10 | Structural basis of recognition and destabilization of the histone H2B ubiquitinated nucleosome by the DOT1L histone H3 Lys79 methyltransferase. Genes and Development, 2019, 33, 620-625. | 2.7 | 73 |
| 11 | Granule-stored MUC5B mucins are packed by the non-covalent formation of N-terminal head-to-head tetramers. Journal of Biological Chemistry, 2018, 293, 5746-5754. | 1.6 | 50 |
| 12 | A spidroinâ€derived solubility tag enables controlled aggregation of a designed amyloid protein. FEBS Journal, 2018, 285, 1873-1885. | 2.2 | 32 |
| 13 | 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. | 2.0 | 17 |
| 14 | Structural modelling of the DNAJB6 oligomeric chaperone shows a peptide-binding cleft lined with conserved S/T-residues at the dimer interface. Scientific Reports, 2018, 8, 5199. | 1.6 | 43 |
| 15 | Biomimetic spinning of artificial spider silk from a chimeric minispidroin. Nature Chemical Biology, 2017, 13, 262-264. | 3.9 | 231 |
| 16 | Efficient protein production inspired by how spiders make silk. Nature Communications, 2017, 8, 15504. | 5.8 | 102 |
| 17 | RNA activationâ€independent DNA targeting of the Type III CRISPRâ€Cas system by a Csm complex. EMBO Reports, 2017, 18, 826-840. | 2.0 | 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. Journal of Biological Chemistry, 2017, 292, 8103-8121. | 1.6 | 24 |

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|---|---|---|---|
| 19 | The normal trachea is cleaned by MUC5B mucin bundles from the submucosal glands coated with the MUC5AC mucin. Biochemical and Biophysical Research Communications, 2017, 492, 331-337. | 1.0 | 92 |
| 20 | Dead-end complex, lipid interactions and catalytic mechanism of microsomal glutathione transferase 1, an electron crystallography and mutagenesis investigation. Scientific Reports, 2017, 7, 7897. | 1.6 | 14 |
| 21 | 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. | 1.1 | 2 |
| 22 | Bri2 BRICHOS client specificity and chaperone activity are governed by assembly state. Nature Communications, 2017, 8, 2081. | 5.8 | 67 |
| 23 | Method to Visualize and Analyze Membrane Interacting Proteins by Transmission Electron Microscopy. Journal of Visualized Experiments, 2017, , . | 0.2 | 7 |
| 24 | Structural and Functional Analysis of Calcium Ion Mediated Binding of 5-Lipoxygenase to Nanodiscs. PLoS ONE, 2016, 11, e0152116. | 1.1 | 8 |
| 25 | Molecular Architecture of Yeast Chromatin Assembly Factor 1. Scientific Reports, 2016, 6, 26702. | 1.6 | 26 |
| 26 | Shell thickness determination of polymer-shelled microbubbles using transmission electron microscopy. Micron, 2016, 85, 39-43. | 1.1 | 9 |
| 27 | Huntingtinâ€™s spherical solenoid structure enables polyglutamine tract-dependent modulation of its structure and function. ELife, 2016, 5, e11184. | 2.8 | 52 |
| 28 | A Refined Single-Particle Reconstruction Procedure to Process Two-Dimensional Crystal Images from Transmission Electron Microscopy. Microscopy and Microanalysis, 2015, 21, 876-885. | 0.2 | 5 |
| 29 | Two-Dimensional Crystallization Procedure, from Protein Expression to Sample Preparation. BioMed Research International, 2015, 2015, 1-10. | 0.9 | 2 |
| 30 | Investigation of the elimination process of a multimodal polymer-shelled contrast agent in rats using ultrasound and transmission electron microscopy. Biomedical Spectroscopy and Imaging, 2015, 4, 81-93. | 1.2 | 7 |
| 31 | Free RCK Arrangement in Kch, a Putative Escherichia coli Potassium Channel, as Suggested by Electron Crystallography. Structure, 2015, 23, 199-205. | 1.6 | 3 |
| 32 | Peptide Anchor for Folate-Targeted Liposomal Delivery. Biomacromolecules, 2015, 16, 2904-2910. | 2.6 | 34 |
| 33 | Size controlled protein nanoemulsions for active targeting of folate receptor positive cells. Colloids and Surfaces B: Biointerfaces, 2015, 135, 90-98. | 2.5 | 26 |
| 34 | Structure of potassium channels. Cellular and Molecular Life Sciences, 2015, 72, 3677-3693. | 2.4 | 187 |
| 35 | The gut microbiota influences blood-brain barrier permeability in mice. Science Translational Medicine, 2014, 6, 263ra158. | 5.8 | 1,589 |
| 36 | The projection structure of Kch, a putative potassium channel in Escherichia coli, by electron crystallography. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 237-243. | 1.4 | 6 |

