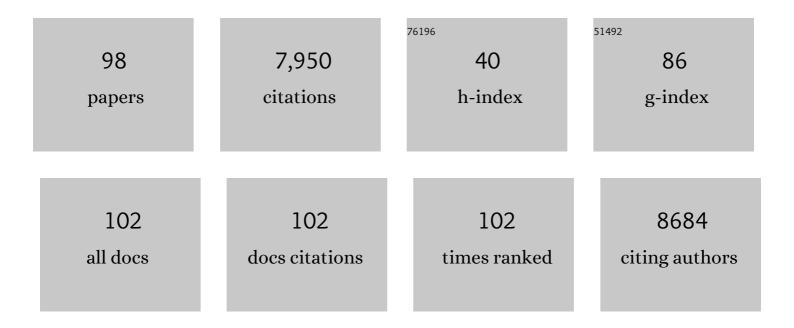
J Bernard Heymann

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6641156/publications.pdf Version: 2024-02-01



I REDNADD HEVMANN

#	Article	IF	CITATIONS
1	The progressive spectral signal-to-noise ratio of cryo-electron micrograph movies as a tool to assess quality and radiation damage. Computer Methods and Programs in Biomedicine, 2022, 220, 106799.	2.6	2
2	High resolution electron tomography and segmentationâ€byâ€modeling interpretation in Bsoft. Protein Science, 2021, 30, 44-59.	3.1	7
3	FSC-Q: a CryoEM map-to-atomic model quality validation based on the local Fourier shell correlation. Nature Communications, 2021, 12, 42.	5.8	28
4	Cryo-Electron Tomography of the Herpesvirus Procapsid Reveals Interactions of the Portal with the Scaffold and a Shift on Maturation. MBio, 2021, 12, .	1.8	8
5	The Mottled Capsid of the Salmonella Giant Phage SPN3US, a Likely Maturation Intermediate with a Novel Internal Shell. Viruses, 2020, 12, 910.	1.5	8
6	Nested Protein Lattices in a Giant Phage Capsid Suggest Partial Maturation and a Residual Scaffold. Microscopy and Microanalysis, 2020, 26, 570-572.	0.2	0
7	Protocols for Processing and Interpreting cryoEM Data Using Bsoft: A Case Study of the Retinal Adhesion Protein, Retinoschisin. Bio-protocol, 2020, 10, e3491.	0.2	1
8	Atomic structures of an entire contractile injection system in both the extended and contracted states. Nature Microbiology, 2019, 4, 1885-1894.	5.9	45
9	Localization of the Herpesvirus Portal. Microscopy and Microanalysis, 2019, 25, 1162-1163.	0.2	1
10	Hunting for the Adhesion Molecule, Retinoschisin, in Retina using CEMOVIS. Microscopy and Microanalysis, 2019, 25, 1308-1309.	0.2	1
11	Carbon replicas reveal double stranded structure of tight junctions in phase-contrast electron microscopy. Communications Biology, 2019, 2, 98.	2.0	13
12	Single-particle reconstruction statistics: a diagnostic tool in solving biomolecular structures by cryo-EM. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 33-44.	0.4	10
13	Cryo-EM of retinoschisin branched networks suggests an intercellular adhesive scaffold in the retina. Journal of Cell Biology, 2019, 218, 1027-1038.	2.3	17
14	Guidelines for using Bsoft for high resolution reconstruction and validation of biomolecular structures from electron micrographs. Protein Science, 2018, 27, 159-171.	3.1	99
15	Using Reconstruction Statistics to Predict the Number of Images Required for Single Particle Analysis. Microscopy and Microanalysis, 2018, 24, 1216-1217.	0.2	0
16	Single particle reconstruction and validation using Bsoft for the map challenge. Journal of Structural Biology, 2018, 204, 90-95.	1.3	21
17	Map Challenge assessment: Fair comparison of single particle cryoEM reconstructions. Journal of Structural Biology, 2018, 204, 360-367.	1.3	10
18	The first single particle analysis Map Challenge: A summary of the assessments. Journal of Structural Biology, 2018, 204, 291-300.	1.3	17

