

# Wim J H Hagen

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

47  
papers

5,717  
citations

30  
h-index

55  
g-index

55  
ext. papers

8,196  
ext. citations

18.4  
avg, IF

6.1  
L-index

#	Paper	IF	Citations
47	Exploring high-resolution cryo-ET and subtomogram averaging capabilities of contemporary DEDs.. <i>Journal of Structural Biology</i> , <b>2022</b> , 214, 107852	3.4	1
46	Defocus-dependent Thon-ring fading. <i>Ultramicroscopy</i> , <b>2021</b> , 222, 113213	3.1	4
45	TEM bright field imaging of thick specimens: nodes in Thon ring patterns. <i>Ultramicroscopy</i> , <b>2020</b> , 216, 113023	3.1	4
44	Benchmarking tomographic acquisition schemes for high-resolution structural biology. <i>Nature Communications</i> , <b>2020</b> , 11, 876	17.4	18
43	Structural basis for RNA polymerase III transcription repression by Maf1. <i>Nature Structural and Molecular Biology</i> , <b>2020</b> , 27, 229-232	17.6	16
42	Structural basis of p62/SQSTM1 helical filaments and their role in cellular cargo uptake. <i>Nature Communications</i> , <b>2020</b> , 11, 440	17.4	33
41	Combining high throughput and high quality for cryo-electron microscopy data collection. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2020</b> , 76, 724-728	5.5	9
40	In-cell architecture of an actively transcribing-translating expressome. <i>Science</i> , <b>2020</b> , 369, 554-557	33.3	82
39	In-cell architecture of the nuclear pore and snapshots of its turnover. <i>Nature</i> , <b>2020</b> , 586, 796-800	50.4	71
38	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> , <b>2020</b> , 117, 22157-22166	11.5	7
37	In situ structural analysis of SARS-CoV-2 spike reveals flexibility mediated by three hinges. <i>Science</i> , <b>2020</b> , 370, 203-208	33.3	287
36	Software tools for automated transmission electron microscopy. <i>Nature Methods</i> , <b>2019</b> , 16, 471-477	21.6	187
35	Molecular mechanism of promoter opening by RNA polymerase III. <i>Nature</i> , <b>2018</b> , 553, 295-300	50.4	70
34	New tools for automated high-resolution cryo-EM structure determination in RELION-3. <i>ELife</i> , <b>2018</b> , 7,	8.9	2049
33	Author response: New tools for automated high-resolution cryo-EM structure determination in RELION-3 <b>2018</b> ,		36
32	Structure of the hexagonal surface layer on <i>Caulobacter crescentus</i> cells. <i>Nature Microbiology</i> , <b>2017</b> , 2, 17059	26.6	60
31	Structural insights into transcription initiation by yeast RNA polymerase I. <i>EMBO Journal</i> , <b>2017</b> , 36, 2698-2709	13	45

30	Capturing protein communities by structural proteomics in a thermophilic eukaryote. <i>Molecular Systems Biology</i> , <b>2017</b> , 13, 936	12.2	79
29	Implementation of a cryo-electron tomography tilt-scheme optimized for high resolution subtomogram averaging. <i>Journal of Structural Biology</i> , <b>2017</b> , 197, 191-198	3.4	272
28	Structure of the COPI coat reveals that the Arf1 GTPase occupies two contrasting molecular environments. <i>ELife</i> , <b>2017</b> , 6,	8.9	61
27	An atomic model of HIV-1 capsid-SP1 reveals structures regulating assembly and maturation. <i>Science</i> , <b>2016</b> , 353, 506-8	33.3	250
26	Molecular Structures of Transcribing RNA Polymerase I. <i>Molecular Cell</i> , <b>2016</b> , 64, 1135-1143	17.6	60
25	The structure and flexibility of conical HIV-1 capsids determined within intact virions. <i>Science</i> , <b>2016</b> , 354, 1434-1437	33.3	149
24	Higher-order assemblies of oligomeric cargo receptor complexes form the membrane scaffold of the Cvt vesicle. <i>EMBO Reports</i> , <b>2016</b> , 17, 1044-60	6.5	20
23	Molecular architecture of the inner ring scaffold of the human nuclear pore complex. <i>Science</i> , <b>2016</b> , 352, 363-5	33.3	216
22	VESICULAR TRANSPORT. A structure of the COPI coat and the role of coat proteins in membrane vesicle assembly. <i>Science</i> , <b>2015</b> , 349, 195-8	33.3	116
21	The selective autophagy receptor p62 forms a flexible filamentous helical scaffold. <i>Cell Reports</i> , <b>2015</b> , 11, 748-58	10.6	136
20	An organized co-assembly of clathrin adaptors is essential for endocytosis. <i>Developmental Cell</i> , <b>2015</b> , 33, 150-62	10.2	51
19	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> , <b>2015</b> , 89, 10294-302	6.6	46
18	In situ structural analysis of the human nuclear pore complex. <i>Nature</i> , <b>2015</b> , 526, 140-143	50.4	267
17	Molecular structures of unbound and transcribing RNA polymerase III. <i>Nature</i> , <b>2015</b> , 528, 231-6	50.4	127
16	Seeing tobacco mosaic virus through direct electron detectors. <i>Journal of Structural Biology</i> , <b>2015</b> , 189, 87-97	3.4	67
15	Structure of the immature HIV-1 capsid in intact virus particles at 8.8 Å resolution. <i>Nature</i> , <b>2015</b> , 517, 505-8	50.4	212
14	Automated cryo electron tomography and sub-tomogram averaging with the FEI Volta phase plate. <i>Microscopy and Microanalysis</i> , <b>2015</b> , 21, 1833-1834	0.5	
13	The dynamic conformational landscape of gamma-secretase. <i>Journal of Cell Science</i> , <b>2015</b> , 128, 589-98	5.3	51

12	SNARE and regulatory proteins induce local membrane protrusions to prime docked vesicles for fast calcium-triggered fusion. <i>EMBO Reports</i> , <b>2014</b> , 15, 308-14	6.5	39
11	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> , <b>2014</b> , 111, 8233-8	11.5	69
10	Determination of protein structure at 8.5Å resolution using cryo-electron tomography and sub-tomogram averaging. <i>Journal of Structural Biology</i> , <b>2013</b> , 184, 394-400	3.4	77
9	Integrated structural analysis of the human nuclear pore complex scaffold. <i>Cell</i> , <b>2013</b> , 155, 1233-43	56.2	273
8	Open membranes are the precursors for assembly of large DNA viruses. <i>Cellular Microbiology</i> , <b>2013</b> , 15, 1883-95	3.9	28
7	Software tools for automated transmission electron microscopy		1
6	Benchmarking tomographic acquisition schemes for high-resolution structural biology		1
5	Artificial intelligence reveals nuclear pore complexity		7
4	In cell architecture of the nuclear pore complex and snapshots of its turnover		4
3	In-cell architecture of an actively transcribing-translating expressome		9
2	In situ structural analysis of SARS-CoV-2 spike reveals flexibility mediated by three hinges		19
1	RELION-3: new tools for automated high-resolution cryo-EM structure determination		21