

Wim J H Hagen

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

9,792
citations

147566

31
h-index

288905

40
g-index

55
all docs

55
docs citations

55
times ranked

13494
citing authors

#	ARTICLE	IF	CITATIONS
1	New tools for automated high-resolution cryo-EM structure determination in RELION-3. <i>ELife</i> , 2018, 7, .	2.8	3,965
2	Implementation of a cryo-electron tomography tilt-scheme optimized for high resolution subtomogram averaging. <i>Journal of Structural Biology</i> , 2017, 197, 191-198.	1.3	556
3	In situ structural analysis of SARS-CoV-2 spike reveals flexibility mediated by three hinges. <i>Science</i> , 2020, 370, 203-208.	6.0	531
4	An atomic model of HIV-1 capsid-SP1 reveals structures regulating assembly and maturation. <i>Science</i> , 2016, 353, 506-508.	6.0	375
5	Software tools for automated transmission electron microscopy. <i>Nature Methods</i> , 2019, 16, 471-477.	9.0	367
6	In situ structural analysis of the human nuclear pore complex. <i>Nature</i> , 2015, 526, 140-143.	13.7	361
7	Integrated Structural Analysis of the Human Nuclear Pore Complex Scaffold. <i>Cell</i> , 2013, 155, 1233-1243.	13.5	321
8	Molecular architecture of the inner ring scaffold of the human nuclear pore complex. <i>Science</i> , 2016, 352, 363-365.	6.0	284
9	Structure of the immature HIV-1 capsid in intact virus particles at 8.8Å... resolution. <i>Nature</i> , 2015, 517, 505-508.	13.7	277
10	The structure and flexibility of conical HIV-1 capsids determined within intact virions. <i>Science</i> , 2016, 354, 1434-1437.	6.0	229
11	In-cell architecture of an actively transcribing-translating expressome. <i>Science</i> , 2020, 369, 554-557.	6.0	192
12	The Selective Autophagy Receptor p62 Forms a Flexible Filamentous Helical Scaffold. <i>Cell Reports</i> , 2015, 11, 748-758.	2.9	190
13	Molecular structures of unbound and transcribing RNA polymerase III. <i>Nature</i> , 2015, 528, 231-236.	13.7	167
14	A structure of the COPI coat and the role of coat proteins in membrane vesicle assembly. <i>Science</i> , 2015, 349, 195-198.	6.0	159
15	In-cell architecture of the nuclear pore and snapshots of its turnover. <i>Nature</i> , 2020, 586, 796-800.	13.7	139
16	AI-based structure prediction empowers integrative structural analysis of human nuclear pores. <i>Science</i> , 2022, 376, .	6.0	136
17	Capturing protein communities by structural proteomics in a thermophilic eukaryote. <i>Molecular Systems Biology</i> , 2017, 13, 936.	3.2	108
18	9Å... structure of the COPI coat reveals that the Arf1 GTPase occupies two contrasting molecular environments. <i>ELife</i> , 2017, 6, .	2.8	103

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19	Molecular mechanism of promoter opening by RNA polymerase III. <i>Nature</i> , 2018, 553, 295-300.	13.7	101
20	Cryo-electron microscopy of tubular arrays of HIV-1 Gag resolves structures essential for immature virus assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8233-8238.	3.3	98
21	Determination of protein structure at 8.5 Å... resolution using cryo-electron tomography and sub-tomogram averaging. <i>Journal of Structural Biology</i> , 2013, 184, 394-400.	1.3	85
22	Molecular Structures of Transcribing RNA Polymerase I. <i>Molecular Cell</i> , 2016, 64, 1135-1143.	4.5	85
23	Structure of the hexagonal surface layer on <i>Caulobacter crescentus</i> cells. <i>Nature Microbiology</i> , 2017, 2, 17059.	5.9	85
24	Seeing tobacco mosaic virus through direct electron detectors. <i>Journal of Structural Biology</i> , 2015, 189, 87-97.	1.3	82
25	An Organized Co-assembly of Clathrin Adaptors Is Essential for Endocytosis. <i>Developmental Cell</i> , 2015, 33, 150-162.	3.1	75
26	Structural basis of p62/SQSTM1 helical filaments and their role in cellular cargo uptake. <i>Nature Communications</i> , 2020, 11, 440.	5.8	71
27	The dynamic conformational landscape of β -secretase. <i>Journal of Cell Science</i> , 2015, 128, 589-98.	1.2	63
28	The Structure of Immature Virus-Like Rous Sarcoma Virus Gag Particles Reveals a Structural Role for the p10 Domain in Assembly. <i>Journal of Virology</i> , 2015, 89, 10294-10302.	1.5	61
29	Structural insights into transcription initiation by yeast RNA polymerase I. <i>EMBO Journal</i> , 2017, 36, 2698-2709.	3.5	58
30	Benchmarking tomographic acquisition schemes for high-resolution structural biology. <i>Nature Communications</i> , 2020, 11, 876.	5.8	49
31	<scp>SNARE</scp> and regulatory proteins induce local membrane protrusions to prime docked vesicles for fast calcium-triggered fusion. <i>EMBO Reports</i> , 2014, 15, 308-314.	2.0	46
32	Combining high throughput and high quality for cryo-electron microscopy data collection. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 724-728.	1.1	42
33	Structural basis for RNA polymerase III transcription repression by Maf1. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 229-232.	3.6	37
34	Open membranes are the precursors for assembly of large DNA viruses. <i>Cellular Microbiology</i> , 2013, 15, n/a-n/a.	1.1	31
35	Higher-order assemblies of oligomeric cargo receptor complexes form the membrane scaffold of the Cvt vesicle. <i>EMBO Reports</i> , 2016, 17, 1044-1060.	2.0	26
36	Structural impact of K63 ubiquitin on yeast translocating ribosomes under oxidative stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22157-22166.	3.3	21

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37	Exploring high-resolution cryo-ET and subtomogram averaging capabilities of contemporary DEDs. Journal of Structural Biology, 2022, 214, 107852.	1.3	18
38	Defocus-dependent Thon-ring fading. Ultramicroscopy, 2021, 222, 113213.	0.8	11
39	TEM bright field imaging of thick specimens: nodes in Thon ring patterns. Ultramicroscopy, 2020, 216, 113023.	0.8	10
40	Strategies for Optimization of Cryogenic Electron Tomography Data Acquisition. Journal of Visualized Experiments, 2021, , .	0.2	4
41	Automated cryo electron tomography and sub-tomogram averaging with the FEI Volta phase plate. Microscopy and Microanalysis, 2015, 21, 1833-1834.	0.2	0
42	Location and Identification of Macromolecular Complexes within Cellular Environments by High-Resolution Template Matching. Biophysical Journal, 2020, 118, 3a.	0.2	0