#	Article	IF	CITATIONS
19	Tomographic Reconstruction from Electron Micrographs. Biological and Medical Physics Series, 2018, , 209-236.	0.3	0
20	The Primary Enveloped Virion of Herpes Simplex Virus 1: Its Role in Nuclear Egress. MBio, 2017, 8, .	1.8	44
21	Galactose Induces Formation of Chains of the Retinal Adhesion Protein, Retinoschisin. Microscopy and Microanalysis, 2017, 23, 1112-1113.	0.2	0
22	Primary Envelopment of the Herpes Simplex 1 Virion. Microscopy and Microanalysis, 2017, 23, 1224-1225.	0.2	0
23	A Polymerase-Activating Host Factor, YajQ, Bound to the Bacteriophage ϕ6 Capsid. Microscopy and Microanalysis, 2016, 22, 1110-1111.	0.2	1
24	Paired octamer rings of retinoschisin suggest a junctional model for cell–cell adhesion in the retina. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5287-5292.	3.3	49
25	The Structure of HIV-1 Rev Filaments Suggests a Bilateral Model for Rev-RRE Assembly. Structure, 2016, 24, 1068-1080.	1.6	22
26	The Electron Microscopy eXchange (EMX) initiative. Journal of Structural Biology, 2016, 194, 156-163.	1.3	12
27	Retinoschisin at 4 Ã Resolution from cryo-EM: A Junctional Model of Back-to-Back Octamers for Adhesion in the Retina. Biophysical Journal, 2016, 110, 348a.	0.2	Ο
28	α-Synuclein Amyloid Fibrils with Two Entwined, Asymmetrically Associated Protofibrils. Journal of Biological Chemistry, 2016, 291, 2310-2318.	1.6	48
29	Subassemblies and Asymmetry in Assembly of Herpes Simplex Virus Procapsid. MBio, 2015, 6, e01525-15.	1.8	28
30	α-Synuclein Amyloid Fibrils Formed of Two Protofibrils. Microscopy and Microanalysis, 2015, 21, 1285-1286.	0.2	0
31	CTF Challenge: Result summary. Journal of Structural Biology, 2015, 190, 348-359.	1.3	34
32	Validation of 3D EM Reconstructions: The Phantom in the Noise. AIMS Biophysics, 2015, 2, 21-35.	0.3	19
33	A virus capsidâ€like nanocompartment that stores iron and protects bacteria from oxidative stress. EMBO Journal, 2014, 33, 1896-1911.	3.5	153
34	The Phantom in the Noise and Validation of 3D EM Reconstructions. Microscopy and Microanalysis, 2014, 20, 792-793.	0.2	3
35	Phage Capsid-like Structure of Myxococcus xanthus Encapsulin, a Protein Shell That Stores Iron. Microscopy and Microanalysis, 2014, 20, 1244-1245.	0.2	3
36	Clathrin-coated vesicles from brain have small payloads: A cryo-electron tomographic study. Journal of Structural Biology, 2013, 184, 43-51.	1.3	19

#	Article	IF	CITATIONS
37	Subunit Folds and Maturation Pathway of a dsRNA Virus Capsid. Structure, 2013, 21, 1374-1383.	1.6	46
38	One number does not fit all: Mapping local variations in resolution in cryo-EM reconstructions. Journal of Structural Biology, 2013, 184, 226-236.	1.3	340
39	A Two-Pronged Structural Analysis of Retroviral Maturation Indicates that Core Formation Proceeds by a Disassembly-Reassembly Pathway Rather than a Displacive Transition. Journal of Virology, 2013, 87, 13655-13664.	1.5	68
40	Three-dimensional Structure of the Toxin-delivery Particle Antifeeding Prophage of Serratia entomophila. Journal of Biological Chemistry, 2013, 288, 25276-25284.	1.6	57
41	Packaging Accessory Protein P7 and Polymerase P2 Have Mutually Occluding Binding Sites inside the Bacteriophage ϕ6 Procapsid. Journal of Virology, 2012, 86, 11616-11624.	1.5	28
42	Data management challenges in three-dimensional EM. Nature Structural and Molecular Biology, 2012, 19, 1203-1207.	3.6	49
43	Towards an atlas of mammalian cell ultrastructure by cryo soft X-ray tomography. Journal of Structural Biology, 2012, 177, 179-192.	1.3	57
44	Structural Changes in Influenza Virus at Low pH Characterized by Cryo-Electron Tomography. Journal of Virology, 2012, 86, 2919-2929.	1.5	109
45	Procapsid Assembly, Maturation, Nuclear Exit: Dynamic Steps in the Production of Infectious Herpesvirions. Advances in Experimental Medicine and Biology, 2012, 726, 423-439.	0.8	68
46	Stepwise Expansion of the Bacteriophage ϕ6 Procapsid: Possible Packaging Intermediates. Journal of Molecular Biology, 2011, 414, 260-271.	2.0	28
47	HIV-1 Maturation Inhibitor Bevirimat Stabilizes the Immature Gag Lattice. Journal of Virology, 2011, 85, 1420-1428.	1.5	107
48	Three-dimensional cellular ultrastructure resolved by X-ray microscopy. Nature Methods, 2010, 7, 985-987.	9.0	318
49	Cryo-electron tomography of bacteriophage φ6 procapsids shows random occupancy of the binding sites for RNA polymerase and packaging NTPase. Journal of Structural Biology, 2010, 171, 389-396.	1.3	29
50	Initial Stages of V(D)J Recombination: The Organization of RAG1/2 and RSS DNA in the Postcleavage Complex. Molecular Cell, 2009, 35, 217-227.	4.5	44
51	Image Processing and Interpretation in Structural Electron Microscopy. Microscopy and Microanalysis, 2009, 15, 1536-1537.	0.2	Ο
52	Expansion of the Bacteriophage φ6 Procapsid Revealed by Electron Cryo-Microscopy. Microscopy and Microanalysis, 2009, 15, 586-587.	0.2	0
53	Analysis of Simian Virus 40 Chromatin Structure by Cryo-Electron Tomography. Microscopy and Microanalysis, 2009, 15, 644-645.	0.2	1
54	Electron Cryo-Tomography Demonstrates Variable Distributions of the Viral NTPase and RNA Polymerase in Bacteriophage I†6 Procapsids. Microscopy and Microanalysis, 2009, 15, 588-589.	0.2	0