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|---|---|---|---|
| 37 | On the interplay of shell structure with low- and high-frequency mechanics of multifunctional magnetic microbubbles. Soft Matter, 2014, 10, 214-226. | 1.2 | 44 |
| 38 | Intestinal MUC2 Mucin Supramolecular Topology by Packing and Release Resting on D3 Domain Assembly. Journal of Molecular Biology, 2014, 426, 2567-2579. | 2.0 | 36 |
| 39 | Liposome and protein based stealth nanoparticles. Faraday Discussions, 2013, 166, 417. | 1.6 | 26 |
| 40 | Calcium and pH-dependent packing and release of the gel-forming MUC2 mucin. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5645-5650. | 3.3 | 265 |
| 41 | Magnetite Nanoparticles Can Be Coupled to Microbubbles to Support Multimodal Imaging. Biomacromolecules, 2012, 13, 1390-1399. | 2.6 | 73 |
| 42 | Bicarbonate and functional CFTR channel are required for proper mucin secretion and link cystic fibrosis with its mucus phenotype. Journal of Experimental Medicine, 2012, 209, 1263-1272. | 4.2 | 292 |
| 43 | Structural properties of functional HDL and variants of apoAâ€¹. FASEB Journal, 2012, 26, 997.5. | 0.2 | 0 |
| 44 | Subunit arrangement in the dodecameric chloroplast small heat shock protein Hsp21. Protein Science, 2011, 20, 291-301. | 3.1 | 29 |
| 45 | ATP-Induced Conformational Dynamics in the AAA+ Motor Unit of Magnesium Chelatase. Structure, 2010, 18, 354-365. | 1.6 | 70 |
| 46 | Single-particle cryoelectron microscopy analysis reveals the HIV-1 spike as a tripod structure. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18844-18849. | 3.3 | 55 |
| 47 | Identification of Key Residues Determining Species Differences in Inhibitor Binding of Microsomal Prostaglandin E Synthase-1*. Journal of Biological Chemistry, 2010, 285, 29254-29261. | 1.6 | 68 |
| 48 | Cryo-EM Reveals Promoter DNA Binding and Conformational Flexibility of the General Transcription Factor TFIID. Structure, 2009, 17, 1442-1452. | 1.6 | 31 |
| 49 | Two-Dimensional Crystallization of Biological Macromolecules. , 2009, , 95-111. | | 0 |
| 50 | Assembly of Kch, a putative potassium channel from Escherichia coli. Journal of Structural Biology, 2009, 168, 288-293. | 1.3 | 4 |
| 51 | Microsomal glutathione transferase 1 exhibits one-third-of-the-sites-reactivity towards glutathione. Archives of Biochemistry and Biophysics, 2009, 487, 42-48. | 1.4 | 31 |
| 52 | Exploring the activity of tobacco etch virus protease in detergent solutions. Analytical Biochemistry, 2008, 382, 69-71. | 1.1 | 25 |
| 53 | Turning of the receptor-binding domains opens up the murine leukaemia virus Env for membrane fusion. EMBO Journal, 2008, 27, 2799-2808. | 3.5 | 15 |
| 54 | A New Cryo-EM Single-Particle Ab Initio Reconstruction Method Visualizes Secondary Structure Elements in an ATP-Fueled AAA+ Motor. Journal of Molecular Biology, 2008, 375, 934-947. | 2.0 | 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. | 3.3 | 139 |
| 56 | Location of Substrate Binding Sites within the Integral Membrane Protein Microsomal Glutathione Transferase-1â€. Biochemistry, 2007, 46, 2812-2822. | 1.2 | 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. | 2.6 | 25 |
| 58 | Structural Basis for Detoxification and Oxidative Stress Protection in Membranes. Journal of Molecular Biology, 2006, 360, 934-945. | 2.0 | 129 |
| 59 | Transmembrane topology of FRO2, a ferric chelate reductase from Arabidopsis thaliana. Plant Molecular Biology, 2006, 62, 215-221. | 2.0 | 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. | 3.3 | 186 |
| 61 | Twoâ€Dimensional Crystallization and Electron Crystallography of MAPEG Proteins. Methods in Enzymology, 2005, 401, 161-168. | 0.4 | 3 |
| 62 | Renal Na,Kâ€ATPase Structure from Cryoâ€electron Microscopy of Twoâ€Dimensional Crystals. Annals of the New York Academy of Sciences, 2003, 986, 9-16. | 1.8 | 10 |
| 63 | Human Microsomal Prostaglandin E Synthase-1. Journal of Biological Chemistry, 2003, 278, 22199-22209. | 1.6 | 153 |
| 64 | Projection structure at 8 A resolution of the melibiose permease, an Na-sugar co-transporter from Escherichia coli. EMBO Journal, 2002, 21, 3569-3574. | 3.5 | 44 |
| 65 | Three-dimensional structure of renal Na,K-ATPase from cryo-electron microscopy of two-dimensional crystals 1 1Edited by M. F. Moody. Journal of Molecular Biology, 2001, 314, 479-494. | 2.0 | 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. | 0.2 | 0 |
| 68 | The projection structure of the membrane protein microsomal glutathione transferase at 3 Ã... resolution as determined from two-dimensional hexagonal crystals. Journal of Molecular Biology, 1999, 288, 243-253. | 2.0 | 34 |
| 69 | The 3.0 Ã... 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. | 2.0 | 40 |
| 70 | The projection structure of Perfringolysin O (Clostridium perfringensÎ¸-toxin). FEBS Letters, 1993, 319, 125-127. | 1.3 | 81 |
| 71 | Cryo-electron microscope analysis of frozen-hydrated crystals of Na, K-ATPase.. Acta Histochemica Et Cytochemica, 1992, 25, 279-285. | 0.8 | 8 |
| 72 | Two-dimensional crystals of membrane-bound gastric H,K-ATPase. FEBS Letters, 1992, 299, 159-162. | 1.3 | 55 |

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| 73 | Crystalline layers and three-dimensional structure ofStaphylococcus aureus Î±-toxin. Journal of Molecular Biology, 1990, 214, 299-306. | 2.0 | 43 |
| 74 | Coexistence of different forms ofNa,K-ATPase in two-dimensional membrane crystals. FEBS Letters, 1990, 268, 83-87. | 1.3 | 11 |
| 75 | Structure analysis of fibrinogen by electron microscopy and image processing. Journal of Structural Biology, 1988, 98, 312-319. | 0.9 | 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. | 0.9 | 20 |
| 78 | Assembly of two-dimensional membrane crystals of Na,K-ATPase. Journal of Structural Biology, 1988, 99, 234-243. | 0.9 | 8 |
| 79 | | | |