#	Article	IF	CITATIONS
55	Computational resources for cryo-electron tomography in Bsoft. Journal of Structural Biology, 2008, 161, 232-242.	1.3	128
56	RSV Capsid Polymorphism Correlates with Polymerization Efficiency and Envelope Glycoprotein Content: Implications that Nucleation Controls Morphogenesis. Journal of Molecular Biology, 2008, 376, 1168-1181.	2.0	58
57	Initial Location of the RNA-dependent RNA Polymerase in the Bacteriophage Φ6 Procapsid Determined by Cryo-electron Microscopy. Journal of Biological Chemistry, 2008, 283, 12227-12231.	1.6	40
58	Irregular and Semi-Regular Polyhedral Models for Rous Sarcoma Virus Cores. Computational and Mathematical Methods in Medicine, 2008, 9, 197-210.	0.7	29
59	Cryo-Electron Tomography of Coated Vesicles and Modeling the Polyhedral Clathrin Network. Microscopy and Microanalysis, 2008, 14, 1064-1065.	0.2	1
60	Packaging of Proteins into Viral Capsids and their Activation. Microscopy and Microanalysis, 2008, 14, 160-161.	0.2	0
61	Capsid Polymorphism of Rous Sarcoma Virus Correlates with Assembly Efficiency and Envelope Glycoprotein Content. Microscopy and Microanalysis, 2008, 14, 1546-1547.	0.2	0
62	Bsoft: Image processing and molecular modeling for electron microscopy. Journal of Structural Biology, 2007, 157, 3-18.	1.3	493
63	A comparison of liquid nitrogen and liquid helium as cryogens for electron cryotomography. Journal of Structural Biology, 2006, 153, 231-240.	1.3	84
64	Visualizing the Clathrin and Assembly-Regulating Proteins of Coated Vesicles by Cryo-Electron Tomography. Microscopy and Microanalysis, 2006, 12, 374-375.	0.2	2
65	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. Structure, 2006, 14, 1211-1217.	1.6	60
66	Influenza virus pleiomorphy characterized by cryoelectron tomography. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19123-19127.	3.3	426
67	Peach: A Simple Perl-Based System for Distributed Computation and Its Application to Cryo-EM Data Processing. Structure, 2005, 13, 505-511.	1.6	13
68	Virus maturation: dynamics and mechanism of a stabilizing structural transition that leads to infectivity. Current Opinion in Structural Biology, 2005, 15, 227-236.	2.6	160
69	Visualization of the Binding of Hsc70 ATPase to Clathrin Baskets. Journal of Biological Chemistry, 2005, 280, 7156-7161.	1.6	28
70	The Axial Channel of the 20S Proteasome Opens Upon Binding of the PA200 Activator. Journal of Molecular Biology, 2005, 346, 1221-1227.	2.0	102
71	Common conventions for interchange and archiving of three-dimensional electron microscopy information in structural biology. Journal of Structural Biology, 2005, 151, 196-207.	1.3	61
72	A "flip–flop―rotation stage for routine dual-axis electron cryotomography. Journal of Structural Biology, 2005, 151, 288-297.	1.3	61

J Bernard Heymann

#	Article	IF	CITATIONS
73	Molecular dynamics of protein complexes from four-dimensional cryo-electron microscopy. Journal of Structural Biology, 2004, 147, 291-301.	1.3	37
74	Macro Molecular Dynamics by Multiple Particle Analysis: Classifying Distinct Conformational States by Generalized Projection Matching. Microscopy and Microanalysis, 2004, 10, 30-31.	0.2	0
75	Dynamics of herpes simplex virus capsid maturation visualized by time-lapse cryo-electron microscopy. Nature Structural and Molecular Biology, 2003, 10, 334-341.	3.6	158
76	Three-Dimensional Structure of Herpes Simplex Virus from Cryo-Electron Tomography. Science, 2003, 302, 1396-1398.	6.0	507
77	Sampling effects influence heights measured with atomic force microscopy. Journal of Microscopy, 2002, 207, 43-51.	0.8	13
78	Bsoft: Image and Molecular Processing in Electron Microscopy. Journal of Structural Biology, 2001, 133, 156-169.	1.3	222
79	Chapter 2 The aquaporin superfamily: Structure and function. Current Topics in Membranes, 2001, 51, 39-119.	0.5	3
80	Molecular basis of water selectivity on aquaporin-1. Kidney International, 2001, 60, 399.	2.6	1
81	Capsid Structure of Kaposi's Sarcoma-Associated Herpesvirus, a Gammaherpesvirus, Compared to Those of an Alphaherpesvirus, Herpes Simplex Virus Type 1, and a Betaherpesvirus, Cytomegalovirus. Journal of Virology, 2001, 75, 2879-2890.	1.5	79
82	Structural determinants of water permeation through aquaporin-1. Nature, 2000, 407, 599-605.	13.7	1,584
83	Conformations of the rhodopsin third cytoplasmic loop grafted onto bacteriorhodopsin. Structure, 2000, 8, 643-653.	1.6	23
84	Structural clues in the sequences of the aquaporins. Journal of Molecular Biology, 2000, 295, 1039-1053.	2.0	147
85	The Fold of Human Aquaporin 1. Journal of Molecular Biology, 2000, 300, 987-994.	2.0	34
86	Atomic force microscopy of native purple membrane. Biochimica Et Biophysica Acta - Bioenergetics, 2000, 1460, 27-38.	0.5	121
87	Folded State of the Integral Membrane Colicin E1 Immunity Protein in Solvents of Mixed Polarity. Biochemistry, 2000, 39, 12131-12139.	1.2	20
88	Aquaporins: Phylogeny, Structure, and Physiology of Water Channels. Physiology, 1999, 14, 187-193.	1.6	114
89	Organising multi-dimensional biological image information: The Biolmage Database. Nucleic Acids Research, 1999, 27, 280-283.	6.5	28
90	Imaging streptavidin 2D crystals on biotinylated lipid monolayers at high resolution with the atomic force microscope. Journal of Microscopy, 1999, 193, 28-35.	0.8	102

#	Article	IF	CITATIONS
91	Visualizing 3D Data Obtained from Microscopy on the Internet. Journal of Structural Biology, 1999, 125, 123-132.	1.3	23
92	The Structure of Aquaporin-1 at 4.5-à Resolution Reveals Short α-Helices in the Center of the Monomer. Journal of Structural Biology, 1999, 128, 34-43.	1.3	122
93	Charting the Surfaces of the Purple Membrane. Journal of Structural Biology, 1999, 128, 243-249.	1.3	60
94	Progress on the Structure and Function of Aquaporin 1. Journal of Structural Biology, 1998, 121, 191-206.	1.3	90
95	2D Crystallization of Membrane Proteins: Rationales and Examples. Journal of Structural Biology, 1998, 121, 162-171.	1.3	98
96	Electron and atomic force microscopy of membrane proteins. Current Opinion in Structural Biology, 1997, 7, 543-549.	2.6	37
97	The three-dimensional structure of aquaporin-1. Nature, 1997, 387, 624-627.	13.7	441
98	Structural aspects of the cytochromeb 6 f complex; structure of the lumen-side domain of cytochromef. Journal of Bioenergetics and Biomembranes, 1994, 26, 31-47.	1.0	62